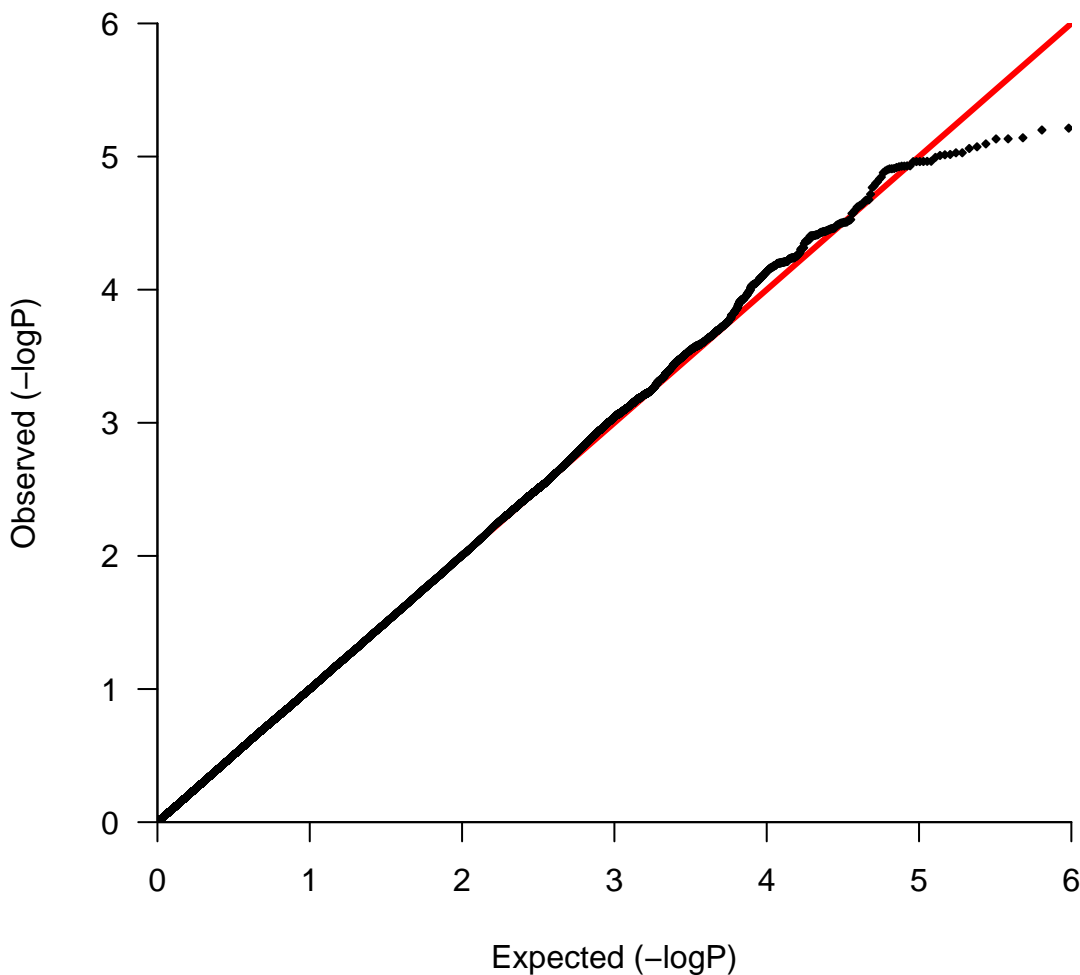
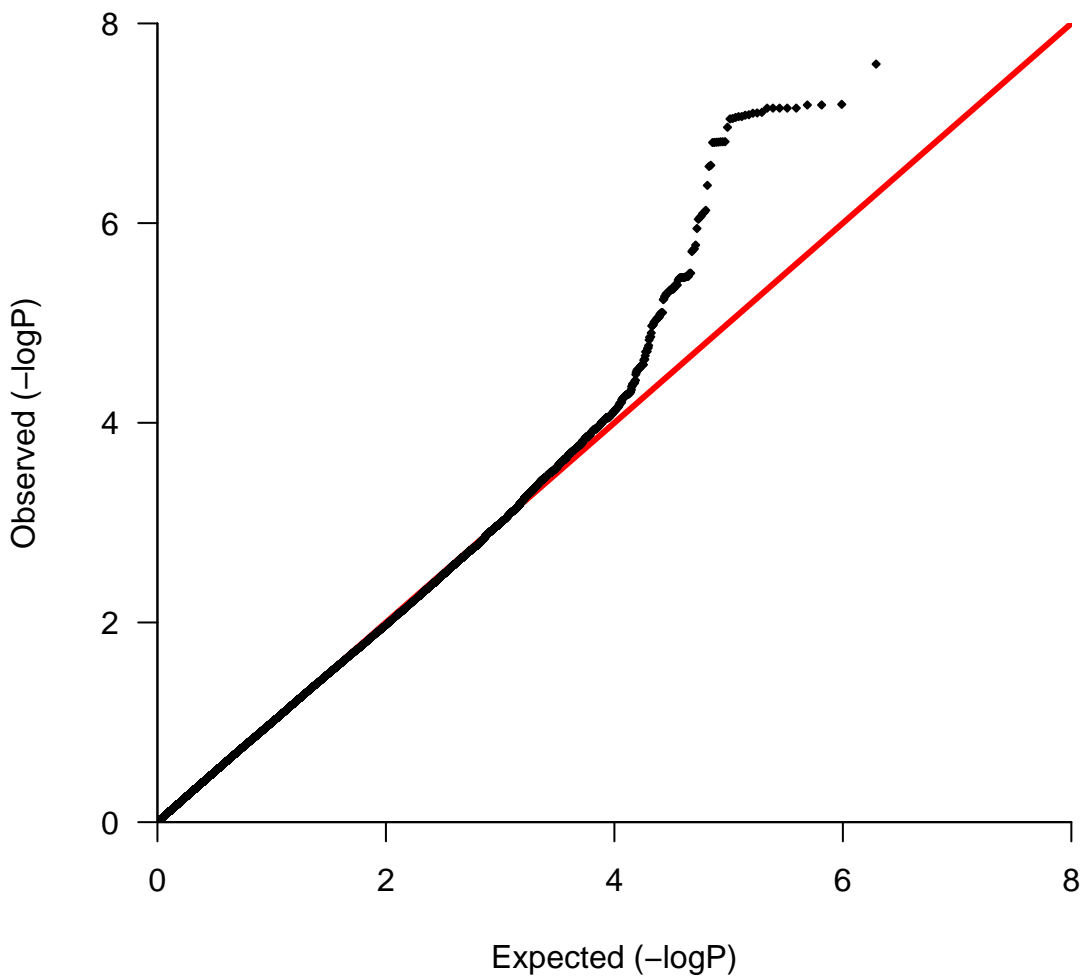


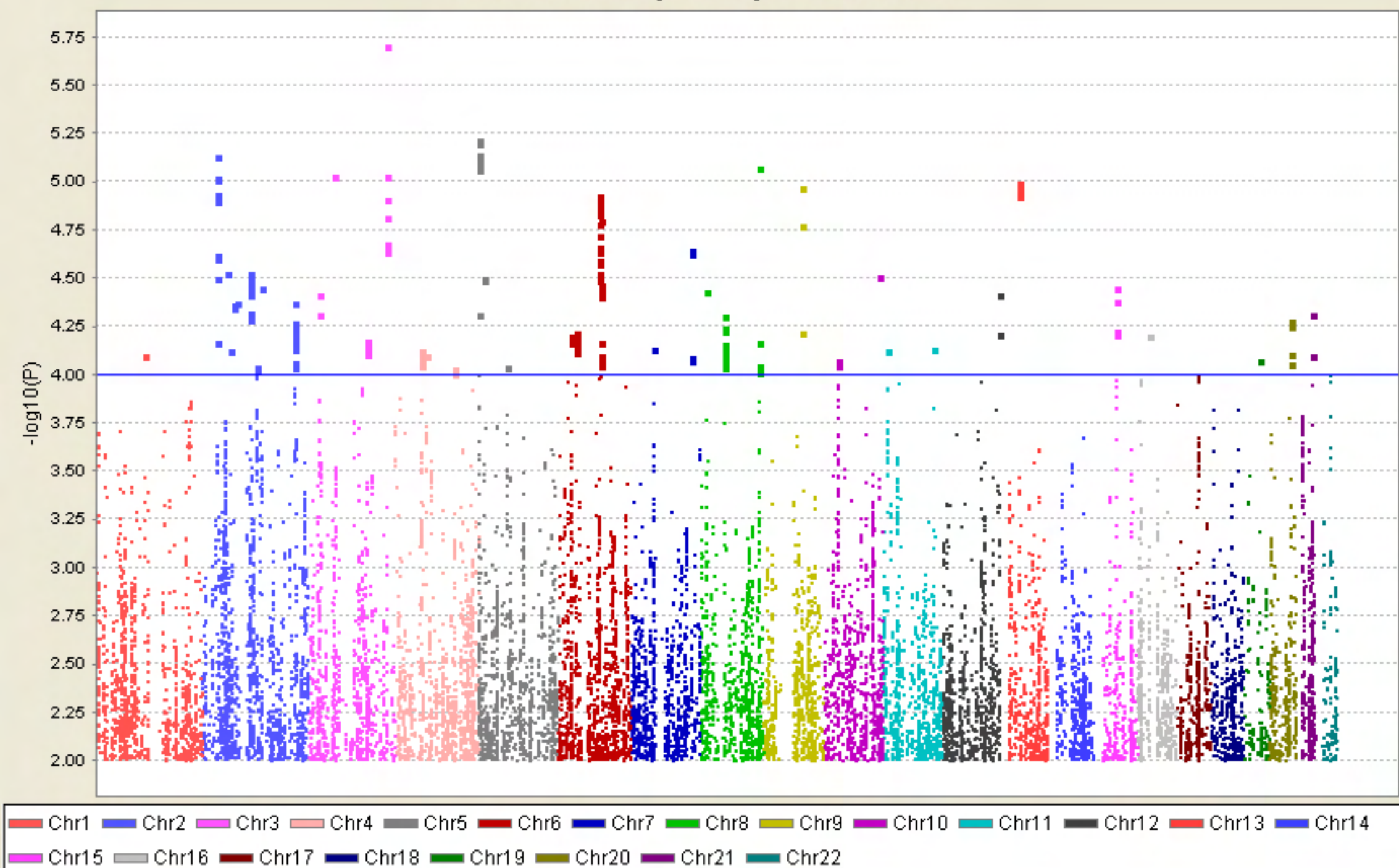
step_n_uk.SA.mach.R8
 $\lambda = 1.003$



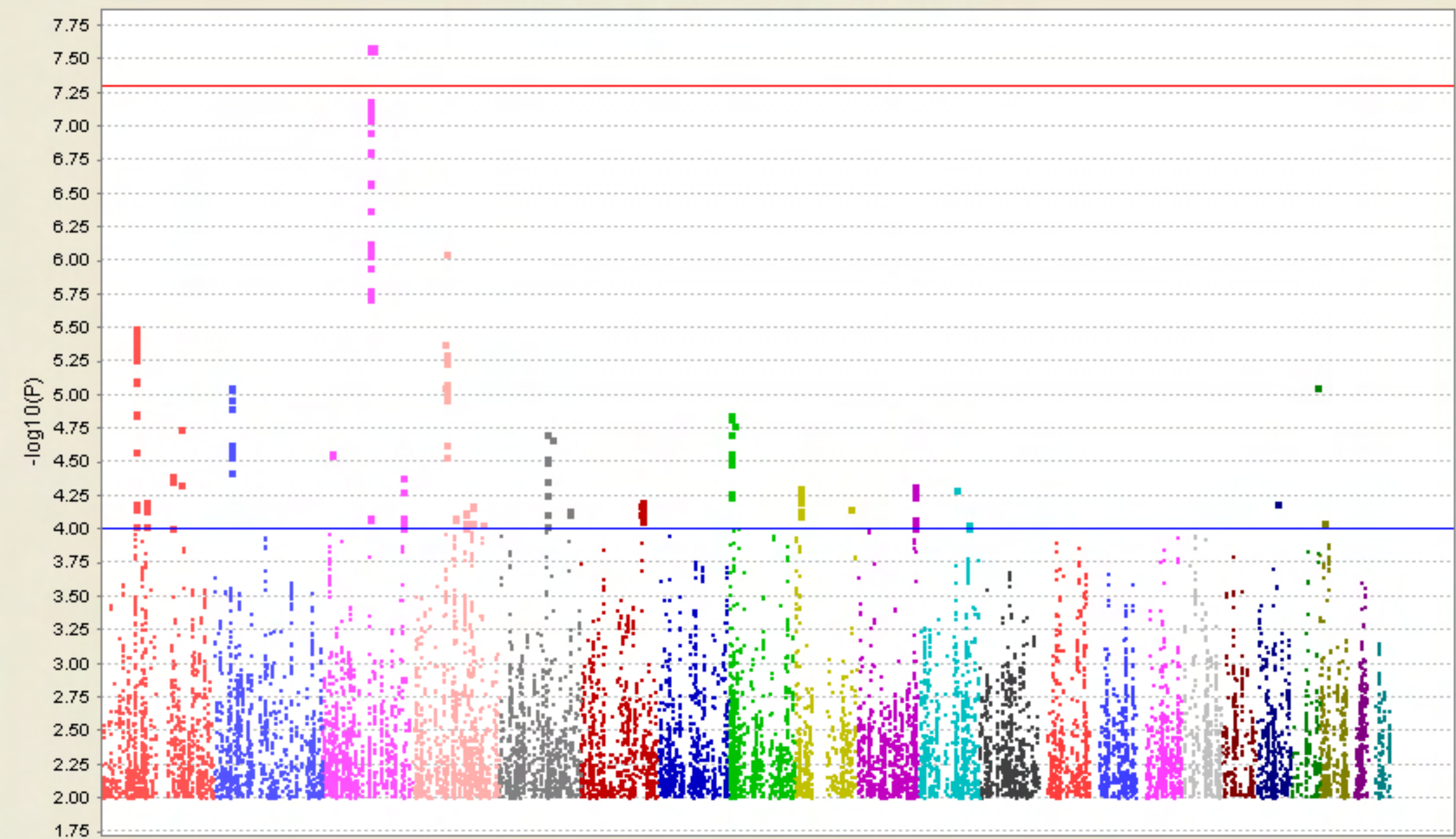
stard.SA.mach.R8
 $\lambda = 1.017$



Suicide attempt in bipolar disorder



Suicide attempt in MDD (STAR*D)



Chr1 Chr2 Chr3 Chr4 Chr5 Chr6 Chr7 Chr8 Chr9 Chr10 Chr11 Chr12 Chr13 Chr14
Chr15 Chr16 Chr17 Chr18 Chr19 Chr20 Chr21 Chr22

Supplemental Methods

Genotyping and Imputation

STEP-BD/WTCCC/UCL

DNA for the STEP-BD and UCL samples was extracted from lymphoblastoid cell lines or whole blood at the Rutgers DNA repository. As previously described(1), all genotyping was performed at the Broad Institute of MIT and Harvard using the Affymetrix GeneChip Human Mapping 500K array and standard protocols. Genotypes were called using the Bayesian Robust Linear Model with Mahalanobis distance classifier (BRLMM) (2). Quality control was performed using PLINK v1.04 (<http://pngu.mgh.harvard.edu/~purcell/plink/>)(3). Individuals were excluded if they had overall call rates <85%; for excess or insufficient heterozygosity (outliers approximately three standard deviations from the mean estimated inbreeding coefficient) or for apparent relatedness. Individuals with apparent non-Caucasian ancestry were also excluded if they did not overlap with CEU samples when plotting the first two quantitative ancestry indices after merging the STEP-BD, UCL, and NIMH control samples with the HapMap phase III dataset. SNPs were excluded if they had a call rate <95%; minor allele frequency <1%, were inconsistent with Hardy-Weinberg Equilibrium at $p < 1 \times 10^{-6}$ or showed differential rates of missingness in bipolar subjects and controls(3). After this quality control, ~325,600 genotyped markers were retained for analysis, with a total genotyping rate in the final sample >99%.

Details of genotyping and quality control for the WTCCC samples are described elsewhere(4).

Briefly, DNA for the WTCCC samples was extracted from whole blood and genotyped using the

Affymetrix GeneChip 500K array at Affymetrix Services Lab with standard protocols. Genotypes were called using CHIAMO(4). SNPs were excluded if they had a call rate <95% (or <99% for SNPs with MAF <5%), or were inconsistent with Hardy-Weinberg Equilibrium at $p < 5.7 \times 10^{-7}$. In all, 469,557 SNPs were originally retained for analysis. As with the STEP-BD cohort, subjects were excluded if the first two quantitative ancestry indices indicated they did not cluster with the primary Caucasian WTCCC group. For the present analysis, WTCCC genotypes were downloaded from the WTCCC website (2007-02-05 CHIAMO data freeze calls, confidence score >0.9) and further cleaned as described in Ferreira(5); after exclusion of SNPs with MAF <0.01, ~405,800 SNPs were retained, then merged with the STEP-BD SNPs to form a single data set.

Imputation was then performed for the autosomes from the combined STEP-BD/UCL/WTCCC data using the MACH software package (<http://www.sph.umich.edu/csg/abecasis/MACH>) (6). Imputation utilized a HapMap reference panel (release 22, 60 Caucasian-European (CEU) founders). SNPs with $r^2 > 0.8$ were retained for further analysis, yielding 1,922,309 SNPs.

MDD

Genotyping for the STAR*D cohort also utilized Affymetrix 500k platforms – half on the Affymetrix GeneChip Human Mapping 500K Array Set, half with the Affymetrix Human SNP Array 5.0. Details of genotype calling methodology and initial quality control processing are in Garriock(7). Genotypes for samples run on the Affymetrix 500K Array (n=969) were called using the BRLMM algorithm, and those analyzed on Affymetrix Array 5.0 (n=979) were called using the BRLMM-P algorithm. Further quality control was performed using PLINK v1.04, with exclusion of individuals with overall call-rates <95% or apparent relatedness and SNPs with call rate <98%,

MAF<1%, or out of Hardy-Weinberg equilibrium ($p < 1 \times 10^{-6}$). This yielded a total of 229,703 genotyped SNPs, with call rates >99%. In addition, as with the STEP-BD/UCL cohort, to minimize the risk of population stratification, the STAR*D data set was merged with the HapMap phase III dataset and the first two quantitative indices of ancestry were plotted. Those subjects who did not overlap with CEU samples were then excluded, yielding 1,273 subjects. Finally, as with STEP-BD, we imputed missing genotypes using MACH and retained SNPs with $r^2 > 0.8$, yielding 1,954,455 SNPs.

References

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7. Garriock HA, Kraft JB, Shyn SI, Peters EJ, Yokoyama JS, Jenkins GD, et al. A Genomewide Association Study of Citalopram Response in Major Depressive Disorder. *Biol Psychiatry*. 2009.

| CHR | SNP | POS | GENE | DISTANCE | BAND | A1/A2 | A1 | OR | P |
|-----|------------|-----------|-----------|------------------------|--------|-------|--------|-------|----------|
| 3 | rs1466846 | 178815700 | TBL1XR1 | 417958 base downstream | q26.32 | AG | 0.285 | 0.738 | 1.98E-06 |
| 5 | rs924134 | 2521375 | IRX2 | 278504 base upstream | p15.33 | AC | 0.3736 | 0.776 | 6.12E-06 |
| 5 | rs6555113 | 2525928 | IRX2 | 273951 base upstream | p15.33 | AT | 0.639 | 1.296 | 6.32E-06 |
| 5 | rs3104229 | 2526843 | IRX2 | 273036 base upstream | p15.33 | CG | 0.6177 | 1.279 | 7.23E-06 |
| 5 | rs6880842 | 2522415 | IRX2 | 277464 base upstream | p15.33 | AG | 0.6181 | 1.277 | 7.36E-06 |
| 2 | rs6548036 | 30860228 | CAPN13 | intron 21 | p23.1 | CG | 0.3395 | 1.303 | 7.37E-06 |
| 5 | rs3112426 | 2534088 | IRX2 | 265791 base upstream | p15.33 | AC | 0.6161 | 1.282 | 8.03E-06 |
| 8 | rs1457463 | 135168960 | ZNF406 | 390253 base upstream | q24.22 | AG | 0.5398 | 0.793 | 8.45E-06 |
| 5 | rs1992827 | 2541341 | IRX2 | 258538 base upstream | p15.33 | CT | 0.3844 | 0.781 | 8.70E-06 |
| 3 | rs9825151 | 178817943 | TBL1XR1 | 420201 base downstream | q26.32 | CT | 0.6024 | 1.266 | 9.37E-06 |
| 3 | rs11130703 | 59333230 | FLJ42117 | 322475 base downstream | p14.2 | CT | 0.3125 | 1.281 | 9.37E-06 |
| 2 | rs1568403 | 30854671 | CAPN13 | intron 21 | p23.1 | AG | 0.3284 | 1.277 | 9.64E-06 |
| 2 | rs17010264 | 30855109 | CAPN13 | intron 21 | p23.1 | CG | 0.6703 | 0.784 | 9.70E-06 |
| 2 | rs4952181 | 30855725 | CAPN13 | intron 21 | p23.1 | AT | 0.6702 | 0.784 | 9.82E-06 |
| 13 | rs17067344 | 45344451 | LOC283514 | 20604 base downstream | q14.12 | CT | 0.044 | 0.553 | 1.01E-05 |
| 9 | rs4877830 | 86066135 | SLC28A3 | 16776 base upstream | q21.32 | GT | 0.0879 | 1.486 | 1.09E-05 |
| 13 | rs17067329 | 45341521 | LOC283514 | 17674 base downstream | q14.12 | AT | 0.0443 | 0.553 | 1.09E-05 |
| 13 | rs7982931 | 45343013 | LOC283514 | 19166 base downstream | q14.12 | CT | 0.9564 | 1.794 | 1.09E-05 |
| 13 | rs4942456 | 45339590 | LOC283514 | 15743 base downstream | q14.12 | AG | 0.0444 | 0.552 | 1.09E-05 |
| 13 | rs7998666 | 45341888 | LOC283514 | 18041 base downstream | q14.12 | GT | 0.9561 | 1.8 | 1.09E-05 |
| 13 | rs4941534 | 45339540 | LOC283514 | 15693 base downstream | q14.12 | AT | 0.0445 | 0.552 | 1.09E-05 |
| 2 | rs2030385 | 30858633 | CAPN13 | intron 21 | p23.1 | CT | 0.3294 | 1.273 | 1.17E-05 |
| 2 | rs6710242 | 30859637 | CAPN13 | intron 21 | p23.1 | CT | 0.6688 | 0.779 | 1.18E-05 |
| 6 | rs1338341 | 94830027 | EPHA7 | 644034 base downstream | q16.1 | AG | 0.6732 | 0.785 | 1.18E-05 |
| 6 | rs1538283 | 94824189 | EPHA7 | 638196 base downstream | q16.1 | AG | 0.6732 | 0.785 | 1.18E-05 |
| 13 | rs7983269 | 45343085 | LOC283514 | 19238 base downstream | q14.12 | AG | 0.0436 | 0.559 | 1.19E-05 |
| 6 | rs9354082 | 94830432 | EPHA7 | 644439 base downstream | q16.1 | CT | 0.6732 | 0.786 | 1.21E-05 |
| 3 | rs9880740 | 178817999 | TBL1XR1 | 420257 base downstream | q26.32 | AG | 0.6092 | 1.262 | 1.23E-05 |
| 2 | rs6548035 | 30859375 | CAPN13 | intron 21 | p23.1 | AG | 0.3299 | 1.275 | 1.24E-05 |
| 6 | rs9445199 | 94830956 | EPHA7 | 644963 base downstream | q16.1 | AG | 0.6732 | 0.786 | 1.24E-05 |
| 2 | rs2030386 | 30858916 | CAPN13 | intron 21 | p23.1 | AG | 0.6708 | 0.787 | 1.26E-05 |
| 6 | rs2787944 | 94821751 | EPHA7 | 635758 base downstream | q16.1 | CT | 0.3274 | 1.272 | 1.28E-05 |
| 6 | rs9351405 | 94834038 | EPHA7 | 648045 base downstream | q16.1 | AG | 0.6732 | 0.786 | 1.32E-05 |
| 6 | rs1416058 | 94825178 | EPHA7 | 639185 base downstream | q16.1 | AT | 0.3265 | 1.27 | 1.43E-05 |
| 6 | rs9354083 | 94830671 | EPHA7 | 644678 base downstream | q16.1 | CT | 0.6734 | 0.787 | 1.48E-05 |
| 3 | rs1875102 | 178825162 | TBL1XR1 | 427420 base downstream | q26.32 | CT | 0.609 | 1.258 | 1.55E-05 |

| | | | | | | | | | |
|----|------------|-----------|----------|------------------------|--------|----|--------|-------|----------|
| 6 | rs9482753 | 99029526 | POU3F2 | 359774 base upstream | q16.2 | AG | 0.9535 | 1.925 | 1.59E-05 |
| 6 | rs1488307 | 94772045 | EPHA7 | 586052 base downstream | q16.1 | CT | 0.3493 | 1.28 | 1.67E-05 |
| 9 | rs17427184 | 86103553 | SLC28A3 | intron 12 | q21.33 | AG | 0.0806 | 1.515 | 1.71E-05 |
| 6 | rs669021 | 94855791 | EPHA7 | 669798 base downstream | q16.1 | CT | 0.3255 | 1.27 | 1.92E-05 |
| 3 | rs11716881 | 178804169 | TBL1XR1 | 406427 base downstream | q26.32 | AG | 0.599 | 1.262 | 2.11E-05 |
| 3 | rs4241484 | 178798779 | TBL1XR1 | 401037 base downstream | q26.32 | AC | 0.599 | 1.263 | 2.12E-05 |
| 3 | rs6766914 | 178805561 | TBL1XR1 | 407819 base downstream | q26.32 | CT | 0.599 | 1.258 | 2.13E-05 |
| 6 | rs582835 | 94785340 | EPHA7 | 599347 base downstream | q16.1 | CT | 0.662 | 0.792 | 2.19E-05 |
| 7 | rs706568 | 136935020 | DGKI | intron 23 | q33 | AT | 0.0538 | 1.671 | 2.26E-05 |
| 3 | rs4857716 | 178795570 | TBL1XR1 | 397828 base downstream | q26.32 | CT | 0.4009 | 0.79 | 2.31E-05 |
| 6 | rs1586510 | 94789896 | EPHA7 | 603903 base downstream | q16.1 | CT | 0.338 | 1.261 | 2.33E-05 |
| 7 | rs6949094 | 136934899 | DGKI | intron 23 | q33 | CT | 0.048 | 1.681 | 2.38E-05 |
| 2 | rs2030383 | 30858582 | CAPN13 | intron 21 | p23.1 | GT | 0.6891 | 0.787 | 2.40E-05 |
| 2 | rs2030384 | 30858583 | CAPN13 | intron 21 | p23.1 | GT | 0.6892 | 0.787 | 2.50E-05 |
| 6 | rs667243 | 94818482 | EPHA7 | 632489 base downstream | q16.1 | AG | 0.3357 | 1.261 | 2.56E-05 |
| 6 | rs679881 | 94799746 | EPHA7 | 613753 base downstream | q16.1 | AG | 0.338 | 1.259 | 2.66E-05 |
| 6 | rs1463678 | 94800718 | EPHA7 | 614725 base downstream | q16.1 | AG | 0.338 | 1.259 | 2.68E-05 |
| 2 | rs12474717 | 55796721 | PNPT1 | 22258 base downstream | p16.1 | GT | 0.887 | 0.686 | 2.98E-05 |
| 6 | rs2875662 | 94807741 | EPHA7 | 621748 base downstream | q16.1 | CT | 0.6621 | 0.796 | 3.02E-05 |
| 2 | rs2377685 | 106754304 | ST6GAL2 | 35235 base upstream | q12.3 | GT | 0.2968 | 0.784 | 3.02E-05 |
| 10 | rs10887132 | 124083263 | C10orf87 | intron 13 | q26.13 | CT | 0.2681 | 0.766 | 3.10E-05 |
| 2 | rs1349065 | 106754740 | ST6GAL2 | 34799 base upstream | q12.3 | CG | 0.7032 | 1.275 | 3.11E-05 |
| 6 | rs6919516 | 94816613 | EPHA7 | 630620 base downstream | q16.1 | AG | 0.3376 | 1.257 | 3.12E-05 |
| 10 | rs10887131 | 124083189 | C10orf87 | intron 13 | q26.13 | CG | 0.2681 | 0.766 | 3.12E-05 |
| 2 | rs17010236 | 30846223 | CAPN13 | intron 18 | p23.1 | GT | 0.325 | 1.256 | 3.15E-05 |
| 2 | rs17324843 | 30846381 | CAPN13 | intron 18 | p23.1 | AG | 0.6751 | 0.796 | 3.16E-05 |
| 5 | rs151152 | 13541800 | DNAH5 | 201636 base upstream | p15.2 | CT | 0.853 | 0.722 | 3.17E-05 |
| 2 | rs11894298 | 106754935 | ST6GAL2 | 34604 base upstream | q12.3 | CT | 0.2968 | 0.785 | 3.20E-05 |
| 6 | rs678036 | 94814119 | EPHA7 | 628126 base downstream | q16.1 | CG | 0.6621 | 0.796 | 3.24E-05 |
| 5 | rs3853117 | 13541819 | DNAH5 | 201617 base upstream | p15.2 | CT | 0.853 | 0.723 | 3.26E-05 |
| 2 | rs11894451 | 106755254 | ST6GAL2 | 34285 base upstream | q12.3 | CT | 0.2969 | 0.785 | 3.29E-05 |
| 2 | rs11887836 | 106755321 | ST6GAL2 | 34218 base upstream | q12.3 | CG | 0.7031 | 1.273 | 3.39E-05 |
| 2 | rs11888992 | 106755485 | ST6GAL2 | 34054 base upstream | q12.3 | CG | 0.703 | 1.273 | 3.44E-05 |
| 2 | rs6747891 | 106756383 | ST6GAL2 | 33156 base upstream | q12.3 | AG | 0.297 | 0.786 | 3.46E-05 |
| 6 | rs9491646 | 99034084 | POU3F2 | 355216 base upstream | q16.2 | AG | 0.0424 | 0.531 | 3.47E-05 |
| 6 | rs9491645 | 99032544 | POU3F2 | 356756 base upstream | q16.2 | CT | 0.9577 | 1.881 | 3.48E-05 |
| 6 | rs9491644 | 99032521 | POU3F2 | 356779 base upstream | q16.2 | AG | 0.9577 | 1.881 | 3.49E-05 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|----------|
| 2 | rs1448103 | 106757512 | ST6GAL2 | 32027 base upstream | q12.3 | AG | 0.2971 | 0.786 | 3.52E-05 |
| 6 | rs11154359 | 99031598 | POU3F2 | 357702 base upstream | q16.2 | AG | 0.0422 | 0.533 | 3.54E-05 |
| 2 | rs16830280 | 134733887 | MGAT5 | intron 1 | q21.2 | AT | 0.9361 | 0.631 | 3.57E-05 |
| 15 | rs10518706 | 51240801 | WDR72 | 352428 base upstream | q21.3 | CT | 0.8207 | 0.752 | 3.59E-05 |
| 15 | rs11070957 | 51238288 | WDR72 | 354941 base upstream | q21.3 | GT | 0.8207 | 0.752 | 3.60E-05 |
| 6 | rs9482751 | 99028026 | POU3F2 | 361274 base upstream | q16.2 | CT | 0.958 | 1.868 | 3.65E-05 |
| 6 | rs1494770 | 99026958 | POU3F2 | 362342 base upstream | q16.2 | CT | 0.042 | 0.536 | 3.65E-05 |
| 6 | rs9482752 | 99028948 | POU3F2 | 360352 base upstream | q16.2 | AC | 0.042 | 0.535 | 3.66E-05 |
| 6 | rs9491640 | 99025985 | POU3F2 | 363315 base upstream | q16.2 | AC | 0.042 | 0.536 | 3.66E-05 |
| 8 | rs7817295 | 14915797 | SGCZ | intron 7 | p22 | AT | 0.516 | 0.805 | 3.70E-05 |
| 6 | rs9885878 | 99023244 | POU3F2 | 366056 base upstream | q16.2 | AC | 0.0419 | 0.537 | 3.71E-05 |
| 6 | rs9491637 | 99024090 | POU3F2 | 365210 base upstream | q16.2 | AG | 0.9581 | 1.863 | 3.71E-05 |
| 6 | rs9482747 | 99023189 | POU3F2 | 366111 base upstream | q16.2 | CT | 0.9582 | 1.86 | 3.75E-05 |
| 2 | rs17033251 | 106759973 | ST6GAL2 | 29566 base upstream | q12.3 | CT | 0.2984 | 0.784 | 3.78E-05 |
| 6 | rs1908399 | 99021767 | POU3F2 | 367533 base upstream | q16.2 | AG | 0.9583 | 1.854 | 3.83E-05 |
| 2 | rs1448105 | 106761667 | ST6GAL2 | 27872 base upstream | q12.3 | AT | 0.2989 | 0.783 | 3.86E-05 |
| 12 | rs11060565 | 128857653 | TMEM132D | intron 8 | q24.33 | CT | 0.1757 | 1.326 | 3.87E-05 |
| 3 | rs1984870 | 24690139 | THRB | 178822 base downstream | p24.2 | GT | 0.5299 | 1.241 | 3.87E-05 |
| 6 | rs9491633 | 99021401 | POU3F2 | 367899 base upstream | q16.2 | AC | 0.0416 | 0.54 | 3.90E-05 |
| 3 | rs1984874 | 24690109 | THRB | 178792 base downstream | p24.2 | CT | 0.5297 | 1.241 | 3.91E-05 |
| 6 | rs9388491 | 99020082 | POU3F2 | 369218 base upstream | q16.2 | AC | 0.9585 | 1.848 | 3.92E-05 |
| 6 | rs9491631 | 99021192 | POU3F2 | 368108 base upstream | q16.2 | CT | 0.9584 | 1.849 | 3.93E-05 |
| 6 | rs9401880 | 99020505 | POU3F2 | 368795 base upstream | q16.2 | CG | 0.9584 | 1.848 | 3.94E-05 |
| 6 | rs9491632 | 99021290 | POU3F2 | 368010 base upstream | q16.2 | AT | 0.0416 | 0.541 | 3.94E-05 |
| 6 | rs9491625 | 99016428 | POU3F2 | 372872 base upstream | q16.2 | AG | 0.0415 | 0.542 | 3.95E-05 |
| 6 | rs9482746 | 99021203 | POU3F2 | 368097 base upstream | q16.2 | CT | 0.0416 | 0.541 | 3.95E-05 |
| 6 | rs12213284 | 99015010 | POU3F2 | 374290 base upstream | q16.2 | GT | 0.0414 | 0.543 | 3.97E-05 |
| 15 | rs17545312 | 51214304 | ONECUT1 | 344803 base downstream | q21.3 | AG | 0.8215 | 0.755 | 4.22E-05 |
| 15 | rs17627721 | 51214080 | ONECUT1 | 344579 base downstream | q21.3 | GT | 0.8215 | 0.755 | 4.23E-05 |
| 2 | rs13010864 | 210430270 | C2orf21 | 60754 base downstream | q34 | AG | 0.8693 | 0.718 | 4.24E-05 |
| 2 | rs17014915 | 78148150 | LRRTM4 | 545140 base downstream | p12 | CT | 0.2444 | 1.278 | 4.25E-05 |
| 2 | rs17014922 | 78149582 | LRRTM4 | 546572 base downstream | p12 | CT | 0.2444 | 1.278 | 4.28E-05 |
| 2 | rs10188275 | 71088630 | TEX261 | 13121 base downstream | p13.3 | CT | 0.0543 | 0.58 | 4.32E-05 |
| 2 | rs10196871 | 71088542 | TEX261 | 13033 base downstream | p13.3 | AG | 0.9457 | 1.726 | 4.32E-05 |
| 2 | rs10189222 | 71089555 | TEX261 | 14046 base downstream | p13.3 | CT | 0.0543 | 0.577 | 4.45E-05 |
| 2 | rs10179209 | 71089580 | TEX261 | 14071 base downstream | p13.3 | AG | 0.0544 | 0.575 | 4.51E-05 |
| 2 | rs728241 | 106764565 | ST6GAL2 | 24974 base upstream | q12.3 | AG | 0.3041 | 0.776 | 4.84E-05 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|----------|
| 3 | rs2362756 | 24691768 | THRB | 180451 base downstream | p24.2 | GT | 0.5305 | 1.241 | 4.87E-05 |
| 21 | rs2837220 | 40082808 | LOC150084 | intron 6 | q22.2 | CT | 0.3851 | 1.24 | 4.88E-05 |
| 2 | rs728239 | 106764687 | ST6GAL2 | 24852 base upstream | q12.3 | CT | 0.3043 | 0.776 | 4.88E-05 |
| 5 | rs2453814 | 2546280 | IRX2 | 253599 base upstream | p15.33 | AC | 0.5845 | 1.24 | 4.92E-05 |
| 8 | rs16918988 | 54353550 | OPRK1 | 26803 base downstream | q11.23 | CT | 0.8823 | 1.453 | 5.00E-05 |
| 2 | rs728240 | 106764888 | ST6GAL2 | 24651 base upstream | q12.3 | GT | 0.6947 | 1.291 | 5.23E-05 |
| 20 | rs6019695 | 47271275 | DDX27 | intron 1 | q13.13 | AG | 0.0611 | 1.544 | 5.31E-05 |
| 2 | rs10194322 | 210423419 | C2orf21 | 53903 base downstream | q34 | AG | 0.1212 | 1.391 | 5.40E-05 |
| 2 | rs7593426 | 210442080 | C2orf21 | 72564 base downstream | q34 | AG | 0.1216 | 1.382 | 5.40E-05 |
| 2 | rs10194333 | 210423552 | C2orf21 | 54036 base downstream | q34 | AC | 0.1212 | 1.39 | 5.43E-05 |
| 20 | rs6012627 | 47306203 | ZNFX1 | intron 6 | q13.13 | AG | 0.9388 | 0.65 | 5.57E-05 |
| 2 | rs13013030 | 210425175 | C2orf21 | 55659 base downstream | q34 | CG | 0.8784 | 0.721 | 5.58E-05 |
| 2 | rs7584039 | 210425771 | C2orf21 | 56255 base downstream | q34 | CT | 0.1216 | 1.387 | 5.60E-05 |
| 2 | rs2191909 | 210427017 | C2orf21 | 57501 base downstream | q34 | CG | 0.8783 | 0.721 | 5.64E-05 |
| 2 | rs7566741 | 210442197 | C2orf21 | 72681 base downstream | q34 | AG | 0.8786 | 0.723 | 5.67E-05 |
| 2 | rs2159747 | 210427142 | C2orf21 | 57626 base downstream | q34 | CT | 0.1219 | 1.384 | 5.75E-05 |
| 8 | rs2376420 | 54356965 | OPRK1 | 30218 base downstream | q11.23 | AT | 0.1062 | 0.693 | 5.75E-05 |
| 8 | rs2376419 | 54357042 | OPRK1 | 30295 base downstream | q11.23 | AG | 0.1062 | 0.693 | 5.75E-05 |
| 8 | rs4565474 | 54357197 | OPRK1 | 30450 base downstream | q11.23 | AG | 0.894 | 1.445 | 5.77E-05 |
| 8 | rs2376418 | 54357083 | OPRK1 | 30336 base downstream | q11.23 | AT | 0.894 | 1.445 | 5.77E-05 |
| 8 | rs2059547 | 54355648 | OPRK1 | 28901 base downstream | q11.23 | CT | 0.1064 | 0.693 | 5.77E-05 |
| 8 | rs2376422 | 54356785 | OPRK1 | 30038 base downstream | q11.23 | AG | 0.8936 | 1.442 | 5.78E-05 |
| 2 | rs10490027 | 210442707 | C2orf21 | 73191 base downstream | q34 | AT | 0.1213 | 1.383 | 5.80E-05 |
| 8 | rs9792384 | 54352922 | OPRK1 | 26175 base downstream | q11.23 | AG | 0.1068 | 0.695 | 5.82E-05 |
| 8 | rs9792266 | 54352873 | OPRK1 | 26126 base downstream | q11.23 | AT | 0.1068 | 0.695 | 5.84E-05 |
| 8 | rs9792157 | 54348944 | OPRK1 | 22197 base downstream | q11.23 | AC | 0.1068 | 0.696 | 5.87E-05 |
| 2 | rs7579121 | 210429691 | C2orf21 | 60175 base downstream | q34 | CT | 0.1221 | 1.382 | 5.87E-05 |
| 15 | rs7168646 | 51305758 | WDR72 | 287471 base upstream | q21.3 | AG | 0.8081 | 0.759 | 5.93E-05 |
| 8 | rs2162181 | 54346783 | OPRK1 | 20036 base downstream | q11.23 | CT | 0.893 | 1.435 | 5.96E-05 |
| 9 | rs10868141 | 86111098 | SLC28A3 | intron 15 | q21.33 | CT | 0.9065 | 0.697 | 6.12E-05 |
| 2 | rs9631001 | 210433939 | C2orf21 | 64423 base downstream | q34 | CT | 0.8776 | 0.725 | 6.13E-05 |
| 6 | rs9471557 | 41399757 | NCR2 | 11748 base upstream | p21.1 | CT | 0.4283 | 1.238 | 6.14E-05 |
| 6 | rs9471560 | 41399986 | NCR2 | 11519 base upstream | p21.1 | AG | 0.5717 | 0.807 | 6.14E-05 |
| 6 | rs10807260 | 41400115 | NCR2 | 11390 base upstream | p21.1 | CT | 0.5717 | 0.808 | 6.16E-05 |
| 6 | rs12198812 | 41401304 | NCR2 | 10201 base upstream | p21.1 | CT | 0.5718 | 0.808 | 6.16E-05 |
| 6 | rs10807261 | 41400213 | NCR2 | 11292 base upstream | p21.1 | AC | 0.5718 | 0.808 | 6.16E-05 |
| 6 | rs9462699 | 41402041 | NCR2 | 9464 base upstream | p21.1 | AG | 0.4282 | 1.238 | 6.18E-05 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|----------|
| 12 | rs1376797 | 128850548 | TMEM132D | intron 8 | q24.33 | CT | 0.1787 | 1.316 | 6.20E-05 |
| 6 | rs13219519 | 41402893 | NCR2 | 8612 base upstream | p21.1 | AT | 0.5719 | 0.808 | 6.22E-05 |
| 6 | rs13203392 | 41402924 | NCR2 | 8581 base upstream | p21.1 | CT | 0.4281 | 1.238 | 6.23E-05 |
| 2 | rs10178431 | 210413152 | C2orf21 | 43636 base downstream | q34 | GT | 0.8784 | 0.711 | 6.24E-05 |
| 6 | rs2395773 | 41403590 | NCR2 | 7915 base upstream | p21.1 | CT | 0.4281 | 1.238 | 6.24E-05 |
| 15 | rs16965587 | 51225655 | ONECUT1 | 356154 base downstream | q21.3 | GT | 0.8314 | 0.748 | 6.25E-05 |
| 6 | rs4605877 | 41403756 | NCR2 | 7749 base upstream | p21.1 | GT | 0.572 | 0.808 | 6.27E-05 |
| 6 | rs2395774 | 41403603 | NCR2 | 7902 base upstream | p21.1 | AG | 0.428 | 1.238 | 6.27E-05 |
| 2 | rs12328328 | 210443088 | C2orf21 | 73572 base downstream | q34 | CT | 0.8789 | 0.724 | 6.29E-05 |
| 6 | rs9261043 | 30074705 | HCG9 | 20557 base downstream | p21.33 | CT | 0.9386 | 0.639 | 6.30E-05 |
| 2 | rs9973787 | 210437244 | C2orf21 | 67728 base downstream | q34 | AG | 0.8774 | 0.727 | 6.30E-05 |
| 6 | rs9471568 | 41404359 | NCR2 | 7146 base upstream | p21.1 | CT | 0.4279 | 1.237 | 6.31E-05 |
| 6 | rs13208294 | 41404430 | NCR2 | 7075 base upstream | p21.1 | AG | 0.4279 | 1.237 | 6.32E-05 |
| 2 | rs12329111 | 210443100 | C2orf21 | 73584 base downstream | q34 | AC | 0.8789 | 0.724 | 6.34E-05 |
| 16 | rs12925611 | 26198350 | HS3ST4 | 141841 base downstream | p12.1 | CT | 0.7251 | 0.775 | 6.34E-05 |
| 6 | rs13208406 | 41404488 | NCR2 | 7017 base upstream | p21.1 | AC | 0.4279 | 1.237 | 6.35E-05 |
| 6 | rs12525710 | 41404657 | NCR2 | 6848 base upstream | p21.1 | CT | 0.4279 | 1.237 | 6.35E-05 |
| 2 | rs12328346 | 210443331 | C2orf21 | 73815 base downstream | q34 | AG | 0.1211 | 1.381 | 6.40E-05 |
| 2 | rs7595063 | 210437762 | C2orf21 | 68246 base downstream | q34 | AC | 0.1228 | 1.374 | 6.45E-05 |
| 2 | rs7598071 | 210437956 | C2orf21 | 68440 base downstream | q34 | CG | 0.1228 | 1.374 | 6.51E-05 |
| 2 | rs10490028 | 210443405 | C2orf21 | 73889 base downstream | q34 | CT | 0.8789 | 0.725 | 6.55E-05 |
| 2 | rs9973848 | 210438805 | C2orf21 | 69289 base downstream | q34 | AG | 0.8772 | 0.728 | 6.58E-05 |
| 2 | rs12328869 | 210444413 | C2orf21 | 74897 base downstream | q34 | AT | 0.1211 | 1.38 | 6.61E-05 |
| 2 | rs12328884 | 210444633 | C2orf21 | 75117 base downstream | q34 | CT | 0.1211 | 1.38 | 6.62E-05 |
| 2 | rs9973317 | 210439257 | C2orf21 | 69741 base downstream | q34 | CT | 0.8772 | 0.728 | 6.63E-05 |
| 2 | rs12329303 | 210444857 | C2orf21 | 75341 base downstream | q34 | AG | 0.879 | 0.725 | 6.64E-05 |
| 3 | rs8177203 | 134952715 | TF | intron 2 | q22.1 | AG | 0.9525 | 0.627 | 6.66E-05 |
| 2 | rs7581628 | 210446076 | C2orf21 | 76560 base downstream | q34 | AG | 0.879 | 0.725 | 6.72E-05 |
| 6 | rs1905568 | 41405925 | NCR2 | 5580 base upstream | p21.1 | CT | 0.4274 | 1.239 | 6.76E-05 |
| 2 | rs7581974 | 210446334 | C2orf21 | 76818 base downstream | q34 | AG | 0.879 | 0.725 | 6.78E-05 |
| 6 | rs12208867 | 30134215 | ZNRD1 | 2799 base upstream | p21.33 | AG | 0.0618 | 1.558 | 6.83E-05 |
| 2 | rs17748674 | 210447096 | C2orf21 | 77580 base downstream | q34 | CT | 0.121 | 1.379 | 6.84E-05 |
| 2 | rs4952179 | 30848531 | CAPN13 | intron 19 | p23.1 | CT | 0.7132 | 0.797 | 6.86E-05 |
| 8 | rs7830450 | 135176557 | ZNF406 | 382656 base upstream | q24.22 | CT | 0.5706 | 0.811 | 6.87E-05 |
| 6 | rs12208539 | 99010182 | POU3F2 | 379118 base upstream | q16.2 | GT | 0.9607 | 1.805 | 6.87E-05 |
| 2 | rs17748692 | 210447119 | C2orf21 | 77603 base downstream | q34 | CT | 0.121 | 1.379 | 6.93E-05 |
| 6 | rs2395775 | 41405993 | NCR2 | 5512 base upstream | p21.1 | CG | 0.4272 | 1.24 | 6.99E-05 |

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|----|------------|-----------|---------------|-------------------------|--------|----|--------|-------|----------|
| 2 | rs1558474 | 210447598 | C2orf21 | 78082 base downstream | q34 | CT | 0.879 | 0.726 | 7.00E-05 |
| 8 | rs9792306 | 54353314 | OPRK1 | 26567 base downstream | q11.23 | CT | 0.1204 | 0.701 | 7.00E-05 |
| 2 | rs16843893 | 210449837 | C2orf21 | 80321 base downstream | q34 | CT | 0.879 | 0.726 | 7.09E-05 |
| 2 | rs11682914 | 210450278 | C2orf21 | 80762 base downstream | q34 | AG | 0.1209 | 1.378 | 7.12E-05 |
| 8 | rs16918960 | 54337603 | OPRK1 | 10856 base downstream | q11.23 | AT | 0.1078 | 0.705 | 7.16E-05 |
| 2 | rs2109970 | 210450498 | C2orf21 | 80982 base downstream | q34 | AG | 0.8791 | 0.726 | 7.17E-05 |
| 3 | rs4532136 | 134949575 | TF | intron 1 | q22.1 | AG | 0.0485 | 1.589 | 7.25E-05 |
| 7 | rs1689304 | 52979122 | DKFZp564N2472 | 91720 base upstream | p12.1 | AC | 0.2106 | 1.29 | 7.35E-05 |
| 2 | rs17748818 | 210454100 | C2orf21 | 84584 base downstream | q34 | CT | 0.8791 | 0.726 | 7.35E-05 |
| 7 | rs1689306 | 52979766 | DKFZp564N2472 | 91076 base upstream | p12.1 | AG | 0.2106 | 1.289 | 7.39E-05 |
| 11 | rs427875 | 115309136 | CADM1 | 428685 base downstream | q23.2 | AC | 0.2656 | 1.273 | 7.42E-05 |
| 11 | rs4243917 | 10804775 | EIF4G2 | 17617 base downstream | p15.3 | CT | 0.0861 | 0.678 | 7.51E-05 |
| 2 | rs17028360 | 64129701 | VPS54 | 29983 base downstream | p14 | AG | 0.9461 | 0.64 | 7.57E-05 |
| 6 | rs10755717 | 41406187 | NCR2 | 5318 base upstream | p21.1 | AG | 0.4266 | 1.243 | 7.60E-05 |
| 4 | rs2570071 | 58784187 | IGFBP7 | 1112891 base downstream | q12 | GT | 0.7147 | 1.262 | 7.62E-05 |
| 3 | rs8177186 | 134947891 | TF | 33 base upstream | q22.1 | GT | 0.9512 | 0.631 | 7.66E-05 |
| 6 | rs7771870 | 41406742 | NCR2 | 4763 base upstream | p21.1 | AT | 0.4265 | 1.244 | 7.74E-05 |
| 8 | rs7819906 | 54411642 | OPRK1 | 84895 base downstream | q11.23 | CT | 0.89 | 1.415 | 7.75E-05 |
| 20 | rs761498 | 47349857 | ZNFX1 | 21694 base downstream | q13.13 | CT | 0.9391 | 0.654 | 7.78E-05 |
| 3 | rs8177185 | 134947308 | TF | 616 base upstream | q22.1 | AG | 0.0489 | 1.582 | 7.91E-05 |
| 4 | rs2570089 | 58794368 | IGFBP7 | 1123072 base downstream | q12 | CT | 0.7147 | 1.261 | 8.00E-05 |
| 1 | rs903050 | 110900289 | KCNA10 | 36969 base downstream | p13.3 | CT | 0.1002 | 1.451 | 8.01E-05 |
| 4 | rs4460073 | 71142292 | CSN3 | 629 base upstream | q13.3 | CT | 0.1173 | 0.723 | 8.01E-05 |
| 6 | rs12200527 | 99009252 | POU3F2 | 380048 base upstream | q16.2 | AT | 0.9611 | 1.794 | 8.03E-05 |
| 21 | rs2837202 | 40065876 | LOC150084 | intron 4 | q22.2 | AT | 0.5532 | 0.807 | 8.08E-05 |
| 6 | rs9482736 | 99007342 | POU3F2 | 381958 base upstream | q16.2 | CT | 0.9611 | 1.793 | 8.09E-05 |
| 8 | rs11995645 | 54427066 | OPRK1 | 100319 base downstream | q11.23 | CT | 0.89 | 1.413 | 8.15E-05 |
| 6 | rs6941388 | 99031254 | POU3F2 | 358046 base upstream | q16.2 | AT | 0.0469 | 0.571 | 8.16E-05 |
| 8 | rs11985025 | 54427119 | OPRK1 | 100372 base downstream | q11.23 | AT | 0.89 | 1.413 | 8.22E-05 |
| 7 | rs706567 | 136933752 | DGKI | intron 23 | q33 | CT | 0.0514 | 1.661 | 8.22E-05 |
| 7 | rs706562 | 136927210 | DGKI | intron 22 | q33 | CG | 0.0517 | 1.665 | 8.45E-05 |
| 19 | rs870379 | 40235596 | HPN | intron 5 | q13.11 | AG | 0.6439 | 0.806 | 8.47E-05 |
| 10 | rs1360550 | 30527766 | PAPD1 | 113998 base upstream | p11.23 | AG | 0.6449 | 0.808 | 8.49E-05 |
| 4 | rs11133552 | 58818055 | IGFBP7 | 1146759 base downstream | q12 | AG | 0.7147 | 1.259 | 8.52E-05 |
| 6 | rs3125579 | 99015679 | POU3F2 | 373621 base upstream | q16.2 | AG | 0.9538 | 1.729 | 8.62E-05 |
| 4 | rs2412885 | 58821899 | IGFBP7 | 1150603 base downstream | q12 | CT | 0.2853 | 0.794 | 8.62E-05 |
| 2 | rs11688226 | 210478772 | RPE | 96824 base upstream | q34 | CT | 0.8793 | 0.727 | 8.68E-05 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs2244536 | 58824709 | IGFBP7 | 1153413 base downstream | q12 | AC | 0.7147 | 1.259 | 8.69E-05 |
| 4 | rs1368608 | 58828880 | IGFBP7 | 1157584 base downstream | q12 | AG | 0.2853 | 0.795 | 8.79E-05 |
| 8 | rs7465082 | 54386635 | OPRK1 | 59888 base downstream | q11.23 | GT | 0.89 | 1.411 | 8.81E-05 |
| 20 | rs11907908 | 47357021 | ZNFX1 | 28858 base downstream | q13.13 | CT | 0.9392 | 0.655 | 8.91E-05 |
| 6 | rs9491610 | 99006740 | POU3F2 | 382560 base upstream | q16.2 | AG | 0.9606 | 1.806 | 8.91E-05 |
| 8 | rs765847 | 135205190 | ZNF406 | 354023 base upstream | q24.22 | AG | 0.4854 | 1.224 | 8.94E-05 |
| 8 | rs7011020 | 135210399 | ZNF406 | 348814 base upstream | q24.22 | AG | 0.5146 | 0.817 | 8.98E-05 |
| 6 | rs3104078 | 99010723 | POU3F2 | 378577 base upstream | q16.2 | AT | 0.0454 | 0.578 | 8.98E-05 |
| 4 | rs2553297 | 58833846 | IGFBP7 | 1162550 base downstream | q12 | CT | 0.2853 | 0.795 | 9.04E-05 |
| 10 | rs2462021 | 30530710 | PAPD1 | 111054 base upstream | p11.23 | CT | 0.3552 | 1.237 | 9.06E-05 |
| 8 | rs1124525 | 135192071 | ZNF406 | 367142 base upstream | q24.22 | AG | 0.5147 | 0.817 | 9.09E-05 |
| 2 | rs4848185 | 123110875 | TSN | 868979 base downstream | q14.3 | AG | 0.652 | 1.257 | 9.12E-05 |
| 5 | rs266581 | 64346595 | SDCCAG10 | intron 13 | q12.3 | AT | 0.8249 | 0.754 | 9.14E-05 |
| 8 | rs1446995 | 135211030 | ZNF406 | 348183 base upstream | q24.22 | GT | 0.4854 | 1.223 | 9.14E-05 |
| 2 | rs11694132 | 210480528 | RPE | 95068 base upstream | q34 | AG | 0.8794 | 0.727 | 9.15E-05 |
| 2 | rs6739769 | 210481545 | RPE | 94051 base upstream | q34 | CT | 0.8794 | 0.727 | 9.23E-05 |
| 8 | rs4897681 | 135212703 | ZNF406 | 346510 base upstream | q24.22 | CT | 0.4854 | 1.223 | 9.25E-05 |
| 8 | rs11995818 | 54378028 | OPRK1 | 51281 base downstream | q11.23 | AT | 0.89 | 1.409 | 9.26E-05 |
| 2 | rs17039782 | 123110041 | TSN | 868145 base downstream | q14.3 | CT | 0.3485 | 0.797 | 9.31E-05 |
| 4 | rs1038151 | 136732205 | PABPC4L | 1389852 base downstream | q28.3 | GT | 0.489 | 1.225 | 9.34E-05 |
| 8 | rs6994801 | 135214566 | ZNF406 | 344647 base upstream | q24.22 | CG | 0.5146 | 0.818 | 9.37E-05 |
| 2 | rs987707 | 123108773 | TSN | 866877 base downstream | q14.3 | CT | 0.6511 | 1.253 | 9.50E-05 |
| 4 | rs2035293 | 136730586 | PABPC4L | 1388233 base downstream | q28.3 | AG | 0.511 | 0.816 | 9.61E-05 |
| 8 | rs992526 | 135216479 | ZNF406 | 342734 base upstream | q24.22 | CT | 0.5147 | 0.818 | 9.68E-05 |
| 4 | rs2086327 | 136730007 | PABPC4L | 1387654 base downstream | q28.3 | AC | 0.511 | 0.817 | 9.93E-05 |
| 22 | rs5999742 | 33870423 | RAXLX | 57045 base downstream | q12.3 | AG | 0.7176 | 1.265 | 0.000101 |
| 5 | rs3112414 | 2561221 | IRX2 | 238658 base upstream | p15.33 | CG | 0.5862 | 1.232 | 0.0001011 |
| 17 | rs9915451 | 51788210 | ANKFN1 | intron 5 | q22 | AG | 0.2536 | 1.268 | 0.0001019 |
| 2 | rs1371489 | 123098289 | TSN | 856393 base downstream | q14.3 | CT | 0.3428 | 0.802 | 0.0001028 |
| 6 | rs9491608 | 99005624 | POU3F2 | 383676 base upstream | q16.2 | AG | 0.0402 | 0.548 | 0.0001031 |
| 2 | rs11897702 | 123106179 | TSN | 864283 base downstream | q14.3 | CT | 0.6492 | 1.243 | 0.0001032 |
| 17 | rs1547966 | 51779870 | ANKFN1 | intron 3 | q22 | CT | 0.2585 | 1.273 | 0.0001046 |
| 2 | rs1918273 | 123091471 | TSN | 849575 base downstream | q14.3 | GT | 0.3424 | 0.803 | 0.0001051 |
| 6 | rs1488324 | 94792276 | EPHA7 | 606283 base downstream | q16.1 | AG | 0.3256 | 1.239 | 0.0001052 |
| 16 | rs17146172 | 7343080 | A2BP1 | intron 4 | p13.2 | CT | 0.1066 | 1.383 | 0.0001073 |
| 16 | rs9933137 | 7342542 | A2BP1 | intron 4 | p13.2 | GT | 0.1066 | 1.382 | 0.0001074 |
| 15 | rs690535 | 51194001 | ONECUT1 | 324500 base downstream | q21.3 | GT | 0.1901 | 1.302 | 0.0001075 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 12 | rs825959 | 89248606 | C12orf12 | 621517 base upstream | q21.33 | CT | 0.6379 | 1.242 | 0.00011 |
| 16 | rs17842417 | 7340883 | A2BP1 | intron 4 | p13.2 | CT | 0.1066 | 1.38 | 0.0001101 |
| 6 | rs6910965 | 25280013 | LRRCL16 | 107613 base upstream | p22.2 | CG | 0.1856 | 0.764 | 0.0001104 |
| 17 | rs8082579 | 51771638 | ANKFN1 | intron 3 | q22 | GT | 0.7409 | 0.786 | 0.0001106 |
| 22 | rs5750066 | 33870522 | RAXLX | 57144 base downstream | q12.3 | GT | 0.7087 | 1.265 | 0.0001107 |
| 11 | rs836123 | 34519515 | ELF5 | 27609 base downstream | p13 | CT | 0.9311 | 0.654 | 0.0001123 |
| 21 | rs11088495 | 40081547 | LOC150084 | intron 5 | q22.2 | CT | 0.6049 | 0.815 | 0.000113 |
| 10 | rs2482824 | 30517781 | PAPD1 | 123983 base upstream | p11.23 | CT | 0.644 | 0.812 | 0.000114 |
| 16 | rs17143484 | 7339253 | A2BP1 | intron 4 | p13.2 | CT | 0.1067 | 1.377 | 0.0001143 |
| 16 | rs9924010 | 7338996 | A2BP1 | intron 4 | p13.2 | AG | 0.1067 | 1.377 | 0.0001148 |
| 6 | rs9471573 | 41405361 | NCR2 | 6144 base upstream | p21.1 | AG | 0.5624 | 0.812 | 0.0001149 |
| 15 | rs11858823 | 51190404 | ONECUT1 | 320903 base downstream | q21.3 | AG | 0.1947 | 1.297 | 0.0001153 |
| 6 | rs9384246 | 155209126 | RBM16 | 12242 base downstream | q25.2 | CT | 0.0374 | 0.548 | 0.0001156 |
| 10 | rs2505112 | 30517210 | PAPD1 | 124554 base upstream | p11.23 | CT | 0.3561 | 1.231 | 0.0001176 |
| 2 | rs1439724 | 209684516 | MAP2 | 312499 base upstream | q34 | AG | 0.1488 | 1.332 | 0.0001179 |
| 3 | rs820464 | 124839752 | MYLK | intron 6 | q21.1 | CG | 0.0542 | 1.553 | 0.0001187 |
| 3 | rs820460 | 124837883 | MYLK | intron 5 | q21.1 | CT | 0.0542 | 1.554 | 0.0001187 |
| 3 | rs1254401 | 124836431 | MYLK | intron 5 | q21.1 | CG | 0.0542 | 1.554 | 0.0001188 |
| 3 | rs820463 | 124839727 | MYLK | EXON 6 | q21.1 | AG | 0.9458 | 0.644 | 0.0001188 |
| 3 | rs1254397 | 124833978 | MYLK | intron 5 | q21.1 | CT | 0.9458 | 0.644 | 0.0001189 |
| 11 | rs7103202 | 10779614 | EIF4G2 | intron 8 | p15.3 | AG | 0.0758 | 0.681 | 0.0001189 |
| 3 | rs1254403 | 124840968 | MYLK | intron 6 | q21.1 | AC | 0.9458 | 0.644 | 0.000119 |
| 11 | rs4909953 | 10776960 | EIF4G2 | intron 1 | p15.3 | AC | 0.0758 | 0.681 | 0.000119 |
| 3 | rs820470 | 124845546 | MYLK | intron 7 | q21.1 | CT | 0.0542 | 1.553 | 0.0001192 |
| 11 | rs10743150 | 10781116 | EIF4G2 | intron 11 | p15.3 | AG | 0.9242 | 1.468 | 0.0001197 |
| 3 | rs820472 | 124847003 | MYLK | intron 7 | q21.1 | CT | 0.0542 | 1.553 | 0.0001201 |
| 11 | rs7932171 | 10783496 | EIF4G2 | intron 18 | p15.3 | CT | 0.9242 | 1.468 | 0.0001208 |
| 3 | rs820446 | 124831466 | MYLK | intron 5 | q21.1 | CT | 0.0542 | 1.553 | 0.0001214 |
| 4 | rs6811079 | 175703538 | HPGD | 23352 base downstream | q34.1 | AG | 0.0917 | 0.688 | 0.0001221 |
| 3 | rs820455 | 124823568 | MYLK | intron 3 | q21.1 | AG | 0.9458 | 0.644 | 0.0001232 |
| 3 | rs820459 | 124820628 | MYLK | intron 2 | q21.1 | AG | 0.9458 | 0.644 | 0.0001233 |
| 3 | rs848145 | 124819672 | MYLK | intron 1 | q21.1 | AG | 0.0542 | 1.552 | 0.0001234 |
| 2 | rs10490026 | 210441690 | C2orf21 | 72174 base downstream | q34 | AG | 0.1214 | 1.359 | 0.0001268 |
| 2 | rs10490025 | 210441645 | C2orf21 | 72129 base downstream | q34 | AT | 0.8786 | 0.736 | 0.0001268 |
| 6 | rs9357353 | 41385833 | TREM1 | 23398 base downstream | p21.1 | CT | 0.4184 | 1.234 | 0.0001278 |
| 3 | rs1254389 | 124852418 | MYLK | intron 10 | q21.1 | AT | 0.0539 | 1.549 | 0.0001285 |
| 15 | rs10518710 | 51245627 | WDR72 | 347602 base upstream | q21.3 | CG | 0.1871 | 1.294 | 0.0001304 |

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|----|------------|-----------|---------------|-------------------------|--------|----|--------|-------|-----------|
| 2 | rs1439736 | 209659240 | MAP2 | 337775 base upstream | q34 | GT | 0.8516 | 0.752 | 0.0001306 |
| 4 | rs16895934 | 9892151 | KIAA1729 | 158450 base upstream | p16.1 | GT | 0.006 | 3.933 | 0.0001325 |
| 3 | rs2362754 | 24675281 | THRB | 163964 base downstream | p24.2 | CG | 0.4793 | 0.819 | 0.0001358 |
| 4 | rs2553316 | 58802595 | IGFBP7 | 1131299 base downstream | q12 | CG | 0.6927 | 1.253 | 0.0001365 |
| 10 | rs2488010 | 30531413 | PAPD1 | 110351 base upstream | p11.23 | AG | 0.356 | 1.23 | 0.0001372 |
| 8 | rs7842645 | 135163085 | ZNF406 | 396128 base upstream | q24.22 | AG | 0.4783 | 1.219 | 0.000138 |
| 3 | rs4452272 | 24666213 | THRB | 154896 base downstream | p24.2 | CT | 0.479 | 0.819 | 0.0001387 |
| 1 | rs942837 | 214165817 | USH2A | intron 34 | q41 | CT | 0.8333 | 1.319 | 0.0001393 |
| 2 | rs13414802 | 210440931 | C2orf21 | 71415 base downstream | q34 | AG | 0.8644 | 0.739 | 0.0001405 |
| 1 | rs513746 | 214169419 | USH2A | intron 34 | q41 | CT | 0.8336 | 1.318 | 0.0001411 |
| 1 | rs517577 | 214169893 | USH2A | intron 34 | q41 | AG | 0.1664 | 0.759 | 0.0001414 |
| 7 | rs1919945 | 52978744 | DKFZp564N2472 | 92098 base upstream | p12.1 | CT | 0.8061 | 0.766 | 0.0001418 |
| 1 | rs662355 | 214170400 | USH2A | intron 34 | q41 | CG | 0.8339 | 1.318 | 0.000143 |
| 17 | rs7222776 | 787555 | NXN | intron 7 | p13.3 | GT | 0.6938 | 0.806 | 0.0001433 |
| 1 | rs647908 | 214171349 | USH2A | intron 34 | q41 | AC | 0.1659 | 0.759 | 0.0001449 |
| 1 | rs646576 | 214171639 | USH2A | intron 34 | q41 | AG | 0.1658 | 0.759 | 0.0001454 |
| 5 | rs13156277 | 2517988 | IRX2 | 281891 base upstream | p15.33 | CT | 0.6093 | 1.252 | 0.000146 |
| 10 | rs503598 | 30536131 | PAPD1 | 105633 base upstream | p11.23 | AG | 0.6439 | 0.814 | 0.0001469 |
| 10 | rs4918918 | 97112231 | SORBS1 | intron 11 | q23.33 | CT | 0.6364 | 0.814 | 0.000149 |
| 15 | rs17628504 | 51322236 | WDR72 | 270993 base upstream | q21.3 | AG | 0.8454 | 0.754 | 0.000149 |
| 11 | rs369845 | 115308412 | CADM1 | 427961 base downstream | q23.2 | CT | 0.2816 | 1.249 | 0.0001497 |
| 1 | rs1660383 | 212355520 | PROX1 | 79137 base downstream | q41 | AG | 0.0334 | 1.777 | 0.0001509 |
| 5 | rs13175490 | 2517882 | IRX2 | 281997 base upstream | p15.33 | AG | 0.6094 | 1.251 | 0.0001512 |
| 1 | rs492474 | 214178831 | USH2A | intron 35 | q41 | GT | 0.1653 | 0.76 | 0.0001514 |
| 4 | rs16895848 | 9887927 | WDR1 | 160256 base downstream | p16.1 | AT | 0.006 | 3.923 | 0.0001524 |
| 18 | rs2004027 | 64693088 | CCDC102B | intron 7 | q22.1 | AT | 0.2745 | 1.244 | 0.000153 |
| 2 | rs11684281 | 123098501 | TSN | 856605 base downstream | q14.3 | GT | 0.3593 | 0.811 | 0.0001538 |
| 18 | rs2051301 | 64691203 | CCDC102B | intron 6 | q22.1 | CT | 0.2747 | 1.244 | 0.0001538 |
| 18 | rs2051303 | 64690810 | CCDC102B | intron 6 | q22.1 | AT | 0.2748 | 1.244 | 0.0001541 |
| 12 | rs6488934 | 123620722 | NCOR2 | 34620 base downstream | q24.31 | AT | 0.053 | 1.559 | 0.0001544 |
| 18 | rs4797242 | 6397483 | L3MBTL4 | intron 19 | p11.31 | AC | 0.2891 | 0.799 | 0.0001545 |
| 8 | rs1158934 | 135101424 | ST3GAL1 | 448080 base downstream | q24.22 | AG | 0.439 | 0.819 | 0.0001555 |
| 2 | rs2418570 | 123069387 | TSN | 827491 base downstream | q14.3 | AG | 0.3387 | 0.808 | 0.0001585 |
| 4 | rs13105776 | 58828037 | IGFBP7 | 1156741 base downstream | q12 | CT | 0.7761 | 1.284 | 0.0001593 |
| 6 | rs3123337 | 99005968 | POU3F2 | 383332 base upstream | q16.2 | CT | 0.0454 | 0.571 | 0.0001627 |
| 5 | rs1309534 | 64338340 | SDCCAG10 | intron 13 | q12.3 | AG | 0.1766 | 1.311 | 0.000164 |
| 22 | rs9610223 | 33870650 | RAXLX | 57272 base downstream | q12.3 | CT | 0.2621 | 0.796 | 0.0001643 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs10171928 | 123068787 | TSN | 826891 base downstream | q14.3 | CT | 0.3382 | 0.808 | 0.0001655 |
| 21 | rs2823722 | 16557827 | C21orf34 | intron 4 | q21.1 | CT | 0.609 | 0.802 | 0.0001656 |
| 2 | rs1595755 | 123087692 | TSN | 845796 base downstream | q14.3 | CT | 0.6408 | 1.23 | 0.0001673 |
| 21 | rs238946 | 16544957 | C21orf34 | intron 4 | q21.1 | AG | 0.605 | 0.806 | 0.0001675 |
| 2 | rs2043940 | 123083369 | TSN | 841473 base downstream | q14.3 | CT | 0.6408 | 1.23 | 0.0001676 |
| 10 | rs2488003 | 30507811 | KIAA1462 | 131005 base downstream | p11.23 | AG | 0.6411 | 0.816 | 0.0001683 |
| 2 | rs6753885 | 123075396 | TSN | 833500 base downstream | q14.3 | AT | 0.6408 | 1.23 | 0.0001683 |
| 20 | rs6066696 | 46386093 | PREX1 | 288106 base upstream | q13.13 | AT | 0.3237 | 0.803 | 0.0001686 |
| 6 | rs12663706 | 25256945 | LRRC16 | 130681 base upstream | p22.2 | CG | 0.7816 | 1.295 | 0.0001699 |
| 8 | rs13272401 | 12770433 | C8orf79 | 77120 base upstream | p22 | GT | 0.0196 | 2.135 | 0.0001715 |
| 3 | rs11928551 | 24678903 | THRB | 167586 base downstream | p24.2 | GT | 0.52 | 1.218 | 0.0001728 |
| 3 | rs9812637 | 24680225 | THRB | 168908 base downstream | p24.2 | AG | 0.48 | 0.821 | 0.0001736 |
| 3 | rs6794974 | 106404720 | ALCAM | 163682 base upstream | q13.11 | AG | 0.1946 | 0.777 | 0.0001744 |
| 1 | rs4951084 | 202873597 | LRRN5 | intron 1 | q32.1 | CG | 0.2748 | 1.27 | 0.0001748 |
| 21 | rs2823717 | 16555717 | C21orf34 | intron 4 | q21.1 | AT | 0.6041 | 0.818 | 0.0001755 |
| 1 | rs772713 | 214179910 | USH2A | intron 35 | q41 | AC | 0.8344 | 1.314 | 0.0001757 |
| 16 | rs8054432 | 6838730 | A2BP1 | intron 3 | p13.2 | CT | 0.692 | 1.244 | 0.0001758 |
| 3 | rs9843745 | 24661552 | THRB | 150235 base downstream | p24.2 | AG | 0.4786 | 0.821 | 0.0001766 |
| 2 | rs2698029 | 51633763 | NRXN1 | 520585 base downstream | p16.3 | GT | 0.5489 | 0.821 | 0.0001767 |
| 16 | rs8054809 | 6838963 | A2BP1 | intron 3 | p13.2 | CG | 0.692 | 1.245 | 0.0001771 |
| 3 | rs9817530 | 24656887 | THRB | 145570 base downstream | p24.2 | AG | 0.4785 | 0.821 | 0.0001773 |
| 11 | rs11042997 | 10857160 | EIF4G2 | 70002 base downstream | p15.3 | AC | 0.1366 | 0.728 | 0.0001773 |
| 21 | rs2823721 | 16557703 | C21orf34 | intron 4 | q21.1 | AG | 0.3938 | 1.232 | 0.0001774 |
| 21 | rs2823716 | 16555664 | C21orf34 | intron 4 | q21.1 | AG | 0.6042 | 0.818 | 0.0001782 |
| 2 | rs2715079 | 51634538 | NRXN1 | 521360 base downstream | p16.3 | AG | 0.451 | 1.217 | 0.0001784 |
| 3 | rs1568420 | 106400088 | ALCAM | 168314 base upstream | q13.11 | CT | 0.1946 | 0.777 | 0.0001789 |
| 8 | rs7462232 | 54386673 | OPRK1 | 59926 base downstream | q11.23 | AG | 0.8842 | 1.388 | 0.00018 |
| 21 | rs238964 | 16557408 | C21orf34 | intron 4 | q21.1 | CG | 0.605 | 0.815 | 0.000182 |
| 21 | rs1492957 | 16555965 | C21orf34 | intron 4 | q21.1 | CT | 0.3959 | 1.223 | 0.0001822 |
| 21 | rs4337554 | 40078450 | LOC150084 | intron 5 | q22.2 | AG | 0.665 | 0.81 | 0.0001825 |
| 21 | rs2823718 | 16556290 | C21orf34 | intron 4 | q21.1 | AG | 0.3952 | 1.223 | 0.0001834 |
| 21 | rs6517695 | 16557390 | C21orf34 | intron 4 | q21.1 | GT | 0.3953 | 1.225 | 0.0001843 |
| 2 | rs11124131 | 106716044 | ST6GAL2 | 73495 base upstream | q12.3 | AC | 0.6886 | 1.244 | 0.000185 |
| 21 | rs2823720 | 16556577 | C21orf34 | intron 4 | q21.1 | AC | 0.6043 | 0.817 | 0.0001857 |
| 5 | rs7730020 | 40693709 | PTGER4 | 22079 base upstream | p13.1 | CT | 0.6573 | 1.232 | 0.0001859 |
| 4 | rs11248073 | 1707300 | TACC3 | EXON 8 | p16.3 | CT | 0.6523 | 0.799 | 0.0001864 |
| 2 | rs13393451 | 106707725 | ST6GAL2 | 81814 base upstream | q12.3 | AG | 0.3114 | 0.803 | 0.0001874 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs13391600 | 106709532 | ST6GAL2 | 80007 base upstream | q12.3 | CT | 0.3114 | 0.803 | 0.0001874 |
| 4 | rs17148361 | 71114351 | APIN | 9470 base downstream | q13.3 | CT | 0.869 | 1.335 | 0.0001875 |
| 2 | rs898457 | 106705890 | ST6GAL2 | 83649 base upstream | q12.3 | AG | 0.6886 | 1.245 | 0.0001877 |
| 2 | rs898456 | 106706061 | ST6GAL2 | 83478 base upstream | q12.3 | AG | 0.3114 | 0.803 | 0.0001877 |
| 4 | rs1530588 | 1712577 | TACC3 | intron 13 | p16.3 | AG | 0.3494 | 1.258 | 0.0001882 |
| 21 | rs4465860 | 16555455 | C21orf34 | intron 4 | q21.1 | CT | 0.6042 | 0.818 | 0.0001885 |
| 5 | rs11739531 | 40665104 | PTGER4 | 50684 base upstream | p13.1 | CT | 0.3425 | 0.812 | 0.0001901 |
| 5 | rs16869212 | 16935090 | MYO10 | intron 40 | p15.1 | AG | 0.0667 | 1.455 | 0.0001901 |
| 2 | rs1006472 | 106695948 | ST6GAL2 | 93591 base upstream | q12.2 | AC | 0.6886 | 1.245 | 0.0001902 |
| 2 | rs2698028 | 51635357 | NRXN1 | 522179 base downstream | p16.3 | CT | 0.549 | 0.822 | 0.0001902 |
| 18 | rs12961587 | 6394347 | L3MBTL4 | intron 19 | p11.31 | AG | 0.545 | 1.23 | 0.0001904 |
| 5 | rs7716982 | 40682317 | PTGER4 | 33471 base upstream | p13.1 | GT | 0.3426 | 0.812 | 0.0001906 |
| 3 | rs2918217 | 117029070 | LSAMP | intron 1 | q13.31 | CT | 0.8657 | 0.755 | 0.0001916 |
| 11 | rs11042998 | 10857488 | EIF4G2 | 70330 base downstream | p15.3 | GT | 0.1372 | 0.732 | 0.0001923 |
| 21 | rs2251006 | 16555396 | C21orf34 | intron 4 | q21.1 | CT | 0.3957 | 1.222 | 0.0001925 |
| 2 | rs13001767 | 51625919 | NRXN1 | 512741 base downstream | p16.3 | GT | 0.5323 | 0.821 | 0.0001927 |
| 1 | rs1660382 | 212355741 | PROX1 | 79358 base downstream | q41 | AG | 0.0322 | 1.726 | 0.000193 |
| 11 | rs745231 | 11073168 | GALNTL4 | 175833 base upstream | p15.3 | CT | 0.5474 | 1.219 | 0.0001948 |
| 2 | rs1304771 | 123061530 | TSN | 819634 base downstream | q14.3 | AG | 0.6635 | 1.233 | 0.0001965 |
| 1 | rs7512894 | 55469135 | USP24 | 15785 base downstream | p32.3 | AG | 0.7906 | 0.782 | 0.0001969 |
| 2 | rs10864879 | 123058863 | TSN | 816967 base downstream | q14.3 | CG | 0.6635 | 1.233 | 0.0001971 |
| 4 | rs798761 | 1700924 | TACC3 | intron 4 | p16.3 | AG | 0.3433 | 1.238 | 0.0001976 |
| 12 | rs7136505 | 82308633 | TMTC2 | 256439 base downstream | q21.31 | AG | 0.9678 | 0.566 | 0.000198 |
| 2 | rs984521 | 133209220 | NAP5 | intron 4 | q21.2 | AG | 0.3357 | 0.81 | 0.0001984 |
| 1 | rs11264432 | 154309539 | MEX3A | EXON 1 | q22 | AG | 0.5681 | 0.813 | 0.0001992 |
| 6 | rs6457109 | 30041240 | HCG9 | 9630 base upstream | p21.33 | CT | 0.0635 | 1.522 | 0.0001995 |
| 4 | rs2306445 | 71098553 | APIN | intron 4 | q13.3 | AG | 0.1309 | 0.75 | 0.0001999 |
| 5 | rs1309540 | 64329326 | SDCCAG10 | intron 13 | q12.3 | AG | 0.177 | 1.305 | 0.0002001 |
| 21 | rs2823713 | 16555037 | C21orf34 | intron 4 | q21.1 | AT | 0.3957 | 1.221 | 0.0002008 |
| 4 | rs2854917 | 1690348 | TMEM129 | intron 2 | p16.3 | CT | 0.3416 | 1.235 | 0.0002013 |
| 6 | rs9362322 | 87197144 | HTR1E | 506984 base upstream | q14.3 | AT | 0.1776 | 1.295 | 0.0002021 |
| 2 | rs1439838 | 123052210 | TSN | 810314 base downstream | q14.3 | AT | 0.3369 | 0.811 | 0.0002022 |
| 4 | rs6824942 | 21227268 | KCNIP4 | intron 7 | p15.31 | CT | 0.4933 | 0.821 | 0.0002024 |
| 1 | rs241215 | 4503964 | AJAP1 | 111000 base upstream | p36.32 | AT | 0.609 | 1.225 | 0.0002024 |
| 4 | rs6848248 | 21227279 | KCNIP4 | intron 7 | p15.31 | AG | 0.4933 | 0.821 | 0.0002027 |
| 11 | rs2403431 | 10858797 | EIF4G2 | 71639 base downstream | p15.3 | AC | 0.1376 | 0.735 | 0.0002028 |
| 4 | rs2854916 | 1691146 | TMEM129 | intron 2 | p16.3 | AG | 0.3416 | 1.235 | 0.0002035 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs13117892 | 21227551 | KCNIP4 | intron 7 | p15.31 | AT | 0.4932 | 0.821 | 0.0002035 |
| 3 | rs10933810 | 106415848 | ALCAM | 152554 base upstream | q13.11 | CT | 0.7986 | 1.284 | 0.0002035 |
| 4 | rs10000010 | 21227772 | KCNIP4 | intron 7 | p15.31 | CT | 0.4932 | 0.821 | 0.0002037 |
| 1 | rs694935 | 4503184 | AJAP1 | 111780 base upstream | p36.32 | AT | 0.609 | 1.225 | 0.0002042 |
| 2 | rs2272315 | 123050723 | TSN | 808827 base downstream | q14.3 | AG | 0.3371 | 0.811 | 0.0002044 |
| 10 | rs7900095 | 97109039 | SORBS1 | intron 11 | q23.33 | CT | 0.6196 | 0.819 | 0.0002046 |
| 10 | rs7079293 | 97109583 | SORBS1 | intron 11 | q23.33 | CT | 0.6196 | 0.819 | 0.000205 |
| 10 | rs2798920 | 30515649 | PAPD1 | 126115 base upstream | p11.23 | AG | 0.3598 | 1.221 | 0.0002052 |
| 20 | rs6116726 | 5209399 | PROKR2 | 21287 base upstream | p12.3 | CT | 0.609 | 1.229 | 0.0002056 |
| 21 | rs2823712 | 16554963 | C21orf34 | intron 4 | q21.1 | AG | 0.3957 | 1.221 | 0.0002063 |
| 12 | rs10506083 | 32214624 | BICD1 | intron 1 | p11.21 | AG | 0.5852 | 1.239 | 0.0002072 |
| 10 | rs2795863 | 30540273 | PAPD1 | 101491 base upstream | p11.23 | AG | 0.6443 | 0.817 | 0.0002076 |
| 4 | rs743569 | 1689418 | TMEM129 | intron 1 | p16.3 | GT | 0.3414 | 1.234 | 0.0002077 |
| 10 | rs2798906 | 30514592 | PAPD1 | 127172 base upstream | p11.23 | AG | 0.3596 | 1.222 | 0.0002097 |
| 4 | rs17148330 | 71093585 | APIN | 3247 base upstream | q13.3 | AG | 0.1309 | 0.751 | 0.0002097 |
| 1 | rs1660381 | 212356390 | PROX1 | 80007 base downstream | q41 | CT | 0.0318 | 1.711 | 0.0002102 |
| 10 | rs2795859 | 30514493 | PAPD1 | 127271 base upstream | p11.23 | CT | 0.6405 | 0.819 | 0.0002107 |
| 9 | rs1467773 | 77922888 | PCSK5 | intron 9 | q21.13 | AG | 0.8623 | 1.359 | 0.0002115 |
| 4 | rs17148328 | 71088800 | APIN | 8032 base upstream | q13.3 | CT | 0.1309 | 0.751 | 0.0002146 |
| 17 | rs4793818 | 51868565 | ANKFN1 | intron 7 | q22 | GT | 0.2388 | 1.256 | 0.0002149 |
| 2 | rs1405604 | 123070752 | TSN | 828856 base downstream | q14.3 | AG | 0.3576 | 0.815 | 0.000215 |
| 5 | rs325538 | 104081546 | NUDT12 | 1155157 base downstream | q21.2 | AG | 0.8233 | 0.772 | 0.0002152 |
| 14 | rs7160795 | 82451964 | SEL1L | 1382078 base downstream | q31.1 | CT | 0.7323 | 0.796 | 0.0002155 |
| 3 | rs11129156 | 24635868 | THRB | 124551 base downstream | p24.2 | AG | 0.7023 | 1.251 | 0.0002172 |
| 11 | rs771377 | 10824525 | EIF4G2 | 37367 base downstream | p15.3 | CG | 0.9253 | 1.452 | 0.0002175 |
| 12 | rs17010837 | 82371672 | TMTC2 | 319478 base downstream | q21.31 | AG | 0.032 | 1.76 | 0.000218 |
| 2 | rs16844213 | 210787411 | ACADL | intron 7 | q34 | CT | 0.102 | 1.366 | 0.0002184 |
| 2 | rs13415601 | 210788369 | ACADL | intron 7 | q34 | AT | 0.102 | 1.366 | 0.0002186 |
| 2 | rs13009758 | 210810084 | ACADL | 11692 base downstream | q34 | CT | 0.102 | 1.366 | 0.0002193 |
| 2 | rs1554006 | 111320584 | ACOXL | intron 10 | q13 | AG | 0.3063 | 1.239 | 0.0002196 |
| 11 | rs2687489 | 10826485 | EIF4G2 | 39327 base downstream | p15.3 | AG | 0.9253 | 1.451 | 0.0002199 |
| 2 | rs10210955 | 111315753 | ACOXL | intron 10 | q13 | CG | 0.4815 | 0.824 | 0.00022 |
| 15 | rs12442241 | 51195790 | ONECUT1 | 326289 base downstream | q21.3 | AT | 0.8322 | 0.762 | 0.0002203 |
| 2 | rs1509571 | 210781793 | ACADL | intron 6 | q34 | CT | 0.102 | 1.366 | 0.0002214 |
| 5 | rs9312996 | 2527518 | IRX2 | 272361 base upstream | p15.33 | CG | 0.6846 | 1.251 | 0.0002223 |
| 2 | rs1509572 | 210781582 | ACADL | intron 6 | q34 | AT | 0.102 | 1.365 | 0.0002226 |
| 4 | rs1825033 | 71136589 | C4orf7 | 1034 base downstream | q13.3 | AG | 0.1309 | 0.752 | 0.0002227 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs263666 | 210816047 | ACADL | 17655 base downstream | q34 | AG | 0.8981 | 0.732 | 0.0002231 |
| 2 | rs11563162 | 51632112 | NRXN1 | 518934 base downstream | p16.3 | AG | 0.4933 | 1.225 | 0.0002233 |
| 2 | rs1509568 | 210777256 | ACADL | intron 4 | q34 | CT | 0.898 | 0.732 | 0.0002235 |
| 2 | rs6760874 | 210826755 | ACADL | 28363 base downstream | q34 | CT | 0.8981 | 0.732 | 0.0002237 |
| 11 | rs7925687 | 10829758 | EIF4G2 | 42600 base downstream | p15.3 | CT | 0.0747 | 0.689 | 0.0002241 |
| 3 | rs4075988 | 24755270 | THRB | 243953 base downstream | p24.2 | AG | 0.8474 | 1.328 | 0.0002245 |
| 21 | rs2823692 | 16548642 | C21orf34 | intron 4 | q21.1 | AC | 0.609 | 0.814 | 0.0002252 |
| 4 | rs3775747 | 71147532 | CSN3 | intron 2 | q13.3 | CT | 0.1301 | 0.744 | 0.0002252 |
| 17 | rs4794639 | 51825310 | ANKFN1 | intron 7 | q22 | AG | 0.7525 | 0.797 | 0.0002263 |
| 1 | rs1660380 | 212356402 | PROX1 | 80019 base downstream | q41 | AG | 0.9686 | 0.59 | 0.0002265 |
| 1 | rs1660378 | 212356865 | PROX1 | 80482 base downstream | q41 | CT | 0.0313 | 1.696 | 0.0002268 |
| 4 | rs1817460 | 71136840 | C4orf7 | 1285 base downstream | q13.3 | AT | 0.1309 | 0.752 | 0.000227 |
| 2 | rs263680 | 210775646 | ACADL | intron 3 | q34 | AG | 0.102 | 1.365 | 0.0002271 |
| 21 | rs2823710 | 16554494 | C21orf34 | intron 4 | q21.1 | AG | 0.6044 | 0.82 | 0.0002279 |
| 2 | rs263681 | 210771597 | ACADL | intron 3 | q34 | CG | 0.102 | 1.365 | 0.0002279 |
| 2 | rs2405635 | 128353695 | MGC4268 | intron 6 | q14.3 | AG | 0.5892 | 0.822 | 0.0002282 |
| 20 | rs6116721 | 5203078 | PROKR2 | 27608 base upstream | p12.3 | GT | 0.3915 | 0.815 | 0.0002285 |
| 16 | rs13330100 | 7338030 | A2BP1 | intron 4 | p13.2 | CT | 0.8864 | 0.747 | 0.0002297 |
| 7 | rs11979834 | 52115801 | COBL | 763811 base downstream | p12.1 | AG | 0.2274 | 0.794 | 0.0002298 |
| 2 | rs2715081 | 51629318 | NRXN1 | 516140 base downstream | p16.3 | CT | 0.531 | 0.824 | 0.0002302 |
| 7 | rs6965611 | 52134879 | COBL | 782889 base downstream | p12.1 | GT | 0.2309 | 0.779 | 0.0002306 |
| 5 | rs13178969 | 64299723 | SDCCAG10 | intron 11 | q12.3 | CT | 0.1774 | 1.3 | 0.0002309 |
| 1 | rs1440619 | 212357674 | PROX1 | 81291 base downstream | q41 | AG | 0.0297 | 1.736 | 0.0002312 |
| 11 | rs2232928 | 10831170 | EIF4G2 | 44012 base downstream | p15.3 | AG | 0.9253 | 1.45 | 0.0002313 |
| 1 | rs1660377 | 212356924 | PROX1 | 80541 base downstream | q41 | AT | 0.0313 | 1.694 | 0.000232 |
| 2 | rs7566163 | 128352457 | MGC4268 | intron 6 | q14.3 | AG | 0.4107 | 1.216 | 0.0002324 |
| 1 | rs1795037 | 212357165 | PROX1 | 80782 base downstream | q41 | AG | 0.0313 | 1.694 | 0.0002324 |
| 2 | rs6716836 | 210826582 | ACADL | 28190 base downstream | q34 | AG | 0.108 | 1.366 | 0.0002329 |
| 7 | rs2953422 | 52131614 | COBL | 779624 base downstream | p12.1 | AG | 0.514 | 0.82 | 0.0002344 |
| 1 | rs2556 | 206126982 | CD34 | EXON 1 | q32.2 | AG | 0.0804 | 0.701 | 0.0002354 |
| 9 | rs2185227 | 77923214 | PCSK5 | intron 9 | q21.13 | AG | 0.8631 | 1.352 | 0.0002357 |
| 2 | rs6548032 | 30841879 | CAPN13 | intron 18 | p23.1 | AG | 0.3163 | 1.231 | 0.0002359 |
| 2 | rs1155845 | 210762844 | ACADL | intron 1 | q34 | CT | 0.1019 | 1.364 | 0.000236 |
| 1 | rs542688 | 4500481 | AJAP1 | 114483 base upstream | p36.32 | CG | 0.3915 | 0.817 | 0.000237 |
| 10 | rs2798907 | 30512779 | PAPD1 | 128985 base upstream | p11.23 | AG | 0.64 | 0.819 | 0.0002375 |
| 2 | rs4558528 | 210842791 | MYL1 | 20322 base upstream | q34 | AT | 0.1018 | 1.367 | 0.0002378 |
| 17 | rs7220133 | 51873068 | ANKFN1 | intron 8 | q22 | CT | 0.2384 | 1.253 | 0.000238 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 1 | rs498911 | 214171603 | USH2A | intron 34 | q41 | AC | 0.1585 | 0.76 | 0.0002382 |
| 2 | rs1396830 | 210844857 | MYL1 | 18256 base upstream | q34 | AG | 0.8982 | 0.732 | 0.0002384 |
| 21 | rs2823709 | 16554235 | C21orf34 | intron 4 | q21.1 | AG | 0.3955 | 1.218 | 0.0002385 |
| 21 | rs2823725 | 16558862 | C21orf34 | intron 4 | q21.1 | AT | 0.384 | 1.247 | 0.0002388 |
| 1 | rs12568811 | 212358567 | PROX1 | 82184 base downstream | q41 | AG | 0.9706 | 0.575 | 0.0002395 |
| 2 | rs10445851 | 123052783 | TSN | 810887 base downstream | q14.3 | GT | 0.6435 | 1.225 | 0.0002413 |
| 1 | rs592726 | 4499103 | AJAP1 | 115861 base upstream | p36.32 | CT | 0.3916 | 0.817 | 0.0002413 |
| 22 | rs4821368 | 33864933 | RAXLX | 51555 base downstream | q12.3 | CG | 0.7462 | 1.264 | 0.000243 |
| 15 | rs4887337 | 86294466 | NTRK3 | intron 6 | q25.3 | AC | 0.1054 | 1.369 | 0.0002435 |
| 10 | rs2482828 | 30500212 | KIAA1462 | 123406 base downstream | p11.23 | AG | 0.3581 | 1.225 | 0.0002437 |
| 21 | rs9982468 | 32336948 | HUNK | 38701 base downstream | q22.11 | CT | 0.8505 | 1.324 | 0.0002437 |
| 2 | rs1396831 | 210844923 | MYL1 | 18190 base upstream | q34 | AT | 0.1017 | 1.367 | 0.0002439 |
| 13 | rs7325881 | 89560729 | GPC5 | 1288158 base upstream | q31.3 | CT | 0.1993 | 0.772 | 0.0002447 |
| 2 | rs11563043 | 51630745 | NRXN1 | 517567 base downstream | p16.3 | CG | 0.5453 | 0.825 | 0.0002451 |
| 4 | rs4583737 | 154181234 | KIAA1727 | 60936 base downstream | q31.3 | AC | 0.319 | 1.224 | 0.0002453 |
| 21 | rs4381854 | 16553692 | C21orf34 | intron 4 | q21.1 | CT | 0.6045 | 0.821 | 0.0002455 |
| 18 | rs9948116 | 64676889 | CCDC102B | intron 6 | q22.1 | AG | 0.7248 | 0.809 | 0.0002457 |
| 7 | rs6944484 | 157012904 | PTPRN2 | 11611 base upstream | q36.3 | AC | 0.8832 | 1.364 | 0.0002464 |
| 2 | rs2715084 | 51632158 | NRXN1 | 518980 base downstream | p16.3 | CT | 0.4546 | 1.212 | 0.0002471 |
| 8 | rs1457473 | 135194786 | ZNF406 | 364427 base upstream | q24.22 | AG | 0.4644 | 1.211 | 0.0002475 |
| 5 | rs17065434 | 164985118 | MAT2B | 2106215 base downstream | q34 | CT | 0.7715 | 0.793 | 0.0002479 |
| 2 | rs999492 | 123048824 | TSN | 806928 base downstream | q14.3 | AC | 0.3572 | 0.817 | 0.0002482 |
| 4 | rs2406144 | 154185069 | KIAA1727 | 64771 base downstream | q31.3 | CT | 0.319 | 1.224 | 0.0002486 |
| 18 | rs12969887 | 6392671 | L3MBTL4 | intron 19 | p11.31 | AC | 0.5391 | 1.224 | 0.0002486 |
| 2 | rs6752217 | 210419671 | C2orf21 | 50155 base downstream | q34 | GT | 0.8891 | 0.734 | 0.0002489 |
| 4 | rs908535 | 154187592 | KIAA1727 | 67294 base downstream | q31.3 | AG | 0.6812 | 0.817 | 0.0002489 |
| 11 | rs2232919 | 10832929 | EIF4G2 | 45771 base downstream | p15.3 | CT | 0.0748 | 0.69 | 0.0002494 |
| 13 | rs9588875 | 89566249 | GPC5 | 1282638 base upstream | q31.3 | AT | 0.1992 | 0.772 | 0.0002501 |
| 11 | rs2232918 | 10833019 | EIF4G2 | 45861 base downstream | p15.3 | AG | 0.0748 | 0.69 | 0.0002507 |
| 13 | rs9805500 | 89566889 | GPC5 | 1281998 base upstream | q31.3 | CT | 0.8008 | 1.295 | 0.0002512 |
| 21 | rs9974134 | 32329234 | HUNK | 30987 base downstream | q22.11 | AC | 0.1494 | 0.756 | 0.0002512 |
| 2 | rs1527253 | 123048317 | TSN | 806421 base downstream | q14.3 | CT | 0.6426 | 1.224 | 0.0002514 |
| 2 | rs2715086 | 51632225 | NRXN1 | 519047 base downstream | p16.3 | AT | 0.4544 | 1.212 | 0.0002517 |
| 2 | rs7574002 | 172832429 | DLX2 | 156705 base downstream | q31.1 | CT | 0.3525 | 1.221 | 0.000252 |
| 2 | rs10195812 | 123046194 | TSN | 804298 base downstream | q14.3 | CT | 0.3574 | 0.817 | 0.0002526 |
| 2 | rs13425998 | 123045361 | TSN | 803465 base downstream | q14.3 | CT | 0.6425 | 1.224 | 0.0002535 |
| 11 | rs2291840 | 9123690 | RAB6IP1 | intron 6 | p15.4 | AC | 0.1693 | 1.28 | 0.0002539 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 21 | rs1389071 | 16553672 | C21orf34 | intron 4 | q21.1 | AT | 0.3955 | 1.217 | 0.0002542 |
| 3 | rs6770162 | 24686017 | THRB | 174700 base downstream | p24.2 | AG | 0.5023 | 0.824 | 0.0002543 |
| 8 | rs16905053 | 135108870 | ZNF406 | 450343 base upstream | q24.22 | AT | 0.137 | 0.751 | 0.0002546 |
| 8 | rs16905054 | 135109347 | ZNF406 | 449866 base upstream | q24.22 | AG | 0.863 | 1.331 | 0.0002549 |
| 4 | rs17029545 | 154191355 | KIAA1727 | 71057 base downstream | q31.3 | CT | 0.3185 | 1.223 | 0.000255 |
| 17 | rs980080 | 51864068 | ANKFN1 | intron 7 | q22 | CT | 0.7615 | 0.799 | 0.0002566 |
| 2 | rs2715088 | 51632332 | NRXN1 | 519154 base downstream | p16.3 | CT | 0.4542 | 1.212 | 0.0002574 |
| 4 | rs2412887 | 58862866 | IGFBP7 | 1191570 base downstream | q12 | AG | 0.7211 | 1.237 | 0.0002577 |
| 2 | rs1568213 | 98798495 | MGC42367 | intron 3 | q11.2 | AT | 0.3719 | 1.24 | 0.0002577 |
| 2 | rs2715089 | 51632624 | NRXN1 | 519446 base downstream | p16.3 | AC | 0.4541 | 1.212 | 0.0002578 |
| 3 | rs2972491 | 116985171 | LSAMP | 26668 base upstream | q13.31 | AG | 0.8687 | 0.738 | 0.000258 |
| 5 | rs11134531 | 168144746 | SLIT3 | intron 24 | q35.1 | AG | 0.5645 | 0.809 | 0.0002581 |
| 17 | rs10852984 | 51864305 | ANKFN1 | intron 7 | q22 | AG | 0.2384 | 1.252 | 0.0002583 |
| 6 | rs2844833 | 29810185 | HLA-F | 7903 base downstream | p22.1 | CG | 0.8571 | 0.758 | 0.0002589 |
| 10 | rs11015025 | 26606462 | GAD2 | intron 11 | p12.1 | CT | 0.9003 | 1.381 | 0.0002589 |
| 1 | rs608492 | 4497861 | AJAP1 | 117103 base upstream | p36.32 | CG | 0.6082 | 1.223 | 0.0002592 |
| 1 | rs4654974 | 21826881 | RAP1GA1 | intron 23 | p36.12 | CT | 0.3787 | 0.813 | 0.0002593 |
| 5 | rs3099592 | 2563027 | IRX2 | 236852 base upstream | p15.33 | AG | 0.5632 | 1.224 | 0.0002594 |
| 2 | rs9288414 | 210412445 | C2orf21 | 42929 base downstream | q34 | AC | 0.1089 | 1.368 | 0.0002596 |
| 2 | rs7574225 | 172832483 | DLX2 | 156759 base downstream | q31.1 | AG | 0.6478 | 0.818 | 0.0002605 |
| 1 | rs9426770 | 21828331 | RAP1GA1 | intron 23 | p36.12 | CG | 0.3787 | 0.813 | 0.0002605 |
| 2 | rs6754923 | 30855634 | CAPN13 | intron 21 | p23.1 | CG | 0.3978 | 1.215 | 0.0002609 |
| 2 | rs13028068 | 210418651 | C2orf21 | 49135 base downstream | q34 | GT | 0.1107 | 1.36 | 0.0002614 |
| 5 | rs10055939 | 2530430 | IRX2 | 269449 base upstream | p15.33 | GT | 0.6923 | 1.245 | 0.0002615 |
| 4 | rs2140072 | 58863520 | IGFBP7 | 1192224 base downstream | q12 | AG | 0.7211 | 1.236 | 0.0002623 |
| 3 | rs4131483 | 24666496 | THRB | 155179 base downstream | p24.2 | AT | 0.5275 | 1.213 | 0.0002624 |
| 7 | rs221238 | 157015643 | PTPRN2 | 8872 base upstream | q36.3 | CT | 0.1165 | 0.735 | 0.0002627 |
| 2 | rs6759289 | 123043417 | TSN | 801521 base downstream | q14.3 | AC | 0.3393 | 0.815 | 0.0002629 |
| 1 | rs11588634 | 150047310 | RORC | intron 1 | q21.3 | AT | 0.1325 | 0.724 | 0.0002635 |
| 7 | rs9690478 | 52133795 | COBL | 781805 base downstream | p12.1 | CG | 0.2224 | 0.78 | 0.0002636 |
| 4 | rs13148519 | 58861907 | IGFBP7 | 1190611 base downstream | q12 | AG | 0.2789 | 0.809 | 0.0002637 |
| 2 | rs10178425 | 210413138 | C2orf21 | 43622 base downstream | q34 | GT | 0.8906 | 0.733 | 0.0002641 |
| 2 | rs12386218 | 210418038 | C2orf21 | 48522 base downstream | q34 | CG | 0.8893 | 0.735 | 0.0002648 |
| 21 | rs1389073 | 16553507 | C21orf34 | intron 4 | q21.1 | GT | 0.6046 | 0.822 | 0.0002651 |
| 2 | rs7581875 | 123038464 | TSN | 796568 base downstream | q14.3 | CT | 0.3393 | 0.815 | 0.0002652 |
| 2 | rs1527255 | 123038857 | TSN | 796961 base downstream | q14.3 | AC | 0.6607 | 1.227 | 0.0002652 |
| 2 | rs766757 | 123037185 | TSN | 795289 base downstream | q14.3 | CT | 0.3393 | 0.815 | 0.0002652 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 2 | rs6541834 | 123041003 | TSN | 799107 base downstream | q14.3 | GT | 0.3393 | 0.815 | 0.0002653 |
| 2 | rs11122916 | 123042613 | TSN | 800717 base downstream | q14.3 | CT | 0.3393 | 0.815 | 0.0002653 |
| 4 | rs11933359 | 58866156 | IGFBP7 | 1194860 base downstream | q12 | CT | 0.2789 | 0.809 | 0.0002657 |
| 17 | rs7213627 | 51862430 | ANKFN1 | intron 7 | q22 | GT | 0.7619 | 0.799 | 0.0002659 |
| 1 | rs11588258 | 150047352 | RORC | intron 1 | q21.3 | AT | 0.8676 | 1.381 | 0.0002659 |
| 2 | rs4953986 | 133199169 | NAP5 | intron 1 | q21.2 | CT | 0.6655 | 1.228 | 0.000266 |
| 6 | rs12181054 | 30192566 | TRIM31 | 3720 base downstream | p21.33 | GT | 0.0533 | 1.537 | 0.0002662 |
| 21 | rs1389074 | 16553299 | C21orf34 | intron 4 | q21.1 | CT | 0.6046 | 0.822 | 0.0002667 |
| 4 | rs7690084 | 58860984 | IGFBP7 | 1189688 base downstream | q12 | AG | 0.2789 | 0.809 | 0.0002669 |
| 2 | rs2715077 | 51635788 | NRXN1 | 522610 base downstream | p16.3 | AC | 0.4498 | 1.211 | 0.000267 |
| 1 | rs1795036 | 212358932 | PROX1 | 82549 base downstream | q41 | AG | 0.0289 | 1.741 | 0.0002673 |
| 2 | rs17041560 | 30856523 | CAPN13 | intron 21 | p23.1 | AG | 0.6024 | 0.823 | 0.0002679 |
| 6 | rs7748376 | 6092415 | F13A1 | intron 1 | p25.1 | CG | 0.8373 | 0.772 | 0.0002682 |
| 11 | rs6484557 | 32220627 | RCN1 | 136974 base downstream | p13 | AC | 0.3238 | 0.813 | 0.0002684 |
| 1 | rs9426674 | 21829826 | RAP1GA1 | intron 23 | p36.12 | CG | 0.3791 | 0.814 | 0.0002685 |
| 11 | rs2418587 | 32220968 | RCN1 | 137315 base downstream | p13 | CT | 0.3238 | 0.813 | 0.0002691 |
| 3 | rs12639365 | 106423032 | ALCAM | 145370 base upstream | q13.11 | AT | 0.8191 | 1.312 | 0.0002694 |
| 2 | rs2698026 | 51636011 | NRXN1 | 522833 base downstream | p16.3 | AG | 0.4498 | 1.211 | 0.0002698 |
| 22 | rs5755606 | 33869717 | RAXLX | 56339 base downstream | q12.3 | CT | 0.2557 | 0.803 | 0.0002699 |
| 4 | rs11945898 | 58866253 | IGFBP7 | 1194957 base downstream | q12 | CT | 0.7211 | 1.236 | 0.0002706 |
| 11 | rs1033627 | 32223435 | RCN1 | 139782 base downstream | p13 | AG | 0.3238 | 0.813 | 0.0002709 |
| 1 | rs1795035 | 212358976 | PROX1 | 82593 base downstream | q41 | CT | 0.9712 | 0.574 | 0.0002718 |
| 7 | rs221242 | 157017352 | PTPRN2 | 7163 base upstream | q36.3 | AC | 0.1163 | 0.736 | 0.0002722 |
| 11 | rs1589596 | 10861334 | EIF4G2 | 74176 base downstream | p15.3 | GT | 0.1397 | 0.75 | 0.0002724 |
| 2 | rs9308638 | 123036498 | TSN | 794602 base downstream | q14.3 | GT | 0.6607 | 1.226 | 0.0002729 |
| 10 | rs2488035 | 30497139 | KIAA1462 | 120333 base downstream | p11.23 | AC | 0.358 | 1.225 | 0.0002739 |
| 5 | rs10058639 | 2532184 | IRX2 | 267695 base upstream | p15.33 | AG | 0.3078 | 0.804 | 0.0002742 |
| 4 | rs2247341 | 1671115 | SLBP | EXON 4 | p16.3 | AG | 0.3404 | 1.225 | 0.0002747 |
| 2 | rs263675 | 210745449 | FLJ23861 | 1153 base downstream | q34 | AG | 0.8984 | 0.734 | 0.0002753 |
| 2 | rs17021776 | 107791059 | SLC5A7 | 178367 base upstream | q12.3 | CT | 0.0601 | 0.651 | 0.0002753 |
| 5 | rs10075636 | 2532446 | IRX2 | 267433 base upstream | p15.33 | CT | 0.6921 | 1.244 | 0.0002758 |
| 2 | rs11692408 | 133201434 | NAP5 | intron 2 | q21.2 | AG | 0.3344 | 0.815 | 0.000276 |
| 1 | rs1795034 | 212359212 | PROX1 | 82829 base downstream | q41 | CT | 0.0288 | 1.74 | 0.0002762 |
| 2 | rs10183605 | 128358837 | MGC4268 | EXON 8 | q14.3 | CG | 0.575 | 0.815 | 0.0002765 |
| 2 | rs16843780 | 210417278 | C2orf21 | 47762 base downstream | q34 | CG | 0.1105 | 1.357 | 0.0002766 |
| 7 | rs221250 | 157023027 | PTPRN2 | 1488 base upstream | q36.3 | AG | 0.8836 | 1.359 | 0.0002768 |
| 5 | rs16869822 | 2532515 | IRX2 | 267364 base upstream | p15.33 | AG | 0.6921 | 1.244 | 0.0002768 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 17 | rs2215759 | 51856204 | ANKFN1 | intron 7 | q22 | AG | 0.2387 | 1.251 | 0.0002773 |
| 11 | rs4396289 | 9273306 | TMEM41B | intron 5 | p15.4 | CT | 0.1662 | 1.311 | 0.0002773 |
| 11 | rs1115704 | 32219434 | RCN1 | 135781 base downstream | p13 | CT | 0.6761 | 1.229 | 0.0002775 |
| 2 | rs10188289 | 210416012 | C2orf21 | 46496 base downstream | q34 | AG | 0.1105 | 1.357 | 0.0002781 |
| 2 | rs7573865 | 123035921 | TSN | 794025 base downstream | q14.3 | CG | 0.6607 | 1.226 | 0.0002782 |
| 6 | rs10947055 | 30201343 | TRIM40 | 11145 base upstream | p21.33 | CT | 0.0531 | 1.534 | 0.0002793 |
| 11 | rs10835876 | 32218732 | RCN1 | 135079 base downstream | p13 | AT | 0.324 | 0.814 | 0.0002797 |
| 2 | rs10490024 | 210415606 | C2orf21 | 46090 base downstream | q34 | AG | 0.1105 | 1.357 | 0.0002798 |
| 2 | rs6754455 | 30861183 | CAPN13 | intron 21 | p23.1 | CT | 0.4 | 1.237 | 0.00028 |
| 2 | rs10178675 | 210413593 | C2orf21 | 44077 base downstream | q34 | CG | 0.8895 | 0.737 | 0.0002805 |
| 2 | rs2090734 | 30860893 | CAPN13 | intron 21 | p23.1 | AT | 0.3996 | 1.234 | 0.0002809 |
| 8 | rs6586642 | 17655354 | MTUS1 | intron 13 | p22 | CT | 0.1839 | 0.767 | 0.000281 |
| 4 | rs3958122 | 1663729 | SLBP | 595 base upstream | p16.3 | CT | 0.6596 | 0.816 | 0.0002815 |
| 17 | rs7218500 | 51884770 | ANKFN1 | intron 10 | q22 | CT | 0.7463 | 0.804 | 0.0002815 |
| 9 | rs4258076 | 19654081 | SLC24A2 | intron 9 | p22.1 | GT | 0.6704 | 1.223 | 0.0002822 |
| 4 | rs3733552 | 82333327 | PRKG2 | intron 17 | q21.21 | CG | 0.947 | 0.642 | 0.0002829 |
| 2 | rs1561552 | 123035471 | TSN | 793575 base downstream | q14.3 | GT | 0.6606 | 1.226 | 0.0002839 |
| 2 | rs2950942 | 51639121 | NRXN1 | 525943 base downstream | p16.3 | CT | 0.5502 | 0.826 | 0.0002846 |
| 11 | rs2207820 | 32217307 | RCN1 | 133654 base downstream | p13 | AC | 0.676 | 1.229 | 0.0002849 |
| 5 | rs2240785 | 149561777 | SLC6A7 | intron 6 | q33.1 | CT | 0.027 | 1.711 | 0.0002858 |
| 2 | rs4973009 | 232169359 | MGC35154 | 2123 base downstream | q37.1 | AG | 0.0895 | 1.413 | 0.0002862 |
| 2 | rs11675229 | 30859743 | CAPN13 | intron 21 | p23.1 | CT | 0.3983 | 1.223 | 0.000287 |
| 2 | rs17010271 | 30860140 | CAPN13 | intron 21 | p23.1 | CT | 0.3985 | 1.224 | 0.0002872 |
| 21 | rs9977744 | 32322781 | HUNK | 24534 base downstream | q22.11 | CT | 0.149 | 0.758 | 0.0002872 |
| 4 | rs17603347 | 58850166 | IGFBP7 | 1178870 base downstream | q12 | CT | 0.7376 | 1.255 | 0.0002875 |
| 10 | rs1977583 | 30512398 | PAPD1 | 129366 base upstream | p11.23 | AG | 0.3591 | 1.218 | 0.0002881 |
| 2 | rs4597573 | 30858680 | CAPN13 | intron 21 | p23.1 | CT | 0.6029 | 0.824 | 0.0002881 |
| 3 | rs7644196 | 24682368 | THRB | 171051 base downstream | p24.2 | CG | 0.4966 | 1.21 | 0.0002883 |
| 13 | rs285669 | 76023588 | KCTD12 | 328716 base upstream | q22.3 | AG | 0.6869 | 0.803 | 0.0002885 |
| 3 | rs9876727 | 30335858 | TGFBR2 | 287139 base upstream | p24.1 | AC | 0.4024 | 0.823 | 0.0002885 |
| 3 | rs9876671 | 30335640 | TGFBR2 | 287357 base upstream | p24.1 | AG | 0.4024 | 0.823 | 0.0002887 |
| 11 | rs11043009 | 10881592 | EIF4G2 | 94434 base downstream | p15.3 | CT | 0.8634 | 1.355 | 0.0002887 |
| 12 | rs12366571 | 94738697 | NTN4 | 30030 base downstream | q22 | AC | 0.7292 | 0.81 | 0.0002892 |
| 21 | rs2823705 | 16553084 | C21orf34 | intron 4 | q21.1 | AG | 0.6047 | 0.823 | 0.0002902 |
| 3 | rs17787397 | 24683078 | THRB | 171761 base downstream | p24.2 | CT | 0.4966 | 1.21 | 0.0002904 |
| 14 | rs7152314 | 55245765 | KTN1 | 24718 base downstream | q22.3 | CT | 0.8976 | 0.727 | 0.0002909 |
| 2 | rs4597574 | 30858801 | CAPN13 | intron 21 | p23.1 | CT | 0.6029 | 0.824 | 0.000291 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 11 | rs7109202 | 32216841 | RCN1 | 133188 base downstream | p13 | CT | 0.676 | 1.228 | 0.0002911 |
| 5 | rs16902590 | 13526523 | DNAH5 | 216913 base upstream | p15.2 | CT | 0.9206 | 0.695 | 0.0002915 |
| 10 | rs2795858 | 30512209 | PAPD1 | 129555 base upstream | p11.23 | AG | 0.641 | 0.821 | 0.0002926 |
| 11 | rs1884382 | 32216421 | RCN1 | 132768 base downstream | p13 | AG | 0.6759 | 1.228 | 0.0002935 |
| 3 | rs6781057 | 30330791 | TGFBR2 | 292206 base upstream | p24.1 | GT | 0.4023 | 0.824 | 0.0002944 |
| 14 | rs8015301 | 55246211 | KTN1 | 25164 base downstream | q22.3 | CT | 0.8978 | 0.728 | 0.0002946 |
| 3 | rs6780847 | 30330534 | TGFBR2 | 292463 base upstream | p24.1 | CT | 0.4023 | 0.824 | 0.0002948 |
| 2 | rs6548034 | 30858988 | CAPN13 | intron 21 | p23.1 | AG | 0.3971 | 1.214 | 0.0002953 |
| 4 | rs8051 | 1664607 | SLBP | EXON 1 | p16.3 | CT | 0.3306 | 1.23 | 0.0002965 |
| 1 | rs241220 | 4508064 | AJAP1 | 106900 base upstream | p36.32 | AG | 0.6199 | 1.217 | 0.0002966 |
| 21 | rs2823704 | 16553023 | C21orf34 | intron 4 | q21.1 | CT | 0.3953 | 1.215 | 0.0002973 |
| 5 | rs2240787 | 149561988 | SLC6A7 | intron 6 | q33.1 | CT | 0.9731 | 0.583 | 0.0002983 |
| 1 | rs4916005 | 65081975 | JAK1 | intron 8 | p31.3 | CT | 0.126 | 0.744 | 0.0002984 |
| 4 | rs2030549 | 171427766 | AADAT | 179819 base downstream | q33 | AT | 0.9756 | 0.547 | 0.0002992 |
| 17 | rs9913702 | 51893701 | ANKFN1 | intron 13 | q22 | CT | 0.7458 | 0.805 | 0.0002996 |
| 2 | rs7588418 | 172835915 | DLX2 | 160191 base downstream | q31.1 | CT | 0.3511 | 1.225 | 0.0002999 |
| 7 | rs4473990 | 52130574 | COBL | 778584 base downstream | p12.1 | AG | 0.2237 | 0.783 | 0.0003 |
| 1 | rs12093269 | 65104374 | JAK1 | intron 18 | p31.3 | CT | 0.8575 | 1.355 | 0.0003 |
| 3 | rs6767967 | 24683878 | THRB | 172561 base downstream | p24.2 | AG | 0.4966 | 1.21 | 0.0003 |
| 2 | rs12619351 | 46197239 | PRKCE | intron 11 | p21 | GT | 0.2335 | 0.79 | 0.0003006 |
| 17 | rs1548809 | 51894034 | ANKFN1 | intron 13 | q22 | CT | 0.2542 | 1.242 | 0.000301 |
| 2 | rs1533295 | 111314462 | ACOXL | intron 9 | q13 | AG | 0.6698 | 0.816 | 0.0003025 |
| 3 | rs11129397 | 30329364 | TGFBR2 | 293633 base upstream | p24.1 | CT | 0.5976 | 1.214 | 0.0003033 |
| 6 | rs10947056 | 30203582 | TRIM40 | 8906 base upstream | p21.33 | CG | 0.9472 | 0.654 | 0.0003049 |
| 5 | rs2240791 | 149562853 | SLC6A7 | intron 8 | q33.1 | AG | 0.0268 | 1.719 | 0.0003062 |
| 14 | rs2880396 | 55246612 | KTN1 | 25565 base downstream | q22.3 | AC | 0.1013 | 1.367 | 0.0003063 |
| 12 | rs1492348 | 87460779 | KITLG | intron 8 | q21.32 | AG | 0.9489 | 0.645 | 0.000307 |
| 6 | rs9401370 | 121495669 | C6orf170 | intron 8 | q22.31 | AT | 0.8094 | 0.789 | 0.0003073 |
| 3 | rs7641936 | 63489216 | SYNPR | intron 2 | p14.2 | CT | 0.807 | 1.277 | 0.0003076 |
| 6 | rs9375002 | 121498592 | C6orf170 | intron 8 | q22.31 | AC | 0.1906 | 1.267 | 0.0003077 |
| 2 | rs1528816 | 51628765 | NRXN1 | 515587 base downstream | p16.3 | AG | 0.4752 | 1.208 | 0.0003078 |
| 2 | rs4953987 | 133207895 | NAP5 | intron 4 | q21.2 | AG | 0.3341 | 0.816 | 0.000308 |
| 20 | rs2038410 | 5197302 | PROKR2 | 33384 base upstream | p12.3 | CT | 0.559 | 1.219 | 0.0003082 |
| 2 | rs1528815 | 51628777 | NRXN1 | 515599 base downstream | p16.3 | CG | 0.4752 | 1.208 | 0.0003084 |
| 4 | rs17520678 | 71146872 | CSN3 | intron 2 | q13.3 | AC | 0.8738 | 1.335 | 0.0003085 |
| 21 | rs2823703 | 16552797 | C21orf34 | intron 4 | q21.1 | CG | 0.6047 | 0.824 | 0.0003086 |
| 3 | rs6809482 | 30328416 | TGFBR2 | 294581 base upstream | p24.1 | AG | 0.4024 | 0.824 | 0.0003087 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 22 | rs1473816 | 33862734 | RAXLX | 49356 base downstream | q12.3 | AG | 0.7479 | 1.264 | 0.0003089 |
| 2 | rs1358580 | 51626532 | NRXN1 | 513354 base downstream | p16.3 | AG | 0.5243 | 0.828 | 0.0003089 |
| 5 | rs275829 | 64017230 | P18SRP | 32505 base upstream | q12.3 | AT | 0.5241 | 0.816 | 0.0003094 |
| 15 | rs17545973 | 51288845 | WDR72 | 304384 base upstream | q21.3 | CT | 0.8311 | 0.772 | 0.00031 |
| 4 | rs1402960 | 58871935 | IGFBP7 | 1200639 base downstream | q12 | AG | 0.2791 | 0.811 | 0.0003101 |
| 17 | rs12945850 | 51900513 | ANKFN1 | intron 14 | q22 | CT | 0.2543 | 1.242 | 0.0003101 |
| 2 | rs2698031 | 51626312 | NRXN1 | 513134 base downstream | p16.3 | AG | 0.5242 | 0.828 | 0.0003105 |
| 10 | rs3814160 | 47991283 | ZNF488 | EXON 2 | q11.22 | CT | 0.864 | 0.743 | 0.0003121 |
| 3 | rs9848074 | 63489025 | SYNPR | intron 2 | p14.2 | CG | 0.807 | 1.277 | 0.0003134 |
| 21 | rs239010 | 16551998 | C21orf34 | intron 4 | q21.1 | AG | 0.3953 | 1.214 | 0.0003145 |
| 2 | rs9308637 | 123031511 | TSN | 789615 base downstream | q14.3 | CT | 0.3394 | 0.817 | 0.0003148 |
| 18 | rs9962491 | 64661900 | CCDC102B | intron 5 | q22.1 | CT | 0.7177 | 0.807 | 0.0003149 |
| 4 | rs4149 | 82337376 | PRKG2 | intron 17 | q21.21 | CT | 0.9472 | 0.642 | 0.0003152 |
| 3 | rs11921529 | 63488625 | SYNPR | intron 2 | p14.2 | AG | 0.193 | 0.783 | 0.0003171 |
| 7 | rs4498494 | 52130379 | COBL | 778389 base downstream | p12.1 | AG | 0.776 | 1.275 | 0.0003172 |
| 2 | rs3791259 | 134734535 | MGAT5 | intron 1 | q21.2 | CT | 0.957 | 0.624 | 0.0003176 |
| 2 | rs7592480 | 30844445 | CAPN13 | intron 18 | p23.1 | AG | 0.3086 | 1.224 | 0.0003178 |
| 4 | rs1849717 | 71146110 | CSN3 | intron 2 | q13.3 | CT | 0.8686 | 1.32 | 0.0003182 |
| 2 | rs1080548 | 123024644 | TSN | 782748 base downstream | q14.3 | CT | 0.3395 | 0.817 | 0.0003183 |
| 5 | rs275828 | 64018562 | P18SRP | 31173 base upstream | q12.3 | AG | 0.5325 | 0.821 | 0.0003199 |
| 2 | rs13003439 | 30843832 | CAPN13 | intron 18 | p23.1 | GT | 0.3086 | 1.223 | 0.0003207 |
| 1 | rs10789166 | 65085401 | JAK1 | intron 12 | p31.3 | AG | 0.8738 | 1.342 | 0.0003212 |
| 2 | rs1528817 | 51625061 | NRXN1 | 511883 base downstream | p16.3 | AG | 0.5236 | 0.829 | 0.0003213 |
| 8 | rs10888095 | 14906785 | SGCZ | intron 7 | p22 | AC | 0.5213 | 1.208 | 0.0003216 |
| 5 | rs325571 | 104090005 | NUDT12 | 1163616 base downstream | q21.2 | AG | 0.1787 | 1.289 | 0.0003223 |
| 2 | rs1919434 | 51624921 | NRXN1 | 511743 base downstream | p16.3 | CT | 0.4764 | 1.207 | 0.0003224 |
| 3 | rs6793060 | 24671288 | THRB | 159971 base downstream | p24.2 | AG | 0.5157 | 1.208 | 0.0003224 |
| 14 | rs12432019 | 55248459 | KTN1 | 27412 base downstream | q22.3 | CG | 0.1006 | 1.361 | 0.0003226 |
| 2 | rs10201094 | 123022799 | TSN | 780903 base downstream | q14.3 | CG | 0.3392 | 0.816 | 0.0003226 |
| 14 | rs12431962 | 55248246 | KTN1 | 27199 base downstream | q22.3 | AG | 0.1006 | 1.361 | 0.0003227 |
| 14 | rs11621130 | 55251053 | KTN1 | 30006 base downstream | q22.3 | CT | 0.8995 | 0.735 | 0.0003239 |
| 21 | rs2823702 | 16551609 | C21orf34 | intron 4 | q21.1 | AG | 0.6048 | 0.824 | 0.0003245 |
| 4 | rs17089214 | 58848803 | IGFBP7 | 1177507 base downstream | q12 | CT | 0.2791 | 0.812 | 0.000325 |
| 3 | rs6770081 | 63488445 | SYNPR | intron 2 | p14.2 | AG | 0.807 | 1.276 | 0.0003258 |
| 5 | rs11952402 | 13544938 | DNAH5 | 198498 base upstream | p15.2 | CT | 0.0863 | 1.407 | 0.0003268 |
| 3 | rs6549981 | 30323764 | TGFBR2 | 299233 base upstream | p24.1 | CT | 0.5976 | 1.213 | 0.0003268 |
| 5 | rs6877519 | 2516858 | IRX2 | 283021 base upstream | p15.33 | AG | 0.6143 | 1.233 | 0.0003273 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 10 | rs6584994 | 112308514 | CSPG6 | 8924 base upstream | q25.2 | CG | 0.6995 | 0.81 | 0.0003278 |
| 21 | rs2823700 | 16550664 | C21orf34 | intron 4 | q21.1 | CG | 0.3952 | 1.213 | 0.0003286 |
| 8 | rs1125265 | 14907805 | SGCZ | intron 7 | p22 | CT | 0.4786 | 0.828 | 0.000329 |
| 17 | rs2110200 | 51775701 | ANKFN1 | intron 3 | q22 | GT | 0.2915 | 1.235 | 0.0003302 |
| 2 | rs2091427 | 123023527 | TSN | 781631 base downstream | q14.3 | CG | 0.3393 | 0.818 | 0.0003302 |
| 4 | rs1517547 | 82312214 | PRKG2 | intron 16 | q21.21 | CT | 0.9358 | 0.683 | 0.0003308 |
| 4 | rs1546651 | 82313069 | PRKG2 | intron 16 | q21.21 | CT | 0.9357 | 0.683 | 0.0003311 |
| 2 | rs10171434 | 64133110 | VPS54 | 33392 base downstream | p14 | CT | 0.93 | 0.703 | 0.0003314 |
| 4 | rs1972127 | 82313093 | PRKG2 | intron 16 | q21.21 | AG | 0.0643 | 1.464 | 0.0003314 |
| 4 | rs11933194 | 82313570 | PRKG2 | intron 16 | q21.21 | CT | 0.9357 | 0.683 | 0.0003315 |
| 21 | rs239009 | 16549874 | C21orf34 | intron 4 | q21.1 | AG | 0.3991 | 1.218 | 0.0003316 |
| 1 | rs7555006 | 51252846 | CDKN2C | 39951 base downstream | p33 | AG | 0.5919 | 1.217 | 0.0003316 |
| 11 | rs16908503 | 10869437 | EIF4G2 | 82279 base downstream | p15.3 | AG | 0.8591 | 1.316 | 0.0003319 |
| 15 | rs1836592 | 86265806 | NTRK3 | intron 3 | q25.3 | AT | 0.1895 | 0.78 | 0.0003323 |
| 1 | rs2615060 | 223940235 | ENAH | 32767 base downstream | q42.12 | AC | 0.2361 | 1.244 | 0.0003332 |
| 5 | rs2279170 | 40303687 | PTGER4 | 412101 base upstream | p13.1 | CT | 0.3584 | 1.217 | 0.0003333 |
| 4 | rs3943629 | 82314024 | PRKG2 | intron 16 | q21.21 | AT | 0.9357 | 0.683 | 0.0003334 |
| 2 | rs3769450 | 200960600 | LOC26010 | intron 2 | q33.1 | AG | 0.6156 | 1.237 | 0.0003339 |
| 5 | rs182149 | 64028945 | P18SRP | 20790 base upstream | q12.3 | CT | 0.4663 | 1.207 | 0.0003343 |
| 3 | rs11928896 | 63487802 | SYNPR | intron 2 | p14.2 | AG | 0.807 | 1.275 | 0.0003344 |
| 19 | rs7248564 | 17338318 | PLVAP | intron 5 | p13.11 | CT | 0.5478 | 1.213 | 0.0003346 |
| 10 | rs10763789 | 19333212 | ARL5B | 326266 base downstream | p12.33 | CG | 0.8328 | 1.288 | 0.0003351 |
| 3 | rs6807571 | 144997632 | SLC9A9 | intron 13 | q24 | AG | 0.1698 | 1.296 | 0.0003368 |
| 2 | rs10180446 | 111318413 | ACOXL | intron 10 | q13 | CG | 0.3259 | 1.22 | 0.0003369 |
| 11 | rs10840506 | 10865614 | EIF4G2 | 78456 base downstream | p15.3 | CT | 0.1412 | 0.76 | 0.0003371 |
| 10 | rs2488034 | 30494239 | KIAA1462 | 117433 base downstream | p11.23 | AG | 0.3578 | 1.223 | 0.0003381 |
| 17 | rs9899359 | 51850895 | ANKFN1 | intron 7 | q22 | CG | 0.2384 | 1.247 | 0.0003381 |
| 3 | rs7643926 | 24682097 | THRB | 170780 base downstream | p24.2 | CT | 0.5712 | 1.211 | 0.0003384 |
| 10 | rs2779068 | 30543585 | PAPD1 | 98179 base upstream | p11.23 | GT | 0.3596 | 1.217 | 0.0003389 |
| 10 | rs17457528 | 48000055 | RBP3 | 1439 base upstream | q11.22 | AG | 0.8641 | 0.747 | 0.0003396 |
| 10 | rs2505109 | 30508511 | KIAA1462 | 131705 base downstream | p11.23 | CT | 0.642 | 0.824 | 0.0003399 |
| 20 | rs363012 | 10167799 | SNAP25 | intron 1 | p12.2 | AG | 0.6695 | 0.818 | 0.0003403 |
| 3 | rs1495579 | 30322358 | TGFB2 | 300639 base upstream | p24.1 | GT | 0.5975 | 1.212 | 0.0003411 |
| 2 | rs13019266 | 111321113 | ACOXL | intron 10 | q13 | CT | 0.6746 | 0.82 | 0.0003412 |
| 12 | rs17581242 | 115328821 | FLJ42957 | 126788 base upstream | q24.22 | GT | 0.1495 | 1.307 | 0.0003413 |
| 21 | rs2823699 | 16550560 | C21orf34 | intron 4 | q21.1 | CT | 0.6048 | 0.825 | 0.0003414 |
| 3 | rs11706302 | 144996927 | SLC9A9 | intron 13 | q24 | AG | 0.8303 | 0.773 | 0.0003416 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs3791266 | 134735206 | MGAT5 | intron 1 | q21.2 | CG | 0.957 | 0.626 | 0.0003419 |
| 2 | rs2698022 | 51641486 | NRXN1 | 528308 base downstream | p16.3 | AC | 0.4496 | 1.207 | 0.0003422 |
| 5 | rs283612 | 73286248 | RGNEF | 42964 base downstream | q13.2 | CT | 0.3823 | 0.825 | 0.0003426 |
| 4 | rs1545287 | 82314170 | PRKG2 | intron 16 | q21.21 | AG | 0.0642 | 1.465 | 0.0003428 |
| 5 | rs275832 | 64029942 | P18SRP | 19793 base upstream | q12.3 | AG | 0.4662 | 1.206 | 0.0003432 |
| 10 | rs2689216 | 30543961 | PAPD1 | 97803 base upstream | p11.23 | AG | 0.6404 | 0.822 | 0.0003443 |
| 13 | rs9533862 | 43932814 | TSC22D1 | intron 2 | q14.11 | CG | 0.0266 | 0.511 | 0.0003455 |
| 1 | rs12407862 | 110903737 | KCNA10 | 40417 base downstream | p13.3 | CT | 0.8143 | 0.785 | 0.000346 |
| 12 | rs10777108 | 87284400 | KITLG | 126299 base upstream | q21.32 | AC | 0.035 | 1.688 | 0.0003464 |
| 4 | rs11722020 | 82302241 | PRKG2 | intron 13 | q21.21 | CT | 0.0639 | 1.463 | 0.0003466 |
| 3 | rs6766087 | 63490780 | SYNPR | intron 2 | p14.2 | CT | 0.1929 | 0.786 | 0.0003474 |
| 3 | rs7617487 | 63487061 | SYNPR | intron 2 | p14.2 | GT | 0.193 | 0.785 | 0.0003486 |
| 4 | rs6828114 | 82301012 | PRKG2 | intron 13 | q21.21 | CT | 0.0639 | 1.462 | 0.000349 |
| 10 | rs17104653 | 124863434 | HMX3 | 22122 base upstream | q26.13 | CG | 0.9563 | 1.692 | 0.0003491 |
| 5 | rs283615 | 73286880 | RGNEF | 43596 base downstream | q13.2 | AT | 0.3824 | 0.825 | 0.0003494 |
| 2 | rs9917154 | 111323062 | ACOXL | intron 10 | q13 | CG | 0.6753 | 0.82 | 0.0003499 |
| 21 | rs9808741 | 16550380 | C21orf34 | intron 4 | q21.1 | GT | 0.3952 | 1.212 | 0.0003501 |
| 16 | rs7205094 | 47661065 | CBLN1 | 209136 base upstream | q12.1 | GT | 0.4524 | 0.821 | 0.0003501 |
| 3 | rs6777474 | 63490926 | SYNPR | intron 2 | p14.2 | AG | 0.8069 | 1.273 | 0.0003506 |
| 3 | rs6800578 | 144995427 | SLC9A9 | intron 12 | q24 | CT | 0.8306 | 0.774 | 0.0003506 |
| 5 | rs283616 | 73287077 | RGNEF | 43793 base downstream | q13.2 | CG | 0.3824 | 0.825 | 0.0003509 |
| 11 | rs1884379 | 32216036 | RCN1 | 132383 base downstream | p13 | GT | 0.3244 | 0.816 | 0.0003514 |
| 6 | rs2129857 | 94775217 | EPHA7 | 589224 base downstream | q16.1 | CT | 0.4326 | 1.214 | 0.0003514 |
| 4 | rs3733550 | 82292319 | PRKG2 | intron 12 | q21.21 | CT | 0.9361 | 0.684 | 0.0003515 |
| 20 | rs1847326 | 47379153 | KCNB1 | 42758 base upstream | q13.13 | AC | 0.0742 | 1.455 | 0.0003516 |
| 2 | rs3828175 | 134735267 | MGAT5 | intron 1 | q21.2 | AG | 0.957 | 0.626 | 0.0003517 |
| 5 | rs283618 | 73287272 | RGNEF | 43988 base downstream | q13.2 | AT | 0.3824 | 0.825 | 0.0003542 |
| 2 | rs11695611 | 123031238 | TSN | 789342 base downstream | q14.3 | CT | 0.3592 | 0.822 | 0.0003544 |
| 6 | rs9462696 | 41399102 | NCR2 | 12403 base upstream | p21.1 | AT | 0.4472 | 0.822 | 0.0003548 |
| 6 | rs9471555 | 41398747 | NCR2 | 12758 base upstream | p21.1 | CT | 0.4472 | 0.822 | 0.0003553 |
| 21 | rs2823696 | 16549688 | C21orf34 | intron 4 | q21.1 | AT | 0.3945 | 1.215 | 0.0003568 |
| 21 | rs2823697 | 16550037 | C21orf34 | intron 4 | q21.1 | CT | 0.3946 | 1.215 | 0.0003569 |
| 15 | rs1381112 | 86366855 | NTRK3 | intron 6 | q25.3 | AG | 0.875 | 0.755 | 0.0003569 |
| 2 | rs7576541 | 111323872 | ACOXL | intron 10 | q13 | CT | 0.324 | 1.22 | 0.0003573 |
| 6 | rs9401367 | 121445811 | C6orf170 | intron 1 | q22.31 | CT | 0.8054 | 0.791 | 0.0003577 |
| 3 | rs2121775 | 144994842 | SLC9A9 | intron 12 | q24 | AG | 0.8308 | 0.775 | 0.0003578 |
| 5 | rs6874889 | 13551578 | DNAH5 | 191858 base upstream | p15.2 | AG | 0.0863 | 1.401 | 0.0003585 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 5 | rs4867939 | 168156259 | SLIT3 | intron 27 | q35.1 | CT | 0.5417 | 1.213 | 0.0003597 |
| 11 | rs10767925 | 32215762 | RCN1 | 132109 base downstream | p13 | AG | 0.6756 | 1.224 | 0.0003614 |
| 10 | rs955760 | 97113875 | SORBS1 | intron 11 | q23.33 | AG | 0.5661 | 0.827 | 0.0003626 |
| 3 | rs10935083 | 134936517 | TF | 11407 base upstream | q22.1 | CT | 0.0472 | 1.527 | 0.0003629 |
| 3 | rs1495578 | 30322459 | TGFBF2 | 300538 base upstream | p24.1 | AG | 0.4107 | 0.824 | 0.0003642 |
| 2 | rs1528814 | 51629015 | NRXN1 | 515837 base downstream | p16.3 | CT | 0.4817 | 1.208 | 0.0003652 |
| 3 | rs16854336 | 144993002 | SLC9A9 | intron 12 | q24 | CT | 0.8304 | 0.774 | 0.0003659 |
| 4 | rs10516650 | 82315844 | PRKG2 | intron 17 | q21.21 | AC | 0.064 | 1.466 | 0.0003659 |
| 13 | rs9506821 | 21759295 | FGF9 | 585111 base downstream | q12.11 | AG | 0.5909 | 0.822 | 0.0003665 |
| 18 | rs12961437 | 48360097 | DCC | intron 1 | q21.2 | GT | 0.1554 | 0.766 | 0.0003684 |
| 2 | rs3828176 | 134738798 | MGAT5 | intron 1 | q21.2 | AT | 0.9568 | 0.627 | 0.0003691 |
| 18 | rs11665228 | 48349538 | DCC | intron 1 | q21.2 | CT | 0.1554 | 0.767 | 0.0003695 |
| 6 | rs12202131 | 30221529 | TRIM40 | intron 1 | p21.33 | AT | 0.0512 | 1.521 | 0.0003701 |
| 4 | rs10025532 | 174752942 | MORF4 | 20720 base upstream | q34.1 | AG | 0.6865 | 0.807 | 0.0003707 |
| 7 | rs17143423 | 20862587 | SP8 | 69557 base downstream | p15.3 | AG | 0.83 | 0.769 | 0.0003718 |
| 18 | rs9965853 | 6392126 | L3MBTL4 | intron 19 | p11.31 | CT | 0.5403 | 1.22 | 0.0003726 |
| 6 | rs6913743 | 157077339 | ARID1B | 63438 base upstream | q25.3 | AG | 0.948 | 0.662 | 0.0003729 |
| 3 | rs17068905 | 63485884 | SYNPR | intron 2 | p14.2 | CT | 0.807 | 1.272 | 0.0003735 |
| 18 | rs12964400 | 48306360 | DCC | intron 1 | q21.2 | AG | 0.8431 | 1.307 | 0.0003747 |
| 12 | rs10847348 | 126490295 | SLC15A4 | 1353420 base upstream | q24.32 | CT | 0.7422 | 1.24 | 0.0003751 |
| 3 | rs4392438 | 22537241 | UBE2E2 | 682570 base upstream | p24.3 | CT | 0.7317 | 0.795 | 0.0003757 |
| 14 | rs12587803 | 55252880 | KTN1 | 31833 base downstream | q22.3 | AG | 0.0999 | 1.359 | 0.0003763 |
| 8 | rs11136431 | 1778840 | ARHGEF10 | intron 1 | p23.3 | CT | 0.4378 | 1.213 | 0.0003777 |
| 5 | rs183917 | 64047836 | P18SRP | 1899 base upstream | q12.3 | CT | 0.5342 | 0.831 | 0.0003783 |
| 2 | rs1919432 | 51644950 | NRXN1 | 531772 base downstream | p16.3 | CT | 0.5505 | 0.83 | 0.0003796 |
| 6 | rs9351097 | 87194834 | HTR1E | 509294 base upstream | q14.3 | GT | 0.8413 | 0.776 | 0.0003806 |
| 10 | rs7901527 | 112303893 | CSPG6 | 13545 base upstream | q25.2 | AG | 0.6983 | 0.816 | 0.0003807 |
| 3 | rs2944404 | 117034860 | LSAMP | intron 1 | q13.31 | AG | 0.0718 | 1.434 | 0.000382 |
| 11 | rs12287573 | 32214720 | RCN1 | 131067 base downstream | p13 | CT | 0.6755 | 1.223 | 0.0003825 |
| 1 | rs7515605 | 81202644 | LPHN2 | 836025 base upstream | p31.1 | AG | 0.1668 | 0.766 | 0.0003828 |
| 10 | rs17104648 | 124859893 | HMX3 | 25663 base upstream | q26.13 | CG | 0.9564 | 1.659 | 0.000383 |
| 2 | rs6711988 | 105447178 | FHL2 | 25786 base downstream | q12.2 | CT | 0.0735 | 1.47 | 0.0003836 |
| 4 | rs10516651 | 82316475 | PRKG2 | intron 17 | q21.21 | CT | 0.9361 | 0.682 | 0.0003839 |
| 3 | rs16840751 | 134933123 | TF | 14801 base upstream | q22.1 | AG | 0.0477 | 1.517 | 0.0003843 |
| 3 | rs12233446 | 144993820 | SLC9A9 | intron 12 | q24 | CT | 0.8315 | 0.779 | 0.0003844 |
| 21 | rs2205205 | 40071834 | LOC150084 | intron 4 | q22.2 | AG | 0.3174 | 1.219 | 0.000387 |
| 8 | rs10888094 | 14906737 | SGCZ | intron 7 | p22 | AG | 0.5226 | 1.205 | 0.0003871 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs9426771 | 21831326 | RAP1GA1 | intron 23 | p36.12 | GT | 0.5861 | 1.221 | 0.0003872 |
| 4 | rs2073503 | 3505974 | LRPAP1 | 2032 base downstream | p16.2 | CG | 0.6918 | 1.222 | 0.0003875 |
| 5 | rs10061059 | 175193656 | CPLX2 | intron 2 | q35.2 | AG | 0.2175 | 0.796 | 0.0003886 |
| 2 | rs13385109 | 105446439 | FHL2 | 25047 base downstream | q12.2 | AT | 0.9264 | 0.677 | 0.0003889 |
| 1 | rs1660375 | 212361177 | PROX1 | 84794 base downstream | q41 | AG | 0.0278 | 1.721 | 0.000389 |
| 2 | rs1045832 | 128337564 | MGC4268 | EXON 1 | q14.3 | AG | 0.59 | 0.827 | 0.0003893 |
| 2 | rs3791270 | 134738836 | MGAT5 | intron 1 | q21.2 | AG | 0.9567 | 0.629 | 0.0003897 |
| 2 | rs9989768 | 105447653 | FHL2 | 26261 base downstream | q12.2 | CT | 0.0731 | 1.47 | 0.0003897 |
| 11 | rs1155855 | 32214418 | RCN1 | 130765 base downstream | p13 | AG | 0.3245 | 0.818 | 0.0003907 |
| 2 | rs1356424 | 98792270 | MGC42367 | intron 3 | q11.2 | CT | 0.6266 | 0.812 | 0.0003913 |
| 4 | rs6552548 | 183404530 | ODZ3 | 77600 base upstream | q35.1 | AC | 0.6697 | 1.228 | 0.0003914 |
| 2 | rs3791271 | 134738884 | MGAT5 | intron 1 | q21.2 | CT | 0.0433 | 1.59 | 0.0003925 |
| 6 | rs13190874 | 15935221 | DTNBP1 | 163971 base downstream | p22.3 | CT | 0.131 | 1.316 | 0.0003932 |
| 3 | rs11715340 | 134917507 | TF | 30417 base upstream | q22.1 | AT | 0.0484 | 1.516 | 0.0003942 |
| 1 | rs6671533 | 55443484 | USP24 | intron 64 | p32.3 | CG | 0.2111 | 1.271 | 0.0003943 |
| 3 | rs6775133 | 63485004 | SYNPR | intron 2 | p14.2 | AG | 0.807 | 1.271 | 0.0003953 |
| 10 | rs2795857 | 30512070 | PAPD1 | 129694 base upstream | p11.23 | CG | 0.3579 | 1.212 | 0.0003968 |
| 13 | rs9533877 | 43970674 | TSC22D1 | intron 2 | q14.11 | AG | 0.0268 | 0.515 | 0.000398 |
| 17 | rs1442831 | 51907580 | ANKFN1 | intron 14 | q22 | AT | 0.2532 | 1.237 | 0.0003984 |
| 17 | rs8070836 | 51908311 | ANKFN1 | intron 14 | q22 | CT | 0.7468 | 0.809 | 0.0003988 |
| 17 | rs11653462 | 51911802 | ANKFN1 | intron 15 | q22 | GT | 0.7468 | 0.809 | 0.0003998 |
| 3 | rs1390298 | 30319780 | RBMS3 | 298157 base downstream | p24.1 | CT | 0.5973 | 1.21 | 0.0003999 |
| 9 | rs497510 | 91833463 | GADD45G | 422176 base downstream | q22.2 | GT | 0.5306 | 1.204 | 0.0004003 |
| 12 | rs4761007 | 126490843 | SLC15A4 | 1352872 base upstream | q24.32 | CT | 0.2676 | 0.802 | 0.0004014 |
| 6 | rs2523386 | 29819726 | HLA-F | 17444 base downstream | p22.1 | AG | 0.1634 | 1.281 | 0.0004033 |
| 16 | rs1345408 | 47680675 | CBLN1 | 189526 base upstream | q12.1 | CG | 0.4633 | 0.829 | 0.000404 |
| 2 | rs2937600 | 155411014 | KCNJ3 | intron 2 | q24.1 | AG | 0.7094 | 1.227 | 0.0004041 |
| 11 | rs1155856 | 32214070 | RCN1 | 130417 base downstream | p13 | AG | 0.6754 | 1.222 | 0.0004048 |
| 21 | rs7278733 | 40073319 | LOC150084 | intron 5 | q22.2 | AG | 0.6826 | 0.821 | 0.0004048 |
| 2 | rs1900132 | 155411314 | KCNJ3 | intron 2 | q24.1 | AG | 0.7094 | 1.227 | 0.0004049 |
| 1 | rs17123324 | 62513884 | ANKRD38 | intron 8 | p31.3 | AG | 0.0175 | 2.165 | 0.0004072 |
| 1 | rs898386 | 202846320 | LRRN5 | 6607 base upstream | q32.1 | AG | 0.308 | 1.224 | 0.0004072 |
| 3 | rs13067087 | 63483291 | SYNPR | intron 2 | p14.2 | AT | 0.8072 | 1.278 | 0.0004076 |
| 1 | rs898387 | 202845996 | LRRN5 | 6931 base upstream | q32.1 | AG | 0.6919 | 0.817 | 0.0004084 |
| 2 | rs4851165 | 98851853 | MGC42367 | intron 9 | q11.2 | CT | 0.94 | 0.672 | 0.0004086 |
| 2 | rs13025854 | 232149419 | MGC35154 | 16436 base upstream | q37.1 | AC | 0.9163 | 0.717 | 0.0004089 |
| 3 | rs2202492 | 63482702 | SYNPR | intron 2 | p14.2 | CT | 0.1928 | 0.782 | 0.0004091 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 2 | rs6735741 | 134739376 | MGAT5 | intron 1 | q21.2 | AG | 0.9566 | 0.63 | 0.0004092 |
| 8 | rs16893344 | 134275461 | WISP1 | intron 1 | q24.22 | CT | 0.646 | 1.214 | 0.0004097 |
| 10 | rs2505110 | 30510906 | PAPD1 | 130858 base upstream | p11.23 | AG | 0.3578 | 1.211 | 0.00041 |
| 6 | rs4712261 | 15943835 | DTNBP1 | 172585 base downstream | p22.3 | CT | 0.8687 | 0.762 | 0.0004102 |
| 3 | rs2221476 | 63482584 | SYNPR | intron 2 | p14.2 | AG | 0.8072 | 1.28 | 0.0004107 |
| 6 | rs730858 | 29818607 | HLA-F | 16325 base downstream | p22.1 | AG | 0.1634 | 1.281 | 0.0004116 |
| 1 | rs7537835 | 81205753 | LPHN2 | 832916 base upstream | p31.1 | AG | 0.6262 | 1.216 | 0.0004116 |
| 6 | rs13218971 | 15938880 | DTNBP1 | 167630 base downstream | p22.3 | CT | 0.8687 | 0.762 | 0.0004119 |
| 2 | rs1609361 | 51645727 | NRXN1 | 532549 base downstream | p16.3 | AG | 0.5505 | 0.831 | 0.0004123 |
| 1 | rs2184484 | 116602943 | ATP1A1 | 114415 base upstream | p13.1 | AG | 0.6625 | 0.821 | 0.0004126 |
| 6 | rs4712260 | 15935963 | DTNBP1 | 164713 base downstream | p22.3 | AG | 0.1313 | 1.313 | 0.0004135 |
| 13 | rs2038711 | 21757408 | FGF9 | 583224 base downstream | q12.11 | CT | 0.6109 | 0.827 | 0.000414 |
| 5 | rs10475154 | 2532789 | IRX2 | 267090 base upstream | p15.33 | GT | 0.3222 | 0.814 | 0.0004142 |
| 2 | rs3791276 | 134741186 | MGAT5 | intron 1 | q21.2 | AC | 0.9565 | 0.63 | 0.0004147 |
| 13 | rs9533885 | 43987160 | TSC22D1 | intron 2 | q14.11 | AG | 0.9731 | 1.937 | 0.0004147 |
| 5 | rs6859797 | 104016997 | NUDT12 | 1090608 base downstream | q21.2 | AC | 0.1646 | 1.287 | 0.0004148 |
| 12 | rs10751692 | 130809881 | SFRS8 | intron 11 | q24.33 | CT | 0.3825 | 0.829 | 0.0004153 |
| 12 | rs3741526 | 130806294 | SFRS8 | intron 10 | q24.33 | CT | 0.6178 | 1.207 | 0.0004157 |
| 6 | rs2517938 | 29817819 | HLA-F | 15537 base downstream | p22.1 | CT | 0.1634 | 1.281 | 0.000416 |
| 2 | rs3791275 | 134741150 | MGAT5 | intron 1 | q21.2 | AG | 0.9565 | 0.631 | 0.0004163 |
| 2 | rs10182727 | 232148981 | MGC35154 | 16874 base upstream | q37.1 | AT | 0.0839 | 1.391 | 0.0004171 |
| 14 | rs6571636 | 33759807 | C14orf147 | 212088 base upstream | q13.1 | AG | 0.6052 | 1.211 | 0.0004173 |
| 6 | rs9468692 | 30227869 | TRIM10 | EXON 1 | p21.33 | GT | 0.9492 | 0.66 | 0.0004183 |
| 3 | rs3844271 | 146903072 | PLOD2 | 366845 base upstream | q24 | AG | 0.5353 | 0.816 | 0.000419 |
| 2 | rs3791273 | 134740952 | MGAT5 | intron 1 | q21.2 | CG | 0.0435 | 1.585 | 0.00042 |
| 2 | rs333238 | 107970060 | SLC5A7 | intron 1 | q12.3 | AG | 0.1965 | 0.781 | 0.0004201 |
| 10 | rs1571957 | 30509940 | PAPD1 | 131824 base upstream | p11.23 | CT | 0.3577 | 1.21 | 0.000422 |
| 5 | rs10075967 | 64055597 | P18SRP | EXON 1 | q12.3 | CT | 0.4704 | 1.203 | 0.0004221 |
| 5 | rs1863931 | 175189132 | CPLX2 | intron 2 | q35.2 | AG | 0.2164 | 0.795 | 0.000423 |
| 6 | rs2743950 | 29817265 | HLA-F | 14983 base downstream | p22.1 | CT | 0.8366 | 0.781 | 0.0004231 |
| 2 | rs333236 | 107970399 | SLC5A7 | intron 1 | q12.3 | AG | 0.8035 | 1.28 | 0.0004235 |
| 21 | rs11701807 | 17230025 | C21orf34 | 328612 base downstream | q21.1 | CT | 0.2592 | 1.24 | 0.0004237 |
| 3 | rs7614676 | 63482284 | SYNPR | intron 2 | p14.2 | AG | 0.8074 | 1.287 | 0.000425 |
| 2 | rs1528812 | 51646842 | NRXN1 | 533664 base downstream | p16.3 | CG | 0.4493 | 1.203 | 0.0004269 |
| 2 | rs6736839 | 133195447 | NAP5 | intron 1 | q21.2 | CT | 0.5591 | 1.205 | 0.0004277 |
| 6 | rs9468693 | 30228616 | TRIM10 | EXON 1 | p21.33 | CT | 0.0507 | 1.515 | 0.0004281 |
| 3 | rs7629687 | 30361546 | TGFBR2 | 261451 base upstream | p24.1 | AT | 0.3903 | 0.823 | 0.0004283 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 4 | rs10003341 | 82316801 | PRKG2 | intron 17 | q21.21 | AC | 0.9364 | 0.681 | 0.0004296 |
| 10 | rs17103522 | 124167869 | PLEKHA1 | intron 8 | q26.13 | CT | 0.1307 | 0.741 | 0.0004321 |
| 13 | rs9583775 | 89501299 | GPC5 | 1347588 base upstream | q31.3 | AG | 0.1887 | 0.789 | 0.0004344 |
| 1 | rs309543 | 23097909 | EPHB2 | intron 9 | p36.12 | AG | 0.3566 | 1.208 | 0.000435 |
| 8 | rs7012406 | 135219115 | ZNF406 | 340098 base upstream | q24.22 | AT | 0.5239 | 0.834 | 0.0004351 |
| 15 | rs17545046 | 51189302 | ONECUT1 | 319801 base downstream | q21.3 | AG | 0.1714 | 1.297 | 0.0004355 |
| 15 | rs10438404 | 36725309 | FLJ35695 | 50781 base upstream | q14 | GT | 0.4019 | 0.831 | 0.0004365 |
| 6 | rs13211010 | 15945269 | DTNBP1 | 174019 base downstream | p22.3 | CT | 0.1313 | 1.311 | 0.0004367 |
| 9 | rs12237890 | 119033609 | ASTN2 | intron 20 | q33.1 | AT | 0.0572 | 1.501 | 0.0004369 |
| 11 | rs11031664 | 32223969 | RCN1 | 140316 base downstream | p13 | CT | 0.6829 | 1.241 | 0.0004376 |
| 6 | rs2517941 | 29816396 | HLA-F | 14114 base downstream | p22.1 | CG | 0.8366 | 0.782 | 0.0004385 |
| 10 | rs4565845 | 124149040 | PLEKHA1 | intron 3 | q26.13 | AC | 0.8688 | 1.347 | 0.0004404 |
| 17 | rs759107 | 51764470 | ANKFN1 | intron 3 | q22 | AG | 0.2953 | 1.227 | 0.0004425 |
| 15 | rs3923022 | 36725830 | FLJ35695 | 50260 base upstream | q14 | AG | 0.5982 | 1.203 | 0.0004439 |
| 9 | rs1335405 | 119032843 | ASTN2 | intron 20 | q33.1 | CT | 0.9428 | 0.666 | 0.0004444 |
| 2 | rs10498258 | 232145603 | MGC35154 | 20252 base upstream | q37.1 | AG | 0.0843 | 1.383 | 0.000445 |
| 7 | rs10256394 | 52086483 | COBL | 734493 base downstream | p12.1 | CT | 0.2252 | 0.802 | 0.0004455 |
| 2 | rs6727830 | 232144608 | MGC35154 | 21247 base upstream | q37.1 | AG | 0.9158 | 0.723 | 0.000446 |
| 10 | rs17103488 | 124144159 | PLEKHA1 | intron 2 | q26.13 | CT | 0.1315 | 0.743 | 0.000446 |
| 11 | rs355220 | 41020808 | LRR4C | 748568 base downstream | p12 | CT | 0.9644 | 1.752 | 0.0004461 |
| 15 | rs879131 | 86273174 | NTRK3 | intron 3 | q25.3 | AG | 0.8014 | 1.277 | 0.0004465 |
| 2 | rs333235 | 107973532 | SLC5A7 | intron 2 | q12.3 | CT | 0.1969 | 0.781 | 0.0004469 |
| 14 | rs10483393 | 31530235 | ARHGAP5 | 86010 base upstream | q12 | CT | 0.786 | 0.787 | 0.0004484 |
| 21 | rs1475897 | 19398897 | PRSS7 | 701053 base downstream | q21.1 | AG | 0.3396 | 1.238 | 0.0004486 |
| 2 | rs1581667 | 51648256 | NRXN1 | 535078 base downstream | p16.3 | CT | 0.5514 | 0.831 | 0.0004489 |
| 3 | rs12493961 | 11219825 | HRH1 | intron 1 | p25.3 | AG | 0.9645 | 1.806 | 0.000449 |
| 2 | rs2698014 | 51649426 | NRXN1 | 536248 base downstream | p16.3 | GT | 0.4485 | 1.203 | 0.0004522 |
| 2 | rs2715062 | 51639646 | NRXN1 | 526468 base downstream | p16.3 | AG | 0.4523 | 1.203 | 0.0004525 |
| 3 | rs2972481 | 117048396 | LSAMP | intron 3 | q13.31 | AG | 0.0724 | 1.43 | 0.0004531 |
| 10 | rs7895653 | 61813354 | ANK3 | intron 43 | q21.2 | CT | 0.7763 | 0.799 | 0.0004533 |
| 21 | rs2824149 | 17229575 | C21orf34 | 328162 base downstream | q21.1 | CT | 0.7221 | 0.817 | 0.0004534 |
| 1 | rs17514217 | 167156031 | ATP1B1 | 186539 base upstream | q24.2 | AT | 0.1034 | 0.736 | 0.0004538 |
| 4 | rs10005912 | 82316860 | PRKG2 | intron 17 | q21.21 | GT | 0.0635 | 1.469 | 0.0004546 |
| 7 | rs6959643 | 5295742 | SLC29A4 | intron 2 | p22.1 | AT | 0.4131 | 1.208 | 0.000456 |
| 3 | rs9847885 | 134921034 | TF | 26890 base upstream | q22.1 | CT | 0.9512 | 0.671 | 0.0004578 |
| 3 | rs604132 | 54723274 | CACNA2D3 | intron 11 | p14.3 | AT | 0.41 | 0.82 | 0.0004583 |
| 2 | rs3915321 | 51618222 | NRXN1 | 505044 base downstream | p16.3 | CT | 0.581 | 0.821 | 0.0004584 |

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|----|------------|-----------|---------------|-------------------------|--------|----|--------|-------|-----------|
| 9 | rs10869020 | 70346371 | C9orf71 | 768 base downstream | q13 | AG | 0.8557 | 1.305 | 0.0004585 |
| 13 | rs1491005 | 89487776 | GPC5 | 1361111 base upstream | q31.3 | CT | 0.8113 | 1.267 | 0.0004589 |
| 15 | rs1122891 | 36725969 | FLJ35695 | 50121 base upstream | q14 | CG | 0.4016 | 0.832 | 0.0004599 |
| 2 | rs3791261 | 134734676 | MGAT5 | intron 1 | q21.2 | GT | 0.0499 | 1.581 | 0.0004601 |
| 4 | rs2570073 | 58782188 | IGFBP7 | 1110892 base downstream | q12 | AC | 0.7227 | 1.232 | 0.0004605 |
| 3 | rs11717407 | 134920954 | TF | 26970 base upstream | q22.1 | AG | 0.9511 | 0.671 | 0.0004611 |
| 1 | rs6656346 | 110905211 | KCNA10 | 41891 base downstream | p13.3 | AG | 0.2633 | 1.229 | 0.0004613 |
| 2 | rs3915322 | 51618512 | NRXN1 | 505334 base downstream | p16.3 | AG | 0.419 | 1.217 | 0.0004619 |
| 6 | rs12194995 | 51918458 | PKHD1 | intron 31 | p12.2 | CT | 0.2001 | 0.793 | 0.0004622 |
| 10 | rs17700389 | 110680293 | XPNPEP1 | 934220 base upstream | q25.1 | GT | 0.8191 | 1.273 | 0.0004624 |
| 9 | rs10746875 | 70346769 | C9orf71 | 1166 base downstream | q13 | AT | 0.1443 | 0.766 | 0.0004626 |
| 19 | rs8182538 | 13277170 | CACNA1A | intron 32 | p13.13 | AG | 0.4076 | 1.202 | 0.000463 |
| 10 | rs17700354 | 110679319 | XPNPEP1 | 935194 base upstream | q25.1 | CT | 0.8191 | 1.273 | 0.0004631 |
| 2 | rs10460338 | 232142905 | MGC35154 | 22950 base upstream | q37.1 | CT | 0.0836 | 1.386 | 0.0004634 |
| 3 | rs4582061 | 134920716 | TF | 27208 base upstream | q22.1 | AG | 0.0489 | 1.489 | 0.0004641 |
| 12 | rs6580809 | 49895867 | POU6F1 | intron 10 | q13.13 | CT | 0.3455 | 0.818 | 0.0004653 |
| 2 | rs2697239 | 197749763 | ANKRD44 | intron 24 | q33.1 | CT | 0.0342 | 0.582 | 0.0004656 |
| 6 | rs1900554 | 25265596 | LRRC16 | 122030 base upstream | p22.2 | CT | 0.1879 | 0.794 | 0.0004656 |
| 9 | rs10811225 | 19652307 | SLC24A2 | intron 9 | p22.1 | AG | 0.3901 | 0.829 | 0.0004657 |
| 2 | rs2450280 | 107974450 | SLC5A7 | intron 2 | q12.3 | CT | 0.8031 | 1.281 | 0.0004665 |
| 19 | rs4433935 | 13277280 | CACNA1A | intron 32 | p13.13 | CT | 0.5924 | 0.832 | 0.0004669 |
| 12 | rs935537 | 9923537 | CLEC2B | 9812 base downstream | p13.31 | CG | 0.7193 | 0.817 | 0.0004671 |
| 2 | rs2354378 | 51618920 | NRXN1 | 505742 base downstream | p16.3 | CT | 0.5812 | 0.822 | 0.0004672 |
| 2 | rs7579884 | 229854835 | PID1 | 10534 base downstream | q36.3 | AG | 0.9278 | 0.704 | 0.0004675 |
| 7 | rs1689299 | 52977371 | DKFZp564N2472 | 93471 base upstream | p12.1 | AT | 0.8501 | 0.775 | 0.000468 |
| 10 | rs11591352 | 110514731 | XPNPEP1 | 1099782 base upstream | q25.1 | GT | 0.8073 | 1.281 | 0.000469 |
| 3 | rs16840699 | 134920291 | TF | 27633 base upstream | q22.1 | CT | 0.9511 | 0.672 | 0.0004692 |
| 2 | rs2175824 | 111308878 | ACOXL | intron 9 | q13 | GT | 0.6206 | 1.234 | 0.0004704 |
| 10 | rs3934875 | 110674541 | XPNPEP1 | 939972 base upstream | q25.1 | AG | 0.8189 | 1.273 | 0.0004717 |
| 2 | rs13417566 | 111309077 | ACOXL | intron 9 | q13 | AC | 0.3795 | 0.811 | 0.0004718 |
| 19 | rs4499352 | 13277350 | CACNA1A | intron 32 | p13.13 | GT | 0.4076 | 1.202 | 0.0004725 |
| 11 | rs1384641 | 18845442 | MRGPRX1 | 66493 base upstream | p15.1 | CG | 0.8914 | 0.746 | 0.0004734 |
| 11 | rs1384642 | 18846017 | MRGPRX1 | 65918 base upstream | p15.1 | AG | 0.1086 | 1.34 | 0.0004743 |
| 13 | rs2038712 | 21757616 | FGF9 | 583432 base downstream | q12.11 | CT | 0.5874 | 0.826 | 0.0004761 |
| 3 | rs11130939 | 63493103 | SYNPR | intron 2 | p14.2 | GT | 0.8105 | 1.278 | 0.0004767 |
| 20 | rs6019750 | 47380876 | KCNB1 | 41035 base upstream | q13.13 | CG | 0.9258 | 0.695 | 0.0004767 |
| 13 | rs17083114 | 67594394 | PCDH9 | 891930 base downstream | q21.33 | CT | 0.974 | 1.814 | 0.0004767 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 12 | rs576601 | 9937319 | CLEC2B | 23594 base downstream | p13.31 | AC | 0.7262 | 0.817 | 0.0004771 |
| 13 | rs17083120 | 67598341 | PCDH9 | 895877 base downstream | q21.33 | CT | 0.974 | 1.813 | 0.0004771 |
| 13 | rs17083124 | 67599095 | PCDH9 | 896631 base downstream | q21.33 | AT | 0.974 | 1.813 | 0.0004774 |
| 14 | rs10143992 | 31528650 | ARHGAP5 | 87595 base upstream | q12 | CG | 0.2142 | 1.268 | 0.0004775 |
| 4 | rs17055545 | 171439939 | AADAT | 191992 base downstream | q33 | GT | 0.0241 | 1.786 | 0.0004778 |
| 21 | rs2824148 | 17228121 | C21orf34 | 326708 base downstream | q21.1 | AG | 0.2779 | 1.224 | 0.0004779 |
| 6 | rs2844845 | 29820738 | HLA-F | 18456 base downstream | p22.1 | AT | 0.1651 | 1.276 | 0.0004781 |
| 12 | rs2936206 | 17411380 | FLJ22655 | 713689 base upstream | p12.3 | AG | 0.5405 | 1.2 | 0.0004782 |
| 2 | rs1226946 | 229856782 | PID1 | 12481 base downstream | q36.3 | CT | 0.0721 | 1.419 | 0.0004786 |
| 18 | rs1349930 | 48306727 | DCC | intron 1 | q21.2 | CG | 0.8447 | 1.297 | 0.0004802 |
| 9 | rs7860486 | 70347279 | C9orf71 | 1676 base downstream | q13 | AC | 0.1443 | 0.767 | 0.0004807 |
| 12 | rs10751693 | 130839269 | SFRS8 | intron 15 | q24.33 | AG | 0.3851 | 0.83 | 0.0004808 |
| 1 | rs915180 | 154345707 | LMNA | 5377 base upstream | q22 | CT | 0.6107 | 0.82 | 0.000482 |
| 13 | rs2325107 | 67611790 | PCDH9 | 909326 base downstream | q21.33 | AG | 0.026 | 0.552 | 0.0004827 |
| 13 | rs11840273 | 67606518 | PCDH9 | 904054 base downstream | q21.33 | AG | 0.026 | 0.552 | 0.0004828 |
| 4 | rs4434285 | 65093689 | SRD5A2L2 | 135916 base downstream | q13.1 | AT | 0.8118 | 0.787 | 0.0004832 |
| 13 | rs17083164 | 67660291 | PCDH9 | 957827 base downstream | q21.33 | CT | 0.974 | 1.812 | 0.0004833 |
| 20 | rs6019751 | 47381122 | KCNB1 | 40789 base upstream | q13.13 | CT | 0.9258 | 0.696 | 0.0004843 |
| 3 | rs539967 | 178788491 | TBL1XR1 | 390749 base downstream | q26.32 | AC | 0.5946 | 1.214 | 0.0004847 |
| 2 | rs2698024 | 51640024 | NRXN1 | 526846 base downstream | p16.3 | AG | 0.4523 | 1.201 | 0.0004862 |
| 8 | rs10097898 | 14884772 | SGCZ | intron 7 | p22 | AG | 0.4142 | 1.223 | 0.0004863 |
| 6 | rs12196767 | 51884494 | PKHD1 | intron 28 | p12.2 | CT | 0.1897 | 0.785 | 0.0004865 |
| 14 | rs1952969 | 31527434 | ARHGAP5 | 88811 base upstream | q12 | GT | 0.7857 | 0.789 | 0.0004865 |
| 1 | rs17514245 | 167156181 | ATP1B1 | 186389 base upstream | q24.2 | AG | 0.8966 | 1.357 | 0.0004871 |
| 2 | rs2715057 | 51649455 | NRXN1 | 536277 base downstream | p16.3 | CT | 0.5524 | 0.831 | 0.0004873 |
| 12 | rs11059127 | 126488790 | SLC15A4 | 1354925 base upstream | q24.32 | GT | 0.7388 | 1.238 | 0.0004875 |
| 1 | rs7530207 | 167157044 | ATP1B1 | 185526 base upstream | q24.2 | CG | 0.1035 | 0.736 | 0.0004882 |
| 14 | rs8017647 | 31526109 | ARHGAP5 | 90136 base upstream | q12 | CT | 0.2143 | 1.266 | 0.0004885 |
| 12 | rs6598153 | 130815441 | SFRS8 | intron 12 | q24.33 | CT | 0.3821 | 0.831 | 0.0004885 |
| 8 | rs10099567 | 1780249 | ARHGEF10 | intron 2 | p23.3 | AG | 0.5677 | 0.829 | 0.0004886 |
| 17 | rs8076116 | 47289896 | CA10 | intron 6 | q21.33 | GT | 0.0405 | 1.565 | 0.0004893 |
| 21 | rs7282020 | 17225906 | C21orf34 | 324493 base downstream | q21.1 | AC | 0.2725 | 1.229 | 0.0004896 |
| 10 | rs12258030 | 110686488 | XPNPEP1 | 928025 base upstream | q25.1 | AG | 0.819 | 1.272 | 0.000491 |
| 11 | rs12795402 | 32212512 | RCN1 | 128859 base downstream | p13 | CT | 0.6751 | 1.218 | 0.0004917 |
| 4 | rs2358469 | 149810031 | NR3C2 | 226938 base downstream | q31.23 | AG | 0.587 | 0.818 | 0.0004919 |
| 2 | rs11680441 | 51620902 | NRXN1 | 507724 base downstream | p16.3 | AG | 0.4183 | 1.213 | 0.0004924 |
| 12 | rs12424558 | 88790264 | ATP2B1 | 216289 base downstream | q21.33 | CG | 0.9017 | 0.725 | 0.0004944 |

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|----|------------|-----------|---------------|-------------------------|--------|----|--------|-------|-----------|
| 13 | rs17083147 | 67631961 | PCDH9 | 929497 base downstream | q21.33 | CT | 0.0261 | 0.553 | 0.0004947 |
| 13 | rs9510084 | 21757893 | FGF9 | 583709 base downstream | q12.11 | AC | 0.4128 | 1.21 | 0.0004957 |
| 2 | rs1528811 | 51649652 | NRXN1 | 536474 base downstream | p16.3 | CT | 0.5526 | 0.832 | 0.0004971 |
| 2 | rs1226936 | 229863370 | PID1 | 19069 base downstream | q36.3 | GT | 0.928 | 0.706 | 0.000499 |
| 9 | rs1335406 | 119035785 | ASTN2 | intron 20 | q33.1 | AT | 0.9419 | 0.668 | 0.0004992 |
| 16 | rs7202219 | 7375184 | A2BP1 | intron 4 | p13.2 | AT | 0.9086 | 0.732 | 0.0004997 |
| 2 | rs1528810 | 51649771 | NRXN1 | 536593 base downstream | p16.3 | CT | 0.5527 | 0.832 | 0.0005008 |
| 16 | rs7202208 | 7375166 | A2BP1 | intron 4 | p13.2 | AG | 0.9085 | 0.732 | 0.0005012 |
| 2 | rs1528809 | 51649917 | NRXN1 | 536739 base downstream | p16.3 | AG | 0.4472 | 1.203 | 0.0005015 |
| 16 | rs7202052 | 7375151 | A2BP1 | intron 4 | p13.2 | AG | 0.9085 | 0.732 | 0.0005033 |
| 2 | rs4340504 | 232140542 | MGC35154 | 25313 base upstream | q37.1 | AC | 0.0828 | 1.386 | 0.0005041 |
| 7 | rs11769082 | 52974032 | DKFZp564N2472 | 96810 base upstream | p12.1 | CT | 0.1532 | 1.289 | 0.0005043 |
| 1 | rs11583110 | 116595268 | C1orf161 | 115884 base downstream | p13.1 | AC | 0.3325 | 1.217 | 0.0005043 |
| 4 | rs931771 | 109392362 | LEF1 | 83335 base downstream | q25 | CT | 0.734 | 1.247 | 0.0005089 |
| 2 | rs2698011 | 51651289 | NRXN1 | 538111 base downstream | p16.3 | GT | 0.553 | 0.832 | 0.0005135 |
| 16 | rs1424241 | 70636408 | HP | 9600 base upstream | q22.3 | AG | 0.1816 | 0.786 | 0.0005142 |
| 11 | rs360118 | 9802854 | SBF2 | intron 12 | p15.4 | CG | 0.3518 | 1.22 | 0.0005144 |
| 3 | rs16849682 | 141211649 | CLSTN2 | intron 1 | q23 | CT | 0.9409 | 0.672 | 0.0005145 |
| 12 | rs11059124 | 126488548 | SLC15A4 | 1355167 base upstream | q24.32 | AG | 0.7381 | 1.238 | 0.0005146 |
| 1 | rs284172 | 91987439 | TGFBFR3 | intron 13 | p22.2 | AT | 0.1544 | 0.761 | 0.000516 |
| 11 | rs924111 | 10721194 | CTR9 | 8192 base upstream | p15.3 | AG | 0.592 | 1.207 | 0.0005163 |
| 4 | rs10518071 | 71148222 | CSN3 | intron 3 | q13.3 | CT | 0.1328 | 0.766 | 0.0005164 |
| 4 | rs6811318 | 71149965 | CSN3 | intron 4 | q13.3 | CT | 0.8672 | 1.306 | 0.0005171 |
| 2 | rs6732415 | 44191376 | PPM1B | 58127 base upstream | p21 | AG | 0.0209 | 1.927 | 0.0005175 |
| 7 | rs1208998 | 91252060 | MTERF | 87896 base upstream | q21.2 | CT | 0.9431 | 0.669 | 0.0005176 |
| 4 | rs3775739 | 71149649 | CSN3 | EXON 4 | q13.3 | AG | 0.1328 | 0.766 | 0.0005177 |
| 16 | rs7184072 | 7375088 | A2BP1 | intron 4 | p13.2 | CT | 0.0918 | 1.366 | 0.0005181 |
| 10 | rs3847404 | 30429219 | KIAA1462 | 52413 base downstream | p11.23 | CT | 0.6388 | 0.828 | 0.0005183 |
| 15 | rs11852644 | 90026124 | SLCO3A1 | 171825 base upstream | q26.1 | AT | 0.0843 | 1.39 | 0.0005187 |
| 4 | rs6811366 | 71150032 | CSN3 | intron 4 | q13.3 | CT | 0.8672 | 1.306 | 0.0005189 |
| 10 | rs6584909 | 110687591 | XPNPEP1 | 926922 base upstream | q25.1 | AG | 0.819 | 1.27 | 0.0005189 |
| 11 | rs10742274 | 32212217 | RCN1 | 128564 base downstream | p13 | CT | 0.325 | 0.822 | 0.0005213 |
| 6 | rs11752102 | 25262375 | LRRC16 | 125251 base upstream | p22.2 | AG | 0.8065 | 1.282 | 0.0005216 |
| 8 | rs1379440 | 135092624 | ST3GAL1 | 439280 base downstream | q24.22 | CT | 0.5707 | 1.202 | 0.0005232 |
| 6 | rs2517830 | 29937545 | HLA-G | 30667 base downstream | p21.33 | GT | 0.0545 | 1.531 | 0.0005238 |
| 5 | rs4700651 | 64063348 | P18SRP | intron 2 | q12.3 | AT | 0.5345 | 0.835 | 0.000524 |
| 14 | rs162637 | 82831246 | SEL1L | 1761360 base downstream | q31.2 | CT | 0.8043 | 0.79 | 0.0005241 |

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|----|------------|-----------|---------------|-------------------------|--------|----|--------|-------|-----------|
| 21 | rs8129059 | 19396021 | PRSS7 | 698177 base downstream | q21.1 | CT | 0.6696 | 0.808 | 0.0005253 |
| 4 | rs11099460 | 82319684 | PRKG2 | intron 17 | q21.21 | AC | 0.0631 | 1.471 | 0.0005287 |
| 2 | rs10200921 | 210508108 | RPE | 67488 base upstream | q34 | AG | 0.1474 | 1.319 | 0.0005288 |
| 10 | rs473195 | 30510832 | PAPD1 | 130932 base upstream | p11.23 | CT | 0.7163 | 0.819 | 0.0005303 |
| 2 | rs2715076 | 51652775 | NRXN1 | 539597 base downstream | p16.3 | AC | 0.4466 | 1.202 | 0.0005304 |
| 11 | rs4757732 | 18858429 | MRGPRX1 | 53506 base upstream | p15.1 | CT | 0.8912 | 0.748 | 0.0005317 |
| 10 | rs11595032 | 110687958 | XPNPEP1 | 926555 base upstream | q25.1 | AT | 0.1811 | 0.788 | 0.0005317 |
| 4 | rs11737486 | 136740556 | PABPC4L | 1398203 base downstream | q28.3 | AG | 0.1319 | 1.331 | 0.0005318 |
| 13 | rs1570309 | 28458146 | KIAA0774 | 38601 base upstream | q12.3 | AG | 0.8985 | 0.734 | 0.0005338 |
| 6 | rs9397709 | 154732717 | PIP3-E | 13125 base downstream | q25.2 | CT | 0.9475 | 1.546 | 0.000534 |
| 2 | rs4449121 | 232078303 | MGC43122 | 3077 base upstream | q37.1 | AC | 0.9163 | 0.705 | 0.0005343 |
| 6 | rs4960167 | 6095762 | F13A1 | intron 1 | p25.1 | CT | 0.8313 | 0.787 | 0.0005346 |
| 4 | rs2270269 | 8631852 | GPR78 | 1338 base upstream | p16.1 | CT | 0.5652 | 1.199 | 0.0005356 |
| 6 | rs2517897 | 29908080 | HLA-G | 1202 base downstream | p21.33 | AC | 0.1509 | 0.768 | 0.0005359 |
| 11 | rs10742273 | 32212187 | RCN1 | 128534 base downstream | p13 | CG | 0.6749 | 1.217 | 0.0005368 |
| 4 | rs2270270 | 8631775 | GPR78 | 1415 base upstream | p16.1 | CG | 0.5652 | 1.199 | 0.0005383 |
| 6 | rs9362321 | 87192966 | HTR1E | 511162 base upstream | q14.3 | CT | 0.8437 | 0.783 | 0.0005398 |
| 1 | rs589176 | 4560412 | AJAP1 | 54552 base upstream | p36.32 | AG | 0.4638 | 0.827 | 0.0005409 |
| 2 | rs7572242 | 128341634 | MGC4268 | intron 2 | q14.3 | CT | 0.5889 | 0.829 | 0.000542 |
| 5 | rs4463179 | 13558432 | DNAH5 | 185004 base upstream | p15.2 | AG | 0.0936 | 1.35 | 0.0005427 |
| 10 | rs7091393 | 110512008 | XPNPEP1 | 1102505 base upstream | q25.1 | CT | 0.821 | 1.286 | 0.0005442 |
| 6 | rs9384205 | 154734121 | PIP3-E | 14529 base downstream | q25.2 | CT | 0.0527 | 0.649 | 0.0005446 |
| 3 | rs9852024 | 22446750 | ZNF659 | 678930 base downstream | p24.3 | AT | 0.1627 | 1.296 | 0.0005447 |
| 11 | rs7124928 | 32211971 | RCN1 | 128318 base downstream | p13 | CT | 0.3251 | 0.822 | 0.0005448 |
| 18 | rs1031062 | 48292120 | DCC | intron 1 | q21.2 | GT | 0.1523 | 0.771 | 0.0005456 |
| 6 | rs2129859 | 94798859 | EPHA7 | 612866 base downstream | q16.1 | AC | 0.4233 | 1.199 | 0.0005466 |
| 6 | rs9397710 | 154734212 | PIP3-E | 14620 base downstream | q25.2 | AC | 0.0527 | 0.649 | 0.0005467 |
| 7 | rs10250470 | 52238030 | DKFZp564N2472 | 832812 base upstream | p12.1 | AG | 0.6725 | 0.821 | 0.0005488 |
| 6 | rs9371793 | 154734269 | PIP3-E | 14677 base downstream | q25.2 | CT | 0.9472 | 1.54 | 0.0005489 |
| 6 | rs1318638 | 30235852 | TRIM10 | intron 6 | p21.33 | CT | 0.9504 | 0.665 | 0.0005503 |
| 2 | rs10469900 | 38220587 | CYP1B1 | 63791 base downstream | p22.2 | CT | 0.2062 | 1.247 | 0.0005506 |
| 3 | rs2362755 | 24691672 | THRB | 180355 base downstream | p24.2 | GT | 0.5623 | 1.201 | 0.0005506 |
| 20 | rs6099650 | 55492405 | HMG1L1 | 4450 base upstream | q13.31 | CT | 0.4528 | 0.835 | 0.0005523 |
| 6 | rs2171518 | 94798998 | EPHA7 | 613005 base downstream | q16.1 | CT | 0.5767 | 0.834 | 0.0005535 |
| 12 | rs10859960 | 94742289 | NTN4 | 33622 base downstream | q22 | AG | 0.2611 | 1.225 | 0.0005535 |
| 6 | rs12212092 | 30236421 | TRIM10 | EXON 7 | p21.33 | CT | 0.9505 | 0.665 | 0.0005537 |
| 11 | rs4325289 | 18844035 | MRGPRX1 | 67900 base upstream | p15.1 | CG | 0.1081 | 1.336 | 0.0005543 |

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|----|------------|-----------|---------------|------------------------|--------|----|--------|-------|-----------|
| 20 | rs2182970 | 55505059 | CTCFL | 570 base upstream | q13.31 | GT | 0.5702 | 0.834 | 0.0005549 |
| 10 | rs7073756 | 85953055 | PCDH21 | intron 8 | q23.1 | CT | 0.2404 | 0.804 | 0.0005556 |
| 12 | rs10777742 | 94741290 | NTN4 | 32623 base downstream | q22 | CT | 0.7389 | 0.816 | 0.0005565 |
| 2 | rs12463442 | 111311960 | ACOXL | intron 9 | q13 | AG | 0.6188 | 1.225 | 0.0005566 |
| 11 | rs926968 | 32207354 | RCN1 | 123701 base downstream | p13 | CT | 0.6748 | 1.216 | 0.0005568 |
| 12 | rs10859959 | 94740811 | NTN4 | 32144 base downstream | q22 | CT | 0.2611 | 1.225 | 0.0005574 |
| 6 | rs6941417 | 25260653 | LRRC16 | 126973 base upstream | p22.2 | AG | 0.1943 | 0.781 | 0.0005585 |
| 6 | rs9383704 | 154735267 | PIP3-E | 15675 base downstream | q25.2 | AG | 0.9471 | 1.536 | 0.0005596 |
| 10 | rs7070406 | 110697815 | XPNPEP1 | 916698 base upstream | q25.1 | AT | 0.8188 | 1.268 | 0.0005598 |
| 12 | rs7134181 | 94738331 | NTN4 | 29664 base downstream | q22 | CT | 0.7389 | 0.816 | 0.0005606 |
| 12 | rs7955502 | 93474128 | TMCC3 | 12051 base upstream | q22 | AC | 0.1052 | 1.341 | 0.0005609 |
| 10 | rs6583995 | 97100869 | SORBS1 | intron 8 | q23.33 | CT | 0.2961 | 1.219 | 0.0005617 |
| 10 | rs12780390 | 30332480 | KIAA1462 | 10909 base upstream | p11.23 | CT | 0.5583 | 0.827 | 0.0005623 |
| 13 | rs9510085 | 21757961 | FGF9 | 583777 base downstream | q12.11 | GT | 0.583 | 0.827 | 0.0005625 |
| 10 | rs12779954 | 30332299 | KIAA1462 | 11090 base upstream | p11.23 | AT | 0.5584 | 0.827 | 0.0005627 |
| 6 | rs9461270 | 26652089 | HMGNA4 | intron 1 | p22.1 | AG | 0.5732 | 0.826 | 0.0005649 |
| 1 | rs17111725 | 55459204 | USP24 | 5854 base downstream | p32.3 | AG | 0.7537 | 0.809 | 0.0005653 |
| 6 | rs590701 | 94819838 | EPHA7 | 633845 base downstream | q16.1 | GT | 0.4258 | 1.2 | 0.0005654 |
| 8 | rs16904845 | 134268958 | WISP1 | 3535 base upstream | q24.22 | CT | 0.3404 | 0.812 | 0.0005659 |
| 12 | rs7307769 | 94730019 | NTN4 | 21352 base downstream | q22 | AG | 0.261 | 1.225 | 0.0005661 |
| 12 | rs10859956 | 94729110 | NTN4 | 20443 base downstream | q22 | CT | 0.261 | 1.225 | 0.0005678 |
| 2 | rs1919433 | 51644884 | NRXN1 | 531706 base downstream | p16.3 | CG | 0.4522 | 1.199 | 0.000569 |
| 2 | rs17744093 | 29148258 | FLJ34931 | EXON 2 | p23.2 | CG | 0.2342 | 1.245 | 0.0005691 |
| 6 | rs9371795 | 154735852 | PIP3-E | 16260 base downstream | q25.2 | CT | 0.947 | 1.533 | 0.0005694 |
| 1 | rs1105101 | 110906436 | KCNA2 | 40862 base upstream | p13.3 | CG | 0.7411 | 0.815 | 0.0005698 |
| 12 | rs12582105 | 94722758 | NTN4 | 14091 base downstream | q22 | AG | 0.261 | 1.225 | 0.0005705 |
| 11 | rs926967 | 32207798 | RCN1 | 124145 base downstream | p13 | AG | 0.3252 | 0.823 | 0.0005706 |
| 6 | rs10944713 | 94818161 | EPHA7 | 632168 base downstream | q16.1 | AT | 0.4262 | 1.2 | 0.0005708 |
| 6 | rs2535660 | 94838264 | EPHA7 | 652271 base downstream | q16.1 | CT | 0.5832 | 0.834 | 0.0005708 |
| 10 | rs11596345 | 110692416 | XPNPEP1 | 922097 base upstream | q25.1 | AG | 0.8188 | 1.267 | 0.0005713 |
| 2 | rs4849147 | 113545707 | IL1F10 | intron 1 | q13 | AT | 0.2933 | 1.234 | 0.000572 |
| 1 | rs284170 | 91987216 | TGFB3 | intron 13 | p22.2 | CT | 0.8459 | 1.319 | 0.0005723 |
| 13 | rs9550833 | 21758087 | FGF9 | 583903 base downstream | q12.11 | AC | 0.5829 | 0.828 | 0.0005724 |
| 6 | rs9384206 | 154735871 | PIP3-E | 16279 base downstream | q25.2 | CT | 0.9469 | 1.532 | 0.0005733 |
| 7 | rs11238186 | 52237378 | DKFZp564N2472 | 833464 base upstream | p12.1 | AC | 0.3284 | 1.217 | 0.0005735 |
| 1 | rs6537671 | 110908053 | KCNA2 | 39245 base upstream | p13.3 | CT | 0.2589 | 1.226 | 0.0005741 |
| 10 | rs6481661 | 30520525 | PAPD1 | 121239 base upstream | p11.23 | CT | 0.7237 | 0.819 | 0.0005746 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 5 | rs6449751 | 64072297 | P18SRP | intron 2 | q12.3 | CG | 0.4653 | 1.196 | 0.0005746 |
| 4 | rs11133559 | 58909359 | IGFBP7 | 1238063 base downstream | q12 | AC | 0.2759 | 0.812 | 0.0005749 |
| 9 | rs10120859 | 70346115 | C9orf71 | 512 base downstream | q13 | CT | 0.1512 | 0.77 | 0.0005752 |
| 4 | rs12511263 | 58908862 | IGFBP7 | 1237566 base downstream | q12 | AG | 0.2759 | 0.812 | 0.0005762 |
| 2 | rs11126291 | 70819307 | ADD2 | intron 15 | p13.3 | GT | 0.0512 | 0.661 | 0.0005767 |
| 3 | rs517729 | 54683416 | CACNA2D3 | intron 11 | p14.3 | AG | 0.5107 | 0.832 | 0.0005768 |
| 2 | rs1997326 | 51622700 | NRXN1 | 509522 base downstream | p16.3 | GT | 0.5802 | 0.829 | 0.0005768 |
| 8 | rs7465458 | 54439800 | OPRK1 | 113053 base downstream | q11.23 | AG | 0.8362 | 1.283 | 0.0005778 |
| 11 | rs11601578 | 103266219 | PDGFD | 16905 base upstream | q22.3 | CT | 0.6882 | 1.231 | 0.0005781 |
| 1 | rs241221 | 4508910 | AJAP1 | 106054 base upstream | p36.32 | CT | 0.6104 | 1.208 | 0.0005787 |
| 21 | rs2837183 | 40057208 | LOC150084 | intron 2 | q22.2 | CT | 0.3627 | 1.216 | 0.0005791 |
| 2 | rs11676521 | 229863870 | PID1 | 19569 base downstream | q36.3 | GT | 0.9284 | 0.71 | 0.0005803 |
| 2 | rs17198619 | 181898803 | ITGA4 | 131060 base upstream | q31.3 | GT | 0.9023 | 0.733 | 0.0005806 |
| 2 | rs10185903 | 229840402 | PID1 | intron 3 | q36.3 | CT | 0.145 | 1.284 | 0.0005807 |
| 13 | rs9506819 | 21758269 | FGF9 | 584085 base downstream | q12.11 | GT | 0.5829 | 0.828 | 0.0005807 |
| 13 | rs4770264 | 21758866 | FGF9 | 584682 base downstream | q12.11 | AG | 0.4135 | 1.207 | 0.0005808 |
| 2 | rs3755352 | 70823291 | ADD2 | intron 15 | p13.3 | AT | 0.9488 | 1.513 | 0.0005812 |
| 1 | rs504274 | 4548433 | AJAP1 | 66531 base upstream | p36.32 | CT | 0.0733 | 0.706 | 0.0005827 |
| 6 | rs1018846 | 30245628 | TRIM15 | intron 4 | p21.33 | AG | 0.0492 | 1.505 | 0.0005831 |
| 4 | rs4865328 | 58908498 | IGFBP7 | 1237202 base downstream | q12 | CT | 0.7238 | 1.231 | 0.0005831 |
| 16 | rs3924628 | 8571064 | C16orf68 | 51963 base upstream | p13.2 | AG | 0.3747 | 1.202 | 0.0005843 |
| 4 | rs10517438 | 58908183 | IGFBP7 | 1236887 base downstream | q12 | AT | 0.7238 | 1.231 | 0.0005847 |
| 6 | rs4707818 | 94778822 | EPHA7 | 592829 base downstream | q16.1 | CG | 0.5713 | 0.834 | 0.0005854 |
| 22 | rs5992433 | 17962066 | CLDN5 | 69206 base downstream | q11.21 | CT | 0.4587 | 1.199 | 0.0005857 |
| 4 | rs17029520 | 154177648 | KIAA1727 | 57350 base downstream | q31.3 | CT | 0.6908 | 0.827 | 0.0005859 |
| 10 | rs11592721 | 110687487 | XPNPEP1 | 927026 base upstream | q25.1 | AG | 0.1598 | 0.767 | 0.0005865 |
| 3 | rs9861611 | 22448096 | ZNF659 | 680276 base downstream | p24.3 | CT | 0.1719 | 1.277 | 0.000587 |
| 21 | rs2837232 | 40101083 | LOC150084 | 5190 base downstream | q22.2 | AG | 0.3168 | 1.211 | 0.0005875 |
| 4 | rs7656126 | 183403974 | ODZ3 | 78156 base upstream | q35.1 | GT | 0.7159 | 1.226 | 0.0005878 |
| 8 | rs11998140 | 135092194 | ST3GAL1 | 438850 base downstream | q24.22 | AC | 0.4293 | 0.834 | 0.0005879 |
| 11 | rs2418584 | 32208659 | RCN1 | 125006 base downstream | p13 | CT | 0.6748 | 1.215 | 0.0005883 |
| 21 | rs12626544 | 40059369 | LOC150084 | EXON 3 | q22.2 | AG | 0.6375 | 0.823 | 0.0005913 |
| 5 | rs106451 | 104076769 | NUDT12 | 1150380 base downstream | q21.2 | AC | 0.1654 | 1.272 | 0.0005916 |
| 8 | rs13261120 | 14876643 | SGCZ | intron 7 | p22 | CT | 0.4425 | 1.217 | 0.0005917 |
| 2 | rs13429819 | 64137490 | PEL1 | 36009 base upstream | p14 | AG | 0.9327 | 0.704 | 0.0005918 |
| 2 | rs1446521 | 113543867 | IL1F10 | intron 1 | q13 | AG | 0.7086 | 0.812 | 0.0005927 |
| 5 | rs325529 | 104077128 | NUDT12 | 1150739 base downstream | q21.2 | CT | 0.1654 | 1.272 | 0.0005929 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 5 | rs325527 | 104076454 | NUDT12 | 1150065 base downstream | q21.2 | CT | 0.8346 | 0.786 | 0.0005929 |
| 3 | rs11716879 | 22448847 | ZNF659 | 681027 base downstream | p24.3 | AT | 0.1723 | 1.277 | 0.0005931 |
| 10 | rs17778715 | 110707237 | XPNPEP1 | 907276 base upstream | q25.1 | CT | 0.1812 | 0.79 | 0.0005932 |
| 17 | rs4575596 | 68389374 | SLC39A11 | intron 5 | q24.3 | CT | 0.3942 | 1.199 | 0.0005943 |
| 10 | rs11007929 | 30526790 | PAPD1 | 114974 base upstream | p11.23 | CT | 0.7235 | 0.82 | 0.0005946 |
| 2 | rs12463526 | 111312209 | ACOXL | intron 9 | q13 | AG | 0.6185 | 1.219 | 0.0005946 |
| 5 | rs325530 | 104077349 | NUDT12 | 1150960 base downstream | q21.2 | GT | 0.8345 | 0.786 | 0.0005947 |
| 6 | rs583000 | 94846081 | EPHA7 | 660088 base downstream | q16.1 | CT | 0.4168 | 1.198 | 0.0005951 |
| 2 | rs7560803 | 64135002 | VPS54 | 35284 base downstream | p14 | AG | 0.0673 | 1.419 | 0.0005955 |
| 10 | rs11596046 | 110734026 | XPNPEP1 | 880487 base upstream | q25.1 | AG | 0.1808 | 0.79 | 0.000596 |
| 16 | rs2967303 | 47659380 | CBLN1 | 210821 base upstream | q12.1 | CG | 0.4709 | 0.827 | 0.0005961 |
| 5 | rs325526 | 104074988 | NUDT12 | 1148599 base downstream | q21.2 | AG | 0.8347 | 0.786 | 0.0005963 |
| 2 | rs6754229 | 229839689 | PID1 | intron 3 | q36.3 | CT | 0.145 | 1.283 | 0.0005967 |
| 22 | rs5993715 | 17961946 | CLDN5 | 69086 base downstream | q11.21 | GT | 0.4587 | 1.199 | 0.0005967 |
| 8 | rs1519150 | 12893231 | C8orf79 | intron 2 | p22 | AT | 0.265 | 0.814 | 0.0005968 |
| 2 | rs6724667 | 113506112 | IL1F8 | intron 5 | q13 | AG | 0.6942 | 0.817 | 0.0005969 |
| 6 | rs16890179 | 25277765 | LRRRC16 | 109861 base upstream | p22.2 | CT | 0.1891 | 0.793 | 0.0005972 |
| 5 | rs325531 | 104077611 | NUDT12 | 1151222 base downstream | q21.2 | AG | 0.8345 | 0.786 | 0.0005973 |
| 1 | rs915179 | 154344873 | LMNA | 6211 base upstream | q22 | AG | 0.6103 | 0.827 | 0.0005974 |
| 15 | rs1435399 | 86281541 | NTRK3 | intron 5 | q25.3 | AT | 0.1816 | 0.78 | 0.0005976 |
| 4 | rs10012544 | 154177907 | KIAA1727 | 57609 base downstream | q31.3 | AT | 0.3092 | 1.209 | 0.0005979 |
| 22 | rs5993714 | 17961830 | CLDN5 | 68970 base downstream | q11.21 | AG | 0.4587 | 1.199 | 0.0005984 |
| 2 | rs2118204 | 128340581 | MGC4268 | intron 1 | q14.3 | CT | 0.4046 | 1.203 | 0.0005991 |
| 10 | rs17701356 | 110734457 | XPNPEP1 | 880056 base upstream | q25.1 | AG | 0.1808 | 0.79 | 0.0005993 |
| 21 | rs2837178 | 40054313 | LOC150084 | intron 2 | q22.2 | AG | 0.3631 | 1.216 | 0.0005993 |
| 11 | rs1998003 | 32209862 | RCN1 | 126209 base downstream | p13 | AC | 0.6748 | 1.214 | 0.0005995 |
| 5 | rs895658 | 2547273 | IRX2 | 252606 base upstream | p15.33 | CT | 0.6315 | 1.206 | 0.0005996 |
| 5 | rs325532 | 104077750 | NUDT12 | 1151361 base downstream | q21.2 | CT | 0.1655 | 1.272 | 0.0005997 |
| 10 | rs10509885 | 110729755 | XPNPEP1 | 884758 base upstream | q25.1 | CT | 0.8193 | 1.266 | 0.0006003 |
| 2 | rs17744052 | 29142915 | FLJ34931 | intron 1 | p23.2 | AG | 0.7694 | 0.81 | 0.0006006 |
| 16 | rs8057663 | 7371378 | A2BP1 | intron 4 | p13.2 | AG | 0.907 | 0.735 | 0.0006012 |
| 10 | rs17779611 | 110734927 | XPNPEP1 | 879586 base upstream | q25.1 | CT | 0.1808 | 0.79 | 0.0006014 |
| 6 | rs1235830 | 95082112 | EPHA7 | 896119 base downstream | q16.1 | CT | 0.8463 | 1.287 | 0.0006016 |
| 10 | rs12258219 | 110503646 | XPNPEP1 | 1110867 base upstream | q25.1 | GT | 0.8297 | 1.291 | 0.0006023 |
| 10 | rs4314990 | 110724687 | XPNPEP1 | 889826 base upstream | q25.1 | CT | 0.1807 | 0.79 | 0.0006027 |
| 21 | rs2837226 | 40088875 | LOC150084 | intron 8 | q22.2 | AC | 0.3167 | 1.21 | 0.0006032 |
| 10 | rs17779320 | 110723326 | XPNPEP1 | 891187 base upstream | q25.1 | AG | 0.8193 | 1.266 | 0.0006033 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 12 | rs3191064 | 13260841 | EMP1 | EXON 5 | p13.1 | AG | 0.9281 | 1.47 | 0.0006044 |
| 8 | rs1870126 | 135162883 | ZNF406 | 396330 base upstream | q24.22 | CT | 0.5062 | 0.837 | 0.0006045 |
| 1 | rs7529366 | 55457932 | USP24 | 4582 base downstream | p32.3 | AG | 0.2445 | 1.236 | 0.0006045 |
| 8 | rs2896732 | 135087435 | ST3GAL1 | 434091 base downstream | q24.22 | AC | 0.5708 | 1.199 | 0.0006045 |
| 10 | rs11596823 | 110722721 | XPNPEP1 | 891792 base upstream | q25.1 | AG | 0.8193 | 1.266 | 0.0006048 |
| 2 | rs3791278 | 134742338 | MGAT5 | intron 1 | q21.2 | AG | 0.04 | 1.639 | 0.0006051 |
| 8 | rs1379435 | 135087684 | ST3GAL1 | 434340 base downstream | q24.22 | CT | 0.5708 | 1.199 | 0.0006051 |
| 21 | rs2837229 | 40095584 | LOC150084 | EXON 9 | q22.2 | CT | 0.6833 | 0.826 | 0.0006051 |
| 5 | rs325522 | 104073206 | NUDT12 | 1146817 base downstream | q21.2 | CG | 0.1653 | 1.271 | 0.0006061 |
| 20 | rs6025590 | 55503911 | CTCFL | 1718 base upstream | q13.31 | AG | 0.3854 | 1.2 | 0.0006063 |
| 12 | rs12423171 | 94615189 | NTN4 | intron 5 | q22 | AG | 0.7696 | 0.805 | 0.0006065 |
| 2 | rs4953309 | 46176270 | PRKCE | intron 11 | p21 | CG | 0.2159 | 0.796 | 0.0006067 |
| 5 | rs275820 | 64076579 | P18SRP | intron 3 | q12.3 | GT | 0.5348 | 0.836 | 0.0006069 |
| 15 | rs689991 | 51195489 | ONECUT1 | 325988 base downstream | q21.3 | AG | 0.7787 | 0.803 | 0.000607 |
| 10 | rs17779136 | 110717700 | XPNPEP1 | 896813 base upstream | q25.1 | CT | 0.1807 | 0.79 | 0.0006075 |
| 4 | rs11133558 | 58908044 | IGFBP7 | 1236748 base downstream | q12 | AG | 0.7231 | 1.228 | 0.0006079 |
| 1 | rs6703366 | 55446008 | USP24 | intron 64 | p32.3 | GT | 0.2015 | 1.258 | 0.0006079 |
| 12 | rs7966096 | 13268178 | EMP1 | 7204 base downstream | p13.1 | CT | 0.0662 | 0.662 | 0.0006082 |
| 10 | rs7076888 | 97106209 | SORBS1 | intron 10 | q23.33 | CT | 0.4516 | 1.199 | 0.0006083 |
| 17 | rs4476236 | 68391508 | SLC39A11 | intron 5 | q24.3 | AG | 0.3942 | 1.199 | 0.0006084 |
| 2 | rs10432476 | 151933334 | TNFAIP6 | intron 3 | q23.3 | CT | 0.496 | 1.21 | 0.0006085 |
| 17 | rs4969119 | 68392999 | SLC39A11 | intron 5 | q24.3 | CT | 0.6058 | 0.834 | 0.0006088 |
| 12 | rs17286390 | 94615484 | NTN4 | intron 5 | q22 | AT | 0.7695 | 0.805 | 0.0006089 |
| 2 | rs12993888 | 232134007 | NMUR1 | 30560 base downstream | q37.1 | AG | 0.0818 | 1.382 | 0.0006091 |
| 4 | rs2090901 | 58906382 | IGFBP7 | 1235086 base downstream | q12 | CT | 0.7231 | 1.228 | 0.0006091 |
| 12 | rs7962943 | 13267994 | EMP1 | 7020 base downstream | p13.1 | AG | 0.9338 | 1.509 | 0.0006094 |
| 15 | rs584758 | 51195545 | ONECUT1 | 326044 base downstream | q21.3 | AG | 0.7787 | 0.803 | 0.0006094 |
| 17 | rs4494615 | 68392507 | SLC39A11 | intron 5 | q24.3 | CT | 0.6058 | 0.834 | 0.0006096 |
| 5 | rs325533 | 104080504 | NUDT12 | 1154115 base downstream | q21.2 | AG | 0.1656 | 1.272 | 0.0006099 |
| 10 | rs11597293 | 110736026 | XPNPEP1 | 878487 base upstream | q25.1 | AC | 0.1807 | 0.79 | 0.0006112 |
| 1 | rs6661281 | 154341469 | LMNA | 9615 base upstream | q22 | CT | 0.3898 | 1.209 | 0.0006116 |
| 13 | rs754325 | 46486944 | HTR2A | 118768 base downstream | q14.2 | CT | 0.4226 | 0.818 | 0.0006118 |
| 3 | rs884477 | 106367794 | ALCAM | 200608 base upstream | q13.11 | AG | 0.1733 | 0.775 | 0.0006121 |
| 5 | rs275823 | 64088118 | P18SRP | intron 4 | q12.3 | CT | 0.4633 | 1.199 | 0.0006126 |
| 17 | rs4969120 | 68393030 | SLC39A11 | intron 5 | q24.3 | CT | 0.6057 | 0.833 | 0.0006127 |
| 12 | rs2269828 | 45757706 | AMIGO2 | EXON 1 | q13.11 | AG | 0.3359 | 0.811 | 0.0006132 |
| 5 | rs7715910 | 64084924 | P18SRP | intron 3 | q12.3 | CT | 0.5364 | 0.835 | 0.0006133 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 12 | rs2069086 | 13259589 | EMP1 | EXON 5 | p13.1 | GT | 0.0722 | 0.682 | 0.0006134 |
| 5 | rs1684851 | 73293142 | RGNEF | 49858 base downstream | q13.2 | AC | 0.7229 | 1.22 | 0.0006136 |
| 17 | rs4969122 | 68393833 | SLC39A11 | intron 5 | q24.3 | AC | 0.6056 | 0.833 | 0.0006153 |
| 3 | rs12054371 | 63499138 | SYNPR | intron 2 | p14.2 | CT | 0.8255 | 1.286 | 0.0006157 |
| 5 | rs12514766 | 104072799 | NUDT12 | 1146410 base downstream | q21.2 | AT | 0.1653 | 1.27 | 0.0006159 |
| 17 | rs4969123 | 68393953 | SLC39A11 | intron 5 | q24.3 | AG | 0.6056 | 0.833 | 0.000616 |
| 2 | rs2222779 | 51633654 | NRXN1 | 520476 base downstream | p16.3 | AG | 0.5723 | 0.834 | 0.0006162 |
| 6 | rs7744573 | 154739604 | PIP3-E | 20012 base downstream | q25.2 | CT | 0.0536 | 0.658 | 0.0006164 |
| 7 | rs757393 | 26498670 | SNX10 | 118208 base downstream | p15.2 | CT | 0.6469 | 0.826 | 0.0006167 |
| 2 | rs3771895 | 151932585 | TNFAIP6 | intron 3 | q23.3 | AG | 0.4959 | 1.209 | 0.0006174 |
| 10 | rs17700585 | 110707994 | XPNPPEP1 | 906519 base upstream | q25.1 | CT | 0.8189 | 1.266 | 0.0006176 |
| 5 | rs325563 | 104086941 | NUDT12 | 1160552 base downstream | q21.2 | AG | 0.1657 | 1.272 | 0.0006177 |
| 17 | rs4969124 | 68393965 | SLC39A11 | intron 5 | q24.3 | CT | 0.3944 | 1.2 | 0.0006183 |
| 17 | rs4570929 | 68394861 | SLC39A11 | intron 5 | q24.3 | AC | 0.3945 | 1.2 | 0.0006188 |
| 17 | rs8078564 | 68394559 | SLC39A11 | intron 5 | q24.3 | CG | 0.6055 | 0.833 | 0.000619 |
| 17 | rs8078727 | 68394639 | SLC39A11 | intron 5 | q24.3 | CT | 0.6055 | 0.833 | 0.0006191 |
| 8 | rs9650382 | 14879068 | SGCZ | intron 7 | p22 | AG | 0.4391 | 1.219 | 0.0006201 |
| 4 | rs6840036 | 183400923 | ODZ3 | 81207 base upstream | q35.1 | CT | 0.7351 | 1.232 | 0.0006206 |
| 20 | rs2209885 | 55508313 | CTCFL | intron 1 | q13.31 | CG | 0.386 | 1.201 | 0.0006209 |
| 17 | rs4503863 | 68395088 | SLC39A11 | intron 5 | q24.3 | CT | 0.6055 | 0.833 | 0.0006211 |
| 8 | rs4876434 | 120078754 | TNFRSF11B | 45190 base downstream | q24.12 | CT | 0.052 | 1.491 | 0.0006215 |
| 21 | rs2837227 | 40094036 | LOC150084 | intron 8 | q22.2 | CT | 0.6834 | 0.827 | 0.0006216 |
| 2 | rs11678426 | 229865352 | PID1 | 21051 base downstream | q36.3 | AG | 0.0715 | 1.405 | 0.0006225 |
| 17 | rs7223107 | 68395153 | SLC39A11 | intron 5 | q24.3 | CT | 0.6055 | 0.833 | 0.000623 |
| 2 | rs1922458 | 229868175 | PID1 | 23874 base downstream | q36.3 | AG | 0.9285 | 0.712 | 0.0006233 |
| 8 | rs13282289 | 27642120 | CCDC25 | 4631 base upstream | p21.1 | AG | 0.7678 | 1.248 | 0.0006235 |
| 5 | rs6882769 | 40683520 | PTGER4 | 32268 base upstream | p13.1 | CT | 0.3308 | 0.824 | 0.000624 |
| 6 | rs4716002 | 15947234 | DTNBP1 | 175984 base downstream | p22.3 | GT | 0.8689 | 0.768 | 0.0006244 |
| 5 | rs325564 | 104087577 | NUDT12 | 1161188 base downstream | q21.2 | CG | 0.8342 | 0.786 | 0.0006245 |
| 6 | rs2503674 | 48336297 | LOC442213 | 191913 base downstream | p12.3 | CT | 0.8925 | 0.746 | 0.0006245 |
| 8 | rs12335174 | 120041852 | TNFRSF11B | 8288 base downstream | q24.12 | GT | 0.9462 | 0.688 | 0.0006257 |
| 10 | rs17574901 | 115729399 | ADRB1 | 64396 base upstream | q25.3 | CT | 0.9407 | 0.686 | 0.000626 |
| 17 | rs6501572 | 68395857 | SLC39A11 | intron 5 | q24.3 | GT | 0.3946 | 1.2 | 0.000626 |
| 5 | rs17416034 | 104064571 | NUDT12 | 1138182 base downstream | q21.2 | CT | 0.8346 | 0.787 | 0.0006264 |
| 5 | rs188027 | 64077497 | P18SRP | intron 3 | q12.3 | CT | 0.4652 | 1.195 | 0.0006265 |
| 5 | rs325565 | 104087924 | NUDT12 | 1161535 base downstream | q21.2 | GT | 0.1658 | 1.272 | 0.0006267 |
| 1 | rs591545 | 98737106 | SNX7 | 162694 base upstream | p21.3 | CT | 0.072 | 0.686 | 0.0006267 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 10 | rs17653278 | 115728492 | ADRB1 | 65303 base upstream | q25.3 | CG | 0.9399 | 0.684 | 0.0006268 |
| 4 | rs2090900 | 58906337 | IGFBP7 | 1235041 base downstream | q12 | AC | 0.2775 | 0.815 | 0.0006271 |
| 2 | rs17864534 | 51617864 | NRXN1 | 504686 base downstream | p16.3 | CT | 0.4397 | 1.209 | 0.0006271 |
| 17 | rs8069336 | 68396477 | SLC39A11 | intron 5 | q24.3 | AG | 0.3946 | 1.201 | 0.0006272 |
| 8 | rs4876873 | 120039201 | TNFRSF11B | 5637 base downstream | q24.12 | AC | 0.0538 | 1.453 | 0.000628 |
| 16 | rs3924627 | 8571128 | C16orf68 | 51899 base upstream | p13.2 | AG | 0.6257 | 0.831 | 0.0006283 |
| 2 | rs1419948 | 229868406 | PID1 | 24105 base downstream | q36.3 | AC | 0.9285 | 0.712 | 0.0006286 |
| 6 | rs2535672 | 94846661 | EPHA7 | 660668 base downstream | q16.1 | AG | 0.5844 | 0.835 | 0.0006287 |
| 7 | rs473816 | 125570670 | GRM8 | 295222 base upstream | q31.33 | AG | 0.1216 | 0.758 | 0.0006289 |
| 8 | rs10109779 | 14884317 | SGCZ | intron 7 | p22 | AG | 0.5812 | 0.821 | 0.0006298 |
| 3 | rs1505595 | 63505317 | SYNPR | intron 2 | p14.2 | CT | 0.7981 | 1.271 | 0.0006302 |
| 5 | rs12518236 | 104120449 | NUDT12 | 1194060 base downstream | q21.2 | AG | 0.1285 | 1.318 | 0.0006308 |
| 8 | rs4876872 | 120038338 | TNFRSF11B | 4774 base downstream | q24.12 | AG | 0.9461 | 0.688 | 0.000631 |
| 20 | rs2426130 | 47147339 | CSE1L | 448 base downstream | q13.13 | CT | 0.0773 | 1.404 | 0.000631 |
| 14 | rs8013167 | 32679948 | NPAS3 | intron 1 | q13.1 | AG | 0.2801 | 1.219 | 0.0006324 |
| 2 | rs1419947 | 229868477 | PID1 | 24176 base downstream | q36.3 | AG | 0.9286 | 0.712 | 0.0006368 |
| 8 | rs12386956 | 120037209 | TNFRSF11B | 3645 base downstream | q24.12 | AG | 0.0539 | 1.452 | 0.0006379 |
| 5 | rs325567 | 104088490 | NUDT12 | 1162101 base downstream | q21.2 | CT | 0.8341 | 0.786 | 0.0006381 |
| 8 | rs17758011 | 120042745 | TNFRSF11B | 9181 base downstream | q24.12 | GT | 0.0538 | 1.452 | 0.0006387 |
| 12 | rs12824729 | 94627360 | NTN4 | intron 5 | q22 | AG | 0.2308 | 1.236 | 0.0006389 |
| 21 | rs2837176 | 40054216 | LOC150084 | intron 2 | q22.2 | CG | 0.3635 | 1.215 | 0.00064 |
| 10 | rs17653713 | 115736409 | ADRB1 | 57386 base upstream | q25.3 | CT | 0.9429 | 0.691 | 0.0006401 |
| 5 | rs17097481 | 141067873 | CENTD3 | 25889 base downstream | q31.3 | CT | 0.125 | 1.322 | 0.0006401 |
| 10 | rs11593900 | 110740500 | XPNPEP1 | 874013 base upstream | q25.1 | CT | 0.181 | 0.791 | 0.0006401 |
| 12 | rs11108202 | 94624381 | NTN4 | intron 5 | q22 | AG | 0.2308 | 1.237 | 0.0006403 |
| 7 | rs618766 | 125569040 | GRM8 | 296852 base upstream | q31.33 | GT | 0.1215 | 0.758 | 0.0006405 |
| 2 | rs4849121 | 111316177 | ACOXL | intron 10 | q13 | AG | 0.4705 | 0.837 | 0.0006408 |
| 3 | rs1027764 | 63504654 | SYNPR | intron 2 | p14.2 | GT | 0.2019 | 0.788 | 0.0006416 |
| 8 | rs3134073 | 120035902 | TNFRSF11B | 2338 base downstream | q24.12 | AG | 0.9461 | 0.689 | 0.0006417 |
| 5 | rs325569 | 104089373 | NUDT12 | 1162984 base downstream | q21.2 | AT | 0.8341 | 0.786 | 0.0006422 |
| 7 | rs492757 | 125567593 | GRM8 | 298299 base upstream | q31.33 | AT | 0.8785 | 1.319 | 0.0006428 |
| 2 | rs4849143 | 113503827 | IL1F8 | intron 3 | q13 | CG | 0.6875 | 0.824 | 0.0006441 |
| 10 | rs10508745 | 30470812 | KIAA1462 | 94006 base downstream | p11.23 | CT | 0.2475 | 1.226 | 0.0006442 |
| 10 | rs7896890 | 30470483 | KIAA1462 | 93677 base downstream | p11.23 | CT | 0.7525 | 0.816 | 0.0006452 |
| 2 | rs3795980 | 38204318 | CYP1B1 | 47522 base downstream | p22.2 | GT | 0.8762 | 0.767 | 0.0006453 |
| 7 | rs653569 | 125565214 | GRM8 | 300678 base upstream | q31.33 | AG | 0.1215 | 0.758 | 0.0006463 |
| 21 | rs9983659 | 40054047 | LOC150084 | intron 2 | q22.2 | CT | 0.3635 | 1.215 | 0.0006464 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 11 | rs2418583 | 32207093 | RCN1 | 123440 base downstream | p13 | CT | 0.6749 | 1.213 | 0.0006466 |
| 6 | rs658208 | 94849976 | EPHA7 | 663983 base downstream | q16.1 | AG | 0.4153 | 1.197 | 0.0006467 |
| 11 | rs374729 | 115297985 | CADM1 | 417534 base downstream | q23.2 | AG | 0.2878 | 1.221 | 0.0006471 |
| 5 | rs12520736 | 104090901 | NUDT12 | 1164512 base downstream | q21.2 | CT | 0.166 | 1.272 | 0.0006476 |
| 6 | rs2787950 | 94859869 | EPHA7 | 673876 base downstream | q16.1 | AC | 0.5601 | 0.831 | 0.0006483 |
| 10 | rs11007912 | 30461295 | KIAA1462 | 84489 base downstream | p11.23 | CG | 0.2477 | 1.227 | 0.0006488 |
| 10 | rs11007913 | 30463891 | KIAA1462 | 87085 base downstream | p11.23 | AG | 0.2477 | 1.227 | 0.0006489 |
| 8 | rs4585701 | 82125199 | PAG1 | intron 7 | q21.13 | CT | 0.9431 | 1.474 | 0.0006491 |
| 4 | rs4132377 | 166318168 | KLHL2 | 30072 base upstream | q32.3 | CG | 0.9418 | 0.687 | 0.0006492 |
| 4 | rs12648092 | 58905977 | IGFBP7 | 1234681 base downstream | q12 | AG | 0.2781 | 0.816 | 0.0006497 |
| 7 | rs648172 | 125571034 | GRM8 | 294858 base upstream | q31.33 | AT | 0.1217 | 0.759 | 0.0006497 |
| 8 | rs3134072 | 120034718 | TNFRSF11B | 1154 base downstream | q24.12 | CT | 0.9461 | 0.689 | 0.0006499 |
| 10 | rs11194258 | 110501214 | XPNPEP1 | 1113299 base upstream | q25.1 | AG | 0.8175 | 1.269 | 0.0006502 |
| 5 | rs161456 | 104090924 | NUDT12 | 1164535 base downstream | q21.2 | CT | 0.834 | 0.786 | 0.0006505 |
| 10 | rs11007851 | 30332603 | KIAA1462 | 10786 base upstream | p11.23 | CT | 0.5537 | 0.831 | 0.0006506 |
| 10 | rs11599609 | 110714483 | XPNPEP1 | 900030 base upstream | q25.1 | CT | 0.8192 | 1.264 | 0.0006508 |
| 4 | rs12648067 | 58905886 | IGFBP7 | 1234590 base downstream | q12 | AG | 0.2781 | 0.817 | 0.0006517 |
| 5 | rs11950581 | 40304970 | PTGER4 | 410818 base upstream | p13.1 | AG | 0.6639 | 0.825 | 0.0006519 |
| 10 | rs11593939 | 110740736 | XPNPEP1 | 873777 base upstream | q25.1 | CT | 0.1812 | 0.791 | 0.0006519 |
| 5 | rs161782 | 104091358 | NUDT12 | 1164969 base downstream | q21.2 | AG | 0.166 | 1.272 | 0.000652 |
| 21 | rs2837175 | 40053815 | LOC150084 | intron 2 | q22.2 | CT | 0.3636 | 1.215 | 0.0006521 |
| 5 | rs161457 | 104090937 | NUDT12 | 1164548 base downstream | q21.2 | CT | 0.166 | 1.272 | 0.0006522 |
| 6 | rs2523407 | 29829284 | HLA-F | 27002 base downstream | p22.1 | CG | 0.8284 | 0.786 | 0.0006523 |
| 6 | rs546100 | 94860527 | EPHA7 | 674534 base downstream | q16.1 | AC | 0.4316 | 1.201 | 0.0006525 |
| 3 | rs11130944 | 63503954 | SYNPR | intron 2 | p14.2 | CT | 0.202 | 0.79 | 0.0006528 |
| 3 | rs1268623 | 124794918 | PTPLB | 8304 base downstream | q21.1 | GT | 0.1993 | 1.261 | 0.0006536 |
| 6 | rs606061 | 94852999 | EPHA7 | 667006 base downstream | q16.1 | AG | 0.4153 | 1.197 | 0.0006539 |
| 21 | rs4816652 | 40052396 | LOC150084 | intron 2 | q22.2 | CT | 0.6468 | 0.821 | 0.0006541 |
| 6 | rs591551 | 94854912 | EPHA7 | 668919 base downstream | q16.1 | CT | 0.4153 | 1.197 | 0.0006543 |
| 6 | rs694170 | 94854362 | EPHA7 | 668369 base downstream | q16.1 | AG | 0.4153 | 1.197 | 0.0006545 |
| 2 | rs6733018 | 232133520 | NMUR1 | 30073 base downstream | q37.1 | AG | 0.0815 | 1.38 | 0.0006547 |
| 8 | rs3102725 | 120020186 | TNFRSF11B | intron 4 | q24.12 | AG | 0.054 | 1.45 | 0.0006547 |
| 10 | rs12256452 | 110503291 | XPNPEP1 | 1111222 base upstream | q25.1 | CG | 0.8175 | 1.268 | 0.0006547 |
| 2 | rs11886047 | 43704094 | PLEKHH2 | 13856 base upstream | p21 | CT | 0.2492 | 0.796 | 0.0006548 |
| 2 | rs1528813 | 51646400 | NRXN1 | 533222 base downstream | p16.3 | AT | 0.548 | 0.836 | 0.0006553 |
| 19 | rs1864132 | 38737515 | PEPD | 32874 base downstream | q13.11 | AG | 0.1179 | 0.757 | 0.0006553 |
| 8 | rs11990927 | 135092082 | ST3GAL1 | 438738 base downstream | q24.22 | AG | 0.5715 | 1.196 | 0.0006556 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 6 | rs16877105 | 15948412 | DTNBP1 | 177162 base downstream | p22.3 | AG | 0.131 | 1.3 | 0.0006556 |
| 8 | rs3134070 | 120034205 | TNFRSF11B | 641 base downstream | q24.12 | CT | 0.9461 | 0.689 | 0.0006557 |
| 8 | rs2127938 | 82122134 | PAG1 | intron 7 | q21.13 | CT | 0.0569 | 0.677 | 0.000656 |
| 6 | rs3873283 | 30040979 | HCG9 | 9891 base upstream | p21.33 | AG | 0.8635 | 1.311 | 0.0006562 |
| 7 | rs654111 | 125571959 | GRM8 | 293933 base upstream | q31.33 | CT | 0.1217 | 0.759 | 0.0006564 |
| 8 | rs3134069 | 120034169 | TNFRSF11B | 605 base downstream | q24.12 | AC | 0.9461 | 0.689 | 0.0006565 |
| 5 | rs161783 | 104091863 | NUDT12 | 1165474 base downstream | q21.2 | CT | 0.834 | 0.786 | 0.0006566 |
| 6 | rs9363138 | 94814379 | EPHA7 | 628386 base downstream | q16.1 | GT | 0.4232 | 1.196 | 0.0006568 |
| 10 | rs10509877 | 110503533 | XPNPEP1 | 1110980 base upstream | q25.1 | AG | 0.8175 | 1.268 | 0.0006568 |
| 11 | rs12285496 | 2794317 | KCNQ1 | intron 15 | p15.5 | CG | 0.2015 | 1.254 | 0.0006569 |
| 7 | rs651763 | 125565195 | GRM8 | 300697 base upstream | q31.33 | AC | 0.1215 | 0.758 | 0.0006573 |
| 6 | rs16877108 | 15948658 | DTNBP1 | 177408 base downstream | p22.3 | AG | 0.869 | 0.769 | 0.0006576 |
| 8 | rs11998159 | 135092098 | ST3GAL1 | 438754 base downstream | q24.22 | AG | 0.4285 | 0.836 | 0.0006583 |
| 16 | rs2908915 | 47674551 | CBLN1 | 195650 base upstream | q12.1 | CT | 0.4622 | 0.834 | 0.0006585 |
| 7 | rs674616 | 125572333 | GRM8 | 293559 base upstream | q31.33 | CT | 0.1217 | 0.759 | 0.0006585 |
| 5 | rs161785 | 104092841 | NUDT12 | 1166452 base downstream | q21.2 | AC | 0.834 | 0.786 | 0.0006591 |
| 6 | rs546226 | 94860568 | EPHA7 | 674575 base downstream | q16.1 | AG | 0.5683 | 0.833 | 0.0006608 |
| 5 | rs416286 | 73297869 | RGNEF | 54585 base downstream | q13.2 | AG | 0.7228 | 1.219 | 0.0006609 |
| 15 | rs1159895 | 84618315 | FLJ32310 | intron 14 | q25.3 | AG | 0.3296 | 1.215 | 0.000661 |
| 11 | rs2200174 | 18877606 | MRGPRX1 | 34329 base upstream | p15.1 | AG | 0.1071 | 1.339 | 0.0006611 |
| 10 | rs4751138 | 131545202 | EBF3 | intron 6 | q26.3 | CT | 0.7292 | 1.232 | 0.0006619 |
| 6 | rs9320803 | 121666786 | C6orf170 | intron 24 | q22.31 | CT | 0.8241 | 0.795 | 0.0006621 |
| 5 | rs161786 | 104093239 | NUDT12 | 1166850 base downstream | q21.2 | CT | 0.1661 | 1.272 | 0.0006622 |
| 6 | rs16877113 | 15948891 | DTNBP1 | 177641 base downstream | p22.3 | AC | 0.131 | 1.3 | 0.0006626 |
| 6 | rs9260734 | 30040645 | HCG9 | 10225 base upstream | p21.33 | AG | 0.1366 | 0.763 | 0.0006636 |
| 4 | rs984924 | 82339936 | PRKG2 | intron 17 | q21.21 | AG | 0.9374 | 0.679 | 0.000664 |
| 5 | rs161787 | 104093326 | NUDT12 | 1166937 base downstream | q21.2 | CT | 0.8339 | 0.786 | 0.0006656 |
| 2 | rs7568264 | 46182056 | PRKCE | intron 11 | p21 | AG | 0.2371 | 0.801 | 0.0006657 |
| 8 | rs3102734 | 120033197 | TNFRSF11B | intron 4 | q24.12 | AG | 0.0539 | 1.45 | 0.0006662 |
| 9 | rs11138705 | 82311365 | TLE4 | 779888 base downstream | q21.31 | CG | 0.7633 | 0.801 | 0.0006665 |
| 4 | rs11725852 | 109416443 | LEF1 | 107416 base downstream | q25 | CT | 0.7318 | 1.23 | 0.000667 |
| 4 | rs12641535 | 58905741 | IGFBP7 | 1234445 base downstream | q12 | CT | 0.7216 | 1.223 | 0.000667 |
| 5 | rs161788 | 104095776 | NUDT12 | 1169387 base downstream | q21.2 | CT | 0.1661 | 1.272 | 0.0006674 |
| 8 | rs1052873 | 27723712 | PBK | EXON 1 | p21.1 | CT | 0.7969 | 1.26 | 0.0006677 |
| 11 | rs2418582 | 32207041 | RCN1 | 123388 base downstream | p13 | AG | 0.675 | 1.214 | 0.0006678 |
| 7 | rs920802 | 121757354 | CADPS2 | intron 2 | q31.32 | AG | 0.4113 | 0.827 | 0.0006687 |
| 8 | rs3134068 | 120031840 | TNFRSF11B | intron 4 | q24.12 | CT | 0.0539 | 1.45 | 0.0006695 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 8 | rs11986666 | 82124010 | PAG1 | intron 7 | q21.13 | AC | 0.9429 | 1.468 | 0.0006709 |
| 20 | rs2426133 | 47156669 | STAU1 | 6615 base upstream | q13.13 | CT | 0.0606 | 1.477 | 0.0006718 |
| 1 | rs6668777 | 55456395 | USP24 | 3045 base downstream | p32.3 | AC | 0.7566 | 0.811 | 0.0006719 |
| 10 | rs11593385 | 110709762 | XPNPEP1 | 904751 base upstream | q25.1 | CT | 0.181 | 0.791 | 0.0006722 |
| 2 | rs918804 | 38226868 | CYP1B1 | 70072 base downstream | p22.2 | AT | 0.8595 | 0.778 | 0.0006724 |
| 8 | rs16918909 | 54312587 | OPRK1 | intron 2 | q11.23 | AG | 0.9018 | 1.366 | 0.0006732 |
| 7 | rs642710 | 125565143 | GRM8 | 300749 base upstream | q31.33 | CT | 0.8786 | 1.319 | 0.0006753 |
| 8 | rs3102733 | 120031301 | TNFRSF11B | intron 4 | q24.12 | CT | 0.0539 | 1.449 | 0.0006757 |
| 21 | rs4816653 | 40052413 | LOC150084 | intron 2 | q22.2 | CT | 0.6362 | 0.823 | 0.0006761 |
| 6 | rs471348 | 94855506 | EPHA7 | 669513 base downstream | q16.1 | AG | 0.5845 | 0.835 | 0.0006763 |
| 10 | rs7915293 | 30434183 | KIAA1462 | 57377 base downstream | p11.23 | AG | 0.6743 | 0.828 | 0.0006769 |
| 10 | rs17779016 | 110714051 | XPNPEP1 | 900462 base upstream | q25.1 | AG | 0.8191 | 1.263 | 0.0006772 |
| 8 | rs3134067 | 120030619 | TNFRSF11B | intron 4 | q24.12 | CT | 0.9461 | 0.69 | 0.0006777 |
| 6 | rs1927587 | 15953087 | DTNBP1 | 181837 base downstream | p22.3 | CT | 0.8689 | 0.77 | 0.0006779 |
| 2 | rs12712969 | 46185673 | PRKCE | intron 11 | p21 | CT | 0.2441 | 0.803 | 0.000678 |
| 16 | rs2967260 | 47660593 | CBLN1 | 209608 base upstream | q12.1 | AT | 0.5376 | 1.203 | 0.0006782 |
| 5 | rs7723455 | 164229034 | MAT2B | 1350131 base downstream | q34 | AC | 0.2757 | 0.811 | 0.0006788 |
| 3 | rs9850250 | 45188375 | CDCP1 | 25457 base downstream | p21.31 | AT | 0.571 | 0.834 | 0.0006791 |
| 3 | rs7651813 | 172708739 | TNIK | 48193 base downstream | q26.31 | AG | 0.758 | 1.239 | 0.0006792 |
| 3 | rs1994727 | 22206935 | ZNF659 | 439115 base downstream | p24.3 | AT | 0.8227 | 0.797 | 0.0006793 |
| 6 | rs1352380 | 94782808 | EPHA7 | 596815 base downstream | q16.1 | CT | 0.438 | 1.194 | 0.0006798 |
| 5 | rs17348299 | 55358652 | IL6ST | 32132 base downstream | q11.2 | AC | 0.1751 | 1.285 | 0.00068 |
| 8 | rs3134066 | 120029532 | TNFRSF11B | intron 4 | q24.12 | AT | 0.9461 | 0.69 | 0.0006805 |
| 10 | rs4933978 | 85961327 | PCDH21 | intron 13 | q23.1 | AG | 0.2526 | 0.816 | 0.0006823 |
| 4 | rs12647365 | 58905626 | IGFBP7 | 1234330 base downstream | q12 | AG | 0.2788 | 0.818 | 0.0006827 |
| 21 | rs2410182 | 40101946 | LOC150084 | 6053 base downstream | q22.2 | AG | 0.4164 | 0.836 | 0.0006842 |
| 8 | rs3102731 | 120028570 | TNFRSF11B | intron 4 | q24.12 | AG | 0.0539 | 1.448 | 0.0006852 |
| 8 | rs3134062 | 120028459 | TNFRSF11B | intron 4 | q24.12 | AG | 0.9461 | 0.691 | 0.0006861 |
| 6 | rs9398632 | 121702869 | C6orf170 | 5526 base downstream | q22.31 | AC | 0.8237 | 0.796 | 0.0006861 |
| 6 | rs9320809 | 121698543 | C6orf170 | 1200 base downstream | q22.31 | AG | 0.8237 | 0.796 | 0.0006862 |
| 2 | rs1406429 | 51647831 | NRXN1 | 534653 base downstream | p16.3 | CT | 0.5486 | 0.836 | 0.0006865 |
| 2 | rs1116246 | 46183371 | PRKCE | intron 11 | p21 | AG | 0.7561 | 1.245 | 0.0006866 |
| 7 | rs585146 | 125574072 | GRM8 | 291820 base upstream | q31.33 | CT | 0.8781 | 1.316 | 0.0006867 |
| 8 | rs3102726 | 120024531 | TNFRSF11B | intron 4 | q24.12 | AT | 0.9461 | 0.691 | 0.0006871 |
| 13 | rs283982 | 75986324 | KCTD12 | 365980 base upstream | q22.2 | CT | 0.2097 | 1.252 | 0.0006879 |
| 2 | rs4851164 | 98846759 | MGC42367 | intron 9 | q11.2 | CT | 0.9447 | 0.678 | 0.0006889 |
| 8 | rs3134059 | 120025033 | TNFRSF11B | intron 4 | q24.12 | CT | 0.0539 | 1.448 | 0.0006893 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 8 | rs3102729 | 120025686 | TNFRSF11B | intron 4 | q24.12 | AG | 0.0539 | 1.448 | 0.00069 |
| 8 | rs3134060 | 120025224 | TNFRSF11B | intron 4 | q24.12 | AG | 0.9461 | 0.691 | 0.0006909 |
| 8 | rs3134061 | 120025500 | TNFRSF11B | intron 4 | q24.12 | AT | 0.0539 | 1.448 | 0.000692 |
| 21 | rs238962 | 16554814 | C21orf34 | intron 4 | q21.1 | CT | 0.6212 | 0.828 | 0.0006942 |
| 6 | rs6557347 | 154740453 | PIP3-E | 20861 base downstream | q25.2 | CT | 0.0542 | 0.666 | 0.0006942 |
| 6 | rs7772909 | 6092904 | F13A1 | intron 1 | p25.1 | CT | 0.1689 | 1.265 | 0.0006947 |
| 2 | rs10167555 | 46174610 | PRKCE | intron 11 | p21 | GT | 0.8058 | 1.253 | 0.0006954 |
| 2 | rs17022034 | 98853280 | MGC42367 | intron 9 | q11.2 | AT | 0.9448 | 0.677 | 0.0006954 |
| 2 | rs9678578 | 113527418 | IL1F8 | 507 base downstream | q13 | AT | 0.6865 | 0.825 | 0.0006957 |
| 6 | rs7748218 | 6092368 | F13A1 | intron 1 | p25.1 | CT | 0.8311 | 0.791 | 0.0006962 |
| 4 | rs17218140 | 58904343 | IGFBP7 | 1233047 base downstream | q12 | GT | 0.7209 | 1.221 | 0.0006963 |
| 10 | rs560559 | 30537356 | PAPD1 | 104408 base upstream | p11.23 | AG | 0.2701 | 1.225 | 0.0006974 |
| 7 | rs6973468 | 9678156 | NXPH1 | 919039 base downstream | p21.3 | GT | 0.813 | 1.276 | 0.0006974 |
| 5 | rs436777 | 73300336 | RGNEF | 57052 base downstream | q13.3 | AG | 0.7226 | 1.219 | 0.0006983 |
| 2 | rs1797392 | 232130501 | NMUR1 | 27054 base downstream | q37.1 | CT | 0.9195 | 0.724 | 0.0006983 |
| 3 | rs11926493 | 63498351 | SYNPR | intron 2 | p14.2 | CT | 0.8075 | 1.264 | 0.0006986 |
| 15 | rs7181898 | 51234395 | WDR72 | 358834 base upstream | q21.3 | AG | 0.2406 | 1.232 | 0.0006989 |
| 6 | rs9388559 | 127643410 | RNF146 | intron 2 | q22.33 | AG | 0.0364 | 1.533 | 0.0006989 |
| 6 | rs7764180 | 127647360 | RNF146 | intron 3 | q22.33 | AC | 0.9636 | 0.653 | 0.0006989 |
| 6 | rs9401947 | 127643754 | RNF146 | intron 2 | q22.33 | CT | 0.9636 | 0.653 | 0.0006989 |
| 6 | rs9321072 | 127648042 | RNF146 | intron 3 | q22.33 | CT | 0.9636 | 0.653 | 0.0006989 |
| 6 | rs9401948 | 127666637 | ECHDC1 | intron 1 | q22.33 | CT | 0.9636 | 0.653 | 0.0006992 |
| 6 | rs6936084 | 127655994 | ECHDC1 | intron 1 | q22.33 | AG | 0.0364 | 1.532 | 0.0006992 |
| 6 | rs9372862 | 127642939 | RNF146 | intron 1 | q22.33 | CT | 0.0364 | 1.532 | 0.0006992 |
| 6 | rs761842 | 127662563 | ECHDC1 | intron 1 | q22.33 | AT | 0.9636 | 0.653 | 0.0006992 |
| 6 | rs9372863 | 127659891 | ECHDC1 | intron 1 | q22.33 | AG | 0.9636 | 0.653 | 0.0006992 |
| 6 | rs9401949 | 127692809 | ECHDC1 | intron 4 | q22.33 | CT | 0.0364 | 1.532 | 0.0006994 |
| 6 | rs9372865 | 127691077 | ECHDC1 | intron 4 | q22.33 | CT | 0.9636 | 0.653 | 0.0006995 |
| 6 | rs4141423 | 127690339 | ECHDC1 | intron 4 | q22.33 | CT | 0.9636 | 0.653 | 0.0006995 |
| 6 | rs9375500 | 127688899 | ECHDC1 | intron 3 | q22.33 | CT | 0.0364 | 1.532 | 0.0006995 |
| 6 | rs9372861 | 127642888 | RNF146 | intron 1 | q22.33 | CT | 0.9636 | 0.653 | 0.0006997 |
| 21 | rs2837223 | 40085103 | LOC150084 | intron 6 | q22.2 | CT | 0.3166 | 1.207 | 0.0006999 |
| 15 | rs8041239 | 86276360 | NTRK3 | intron 4 | q25.3 | AG | 0.7974 | 1.264 | 0.0007 |
| 7 | rs498875 | 125577694 | GRM8 | 288198 base upstream | q31.33 | CT | 0.122 | 0.76 | 0.0007007 |
| 6 | rs9372866 | 127697120 | ECHDC1 | intron 4 | q22.33 | CT | 0.0364 | 1.533 | 0.000701 |
| 4 | rs11727794 | 58903846 | IGFBP7 | 1232550 base downstream | q12 | AC | 0.2792 | 0.819 | 0.0007011 |
| 20 | rs6012644 | 47381910 | KCNB1 | 40001 base upstream | q13.13 | CG | 0.0661 | 1.471 | 0.0007014 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 2 | rs4851166 | 98860167 | MGC42367 | intron 9 | q11.2 | CT | 0.9448 | 0.677 | 0.0007017 |
| 4 | rs178329 | 189573141 | FLJ36180 | 267498 base downstream | q35.2 | AG | 0.1954 | 1.27 | 0.0007018 |
| 21 | rs11701338 | 40083878 | LOC150084 | intron 6 | q22.2 | CT | 0.6834 | 0.828 | 0.0007022 |
| 11 | rs633683 | 118009952 | PHLDB1 | intron 10 | q23.3 | CT | 0.599 | 0.827 | 0.0007025 |
| 21 | rs760285 | 40083524 | LOC150084 | intron 6 | q22.2 | AG | 0.6834 | 0.828 | 0.0007031 |
| 16 | rs17664315 | 6607296 | A2BP1 | intron 2 | p13.2 | GT | 0.4919 | 1.199 | 0.0007032 |
| 6 | rs9277053 | 33114200 | HLA-DPA1 | 26571 base upstream | p21.32 | AG | 0.292 | 0.811 | 0.0007033 |
| 6 | rs9375502 | 127698485 | ECHDC1 | intron 4 | q22.33 | GT | 0.9637 | 0.652 | 0.000704 |
| 1 | rs10900601 | 202838673 | LRRN5 | 14254 base upstream | q32.1 | AG | 0.2976 | 1.217 | 0.0007043 |
| 5 | rs2962851 | 164230392 | MAT2B | 1351489 base downstream | q34 | AG | 0.2776 | 0.811 | 0.0007059 |
| 4 | rs11735710 | 58903429 | IGFBP7 | 1232133 base downstream | q12 | AG | 0.2794 | 0.819 | 0.0007062 |
| 3 | rs6763775 | 129059205 | MGLL | 34464 base downstream | q21.3 | CG | 0.8434 | 0.771 | 0.0007094 |
| 1 | rs7526907 | 110912891 | KCNA2 | 34407 base upstream | p13.3 | AG | 0.7401 | 0.818 | 0.0007099 |
| 6 | rs7748589 | 14489463 | CD83 | 244338 base downstream | p23 | AG | 0.5263 | 0.835 | 0.0007099 |
| 5 | rs2962852 | 164230439 | MAT2B | 1351536 base downstream | q34 | AG | 0.2776 | 0.811 | 0.0007101 |
| 1 | rs12092511 | 51249676 | CDKN2C | 36781 base downstream | p33 | AG | 0.4286 | 0.836 | 0.0007106 |
| 20 | rs6107609 | 5210119 | PROKR2 | 20567 base upstream | p12.3 | CT | 0.5045 | 0.838 | 0.0007109 |
| 6 | rs749212 | 124525535 | TCBA1 | intron 1 | q22.31 | AG | 0.8762 | 1.308 | 0.000711 |
| 2 | rs13411546 | 128338961 | MGC4268 | EXON 1 | q14.3 | AG | 0.4089 | 1.202 | 0.0007114 |
| 2 | rs1226973 | 229871291 | PID1 | 26990 base downstream | q36.3 | AC | 0.9288 | 0.715 | 0.0007123 |
| 2 | rs17022036 | 98863360 | MGC42367 | intron 9 | q11.2 | GT | 0.9448 | 0.676 | 0.0007124 |
| 20 | rs4580454 | 5210168 | PROKR2 | 20518 base upstream | p12.3 | CG | 0.5046 | 0.838 | 0.000713 |
| 20 | rs2326618 | 5211444 | PROKR2 | 19242 base upstream | p12.3 | AG | 0.4953 | 1.193 | 0.0007137 |
| 8 | rs2511586 | 105323016 | RIMS2 | intron 19 | q22.3 | AG | 0.6871 | 0.826 | 0.0007139 |
| 16 | rs2967255 | 47669016 | CBLN1 | 201185 base upstream | q12.1 | AC | 0.4624 | 0.833 | 0.0007143 |
| 7 | rs635680 | 125578124 | GRM8 | 287768 base upstream | q31.33 | CG | 0.122 | 0.761 | 0.0007153 |
| 1 | rs2166307 | 66825324 | SGIP1 | intron 1 | p31.3 | CT | 0.1269 | 1.324 | 0.0007155 |
| 10 | rs10887255 | 85962578 | PCDH21 | intron 15 | q23.1 | CT | 0.2528 | 0.816 | 0.0007163 |
| 5 | rs161790 | 104100998 | NUDT12 | 1174609 base downstream | q21.2 | CT | 0.8335 | 0.787 | 0.0007164 |
| 5 | rs11133949 | 2515225 | IRX2 | 284654 base upstream | p15.33 | AG | 0.6062 | 1.199 | 0.000717 |
| 5 | rs161791 | 104101159 | NUDT12 | 1174770 base downstream | q21.2 | GT | 0.1665 | 1.271 | 0.0007178 |
| 3 | rs515920 | 54693761 | CACNA2D3 | intron 11 | p14.3 | CT | 0.5122 | 0.833 | 0.0007178 |
| 12 | rs6490059 | 115293528 | THRAP2 | 94002 base downstream | q24.21 | CT | 0.0579 | 1.448 | 0.000718 |
| 2 | rs10182566 | 29141212 | FLJ34931 | EXON 1 | p23.2 | CT | 0.7435 | 0.808 | 0.0007183 |
| 8 | rs2100119 | 3343653 | CSMD1 | intron 60 | p23.2 | AG | 0.7871 | 1.247 | 0.0007184 |
| 2 | rs10188379 | 38224980 | CYP1B1 | 68184 base downstream | p22.2 | CG | 0.2064 | 1.241 | 0.0007191 |
| 20 | rs910970 | 5219710 | PROKR2 | 10976 base upstream | p12.3 | CT | 0.4952 | 1.193 | 0.00072 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs2174394 | 136738151 | PABPC4L | 1395798 base downstream | q28.3 | AG | 0.1339 | 1.321 | 0.0007205 |
| 12 | rs7313246 | 9920781 | CLEC2B | 7056 base downstream | p13.31 | AT | 0.7161 | 0.82 | 0.0007207 |
| 6 | rs9388558 | 127638279 | RNF146 | intron 1 | q22.33 | AT | 0.9636 | 0.653 | 0.0007207 |
| 4 | rs2102279 | 136739022 | PABPC4L | 1396669 base downstream | q28.3 | CT | 0.1339 | 1.321 | 0.0007212 |
| 6 | rs1050783 | 6090691 | F13A1 | EXON 1 | p25.1 | CT | 0.8311 | 0.791 | 0.0007226 |
| 2 | rs1574516 | 98867750 | MGC42367 | intron 9 | q11.2 | CT | 0.9449 | 0.675 | 0.0007228 |
| 4 | rs3913354 | 109399892 | LEF1 | 90865 base downstream | q25 | AT | 0.7318 | 1.227 | 0.0007231 |
| 2 | rs12477409 | 46181464 | PRKCE | intron 11 | p21 | CG | 0.7566 | 1.245 | 0.0007231 |
| 20 | rs6038126 | 5221314 | PROKR2 | 9372 base upstream | p12.3 | CT | 0.495 | 1.193 | 0.0007233 |
| 6 | rs682644 | 94856518 | EPHA7 | 670525 base downstream | q16.1 | CT | 0.416 | 1.198 | 0.0007239 |
| 1 | rs884108 | 202857860 | LRRN5 | intron 1 | q32.1 | AG | 0.2375 | 1.24 | 0.000724 |
| 2 | rs2345955 | 46174384 | PRKCE | intron 11 | p21 | CT | 0.2002 | 0.8 | 0.0007266 |
| 16 | rs2967254 | 47669641 | CBLN1 | 200560 base upstream | q12.1 | CT | 0.5376 | 1.199 | 0.0007278 |
| 3 | rs2366434 | 59332476 | FLJ42117 | 321721 base downstream | p14.2 | AG | 0.3843 | 1.2 | 0.0007283 |
| 6 | rs2787948 | 94856881 | EPHA7 | 670888 base downstream | q16.1 | CT | 0.4161 | 1.198 | 0.0007291 |
| 12 | rs1376795 | 128846223 | TMEM132D | intron 8 | q24.33 | CT | 0.294 | 1.212 | 0.0007297 |
| 2 | rs12477342 | 46181374 | PRKCE | intron 11 | p21 | CT | 0.2433 | 0.804 | 0.0007302 |
| 2 | rs990524 | 113532952 | IL1F5 | intron 1 | q13 | CT | 0.3136 | 1.211 | 0.0007303 |
| 6 | rs3024457 | 6097407 | F13A1 | intron 2 | p25.1 | AC | 0.1707 | 1.262 | 0.0007306 |
| 13 | rs4265682 | 100537995 | VGCNL1 | intron 14 | q33.1 | GT | 0.5957 | 1.213 | 0.0007307 |
| 10 | rs10887256 | 85963395 | PCDH21 | intron 16 | q23.1 | CG | 0.2249 | 0.805 | 0.0007329 |
| 21 | rs2837246 | 40136888 | PCP4 | 24328 base upstream | q22.2 | CT | 0.3119 | 1.209 | 0.0007337 |
| 4 | rs11935719 | 136722837 | PABPC4L | 1380484 base downstream | q28.3 | AG | 0.2032 | 1.244 | 0.0007338 |
| 7 | rs650045 | 125579026 | GRM8 | 286866 base upstream | q31.33 | AG | 0.1221 | 0.761 | 0.0007338 |
| 4 | rs11935664 | 136722856 | PABPC4L | 1380503 base downstream | q28.3 | CT | 0.7968 | 0.804 | 0.0007345 |
| 4 | rs9312697 | 58878691 | IGFBP7 | 1207395 base downstream | q12 | AG | 0.7192 | 1.216 | 0.0007352 |
| 4 | rs11940405 | 136722879 | PABPC4L | 1380526 base downstream | q28.3 | GT | 0.2032 | 1.244 | 0.0007352 |
| 7 | rs626762 | 125563862 | GRM8 | 302030 base upstream | q31.33 | AC | 0.1263 | 0.752 | 0.0007357 |
| 1 | rs1863618 | 81222832 | LPHN2 | 815837 base upstream | p31.1 | AG | 0.6063 | 1.207 | 0.0007365 |
| 4 | rs13145036 | 136727429 | PABPC4L | 1385076 base downstream | q28.3 | AG | 0.7967 | 0.804 | 0.0007384 |
| 4 | rs7667350 | 136726319 | PABPC4L | 1383966 base downstream | q28.3 | AG | 0.7967 | 0.804 | 0.0007384 |
| 7 | rs553952 | 125579136 | GRM8 | 286756 base upstream | q31.33 | CT | 0.8779 | 1.313 | 0.0007384 |
| 11 | rs6483549 | 18884861 | MRGPRX1 | 27074 base upstream | p15.1 | CG | 0.8934 | 0.748 | 0.0007385 |
| 4 | rs7662409 | 136726126 | PABPC4L | 1383773 base downstream | q28.3 | CG | 0.7967 | 0.804 | 0.0007385 |
| 4 | rs13131704 | 136725872 | PABPC4L | 1383519 base downstream | q28.3 | AT | 0.7968 | 0.804 | 0.0007386 |
| 4 | rs12643192 | 136725857 | PABPC4L | 1383504 base downstream | q28.3 | CG | 0.7968 | 0.804 | 0.0007388 |
| 4 | rs1479789 | 136724400 | PABPC4L | 1382047 base downstream | q28.3 | AG | 0.2032 | 1.244 | 0.0007388 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs1479788 | 136724188 | PABPC4L | 1381835 base downstream | q28.3 | AT | 0.7968 | 0.804 | 0.000739 |
| 4 | rs1479787 | 136724155 | PABPC4L | 1381802 base downstream | q28.3 | CT | 0.7968 | 0.804 | 0.0007391 |
| 4 | rs2127459 | 136723951 | PABPC4L | 1381598 base downstream | q28.3 | GT | 0.7968 | 0.804 | 0.0007391 |
| 17 | rs16945089 | 11467738 | DNAH9 | intron 6 | p12 | CG | 0.8325 | 1.297 | 0.0007391 |
| 11 | rs2896547 | 18884296 | MRGPRX1 | 27639 base upstream | p15.1 | AG | 0.1066 | 1.337 | 0.0007393 |
| 4 | rs2054506 | 136723423 | PABPC4L | 1381070 base downstream | q28.3 | CG | 0.7968 | 0.804 | 0.0007395 |
| 4 | rs2054505 | 136723371 | PABPC4L | 1381018 base downstream | q28.3 | CT | 0.7968 | 0.804 | 0.0007398 |
| 6 | rs2073298 | 127720097 | ECHDC1 | 13650 base downstream | q22.33 | CT | 0.9638 | 0.653 | 0.0007399 |
| 6 | rs6569485 | 127717884 | ECHDC1 | 11437 base downstream | q22.33 | CT | 0.9638 | 0.653 | 0.0007399 |
| 6 | rs9375505 | 127739111 | ECHDC1 | 32664 base downstream | q22.33 | CT | 0.0362 | 1.532 | 0.0007399 |
| 11 | rs1384648 | 18886008 | MRGPRX1 | 25927 base upstream | p15.1 | CT | 0.8934 | 0.748 | 0.0007404 |
| 13 | rs9553915 | 26340889 | GPR12 | 108925 base downstream | q12.13 | AG | 0.8674 | 0.763 | 0.0007406 |
| 8 | rs753722 | 134285128 | WISP1 | intron 1 | q24.22 | CG | 0.2951 | 0.822 | 0.0007415 |
| 6 | rs9385420 | 127744028 | ECHDC1 | 37581 base downstream | q22.33 | AG | 0.9638 | 0.653 | 0.0007419 |
| 4 | rs12504808 | 189571301 | FLJ36180 | 265658 base downstream | q35.2 | CT | 0.8039 | 0.789 | 0.0007419 |
| 4 | rs12504780 | 189571191 | FLJ36180 | 265548 base downstream | q35.2 | CT | 0.8039 | 0.789 | 0.000743 |
| 6 | rs4713614 | 33235965 | COL11A2 | 2481 base upstream | p21.32 | AC | 0.5472 | 0.835 | 0.000744 |
| 12 | rs7297205 | 10712107 | STYK1 | intron 10 | p13.2 | CT | 0.637 | 1.208 | 0.0007441 |
| 6 | rs802274 | 124525158 | TCBA1 | intron 1 | q22.31 | AG | 0.1238 | 0.765 | 0.0007444 |
| 12 | rs10507059 | 94629965 | NTN4 | intron 6 | q22 | CT | 0.7683 | 0.811 | 0.000746 |
| 1 | rs3813634 | 51248076 | CDKN2C | 35181 base downstream | p33 | AG | 0.4287 | 0.837 | 0.0007474 |
| 10 | rs12220219 | 30437845 | KIAA1462 | 61039 base downstream | p11.23 | CT | 0.3109 | 1.206 | 0.0007477 |
| 4 | rs11935796 | 136716070 | PABPC4L | 1373717 base downstream | q28.3 | AG | 0.7862 | 0.807 | 0.0007478 |
| 7 | rs556478 | 125579381 | GRM8 | 286511 base upstream | q31.33 | CT | 0.1222 | 0.762 | 0.0007502 |
| 12 | rs1376796 | 128846311 | TMEM132D | intron 8 | q24.33 | GT | 0.7061 | 0.825 | 0.0007504 |
| 12 | rs1031400 | 128845279 | TMEM132D | intron 8 | q24.33 | AG | 0.706 | 0.825 | 0.0007514 |
| 2 | rs12373805 | 46174598 | PRKCE | intron 11 | p21 | AG | 0.7998 | 1.249 | 0.0007518 |
| 4 | rs6823080 | 151134607 | DCLK2 | 84922 base upstream | q31.3 | AC | 0.1629 | 1.265 | 0.0007524 |
| 6 | rs10944710 | 94788810 | EPHA7 | 602817 base downstream | q16.1 | CT | 0.4381 | 1.193 | 0.000753 |
| 2 | rs4849144 | 113516520 | IL1F8 | intron 5 | q13 | AG | 0.323 | 1.209 | 0.0007531 |
| 2 | rs7569284 | 113520034 | IL1F8 | intron 5 | q13 | AG | 0.677 | 0.827 | 0.0007534 |
| 4 | rs11133555 | 58880555 | IGFBP7 | 1209259 base downstream | q12 | AG | 0.7192 | 1.216 | 0.0007538 |
| 2 | rs7557928 | 113514439 | IL1F8 | intron 5 | q13 | GT | 0.677 | 0.827 | 0.0007538 |
| 10 | rs17295031 | 30437462 | KIAA1462 | 60656 base downstream | p11.23 | AG | 0.687 | 0.831 | 0.0007544 |
| 20 | rs4597612 | 5209578 | PROKR2 | 21108 base upstream | p12.3 | GT | 0.5045 | 0.839 | 0.0007545 |
| 8 | rs2012994 | 14907628 | SGCZ | intron 7 | p22 | AG | 0.5076 | 1.195 | 0.0007555 |
| 7 | rs475294 | 125580265 | GRM8 | 285627 base upstream | q31.33 | CT | 0.8778 | 1.312 | 0.0007556 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 2 | rs10196888 | 55889730 | EFEMP1 | 56875 base upstream | p16.1 | AG | 0.9423 | 0.688 | 0.000756 |
| 2 | rs7592062 | 51622416 | NRXN1 | 509238 base downstream | p16.3 | AG | 0.4406 | 1.2 | 0.0007562 |
| 12 | rs3021522 | 2779406 | FKBP4 | intron 6 | p13.33 | CG | 0.9572 | 0.641 | 0.0007573 |
| 2 | rs2862776 | 113514395 | IL1F8 | intron 5 | q13 | AG | 0.6769 | 0.827 | 0.0007582 |
| 2 | rs1569190 | 51645271 | NRXN1 | 532093 base downstream | p16.3 | GT | 0.5753 | 0.83 | 0.0007582 |
| 3 | rs2618115 | 27918162 | EOMES | 179373 base downstream | p24.1 | AG | 0.1161 | 0.728 | 0.0007586 |
| 16 | rs9936914 | 7338583 | A2BP1 | intron 4 | p13.2 | AT | 0.096 | 1.339 | 0.0007587 |
| 16 | rs9934586 | 7338453 | A2BP1 | intron 4 | p13.2 | AG | 0.904 | 0.747 | 0.000759 |
| 8 | rs6981423 | 135164118 | ZNF406 | 395095 base upstream | q24.22 | CT | 0.448 | 1.193 | 0.0007599 |
| 12 | rs10773708 | 128847165 | TMEM132D | intron 8 | q24.33 | AG | 0.7061 | 0.825 | 0.0007612 |
| 7 | rs501483 | 125580852 | GRM8 | 285040 base upstream | q31.33 | AG | 0.8778 | 1.312 | 0.0007612 |
| 6 | rs12206267 | 51868413 | PKHD1 | intron 24 | p12.2 | CT | 0.8131 | 1.27 | 0.0007639 |
| 8 | rs7001769 | 54436653 | OPRK1 | 109906 base downstream | q11.23 | CT | 0.1654 | 0.783 | 0.000764 |
| 9 | rs11138196 | 81214260 | CHCHD9 | 17490 base downstream | q21.31 | AT | 0.0281 | 1.716 | 0.0007648 |
| 2 | rs2950945 | 51622443 | NRXN1 | 509265 base downstream | p16.3 | AG | 0.4405 | 1.2 | 0.0007656 |
| 11 | rs1973238 | 18888602 | MRGPRX1 | 23333 base upstream | p15.1 | CG | 0.8934 | 0.748 | 0.0007665 |
| 1 | rs2811280 | 176952870 | RALGPS2 | 8052 base upstream | q25.2 | AG | 0.6538 | 1.204 | 0.0007673 |
| 9 | rs1217339 | 71237419 | APBA1 | intron 2 | q21.11 | AG | 0.1895 | 0.795 | 0.0007676 |
| 12 | rs7135319 | 2212678 | CACNA1C | intron 3 | p13.33 | AG | 0.9669 | 0.588 | 0.0007677 |
| 9 | rs3737172 | 71237455 | APBA1 | intron 2 | q21.11 | CT | 0.8105 | 1.258 | 0.0007681 |
| 3 | rs658339 | 8907353 | RAD18 | intron 2 | p25.3 | AG | 0.0364 | 0.607 | 0.0007681 |
| 4 | rs13122550 | 136728035 | PABPC4L | 1385682 base downstream | q28.3 | CT | 0.2036 | 1.243 | 0.0007682 |
| 5 | rs2610243 | 64066108 | P18SRP | intron 2 | q12.3 | GT | 0.5247 | 0.838 | 0.0007683 |
| 9 | rs1217338 | 71237918 | APBA1 | intron 2 | q21.11 | CT | 0.1895 | 0.795 | 0.0007687 |
| 12 | rs1981655 | 2777987 | FKBP4 | intron 3 | p13.33 | AT | 0.9571 | 0.642 | 0.0007696 |
| 3 | rs1505600 | 63493882 | SYNPR | intron 2 | p14.2 | CG | 0.202 | 0.801 | 0.0007697 |
| 3 | rs17014951 | 24627817 | THRB | 116500 base downstream | p24.2 | AG | 0.7373 | 1.235 | 0.0007697 |
| 7 | rs505793 | 125581262 | GRM8 | 284630 base upstream | q31.33 | CT | 0.1222 | 0.762 | 0.0007705 |
| 3 | rs1394902 | 63494733 | SYNPR | intron 2 | p14.2 | CT | 0.798 | 1.248 | 0.0007712 |
| 3 | rs6446043 | 59331465 | FLJ42117 | 320710 base downstream | p14.2 | AT | 0.6153 | 0.833 | 0.0007718 |
| 2 | rs2305150 | 113505787 | IL1F8 | EXON 5 | q13 | CT | 0.4426 | 1.196 | 0.0007722 |
| 2 | rs13415031 | 107784033 | SLC5A7 | 185393 base upstream | q12.3 | CG | 0.346 | 0.812 | 0.0007722 |
| 5 | rs315892 | 2511057 | IRX2 | 288822 base upstream | p15.33 | CT | 0.3243 | 0.821 | 0.0007724 |
| 6 | rs9401954 | 127754044 | ECHDC1 | 47597 base downstream | q22.33 | AC | 0.9636 | 0.656 | 0.0007733 |
| 3 | rs1394901 | 63494767 | SYNPR | intron 2 | p14.2 | CT | 0.202 | 0.801 | 0.0007735 |
| 10 | rs2151114 | 30532611 | PAPD1 | 109153 base upstream | p11.23 | AG | 0.2774 | 1.215 | 0.0007738 |
| 3 | rs4392412 | 63495077 | SYNPR | intron 2 | p14.2 | GT | 0.202 | 0.801 | 0.0007742 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 3 | rs652424 | 54720595 | CACNA2D3 | intron 11 | p14.3 | CT | 0.584 | 1.206 | 0.0007742 |
| 12 | rs7980332 | 97115342 | TMPO | 318197 base upstream | q23.1 | AC | 0.8658 | 1.317 | 0.000775 |
| 3 | rs985370 | 63495157 | SYNPR | intron 2 | p14.2 | AG | 0.798 | 1.248 | 0.0007751 |
| 3 | rs589281 | 54722284 | CACNA2D3 | intron 11 | p14.3 | CT | 0.584 | 1.206 | 0.0007751 |
| 21 | rs2837258 | 40145943 | PCP4 | 15273 base upstream | q22.2 | AC | 0.3118 | 1.208 | 0.0007763 |
| 21 | rs8132770 | 39947754 | B3GALT5 | 3369 base upstream | q22.2 | AT | 0.4775 | 0.84 | 0.0007767 |
| 4 | rs7435172 | 58886180 | IGFBP7 | 1214884 base downstream | q12 | CT | 0.7192 | 1.215 | 0.0007773 |
| 3 | rs7653488 | 30343934 | TGFBR2 | 279063 base upstream | p24.1 | CT | 0.3593 | 0.831 | 0.0007774 |
| 3 | rs985368 | 63495430 | SYNPR | intron 2 | p14.2 | CT | 0.798 | 1.248 | 0.0007782 |
| 14 | rs6571583 | 32680251 | NPAS3 | intron 1 | q13.1 | CT | 0.2833 | 1.216 | 0.0007791 |
| 18 | rs4940191 | 48362228 | DCC | intron 1 | q21.2 | AG | 0.1479 | 0.773 | 0.0007795 |
| 6 | rs13212414 | 30248519 | TRIM15 | 67 base downstream | p21.33 | AT | 0.9519 | 0.667 | 0.0007799 |
| 2 | rs6723695 | 55891570 | EFEMP1 | 55035 base upstream | p16.1 | CT | 0.0578 | 1.449 | 0.00078 |
| 20 | rs7261606 | 47387176 | KCNB1 | 34735 base upstream | q13.13 | CT | 0.9258 | 0.71 | 0.00078 |
| 3 | rs985367 | 63495515 | SYNPR | intron 2 | p14.2 | GT | 0.798 | 1.248 | 0.0007805 |
| 4 | rs1522096 | 58882568 | IGFBP7 | 1211272 base downstream | q12 | AG | 0.2809 | 0.823 | 0.0007813 |
| 2 | rs2160020 | 210710058 | FLJ23861 | intron 13 | q34 | CT | 0.0992 | 1.338 | 0.0007816 |
| 5 | rs1562414 | 2550120 | IRX2 | 249759 base upstream | p15.33 | AG | 0.3681 | 0.832 | 0.0007821 |
| 4 | rs4865165 | 57460303 | REST | 8495 base upstream | q12 | CT | 0.5042 | 1.19 | 0.0007827 |
| 2 | rs7594860 | 107931186 | SLC5A7 | 38240 base upstream | q12.3 | CT | 0.19 | 0.793 | 0.0007828 |
| 5 | rs325524 | 104073920 | NUDT12 | 1147531 base downstream | q21.2 | CG | 0.1664 | 1.265 | 0.0007829 |
| 6 | rs9397585 | 153438568 | RGS17 | intron 4 | q25.2 | CT | 0.3442 | 1.206 | 0.0007832 |
| 16 | rs12443717 | 26204460 | HS3ST4 | 147951 base downstream | p12.1 | AT | 0.7741 | 0.803 | 0.0007834 |
| 4 | rs9998008 | 57460809 | REST | 7989 base upstream | q12 | AG | 0.5041 | 1.19 | 0.0007843 |
| 20 | rs4384857 | 5209440 | PROKR2 | 21246 base upstream | p12.3 | CG | 0.5045 | 0.84 | 0.0007858 |
| 2 | rs1226954 | 229880420 | PID1 | 36119 base downstream | q36.3 | CT | 0.935 | 0.698 | 0.0007859 |
| 12 | rs2291060 | 13256321 | EMP1 | intron 2 | p13.1 | AG | 0.9319 | 1.436 | 0.000786 |
| 11 | rs996263 | 41016901 | LRRC4C | 744661 base downstream | p12 | AT | 0.9638 | 1.69 | 0.0007861 |
| 3 | rs1505599 | 63499833 | SYNPR | intron 2 | p14.2 | AC | 0.7979 | 1.248 | 0.0007869 |
| 2 | rs7577580 | 55892233 | EFEMP1 | 54372 base upstream | p16.1 | GT | 0.0578 | 1.449 | 0.0007873 |
| 6 | rs9445968 | 68815788 | BAI3 | 586564 base upstream | q12 | GT | 0.9836 | 2.206 | 0.0007876 |
| 6 | rs802273 | 124523315 | TCBA1 | intron 1 | q22.31 | GT | 0.1236 | 0.765 | 0.0007883 |
| 2 | rs3768752 | 46196507 | PRKCE | intron 11 | p21 | AC | 0.757 | 1.238 | 0.0007884 |
| 2 | rs10202504 | 46174837 | PRKCE | intron 11 | p21 | CG | 0.2002 | 0.801 | 0.0007893 |
| 13 | rs4483759 | 44574009 | GTF2F2 | 18662 base upstream | q14.12 | CG | 0.8409 | 0.792 | 0.0007893 |
| 2 | rs13385188 | 29149180 | FLJ34931 | EXON 2 | p23.2 | AG | 0.2573 | 1.242 | 0.0007896 |
| 3 | rs1505598 | 63499920 | SYNPR | intron 2 | p14.2 | CG | 0.7979 | 1.248 | 0.0007897 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs4435727 | 149818435 | NR3C2 | 235342 base downstream | q31.23 | CG | 0.2445 | 0.812 | 0.0007898 |
| 6 | rs6938872 | 127762249 | KIAA0408 | 41179 base upstream | q22.33 | GT | 0.9636 | 0.656 | 0.00079 |
| 10 | rs10826770 | 30535057 | PAPD1 | 106707 base upstream | p11.23 | AG | 0.7226 | 0.823 | 0.0007905 |
| 12 | rs11062158 | 2196239 | CACNA1C | intron 3 | p13.33 | CT | 0.0307 | 1.679 | 0.000791 |
| 3 | rs4616634 | 63500043 | SYNPR | intron 2 | p14.2 | AG | 0.7979 | 1.247 | 0.0007913 |
| 7 | rs507803 | 125581531 | GRM8 | 284361 base upstream | q31.33 | CT | 0.8777 | 1.311 | 0.0007914 |
| 20 | rs6099656 | 55497673 | HMG1L1 | 184 base downstream | q13.31 | CT | 0.6224 | 0.831 | 0.0007915 |
| 10 | rs17700240 | 110644600 | XPNPEP1 | 969913 base upstream | q25.1 | AG | 0.8184 | 1.261 | 0.0007916 |
| 12 | rs10848640 | 2196430 | CACNA1C | intron 3 | p13.33 | CG | 0.9693 | 0.596 | 0.000792 |
| 10 | rs17778423 | 110644569 | XPNPEP1 | 969944 base upstream | q25.1 | CG | 0.8185 | 1.261 | 0.0007921 |
| 12 | rs10848641 | 2196442 | CACNA1C | intron 3 | p13.33 | CT | 0.0307 | 1.679 | 0.000793 |
| 11 | rs1145180 | 115317381 | CADM1 | 436930 base downstream | q23.2 | AG | 0.6491 | 0.835 | 0.0007936 |
| 6 | rs9277029 | 33106784 | HLA-DOA | 21417 base downstream | p21.32 | CT | 0.709 | 1.227 | 0.0007938 |
| 6 | rs3024466 | 6089856 | F13A1 | EXON 1 | p25.1 | AC | 0.1688 | 1.262 | 0.0007938 |
| 5 | rs17351308 | 104115918 | NUDT12 | 1189529 base downstream | q21.2 | AG | 0.1668 | 1.272 | 0.0007941 |
| 4 | rs11946618 | 136712040 | PABPC4L | 1369687 base downstream | q28.3 | CG | 0.2142 | 1.238 | 0.0007951 |
| 8 | rs2023100 | 109459433 | TTC35 | 65595 base upstream | q23.1 | GT | 0.3534 | 1.2 | 0.0007969 |
| 18 | rs1550567 | 48343516 | DCC | intron 1 | q21.2 | AG | 0.148 | 0.774 | 0.0007971 |
| 2 | rs1900287 | 113514036 | IL1F8 | intron 5 | q13 | AG | 0.6769 | 0.828 | 0.0007973 |
| 7 | rs613484 | 125581817 | GRM8 | 284075 base upstream | q31.33 | AG | 0.8777 | 1.31 | 0.0007974 |
| 5 | rs17156764 | 104004713 | NUDT12 | 1078324 base downstream | q21.2 | AC | 0.1706 | 1.263 | 0.0007975 |
| 2 | rs1797386 | 232122582 | NMUR1 | 19135 base downstream | q37.1 | CT | 0.9204 | 0.726 | 0.0007976 |
| 5 | rs12514247 | 104001831 | NUDT12 | 1075442 base downstream | q21.2 | CT | 0.1706 | 1.263 | 0.0007976 |
| 5 | rs11242529 | 104007471 | NUDT12 | 1081082 base downstream | q21.2 | CT | 0.1706 | 1.263 | 0.0007977 |
| 3 | rs7633928 | 129060018 | MGLL | 35277 base downstream | q21.3 | AG | 0.8448 | 0.775 | 0.0007979 |
| 6 | rs10806484 | 94777061 | EPHA7 | 591068 base downstream | q16.1 | AC | 0.4441 | 1.192 | 0.0007982 |
| 4 | rs13146643 | 136728154 | PABPC4L | 1385801 base downstream | q28.3 | AG | 0.7963 | 0.805 | 0.0007983 |
| 9 | rs10124892 | 7514847 | C9orf123 | 271645 base upstream | p24.1 | CT | 0.5788 | 1.191 | 0.0007984 |
| 6 | rs9277027 | 33106216 | HLA-DOA | 20849 base downstream | p21.32 | AG | 0.7089 | 1.227 | 0.0007989 |
| 21 | rs2833927 | 32930403 | SYNJ1 | intron 2 | q22.11 | CT | 0.9626 | 1.678 | 0.0007989 |
| 12 | rs7305301 | 2212897 | CACNA1C | intron 3 | p13.33 | CG | 0.9671 | 0.587 | 0.0007992 |
| 7 | rs639211 | 125564375 | GRM8 | 301517 base upstream | q31.33 | AC | 0.879 | 1.32 | 0.0007992 |
| 2 | rs2160236 | 40410780 | SLC8A1 | intron 8 | p22.1 | CG | 0.3564 | 1.202 | 0.0008003 |
| 4 | rs13122996 | 136728247 | PABPC4L | 1385894 base downstream | q28.3 | AT | 0.2037 | 1.242 | 0.0008009 |
| 2 | rs10200693 | 29148520 | FLJ34931 | EXON 2 | p23.2 | AG | 0.7441 | 0.807 | 0.000802 |
| 9 | rs4269591 | 7517298 | C9orf123 | 269194 base upstream | p24.1 | CT | 0.4226 | 0.837 | 0.0008024 |
| 5 | rs17057166 | 159180592 | ADRA1B | 95725 base upstream | q33.3 | CT | 0.9288 | 1.422 | 0.0008026 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 6 | rs9375498 | 127637134 | RNF146 | intron 1 | q22.33 | AG | 0.0366 | 1.527 | 0.0008027 |
| 8 | rs6471719 | 59543277 | LOC137886 | 16664 base downstream | q12.1 | CT | 0.2659 | 0.813 | 0.0008037 |
| 12 | rs4077227 | 94632343 | NTN4 | intron 7 | q22 | CT | 0.7679 | 0.812 | 0.0008043 |
| 5 | rs325492 | 104118535 | NUDT12 | 1192146 base downstream | q21.2 | CT | 0.8332 | 0.786 | 0.0008048 |
| 2 | rs12995836 | 51625568 | NRXN1 | 512390 base downstream | p16.3 | CT | 0.5624 | 0.837 | 0.0008052 |
| 8 | rs10089406 | 109516004 | TTC35 | 9024 base upstream | q23.1 | CT | 0.6099 | 0.828 | 0.0008054 |
| 5 | rs161776 | 104119377 | NUDT12 | 1192988 base downstream | q21.2 | CG | 0.1668 | 1.272 | 0.0008062 |
| 3 | rs8177184 | 134947186 | TF | 738 base upstream | q22.1 | AG | 0.8365 | 0.789 | 0.0008063 |
| 4 | rs13101421 | 136728703 | PABPC4L | 1386350 base downstream | q28.3 | CT | 0.7963 | 0.805 | 0.0008068 |
| 5 | rs3915771 | 13536969 | DNAH5 | 206467 base upstream | p15.2 | AG | 0.4421 | 0.836 | 0.0008092 |
| 9 | rs10758876 | 7517476 | C9orf123 | 269016 base upstream | p24.1 | GT | 0.421 | 0.84 | 0.0008111 |
| 2 | rs333217 | 107976696 | SLC5A7 | intron 4 | q12.3 | AG | 0.1847 | 0.776 | 0.0008116 |
| 4 | rs1111986 | 154168497 | KIAA1727 | 48199 base downstream | q31.3 | AG | 0.309 | 1.204 | 0.0008117 |
| 21 | rs743331 | 33329836 | OLIG2 | 6466 base downstream | q22.11 | CT | 0.4545 | 1.194 | 0.0008119 |
| 7 | rs489655 | 125583266 | GRM8 | 282626 base upstream | q31.33 | AG | 0.8776 | 1.31 | 0.0008123 |
| 8 | rs6471720 | 59547229 | CYP7A1 | 18061 base upstream | q12.1 | AG | 0.2658 | 0.813 | 0.0008124 |
| 2 | rs2862772 | 113507953 | IL1F8 | intron 5 | q13 | CG | 0.5573 | 0.837 | 0.0008125 |
| 2 | rs1375055 | 46193882 | PRKCE | intron 11 | p21 | AG | 0.7596 | 1.238 | 0.0008126 |
| 21 | rs9982859 | 40139786 | PCP4 | 21430 base upstream | q22.2 | CT | 0.312 | 1.206 | 0.0008126 |
| 12 | rs17287370 | 94635249 | NTN4 | intron 7 | q22 | AG | 0.7678 | 0.812 | 0.0008128 |
| 6 | rs375912 | 33124706 | HLA-DPA1 | 16065 base upstream | p21.32 | CT | 0.3493 | 0.823 | 0.0008128 |
| 1 | rs2275644 | 66603687 | PDE4B | intron 12 | p31.3 | AG | 0.0699 | 0.695 | 0.0008128 |
| 5 | rs17167077 | 98947056 | CHD1 | 656918 base downstream | q21.1 | CT | 0.0491 | 0.656 | 0.0008131 |
| 1 | rs7538869 | 66603910 | PDE4B | intron 12 | p31.3 | GT | 0.0699 | 0.695 | 0.0008137 |
| 18 | rs1626332 | 21693248 | SS18 | 156968 base upstream | q11.2 | AT | 0.4027 | 0.833 | 0.0008141 |
| 9 | rs10758877 | 7517489 | C9orf123 | 269003 base upstream | p24.1 | CT | 0.579 | 1.191 | 0.0008144 |
| 21 | rs2837218 | 40081847 | LOC150084 | intron 5 | q22.2 | CG | 0.3169 | 1.205 | 0.0008144 |
| 6 | rs6941233 | 127767426 | KIAA0408 | 36002 base upstream | q22.33 | AG | 0.963 | 0.647 | 0.0008145 |
| 4 | rs2035291 | 136730370 | PABPC4L | 1388017 base downstream | q28.3 | CG | 0.2037 | 1.242 | 0.0008151 |
| 9 | rs10758879 | 7517926 | C9orf123 | 268566 base upstream | p24.1 | AG | 0.579 | 1.191 | 0.0008157 |
| 9 | rs10758880 | 7518098 | C9orf123 | 268394 base upstream | p24.1 | AC | 0.579 | 1.191 | 0.0008161 |
| 2 | rs13414755 | 107783958 | SLC5A7 | 185468 base upstream | q12.3 | AC | 0.3479 | 0.816 | 0.0008161 |
| 2 | rs2697236 | 197753891 | ANKRD44 | intron 24 | q33.1 | CG | 0.0346 | 0.599 | 0.0008171 |
| 5 | rs161777 | 104119936 | NUDT12 | 1193547 base downstream | q21.2 | CT | 0.1668 | 1.272 | 0.0008172 |
| 18 | rs8098773 | 21695157 | SS18 | 155059 base upstream | q11.2 | CT | 0.5974 | 1.201 | 0.0008178 |
| 4 | rs7696796 | 183403463 | ODZ3 | 78667 base upstream | q35.1 | AG | 0.243 | 0.817 | 0.0008182 |
| 21 | rs12627540 | 40136828 | PCP4 | 24388 base upstream | q22.2 | AC | 0.3164 | 1.208 | 0.0008184 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 1 | rs2311985 | 66607403 | PDE4B | intron 16 | p31.3 | AG | 0.9301 | 1.437 | 0.0008194 |
| 2 | rs2697235 | 197754509 | ANKRD44 | intron 24 | q33.1 | AG | 0.9654 | 1.671 | 0.0008197 |
| 2 | rs1226959 | 229877443 | PID1 | 33142 base downstream | q36.3 | AC | 0.9299 | 0.717 | 0.00082 |
| 21 | rs2837249 | 40141997 | PCP4 | 19219 base upstream | q22.2 | AG | 0.312 | 1.206 | 0.00082 |
| 9 | rs10815626 | 7518239 | C9orf123 | 268253 base upstream | p24.1 | CT | 0.579 | 1.191 | 0.0008201 |
| 2 | rs2697234 | 197755262 | ANKRD44 | intron 24 | q33.1 | CT | 0.0346 | 0.599 | 0.0008203 |
| 7 | rs2237701 | 107409386 | LAMB1 | intron 27 | q31.1 | AG | 0.4318 | 1.193 | 0.0008206 |
| 7 | rs2237702 | 107409524 | LAMB1 | intron 27 | q31.1 | AG | 0.5682 | 0.838 | 0.0008208 |
| 8 | rs2977527 | 134282867 | WISP1 | intron 1 | q24.22 | AG | 0.292 | 0.824 | 0.0008208 |
| 3 | rs4530474 | 124810365 | MYLK | 3469 base upstream | q21.1 | CT | 0.1765 | 1.25 | 0.0008224 |
| 4 | rs2035292 | 136730572 | PABPC4L | 1388219 base downstream | q28.3 | AG | 0.2037 | 1.241 | 0.0008226 |
| 21 | rs2834072 | 33332334 | OLIG2 | 8964 base downstream | q22.11 | AG | 0.5455 | 0.838 | 0.0008227 |
| 1 | rs11208951 | 66960695 | SGIP1 | intron 19 | p31.3 | CT | 0.6969 | 0.826 | 0.0008235 |
| 4 | rs13129036 | 136728656 | PABPC4L | 1386303 base downstream | q28.3 | CT | 0.2249 | 1.24 | 0.0008253 |
| 2 | rs6542736 | 107782134 | SLC5A7 | 187292 base upstream | q12.3 | AG | 0.3483 | 0.816 | 0.0008261 |
| 17 | rs7224952 | 51880345 | ANKFN1 | intron 9 | q22 | CT | 0.7037 | 0.825 | 0.0008264 |
| 2 | rs12617786 | 159755255 | TANC1 | intron 16 | q24.2 | AG | 0.0141 | 2.133 | 0.0008267 |
| 8 | rs7005262 | 14903851 | SGCZ | intron 7 | p22 | AG | 0.4978 | 1.196 | 0.000827 |
| 22 | rs134406 | 33909346 | HMG2L1 | 74142 base upstream | q12.3 | CT | 0.2738 | 0.823 | 0.0008271 |
| 3 | rs848146 | 124806457 | MYLK | 7377 base upstream | q21.1 | CG | 0.1764 | 1.25 | 0.0008274 |
| 12 | rs12228890 | 2201258 | CACNA1C | intron 3 | p13.33 | AC | 0.0307 | 1.675 | 0.0008276 |
| 7 | rs730497 | 44190246 | GCK | intron 9 | p13 | AG | 0.1785 | 1.263 | 0.0008282 |
| 7 | rs7811868 | 26507861 | SNX10 | 127399 base downstream | p15.2 | AG | 0.3776 | 1.2 | 0.0008289 |
| 10 | rs17769395 | 110505088 | XPNPEP1 | 1109425 base upstream | q25.1 | CT | 0.8132 | 1.266 | 0.0008289 |
| 7 | rs515267 | 125583763 | GRM8 | 282129 base upstream | q31.33 | GT | 0.1224 | 0.764 | 0.000829 |
| 13 | rs2025418 | 44583847 | GTF2F2 | 8824 base upstream | q14.12 | CT | 0.1642 | 1.263 | 0.0008294 |
| 3 | rs2626028 | 124812622 | MYLK | 1212 base upstream | q21.1 | CT | 0.1765 | 1.25 | 0.0008312 |
| 2 | rs1597156 | 46192218 | PRKCE | intron 11 | p21 | CT | 0.24 | 0.808 | 0.0008312 |
| 8 | rs11780184 | 109448088 | TTC35 | 76940 base upstream | q23.1 | CT | 0.3533 | 1.2 | 0.0008332 |
| 7 | rs2908289 | 44190467 | GCK | intron 9 | p13 | AG | 0.1785 | 1.262 | 0.0008333 |
| 6 | rs9490138 | 121574075 | C6orf170 | intron 11 | q22.31 | CT | 0.1665 | 1.257 | 0.0008336 |
| 21 | rs2837225 | 40087332 | LOC150084 | EXON 8 | q22.2 | AC | 0.2958 | 1.219 | 0.0008341 |
| 1 | rs204262 | 166081092 | SAC | intron 12 | q24.2 | AG | 0.2273 | 1.252 | 0.0008344 |
| 10 | rs12146350 | 22883117 | PIP4K2A | intron 4 | p12.2 | CG | 0.398 | 0.837 | 0.0008346 |
| 3 | rs820479 | 124805854 | MYLK | 7980 base upstream | q21.1 | AG | 0.8236 | 0.8 | 0.0008355 |
| 2 | rs6759150 | 55901698 | EFEMP1 | 44907 base upstream | p16.1 | AT | 0.9422 | 0.691 | 0.0008359 |
| 20 | rs2145083 | 5208540 | PROKR2 | 22146 base upstream | p12.3 | AG | 0.4954 | 1.19 | 0.0008363 |

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|----|------------|-----------|---------|-------------------------|--------|----|--------|-------|-----------|
| 1 | rs12038866 | 48006804 | FOXD2 | 327854 base downstream | p33 | CG | 0.5987 | 1.2 | 0.0008363 |
| 20 | rs6038115 | 5209132 | PROKR2 | 21554 base upstream | p12.3 | AG | 0.5045 | 0.84 | 0.0008364 |
| 20 | rs4553880 | 5209206 | PROKR2 | 21480 base upstream | p12.3 | CT | 0.5045 | 0.84 | 0.0008364 |
| 20 | rs6038114 | 5209029 | PROKR2 | 21657 base upstream | p12.3 | AG | 0.5046 | 0.84 | 0.0008364 |
| 11 | rs12294675 | 2799123 | KCNQ1 | intron 15 | p15.5 | AG | 0.164 | 1.275 | 0.0008374 |
| 11 | rs10834744 | 3638426 | ART1 | intron 3 | p15.4 | AG | 0.827 | 0.79 | 0.0008379 |
| 6 | rs811418 | 124526687 | TCBA1 | intron 1 | q22.31 | AC | 0.1232 | 0.766 | 0.000838 |
| 14 | rs10132087 | 31527742 | ARHGAP5 | 88503 base upstream | q12 | CT | 0.2029 | 1.261 | 0.0008384 |
| 6 | rs7762541 | 92124822 | MAP3K7 | 771194 base downstream | q16.1 | CT | 0.4408 | 1.193 | 0.000839 |
| 8 | rs4382455 | 134283373 | WISP1 | intron 1 | q24.22 | AC | 0.292 | 0.824 | 0.0008396 |
| 2 | rs17257436 | 229875214 | PID1 | 30913 base downstream | q36.3 | AG | 0.9292 | 0.72 | 0.0008396 |
| 4 | rs7694930 | 136731046 | PABPC4L | 1388693 base downstream | q28.3 | AC | 0.7962 | 0.806 | 0.0008402 |
| 6 | rs9353824 | 92118422 | MAP3K7 | 764794 base downstream | q16.1 | AG | 0.5592 | 0.838 | 0.0008409 |
| 1 | rs6691740 | 66625390 | PDE4B | 12541 base downstream | p31.3 | AC | 0.0699 | 0.697 | 0.0008413 |
| 1 | rs6703929 | 66624749 | PDE4B | 11900 base downstream | p31.3 | CT | 0.07 | 0.698 | 0.0008414 |
| 1 | rs6701234 | 66624485 | PDE4B | 11636 base downstream | p31.3 | GT | 0.07 | 0.698 | 0.0008415 |
| 8 | rs1597145 | 109444070 | TTC35 | 80958 base upstream | q23.1 | GT | 0.3532 | 1.2 | 0.000842 |
| 13 | rs7984473 | 67662316 | PCDH9 | 959852 base downstream | q21.33 | AG | 0.9771 | 1.91 | 0.0008422 |
| 3 | rs8177181 | 134946488 | TF | 1436 base upstream | q22.1 | AT | 0.1638 | 1.266 | 0.0008431 |
| 2 | rs16825971 | 229875567 | PID1 | 31266 base downstream | q36.3 | CT | 0.9292 | 0.72 | 0.0008433 |
| 3 | rs993668 | 27906342 | EOMES | 167553 base downstream | p24.1 | CG | 0.8915 | 1.384 | 0.0008435 |
| 8 | rs1448160 | 109442301 | TTC35 | 82727 base upstream | q23.1 | CT | 0.6468 | 0.833 | 0.0008438 |
| 20 | rs6085062 | 5207966 | PROKR2 | 22720 base upstream | p12.3 | CG | 0.4953 | 1.19 | 0.0008446 |
| 3 | rs861890 | 124801210 | MYLK | 12624 base upstream | q21.1 | AG | 0.8236 | 0.801 | 0.0008452 |
| 22 | rs134434 | 33921035 | HMG2L1 | 62453 base upstream | q12.3 | AG | 0.7261 | 1.214 | 0.0008454 |
| 4 | rs7654065 | 136731472 | PABPC4L | 1389119 base downstream | q28.3 | AC | 0.2038 | 1.241 | 0.0008456 |
| 4 | rs17148325 | 71084769 | APIN | 12063 base upstream | q13.3 | CT | 0.8444 | 1.303 | 0.0008458 |
| 5 | rs1120480 | 104014181 | NUDT12 | 1087792 base downstream | q21.2 | CT | 0.8297 | 0.793 | 0.0008459 |
| 2 | rs6734993 | 107922950 | SLC5A7 | 46476 base upstream | q12.3 | CT | 0.1902 | 0.794 | 0.0008467 |
| 20 | rs6085061 | 5207931 | PROKR2 | 22755 base upstream | p12.3 | CT | 0.5047 | 0.84 | 0.0008469 |
| 6 | rs7746647 | 154741048 | PIP3-E | 21456 base downstream | q25.2 | AT | 0.945 | 1.475 | 0.0008469 |
| 1 | rs12239708 | 66627158 | PDE4B | 14309 base downstream | p31.3 | AT | 0.0698 | 0.697 | 0.0008471 |
| 14 | rs10132140 | 31529811 | ARHGAP5 | 86434 base upstream | q12 | AG | 0.7972 | 0.793 | 0.0008473 |
| 21 | rs10854398 | 39943622 | B3GALT5 | 7501 base upstream | q22.2 | CT | 0.5182 | 1.198 | 0.0008485 |
| 4 | rs968774 | 34724145 | CENTD1 | 1019871 base upstream | p15.1 | AG | 0.0181 | 2.007 | 0.0008485 |
| 4 | rs11944567 | 136734593 | PABPC4L | 1392240 base downstream | q28.3 | CT | 0.2038 | 1.24 | 0.0008487 |
| 4 | rs11099350 | 136734221 | PABPC4L | 1391868 base downstream | q28.3 | AG | 0.2038 | 1.24 | 0.0008488 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs13142176 | 136736073 | PABPC4L | 1393720 base downstream | q28.3 | CT | 0.2038 | 1.24 | 0.0008491 |
| 4 | rs968773 | 34724210 | CENTD1 | 1019806 base upstream | p15.1 | AC | 0.0181 | 2.007 | 0.0008491 |
| 4 | rs11723306 | 136733600 | PABPC4L | 1391247 base downstream | q28.3 | CT | 0.2038 | 1.24 | 0.0008493 |
| 10 | rs576505 | 30516612 | PAPD1 | 125152 base upstream | p11.23 | CT | 0.2787 | 1.211 | 0.0008494 |
| 10 | rs4749520 | 30336364 | KIAA1462 | 7025 base upstream | p11.23 | AG | 0.4755 | 1.188 | 0.0008495 |
| 4 | rs7692855 | 136735906 | PABPC4L | 1393553 base downstream | q28.3 | CT | 0.7962 | 0.806 | 0.0008496 |
| 2 | rs2198715 | 184920491 | C2orf10 | 250846 base upstream | q32.1 | CT | 0.1912 | 0.799 | 0.0008496 |
| 8 | rs12542624 | 2652265 | CSMD1 | 128016 base upstream | p23.2 | AG | 0.2399 | 1.224 | 0.0008499 |
| 4 | rs11935087 | 136733042 | PABPC4L | 1390689 base downstream | q28.3 | AG | 0.7962 | 0.806 | 0.00085 |
| 4 | rs2016168 | 136732580 | PABPC4L | 1390227 base downstream | q28.3 | CT | 0.2038 | 1.24 | 0.0008502 |
| 4 | rs1038152 | 136732373 | PABPC4L | 1390020 base downstream | q28.3 | AT | 0.7962 | 0.806 | 0.0008505 |
| 1 | rs12406429 | 66628614 | PDE4B | 15765 base downstream | p31.3 | AG | 0.0698 | 0.697 | 0.0008508 |
| 12 | rs10219684 | 9918211 | CLEC2B | 4486 base downstream | p13.31 | CT | 0.3065 | 1.223 | 0.0008512 |
| 12 | rs768860 | 114335802 | THRAP2 | 544963 base upstream | q24.21 | GT | 0.7674 | 1.242 | 0.0008513 |
| 22 | rs4821375 | 33922615 | HMG2L1 | 60873 base upstream | q12.3 | CT | 0.7261 | 1.214 | 0.0008525 |
| 2 | rs12693375 | 184951945 | C2orf10 | 219392 base upstream | q32.1 | CT | 0.8084 | 1.253 | 0.0008527 |
| 2 | rs2579409 | 197769903 | ANKRD44 | intron 25 | q33.1 | GT | 0.0346 | 0.6 | 0.0008536 |
| 22 | rs134386 | 33903856 | HMG2L1 | 79632 base upstream | q12.3 | CT | 0.7262 | 1.214 | 0.0008538 |
| 3 | rs860224 | 124820104 | MYLK | intron 1 | q21.1 | CG | 0.8233 | 0.801 | 0.0008548 |
| 10 | rs11596191 | 110659654 | XPNPEP1 | 954859 base upstream | q25.1 | CT | 0.183 | 0.795 | 0.0008551 |
| 20 | rs6515995 | 5204774 | PROKR2 | 25912 base upstream | p12.3 | GT | 0.5048 | 0.841 | 0.0008556 |
| 5 | rs12522864 | 104015822 | NUDT12 | 1089433 base downstream | q21.2 | AG | 0.8297 | 0.793 | 0.0008558 |
| 4 | rs6816076 | 136737904 | PABPC4L | 1395551 base downstream | q28.3 | AG | 0.7962 | 0.806 | 0.0008558 |
| 10 | rs3793889 | 112017646 | MXI1 | intron 3 | q25.2 | AG | 0.9205 | 1.413 | 0.000856 |
| 12 | rs7964025 | 114336692 | THRAP2 | 544073 base upstream | q24.21 | AG | 0.2326 | 0.806 | 0.0008563 |
| 7 | rs10808041 | 146312527 | CNTNAP2 | intron 3 | q35 | AT | 0.9106 | 0.739 | 0.0008565 |
| 6 | rs2180130 | 92134035 | MAP3K7 | 780407 base downstream | q16.1 | AG | 0.5605 | 0.838 | 0.0008573 |
| 3 | rs7623889 | 11452387 | ATG7 | intron 18 | p25.3 | CT | 0.9543 | 1.587 | 0.0008573 |
| 1 | rs10788998 | 55471611 | USP24 | 18261 base downstream | p32.3 | AG | 0.7478 | 0.817 | 0.0008573 |
| 1 | rs1498354 | 66953077 | SGIP1 | intron 18 | p31.3 | AT | 0.3032 | 1.209 | 0.0008578 |
| 20 | rs6053245 | 5204385 | PROKR2 | 26301 base upstream | p12.3 | CT | 0.5048 | 0.841 | 0.0008579 |
| 3 | rs9841664 | 30348345 | TGFB2 | 274652 base upstream | p24.1 | CT | 0.64 | 1.202 | 0.0008579 |
| 9 | rs16937690 | 19646396 | SLC24A2 | intron 9 | p22.1 | AG | 0.646 | 1.201 | 0.0008583 |
| 5 | rs12189083 | 104017956 | NUDT12 | 1091567 base downstream | q21.2 | CT | 0.8297 | 0.793 | 0.0008586 |
| 10 | rs1418276 | 30337993 | KIAA1462 | 5396 base upstream | p11.23 | CT | 0.4756 | 1.187 | 0.0008592 |
| 13 | rs17064600 | 74984164 | COMMD6 | 13186 base upstream | q22.2 | CT | 0.2977 | 0.809 | 0.0008595 |
| 5 | rs12189097 | 104018213 | NUDT12 | 1091824 base downstream | q21.2 | CT | 0.8297 | 0.793 | 0.0008599 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 21 | rs12233311 | 33331127 | OLIG2 | 7757 base downstream | q22.11 | AG | 0.4487 | 1.193 | 0.0008604 |
| 21 | rs2243683 | 17225142 | C21orf34 | 323729 base downstream | q21.1 | AG | 0.4704 | 1.197 | 0.0008604 |
| 10 | rs1418278 | 30338084 | KIAA1462 | 5305 base upstream | p11.23 | AG | 0.5243 | 0.842 | 0.0008606 |
| 22 | rs5748309 | 17946365 | CLDN5 | 53505 base downstream | q11.21 | CT | 0.274 | 0.808 | 0.0008608 |
| 2 | rs13031086 | 29141985 | FLJ34931 | intron 1 | p23.2 | CT | 0.748 | 0.813 | 0.0008614 |
| 2 | rs12712970 | 46187198 | PRKCE | intron 11 | p21 | AG | 0.7605 | 1.238 | 0.0008615 |
| 5 | rs7445539 | 104020427 | NUDT12 | 1094038 base downstream | q21.2 | AG | 0.1703 | 1.261 | 0.0008623 |
| 10 | rs11592575 | 110748773 | XPNPEP1 | 865740 base upstream | q25.1 | CT | 0.1831 | 0.796 | 0.0008629 |
| 22 | rs134378 | 33899690 | HMG2L1 | 83798 base upstream | q12.3 | GT | 0.7263 | 1.214 | 0.000863 |
| 22 | rs4821376 | 33922689 | HMG2L1 | 60799 base upstream | q12.3 | AG | 0.7261 | 1.214 | 0.0008634 |
| 10 | rs10826749 | 30338528 | KIAA1462 | 4861 base upstream | p11.23 | CT | 0.4757 | 1.187 | 0.0008638 |
| 16 | rs7197967 | 70564733 | DHODH | 35410 base upstream | q22.3 | AG | 0.1321 | 1.318 | 0.000864 |
| 2 | rs13015290 | 184940461 | C2orf10 | 230876 base upstream | q32.1 | AT | 0.1915 | 0.798 | 0.0008643 |
| 2 | rs17429535 | 184931648 | C2orf10 | 239689 base upstream | q32.1 | CT | 0.1913 | 0.799 | 0.0008644 |
| 8 | rs7812466 | 109467321 | TTC35 | 57707 base upstream | q23.1 | AG | 0.3534 | 1.198 | 0.0008645 |
| 10 | rs17697405 | 110517348 | XPNPEP1 | 1097165 base upstream | q25.1 | CT | 0.1828 | 0.792 | 0.0008646 |
| 8 | rs4363174 | 109471830 | TTC35 | 53198 base upstream | q23.1 | CT | 0.3534 | 1.198 | 0.0008647 |
| 2 | rs13394642 | 55903459 | EFEMP1 | 43146 base upstream | p16.1 | AG | 0.9422 | 0.691 | 0.0008651 |
| 8 | rs10108399 | 109466087 | TTC35 | 58941 base upstream | q23.1 | CT | 0.6466 | 0.834 | 0.0008655 |
| 10 | rs11194333 | 110747661 | XPNPEP1 | 866852 base upstream | q25.1 | CT | 0.1836 | 0.797 | 0.0008661 |
| 6 | rs6910080 | 92125869 | MAP3K7 | 772241 base downstream | q16.1 | AG | 0.5591 | 0.838 | 0.0008664 |
| 22 | rs6000718 | 36129946 | LRRC62 | intron 1 | q13.1 | AG | 0.7535 | 0.804 | 0.0008667 |
| 2 | rs10203961 | 184932641 | C2orf10 | 238696 base upstream | q32.1 | CT | 0.8087 | 1.252 | 0.0008672 |
| 4 | rs2089184 | 136739233 | PABPC4L | 1396880 base downstream | q28.3 | CG | 0.7962 | 0.807 | 0.0008675 |
| 3 | rs16840812 | 134945497 | TF | 2427 base upstream | q22.1 | CT | 0.1641 | 1.265 | 0.0008676 |
| 21 | rs225424 | 42619764 | TFF3 | 10989 base downstream | q22.3 | AG | 0.5045 | 1.212 | 0.0008676 |
| 3 | rs820458 | 124821147 | MYLK | intron 2 | q21.1 | CT | 0.1767 | 1.249 | 0.0008683 |
| 6 | rs9379723 | 25253691 | LRRC16 | 133935 base upstream | p22.2 | CT | 0.7977 | 1.265 | 0.0008687 |
| 4 | rs11737477 | 136740519 | PABPC4L | 1398166 base downstream | q28.3 | GT | 0.7962 | 0.807 | 0.000869 |
| 6 | rs9388306 | 124511753 | TCBA1 | intron 1 | q22.31 | CG | 0.8774 | 1.317 | 0.0008692 |
| 22 | rs134443 | 33925528 | HMG2L1 | 57960 base upstream | q12.3 | CT | 0.2739 | 0.824 | 0.0008702 |
| 6 | rs2146252 | 124512460 | TCBA1 | intron 1 | q22.31 | CT | 0.8774 | 1.317 | 0.0008705 |
| 22 | rs134445 | 33926150 | HMG2L1 | 57338 base upstream | q12.3 | CT | 0.2739 | 0.824 | 0.0008705 |
| 9 | rs12339463 | 81273412 | CHCHD9 | 76642 base downstream | q21.31 | AG | 0.0283 | 1.71 | 0.0008707 |
| 2 | rs2579408 | 197777124 | ANKRD44 | 6117 base downstream | q33.1 | AG | 0.9654 | 1.666 | 0.0008708 |
| 21 | rs741866 | 40129825 | PCP4 | 31391 base upstream | q22.2 | CT | 0.6843 | 0.83 | 0.0008708 |
| 8 | rs12544826 | 36281532 | KCNU1 | 479467 base upstream | p12 | AG | 0.8234 | 0.793 | 0.0008712 |

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|----|------------|-----------|---------|-------------------------|--------|----|--------|-------|-----------|
| 8 | rs4735062 | 109492076 | TTC35 | 32952 base upstream | q23.1 | GT | 0.6479 | 0.835 | 0.0008714 |
| 12 | rs11067584 | 114337140 | THRAP2 | 543625 base upstream | q24.21 | CT | 0.7671 | 1.237 | 0.0008716 |
| 3 | rs9813563 | 32247502 | CMTM8 | 7672 base upstream | p22.3 | CG | 0.161 | 1.256 | 0.0008725 |
| 1 | rs10889649 | 66950593 | SGIP1 | intron 18 | p31.3 | AG | 0.3033 | 1.209 | 0.0008726 |
| 22 | rs134442 | 33925331 | HMG2L1 | 58157 base upstream | q12.3 | CT | 0.7261 | 1.213 | 0.0008728 |
| 5 | rs17350038 | 104055382 | NUDT12 | 1128993 base downstream | q21.2 | CG | 0.1694 | 1.261 | 0.0008738 |
| 2 | rs2712900 | 197778099 | ANKRD44 | 7092 base downstream | q33.1 | CT | 0.0347 | 0.6 | 0.0008739 |
| 8 | rs4735063 | 109492672 | TTC35 | 32356 base upstream | q23.1 | AT | 0.6479 | 0.835 | 0.000874 |
| 9 | rs10867388 | 81271470 | CHCHD9 | 74700 base downstream | q21.31 | AG | 0.9717 | 0.585 | 0.000874 |
| 7 | rs518066 | 125584083 | GRM8 | 281809 base upstream | q31.33 | CT | 0.8775 | 1.308 | 0.000874 |
| 20 | rs996389 | 5203899 | PROKR2 | 26787 base upstream | p12.3 | GT | 0.495 | 1.189 | 0.0008752 |
| 6 | rs2146253 | 124512495 | TCBA1 | intron 1 | q22.31 | AG | 0.8774 | 1.316 | 0.0008759 |
| 2 | rs10200357 | 184938744 | C2orf10 | 232593 base upstream | q32.1 | AT | 0.8086 | 1.252 | 0.0008763 |
| 1 | rs1281173 | 110896325 | KCNA10 | 33005 base downstream | p13.3 | CT | 0.9107 | 0.721 | 0.0008765 |
| 21 | rs1004663 | 40131660 | PCP4 | 29556 base upstream | q22.2 | CG | 0.3158 | 1.204 | 0.0008777 |
| 3 | rs2972479 | 117048717 | LSAMP | intron 3 | q13.31 | CT | 0.0702 | 1.407 | 0.0008795 |
| 8 | rs6998163 | 109493977 | TTC35 | 31051 base upstream | q23.1 | CT | 0.3521 | 1.198 | 0.0008797 |
| 8 | rs13249775 | 109494368 | TTC35 | 30660 base upstream | q23.1 | CT | 0.6479 | 0.835 | 0.0008811 |
| 5 | rs1908159 | 2506377 | IRX2 | 293502 base upstream | p15.33 | AG | 0.6068 | 1.193 | 0.0008813 |
| 3 | rs9855198 | 178807690 | TBL1XR1 | 409948 base downstream | q26.32 | AG | 0.2753 | 1.214 | 0.0008818 |
| 6 | rs2008699 | 124512907 | TCBA1 | intron 1 | q22.31 | CT | 0.8775 | 1.315 | 0.0008819 |
| 13 | rs9510082 | 21757174 | FGF9 | 582990 base downstream | q12.11 | AG | 0.3832 | 1.204 | 0.0008826 |
| 8 | rs1955032 | 109495470 | TTC35 | 29558 base upstream | q23.1 | GT | 0.6479 | 0.835 | 0.0008831 |
| 20 | rs6038111 | 5203159 | PROKR2 | 27527 base upstream | p12.3 | AC | 0.505 | 0.841 | 0.0008832 |
| 1 | rs4951409 | 202827613 | LRRN5 | 25314 base upstream | q32.1 | AT | 0.6717 | 0.83 | 0.0008837 |
| 1 | rs3867319 | 98737348 | SNX7 | 162452 base upstream | p21.3 | AG | 0.0711 | 0.703 | 0.0008839 |
| 5 | rs17415237 | 104037774 | NUDT12 | 1111385 base downstream | q21.2 | AC | 0.1697 | 1.261 | 0.000884 |
| 1 | rs9426772 | 21832177 | RAP1GA1 | intron 23 | p36.12 | CT | 0.5377 | 0.831 | 0.0008842 |
| 8 | rs10098022 | 109497697 | TTC35 | 27331 base upstream | q23.1 | AG | 0.3521 | 1.198 | 0.0008845 |
| 8 | rs4543566 | 6812946 | DEFA1 | 9634 base upstream | p23.1 | CG | 0.8862 | 1.322 | 0.0008847 |
| 5 | rs12516369 | 104047674 | NUDT12 | 1121285 base downstream | q21.2 | AG | 0.1696 | 1.26 | 0.0008866 |
| 13 | rs9583770 | 89489076 | GPC5 | 1359811 base upstream | q31.3 | AG | 0.1983 | 0.8 | 0.0008867 |
| 8 | rs13281088 | 109476961 | TTC35 | 48067 base upstream | q23.1 | CT | 0.3534 | 1.198 | 0.0008869 |
| 12 | rs12319878 | 130855942 | SFRS8 | 5707 base downstream | q24.33 | CT | 0.3967 | 0.838 | 0.0008889 |
| 5 | rs6892501 | 104028035 | NUDT12 | 1101646 base downstream | q21.2 | AC | 0.1702 | 1.26 | 0.0008895 |
| 20 | rs2234397 | 5221382 | PROKR2 | 9304 base upstream | p12.3 | AG | 0.5078 | 0.839 | 0.0008895 |
| 10 | rs17769443 | 110506183 | XPNPEP1 | 1108330 base upstream | q25.1 | AG | 0.8231 | 1.266 | 0.0008905 |

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|----|------------|-----------|---------------|-------------------------|--------|----|--------|-------|-----------|
| 8 | rs2156740 | 109477725 | TTC35 | 47303 base upstream | q23.1 | CG | 0.3534 | 1.198 | 0.000891 |
| 5 | rs11134123 | 5754291 | KIAA0947 | 210953 base downstream | p15.32 | CG | 0.0309 | 0.561 | 0.000891 |
| 7 | rs1689330 | 53069533 | DKFZp564N2472 | 1309 base upstream | p12.1 | CG | 0.2067 | 1.239 | 0.0008916 |
| 8 | rs10103966 | 3339206 | CSMD1 | intron 60 | p23.2 | CG | 0.7855 | 1.244 | 0.0008919 |
| 6 | rs17749408 | 73415061 | KCNQ5 | intron 1 | q13 | AG | 0.1825 | 1.249 | 0.0008927 |
| 10 | rs716595 | 111996476 | MXI1 | intron 3 | q25.2 | AG | 0.0798 | 0.71 | 0.0008928 |
| 7 | rs1799884 | 44195593 | YKT6 | 11509 base upstream | p13 | CT | 0.8221 | 0.798 | 0.0008931 |
| 6 | rs2008708 | 124513036 | TCBA1 | intron 1 | q22.31 | AG | 0.1225 | 0.761 | 0.0008938 |
| 6 | rs12664094 | 68836202 | BAI3 | 566150 base upstream | q12 | CT | 0.984 | 2.174 | 0.0008938 |
| 8 | rs1499682 | 3342219 | CSMD1 | intron 60 | p23.2 | AT | 0.2144 | 0.804 | 0.0008942 |
| 10 | rs12250102 | 110625352 | XPNPEP1 | 989161 base upstream | q25.1 | CT | 0.82 | 1.26 | 0.0008942 |
| 20 | rs6038110 | 5202928 | PROKR2 | 27758 base upstream | p12.3 | AG | 0.5051 | 0.841 | 0.0008944 |
| 10 | rs17769499 | 110506325 | XPNPEP1 | 1108188 base upstream | q25.1 | AC | 0.177 | 0.79 | 0.0008953 |
| 7 | rs4947777 | 53069854 | DKFZp564N2472 | 988 base upstream | p12.1 | GT | 0.2067 | 1.239 | 0.0008958 |
| 3 | rs13315037 | 58047511 | FLNB | intron 4 | p14.3 | GT | 0.0747 | 0.702 | 0.0008961 |
| 21 | rs2833934 | 32946315 | SYNJ1 | intron 10 | q22.11 | CT | 0.9626 | 1.664 | 0.0008964 |
| 2 | rs1583938 | 107777551 | SLC5A7 | 191875 base upstream | q12.3 | AC | 0.6461 | 1.216 | 0.0008965 |
| 8 | rs1893887 | 109479131 | TTC35 | 45897 base upstream | q23.1 | CG | 0.3534 | 1.198 | 0.0008977 |
| 4 | rs1842259 | 136723916 | PABPC4L | 1381563 base downstream | q28.3 | AG | 0.7951 | 0.807 | 0.0008982 |
| 22 | rs134370 | 33897413 | RAXLX | 84035 base downstream | q12.3 | CG | 0.7263 | 1.214 | 0.0008988 |
| 16 | rs8062885 | 6609627 | A2BP1 | intron 2 | p13.2 | CG | 0.4877 | 1.193 | 0.0008997 |
| 1 | rs2045624 | 202851008 | LRRN5 | 1919 base upstream | q32.1 | CG | 0.6897 | 0.829 | 0.0009003 |
| 21 | rs9980807 | 40127381 | LOC150084 | 31488 base downstream | q22.2 | CT | 0.6842 | 0.831 | 0.0009004 |
| 8 | rs1893886 | 109479249 | TTC35 | 45779 base upstream | q23.1 | CT | 0.6466 | 0.835 | 0.0009006 |
| 6 | rs6569377 | 124513424 | TCBA1 | intron 1 | q22.31 | CT | 0.1224 | 0.761 | 0.0009016 |
| 2 | rs13036001 | 184952504 | C2orf10 | 218833 base upstream | q32.1 | CT | 0.8057 | 1.262 | 0.0009021 |
| 10 | rs12412423 | 111992160 | MXI1 | intron 2 | q25.2 | CG | 0.9201 | 1.409 | 0.0009022 |
| 20 | rs6038109 | 5202768 | PROKR2 | 27918 base upstream | p12.3 | CT | 0.5052 | 0.841 | 0.0009027 |
| 9 | rs11138240 | 81266134 | CHCHD9 | 69364 base downstream | q21.31 | CT | 0.9716 | 0.586 | 0.0009035 |
| 7 | rs520807 | 125584379 | GRM8 | 281513 base upstream | q31.33 | CT | 0.8774 | 1.306 | 0.0009049 |
| 4 | rs877619 | 9846004 | WDR1 | 118333 base downstream | p16.1 | AG | 0.9897 | 0.45 | 0.0009054 |
| 22 | rs134318 | 33890448 | RAXLX | 77070 base downstream | q12.3 | CT | 0.7263 | 1.214 | 0.0009055 |
| 1 | rs1547644 | 66948145 | SGIP1 | intron 18 | p31.3 | AG | 0.6968 | 0.828 | 0.0009056 |
| 8 | rs2156739 | 109479507 | TTC35 | 45521 base upstream | q23.1 | AC | 0.3534 | 1.197 | 0.0009063 |
| 2 | rs7569095 | 107772978 | SLC5A7 | 196448 base upstream | q12.3 | CG | 0.6448 | 1.214 | 0.0009084 |
| 9 | rs11138238 | 81261735 | CHCHD9 | 64965 base downstream | q21.31 | CT | 0.9716 | 0.587 | 0.0009092 |
| 3 | rs3772968 | 117050666 | LSAMP | intron 3 | q13.31 | AG | 0.0702 | 1.406 | 0.0009094 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 7 | rs2701039 | 107410778 | LAMB1 | intron 27 | q31.1 | AG | 0.4311 | 1.192 | 0.0009102 |
| 12 | rs2334868 | 2805760 | NRIP2 | EXON 1 | p13.33 | AG | 0.9576 | 0.651 | 0.0009107 |
| 3 | rs4613421 | 71412562 | FOXP1 | intron 16 | p14.1 | CG | 0.688 | 0.83 | 0.0009109 |
| 6 | rs6932946 | 124513519 | TCBA1 | intron 1 | q22.31 | GT | 0.8776 | 1.313 | 0.0009123 |
| 12 | rs994302 | 65462660 | GRIP1 | 103640 base downstream | q14.3 | CG | 0.5534 | 1.193 | 0.0009129 |
| 16 | rs500285 | 26654324 | TNT | 331204 base upstream | p12.1 | CG | 0.9436 | 0.675 | 0.0009132 |
| 1 | rs11206524 | 55460604 | USP24 | 7254 base downstream | p32.3 | CT | 0.2534 | 1.224 | 0.0009135 |
| 10 | rs10884688 | 110624642 | XPNPEP1 | 989871 base upstream | q25.1 | AG | 0.82 | 1.259 | 0.0009147 |
| 18 | rs11081233 | 6396037 | L3MBTL4 | intron 19 | p11.31 | AG | 0.3078 | 0.821 | 0.0009155 |
| 7 | rs6975024 | 44198411 | YKT6 | 8691 base upstream | p13 | CT | 0.178 | 1.253 | 0.0009157 |
| 4 | rs10520281 | 175716769 | HPGD | 36583 base downstream | q34.1 | AG | 0.912 | 1.403 | 0.000916 |
| 1 | rs4926672 | 55462173 | USP24 | 8823 base downstream | p32.3 | AG | 0.2534 | 1.224 | 0.0009163 |
| 8 | rs1955025 | 109481042 | TTC35 | 43986 base upstream | q23.1 | AC | 0.3534 | 1.197 | 0.0009174 |
| 2 | rs2113389 | 38221238 | CYP1B1 | 64442 base downstream | p22.2 | CT | 0.862 | 0.783 | 0.0009182 |
| 10 | rs17127166 | 111979315 | MXI1 | intron 2 | q25.2 | AG | 0.0801 | 0.71 | 0.0009182 |
| 10 | rs12258374 | 110629257 | XPNPEP1 | 985256 base upstream | q25.1 | CT | 0.7486 | 1.224 | 0.0009187 |
| 11 | rs2403354 | 18898424 | MRGPRX1 | 13511 base upstream | p15.1 | CT | 0.1065 | 1.337 | 0.000919 |
| 14 | rs10483520 | 39253036 | FBXO33 | 281665 base downstream | q21.1 | AG | 0.1004 | 1.329 | 0.000919 |
| 8 | rs2023107 | 109483397 | TTC35 | 41631 base upstream | q23.1 | AC | 0.3534 | 1.197 | 0.0009198 |
| 7 | rs473762 | 125586751 | GRM8 | 279141 base upstream | q31.33 | AT | 0.8774 | 1.306 | 0.0009198 |
| 10 | rs10884687 | 110618205 | XPNPEP1 | 996308 base upstream | q25.1 | AT | 0.82 | 1.259 | 0.0009208 |
| 8 | rs2977530 | 134284294 | WISP1 | intron 1 | q24.22 | AG | 0.292 | 0.825 | 0.0009221 |
| 6 | rs17749420 | 73415342 | KCNQ5 | intron 1 | q13 | CG | 0.1824 | 1.248 | 0.0009223 |
| 22 | rs4618151 | 33926311 | HMG2L1 | 57177 base upstream | q12.3 | AC | 0.2739 | 0.825 | 0.0009233 |
| 10 | rs960731 | 85956138 | PCDH21 | intron 10 | q23.1 | GT | 0.7553 | 1.226 | 0.0009236 |
| 4 | rs7671048 | 175716127 | HPGD | 35941 base downstream | q34.1 | CT | 0.9119 | 1.4 | 0.000924 |
| 20 | rs6038108 | 5201641 | PROKR2 | 29045 base upstream | p12.3 | CT | 0.5053 | 0.841 | 0.0009241 |
| 10 | rs11194286 | 110617893 | XPNPEP1 | 996620 base upstream | q25.1 | CT | 0.82 | 1.259 | 0.0009244 |
| 12 | rs2160432 | 87296520 | KITLG | 114179 base upstream | q21.32 | CT | 0.9224 | 0.728 | 0.0009254 |
| 12 | rs2407649 | 87295390 | KITLG | 115309 base upstream | q21.32 | CT | 0.9222 | 0.728 | 0.0009255 |
| 7 | rs593446 | 125587627 | GRM8 | 278265 base upstream | q31.33 | CT | 0.8774 | 1.306 | 0.0009255 |
| 2 | rs12467641 | 45955645 | PRKCE | intron 2 | p21 | AT | 0.7733 | 1.244 | 0.0009258 |
| 12 | rs11062164 | 2203913 | CACNA1C | intron 3 | p13.33 | AC | 0.0308 | 1.666 | 0.0009261 |
| 2 | rs6742654 | 160112937 | BAZ2B | intron 35 | q24.2 | CT | 0.8682 | 1.325 | 0.0009261 |
| 3 | rs2972493 | 116979664 | LSAMP | 32175 base upstream | q13.31 | AC | 0.8748 | 0.768 | 0.0009261 |
| 7 | rs4607517 | 44202193 | YKT6 | 4909 base upstream | p13 | AG | 0.178 | 1.253 | 0.0009268 |
| 12 | rs10858718 | 87293574 | KITLG | 117125 base upstream | q21.32 | CG | 0.0779 | 1.372 | 0.0009269 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 14 | rs7155495 | 32679185 | NPAS3 | intron 1 | q13.1 | CT | 0.6687 | 0.835 | 0.0009274 |
| 10 | rs945824 | 110531064 | XPNPEP1 | 1083449 base upstream | q25.1 | CT | 0.8172 | 1.261 | 0.0009281 |
| 2 | rs13012389 | 29141970 | FLJ34931 | intron 1 | p23.2 | CT | 0.2518 | 1.23 | 0.0009288 |
| 7 | rs2971668 | 44209963 | YKT6 | intron 1 | p13 | CG | 0.178 | 1.253 | 0.0009288 |
| 8 | rs3862101 | 17651768 | MTUS1 | intron 13 | p22 | CT | 0.8506 | 1.282 | 0.0009293 |
| 22 | rs867198 | 37038552 | CSNK1E | intron 9 | q13.1 | CT | 0.9455 | 0.683 | 0.0009293 |
| 1 | rs6704254 | 119091964 | TBX15 | 135224 base upstream | p12 | CT | 0.9649 | 1.655 | 0.0009296 |
| 13 | rs9318155 | 72776677 | KLF5 | 227001 base downstream | q22.1 | AC | 0.5935 | 1.2 | 0.0009298 |
| 9 | rs2991695 | 71238297 | APBA1 | intron 2 | q21.11 | AG | 0.1895 | 0.798 | 0.0009329 |
| 14 | rs4982055 | 32677389 | NPAS3 | intron 1 | q13.1 | GT | 0.6681 | 0.832 | 0.000933 |
| 1 | rs2147780 | 119091517 | TBX15 | 135671 base upstream | p12 | AG | 0.9649 | 1.655 | 0.000933 |
| 8 | rs2023104 | 109484593 | TTC35 | 40435 base upstream | q23.1 | AG | 0.3534 | 1.197 | 0.0009341 |
| 15 | rs10852029 | 36730429 | FLJ35695 | 45661 base upstream | q14 | AG | 0.5233 | 1.2 | 0.0009343 |
| 10 | rs17769672 | 110511738 | XPNPEP1 | 1102775 base upstream | q25.1 | CG | 0.8229 | 1.264 | 0.0009344 |
| 9 | rs1340123 | 81242882 | CHCHD9 | 46112 base downstream | q21.31 | CT | 0.0285 | 1.702 | 0.0009351 |
| 10 | rs11196070 | 114461555 | VTI1A | intron 7 | q25.2 | CG | 0.928 | 0.721 | 0.0009356 |
| 4 | rs11723554 | 15282435 | FBXL5 | 16324 base downstream | p15.33 | CG | 0.0999 | 0.741 | 0.000936 |
| 10 | rs12220246 | 30438125 | KIAA1462 | 61319 base downstream | p11.23 | CT | 0.3107 | 1.202 | 0.0009374 |
| 5 | rs17652448 | 149554727 | SLC6A7 | intron 2 | q33.1 | CT | 0.9762 | 0.584 | 0.0009377 |
| 7 | rs2021886 | 107414230 | LAMB1 | intron 29 | q31.1 | AG | 0.4232 | 1.196 | 0.0009377 |
| 4 | rs10516289 | 15281298 | FBXL5 | 15187 base downstream | p15.33 | CT | 0.0999 | 0.741 | 0.0009384 |
| 12 | rs11062165 | 2204109 | CACNA1C | intron 3 | p13.33 | CT | 0.0308 | 1.665 | 0.0009384 |
| 10 | rs12249791 | 110615683 | XPNPEP1 | 998830 base upstream | q25.1 | CT | 0.18 | 0.794 | 0.0009387 |
| 4 | rs4696159 | 154165619 | KIAA1727 | 45321 base downstream | q31.3 | CT | 0.6898 | 0.828 | 0.00094 |
| 8 | rs12375378 | 12897996 | C8orf79 | intron 2 | p22 | AC | 0.9384 | 1.461 | 0.0009402 |
| 2 | rs7570249 | 128371789 | MGC4268 | 12885 base downstream | q14.3 | GT | 0.3251 | 1.2 | 0.0009408 |
| 6 | rs802249 | 124515810 | TCBA1 | intron 1 | q22.31 | CG | 0.8778 | 1.31 | 0.0009409 |
| 2 | rs10495767 | 29140696 | FLJ34931 | EXON 1 | p23.2 | AG | 0.2263 | 1.236 | 0.0009409 |
| 14 | rs8011345 | 32677988 | NPAS3 | intron 1 | q13.1 | AG | 0.6683 | 0.833 | 0.0009412 |
| 8 | rs6469185 | 109508139 | TTC35 | 16889 base upstream | q23.1 | AT | 0.362 | 1.197 | 0.0009416 |
| 1 | rs2887429 | 202831635 | LRRN5 | 21292 base upstream | q32.1 | GT | 0.328 | 1.203 | 0.0009424 |
| 9 | rs12352718 | 81239935 | CHCHD9 | 43165 base downstream | q21.31 | CT | 0.9715 | 0.588 | 0.0009425 |
| 5 | rs2240782 | 149543189 | CDX1 | intron 2 | q33.1 | AC | 0.0235 | 1.727 | 0.0009426 |
| 12 | rs10777110 | 87293154 | KITLG | 117545 base upstream | q21.32 | AG | 0.0779 | 1.371 | 0.0009441 |
| 10 | rs6584895 | 110512515 | XPNPEP1 | 1101998 base upstream | q25.1 | CT | 0.8229 | 1.264 | 0.0009442 |
| 10 | rs11599840 | 110614661 | XPNPEP1 | 999852 base upstream | q25.1 | AG | 0.18 | 0.794 | 0.0009444 |
| 21 | rs1984023 | 40114073 | LOC150084 | 18180 base downstream | q22.2 | AG | 0.3158 | 1.203 | 0.0009448 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 3 | rs820448 | 124830480 | MYLK | intron 4 | q21.1 | CG | 0.8229 | 0.802 | 0.0009454 |
| 8 | rs13275153 | 109488103 | TTC35 | 36925 base upstream | q23.1 | CT | 0.3534 | 1.197 | 0.0009459 |
| 3 | rs17623772 | 30361864 | TGFBR2 | 261133 base upstream | p24.1 | CT | 0.6414 | 1.201 | 0.0009468 |
| 8 | rs4734174 | 109423278 | EIF3S6 | 93143 base downstream | q23.1 | AG | 0.3543 | 1.197 | 0.0009471 |
| 2 | rs2100071 | 113541857 | IL1F10 | 160 base upstream | q13 | AC | 0.6861 | 0.829 | 0.000948 |
| 12 | rs7959834 | 89968187 | KERA | 214 base upstream | q21.33 | CT | 0.0603 | 0.692 | 0.0009495 |
| 7 | rs2952763 | 52130392 | COBL | 778402 base downstream | p12.1 | CT | 0.5363 | 0.842 | 0.0009497 |
| 12 | rs10845199 | 10711585 | STYK1 | intron 10 | p13.2 | CT | 0.3682 | 0.835 | 0.0009501 |
| 2 | rs12714260 | 29141728 | FLJ34931 | intron 1 | p23.2 | CG | 0.2517 | 1.23 | 0.0009504 |
| 7 | rs593517 | 125587676 | GRM8 | 278216 base upstream | q31.33 | AC | 0.8773 | 1.305 | 0.0009508 |
| 12 | rs7973791 | 89968856 | KERA | EXON 1 | q21.33 | AC | 0.9397 | 1.445 | 0.0009509 |
| 3 | rs820450 | 124829191 | MYLK | intron 4 | q21.1 | AT | 0.8229 | 0.802 | 0.000951 |
| 3 | rs12634878 | 30362570 | TGFBR2 | 260427 base upstream | p24.1 | AG | 0.6415 | 1.201 | 0.0009512 |
| 12 | rs7312354 | 2204705 | CACNA1C | intron 3 | p13.33 | CT | 0.0308 | 1.664 | 0.0009513 |
| 22 | rs3918439 | 33934502 | HMG2L1 | 48986 base upstream | q12.3 | CG | 0.2738 | 0.824 | 0.0009515 |
| 2 | rs7599662 | 113541556 | IL1F10 | 461 base upstream | q13 | CT | 0.686 | 0.829 | 0.0009516 |
| 9 | rs11138206 | 81234189 | CHCHD9 | 37419 base downstream | q21.31 | AG | 0.0285 | 1.699 | 0.0009516 |
| 7 | rs917793 | 44212378 | YKT6 | intron 2 | p13 | AT | 0.8219 | 0.799 | 0.0009518 |
| 22 | rs5999766 | 33936111 | HMG2L1 | 47377 base upstream | q12.3 | CT | 0.2738 | 0.824 | 0.000952 |
| 7 | rs639166 | 125564351 | GRM8 | 301541 base upstream | q31.33 | CT | 0.8793 | 1.32 | 0.0009521 |
| 12 | rs10743918 | 10711189 | STYK1 | intron 10 | p13.2 | AC | 0.6319 | 1.197 | 0.0009524 |
| 6 | rs802251 | 124516266 | TCBA1 | intron 1 | q22.31 | GT | 0.1222 | 0.764 | 0.0009526 |
| 6 | rs13208606 | 41404395 | NCR2 | 7110 base upstream | p21.1 | AG | 0.4474 | 0.84 | 0.0009527 |
| 1 | rs6682208 | 202832806 | LRRN5 | 20121 base upstream | q32.1 | CT | 0.672 | 0.831 | 0.0009527 |
| 17 | rs1501259 | 47371272 | CA10 | intron 7 | q21.33 | AT | 0.9737 | 0.558 | 0.0009529 |
| 6 | rs4715472 | 54711017 | C6orf143 | 108510 base upstream | p12.1 | AG | 0.1146 | 0.76 | 0.0009529 |
| 6 | rs802272 | 124523218 | TCBA1 | intron 1 | q22.31 | CT | 0.8771 | 1.303 | 0.0009535 |
| 22 | rs738440 | 33933022 | HMG2L1 | 50466 base upstream | q12.3 | CT | 0.7262 | 1.213 | 0.0009543 |
| 3 | rs820451 | 124828079 | MYLK | intron 3 | q21.1 | CT | 0.1772 | 1.247 | 0.0009547 |
| 6 | rs926924 | 14489412 | CD83 | 244287 base downstream | p23 | CT | 0.4587 | 1.187 | 0.0009548 |
| 2 | rs2433718 | 107969863 | SLC5A7 | intron 1 | q12.3 | AG | 0.1687 | 0.775 | 0.000955 |
| 2 | rs11125041 | 45962449 | PRKCE | intron 2 | p21 | CT | 0.7799 | 1.236 | 0.0009559 |
| 5 | rs17708892 | 149554979 | SLC6A7 | intron 2 | q33.1 | AG | 0.0239 | 1.707 | 0.0009569 |
| 22 | rs7284380 | 33932582 | HMG2L1 | 50906 base upstream | q12.3 | AG | 0.7262 | 1.212 | 0.0009578 |
| 12 | rs7296039 | 2205194 | CACNA1C | intron 3 | p13.33 | CG | 0.0308 | 1.663 | 0.0009579 |
| 2 | rs13431763 | 45964078 | PRKCE | intron 2 | p21 | AG | 0.2199 | 0.809 | 0.000958 |
| 21 | rs9305680 | 40106968 | LOC150084 | 11075 base downstream | q22.2 | CG | 0.684 | 0.832 | 0.000958 |

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|----|------------|-----------|---------------|------------------------|--------|----|--------|-------|-----------|
| 6 | rs802252 | 124516294 | TCBA1 | intron 1 | q22.31 | CT | 0.1222 | 0.764 | 0.0009582 |
| 2 | rs1358578 | 51626897 | NRXN1 | 513719 base downstream | p16.3 | AG | 0.4251 | 1.19 | 0.0009592 |
| 2 | rs12620307 | 29141613 | FLJ34931 | intron 1 | p23.2 | AG | 0.7483 | 0.813 | 0.0009603 |
| 4 | rs9998916 | 175714448 | HPGD | 34262 base downstream | q34.1 | CG | 0.0882 | 0.717 | 0.0009622 |
| 9 | rs17082380 | 81234777 | CHCHD9 | 38007 base downstream | q21.31 | AC | 0.9715 | 0.589 | 0.0009625 |
| 3 | rs552757 | 178791718 | TBL1XR1 | 393976 base downstream | q26.32 | AG | 0.374 | 0.833 | 0.000963 |
| 2 | rs4673461 | 209855352 | MAP2 | 141663 base upstream | q34 | AG | 0.7784 | 0.81 | 0.0009631 |
| 1 | rs11240761 | 202833323 | LRRN5 | 19604 base upstream | q32.1 | AC | 0.6721 | 0.831 | 0.0009633 |
| 22 | rs5999761 | 33929534 | HMG2L1 | 53954 base upstream | q12.3 | CG | 0.7261 | 1.212 | 0.0009635 |
| 7 | rs526981 | 125587892 | GRM8 | 278000 base upstream | q31.33 | CT | 0.8773 | 1.305 | 0.0009641 |
| 14 | rs12147244 | 39252820 | FBXO33 | 281449 base downstream | q21.1 | AG | 0.1005 | 1.327 | 0.0009643 |
| 6 | rs682747 | 117190566 | C6orf189 | intron 2 | q22.2 | AC | 0.5412 | 0.83 | 0.0009645 |
| 2 | rs2515404 | 113537588 | IL1F5 | EXON 5 | q13 | CT | 0.3145 | 1.205 | 0.0009648 |
| 12 | rs2239031 | 2206430 | CACNA1C | intron 3 | p13.33 | GT | 0.9692 | 0.601 | 0.0009658 |
| 5 | rs11743490 | 30094872 | CDH6 | 1134680 base upstream | p13.3 | AG | 0.9107 | 0.735 | 0.0009666 |
| 3 | rs11129059 | 22438352 | ZNF659 | 670532 base downstream | p24.3 | AG | 0.162 | 1.266 | 0.0009675 |
| 12 | rs11067588 | 114340512 | THRAP2 | 540253 base upstream | q24.21 | CG | 0.7659 | 1.235 | 0.0009679 |
| 20 | rs6053263 | 5222381 | PROKR2 | 8305 base upstream | p12.3 | CG | 0.4914 | 1.191 | 0.0009681 |
| 7 | rs4947759 | 52985234 | DKFZp564N247c | 85608 base upstream | p12.1 | AG | 0.8489 | 0.786 | 0.0009682 |
| 6 | rs603540 | 117190939 | C6orf189 | intron 2 | q22.2 | CT | 0.4589 | 1.204 | 0.0009686 |
| 2 | rs6726828 | 67716071 | ETAA16 | 225034 base downstream | p14 | GT | 0.3549 | 1.197 | 0.0009689 |
| 8 | rs13252623 | 12906017 | C8orf79 | intron 2 | p22 | GT | 0.9391 | 1.466 | 0.0009698 |
| 12 | rs2407653 | 87292097 | KITLG | 118602 base upstream | q21.32 | AC | 0.9221 | 0.73 | 0.0009699 |
| 10 | rs4542335 | 97076365 | SORBS1 | intron 3 | q23.33 | CG | 0.3026 | 1.207 | 0.0009704 |
| 22 | rs713969 | 33928993 | HMG2L1 | 54495 base upstream | q12.3 | AC | 0.2739 | 0.826 | 0.0009717 |
| 5 | rs6887917 | 143534973 | KCTD16 | intron 2 | q32 | AG | 0.3554 | 1.199 | 0.0009741 |
| 22 | rs5746794 | 17963106 | CLDN5 | 70246 base downstream | q11.21 | CG | 0.5322 | 0.833 | 0.0009741 |
| 12 | rs12228056 | 89954104 | KERA | 14297 base upstream | q21.33 | CT | 0.9397 | 1.444 | 0.0009743 |
| 13 | rs17215110 | 73018296 | KLF12 | 139854 base upstream | q22.1 | AC | 0.8681 | 0.775 | 0.0009751 |
| 10 | rs11196072 | 114466456 | VTI1A | intron 7 | q25.2 | CT | 0.0721 | 1.385 | 0.0009752 |
| 10 | rs7097972 | 22887793 | PIP4K2A | intron 4 | p12.2 | CT | 0.406 | 0.839 | 0.0009759 |
| 18 | rs9949152 | 40396618 | SETBP1 | 138848 base upstream | q12.3 | CT | 0.1898 | 1.262 | 0.0009763 |
| 7 | rs2953431 | 52155467 | COBL | 803477 base downstream | p12.1 | AG | 0.4338 | 1.188 | 0.0009769 |
| 9 | rs10811336 | 20232344 | MLLT3 | 102623 base upstream | p21.3 | AC | 0.8621 | 1.308 | 0.0009777 |
| 12 | rs12306540 | 114341431 | THRAP2 | 539334 base upstream | q24.21 | AG | 0.7657 | 1.234 | 0.0009784 |
| 1 | rs11240764 | 202835999 | LRRN5 | 16928 base upstream | q32.1 | CT | 0.6721 | 0.832 | 0.0009796 |
| 1 | rs6594019 | 202835233 | LRRN5 | 17694 base upstream | q32.1 | CT | 0.6721 | 0.832 | 0.0009797 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs6594018 | 202834775 | LRRN5 | 18152 base upstream | q32.1 | AG | 0.3279 | 1.202 | 0.0009798 |
| 7 | rs2465796 | 52158227 | COBL | 806237 base downstream | p12.1 | CT | 0.4338 | 1.188 | 0.0009806 |
| 12 | rs10745478 | 87270942 | KITLG | 139757 base upstream | q21.32 | GT | 0.9275 | 0.718 | 0.0009809 |
| 16 | rs7199694 | 6606821 | A2BP1 | intron 2 | p13.2 | AG | 0.5118 | 0.839 | 0.0009816 |
| 6 | rs802270 | 124522342 | TCBA1 | intron 1 | q22.31 | AG | 0.877 | 1.301 | 0.0009818 |
| 12 | rs2111038 | 87296649 | KITLG | 114050 base upstream | q21.32 | CT | 0.076 | 1.382 | 0.0009824 |
| 7 | rs2908282 | 44215353 | YKT6 | intron 5 | p13 | AG | 0.1781 | 1.251 | 0.0009831 |
| 9 | rs10817727 | 117019231 | 1-Dec | intron 1 | q33.1 | AG | 0.8927 | 0.753 | 0.0009833 |
| 6 | rs10872698 | 153444170 | RGS17 | intron 4 | q25.2 | AG | 0.5861 | 0.841 | 0.0009839 |
| 3 | rs4679546 | 59364649 | FHIT | 345428 base upstream | p14.2 | AC | 0.2011 | 1.236 | 0.0009839 |
| 6 | rs802253 | 124516437 | TCBA1 | intron 1 | q22.31 | CG | 0.1221 | 0.765 | 0.0009848 |
| 6 | rs9479502 | 153444391 | RGS17 | intron 4 | q25.2 | CT | 0.4139 | 1.19 | 0.0009854 |
| 6 | rs693602 | 117192477 | C6orf189 | intron 2 | q22.2 | AC | 0.5411 | 0.832 | 0.0009855 |
| 18 | rs9947555 | 6396648 | L3MBTL4 | intron 19 | p11.31 | CT | 0.3159 | 0.822 | 0.000986 |
| 13 | rs9511023 | 23529796 | SPATA13 | 103090 base upstream | q12.12 | AG | 0.2386 | 1.227 | 0.0009865 |
| 15 | rs12915677 | 46652089 | FBN1 | intron 60 | q21.1 | CT | 0.7983 | 0.812 | 0.0009868 |
| 8 | rs11136435 | 1779092 | ARHGEF10 | intron 2 | p23.3 | AG | 0.5032 | 1.189 | 0.000987 |
| 6 | rs802255 | 124517096 | TCBA1 | intron 1 | q22.31 | AG | 0.1221 | 0.765 | 0.0009871 |
| 16 | rs154537 | 22620480 | HS3ST2 | 112880 base upstream | p12.1 | GT | 0.8262 | 1.267 | 0.0009872 |
| 6 | rs9478386 | 153444523 | RGS17 | intron 4 | q25.2 | AG | 0.4139 | 1.19 | 0.0009877 |
| 8 | rs2385523 | 127250276 | FAM84B | 383592 base upstream | q24.13 | AC | 0.7564 | 0.81 | 0.0009878 |
| 2 | rs312052 | 21281690 | APOB | 161240 base downstream | p24.1 | AG | 0.7613 | 0.81 | 0.0009883 |
| 12 | rs10745479 | 87291483 | KITLG | 119216 base upstream | q21.32 | AG | 0.9221 | 0.73 | 0.000989 |
| 3 | rs977305 | 30365684 | TGFB2 | 257313 base upstream | p24.1 | AG | 0.6416 | 1.2 | 0.0009897 |
| 2 | rs6732490 | 67714314 | ETAA16 | 223277 base downstream | p14 | AC | 0.6451 | 0.836 | 0.0009898 |
| 7 | rs3815412 | 115977929 | CAV1 | intron 2 | q31.2 | CT | 0.2498 | 1.21 | 0.0009901 |
| 5 | rs4867706 | 172714540 | STC2 | 25428 base downstream | q35.2 | AG | 0.7144 | 1.232 | 0.0009901 |
| 10 | rs11597369 | 110493441 | XPNPEP1 | 1121072 base upstream | q25.1 | AC | 0.8235 | 1.263 | 0.0009903 |
| 6 | rs10872697 | 153442739 | RGS17 | intron 4 | q25.2 | GT | 0.5862 | 0.841 | 0.0009905 |
| 10 | rs4748813 | 22886741 | PIP4K2A | intron 4 | p12.2 | CT | 0.592 | 1.191 | 0.0009906 |
| 10 | rs11194334 | 110747675 | XPNPEP1 | 866838 base upstream | q25.1 | AC | 0.1621 | 0.778 | 0.0009907 |
| 20 | rs4346455 | 10827336 | JAG1 | 224642 base downstream | p12.2 | CT | 0.4354 | 0.842 | 0.0009908 |
| 12 | rs4842604 | 87297081 | KITLG | 113618 base upstream | q21.32 | CT | 0.0759 | 1.383 | 0.0009925 |
| 15 | rs2940333 | 60544836 | TLN2 | 181965 base upstream | q22.2 | AG | 0.2166 | 0.804 | 0.0009931 |
| 2 | rs6760893 | 67713993 | ETAA16 | 222956 base downstream | p14 | AG | 0.3549 | 1.196 | 0.0009942 |
| 7 | rs1524344 | 146317484 | CNTNAP2 | intron 3 | q35 | CG | 0.0907 | 1.35 | 0.0009955 |
| 1 | rs12409699 | 55456607 | USP24 | 3257 base downstream | p32.3 | AG | 0.763 | 0.813 | 0.0009956 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 10 | rs6583997 | 97117254 | SORBS1 | intron 11 | q23.33 | CT | 0.7163 | 0.826 | 0.0009957 |
| 2 | rs17033996 | 67713787 | ETAA16 | 222750 base downstream | p14 | AG | 0.6451 | 0.836 | 0.0009961 |
| 21 | rs17210470 | 17222789 | C21orf34 | 321376 base downstream | q21.1 | CT | 0.2791 | 1.222 | 0.0009962 |
| 5 | rs12513560 | 104050721 | NUDT12 | 1124332 base downstream | q21.2 | CT | 0.8305 | 0.795 | 0.0009971 |
| 2 | rs6752290 | 209868043 | MAP2 | 128972 base upstream | q34 | CT | 0.2211 | 1.233 | 0.0009972 |
| 6 | rs9479499 | 153441972 | RGS17 | intron 4 | q25.2 | AT | 0.5862 | 0.841 | 0.0009973 |
| 10 | rs7920198 | 110537793 | XPNPEP1 | 1076720 base upstream | q25.1 | AG | 0.8171 | 1.259 | 0.0009975 |
| 4 | rs2877818 | 175712054 | HPGD | 31868 base downstream | q34.1 | CT | 0.9117 | 1.386 | 0.0009977 |
| 10 | rs3006662 | 32469248 | KIF5B | 84027 base downstream | p11.22 | AC | 0.0367 | 1.58 | 0.0009978 |
| 4 | rs10019035 | 175713571 | HPGD | 33385 base downstream | q34.1 | CT | 0.9117 | 1.387 | 0.0009987 |
| 12 | rs10745477 | 87265181 | KITLG | 145518 base upstream | q21.32 | GT | 0.919 | 0.729 | 0.0009989 |
| 10 | rs7084853 | 85956301 | PCDH21 | intron 10 | q23.1 | AG | 0.7556 | 1.224 | 0.0009989 |
| 1 | rs12063029 | 55481326 | USP24 | 27976 base downstream | p32.3 | AG | 0.2422 | 1.23 | 0.0009989 |
| 21 | rs17666683 | 32310264 | HUNK | 12017 base downstream | q22.11 | GT | 0.8553 | 1.284 | 0.0009996 |
| 8 | rs13281642 | 12887282 | C8orf79 | intron 1 | p22 | AT | 0.9382 | 1.456 | 0.001 |
| 10 | rs2998089 | 32470365 | KIF5B | 85144 base downstream | p11.22 | GT | 0.9633 | 0.633 | 0.001 |

| CHR | SNP | POS | GENE | DISTANCE | BAND | A1/A2 | A1 freq | OR | P |
|-----|------------|-----------|--------|-----------------------|-------|-------|---------|-------|----------|
| 3 | rs2576377 | 102130439 | ABI3BP | intron 34 | q12.2 | CT | 0.1657 | 2.307 | 2.55E-08 |
| 3 | rs13072000 | 102108512 | ABI3BP | intron 33 | q12.2 | AG | 0.8508 | 0.439 | 6.56E-08 |
| 3 | rs13079002 | 102112831 | ABI3BP | intron 33 | q12.2 | CT | 0.8509 | 0.438 | 6.47E-08 |
| 3 | rs2713782 | 102111994 | ABI3BP | intron 33 | q12.2 | AG | 0.8508 | 0.439 | 6.56E-08 |
| 3 | rs4060963 | 102107251 | ABI3BP | intron 33 | q12.2 | AG | 0.1495 | 2.272 | 7.06E-08 |
| 3 | rs2713787 | 102107128 | ABI3BP | intron 33 | q12.2 | CG | 0.8505 | 0.44 | 7.05E-08 |
| 3 | rs9832195 | 102105082 | ABI3BP | intron 33 | q12.2 | AC | 0.1495 | 2.271 | 7.05E-08 |
| 3 | rs2576365 | 102104116 | ABI3BP | intron 32 | q12.2 | AC | 0.8505 | 0.44 | 7.05E-08 |
| 3 | rs4928096 | 102102450 | ABI3BP | intron 32 | q12.2 | AG | 0.8505 | 0.44 | 7.05E-08 |
| 3 | rs2713793 | 102101864 | ABI3BP | intron 32 | q12.2 | AG | 0.1495 | 2.27 | 7.77E-08 |
| 3 | rs2245266 | 102101463 | ABI3BP | intron 32 | q12.2 | CT | 0.8506 | 0.441 | 7.88E-08 |
| 3 | rs2576369 | 102100845 | ABI3BP | intron 32 | q12.2 | AG | 0.8506 | 0.441 | 7.93E-08 |
| 3 | rs7431835 | 102125413 | ABI3BP | intron 33 | q12.2 | AT | 0.15 | 2.264 | 8.56E-08 |
| 3 | rs1036467 | 102125494 | ABI3BP | intron 33 | q12.2 | CT | 0.85 | 0.442 | 8.58E-08 |
| 3 | rs17284842 | 102127637 | ABI3BP | intron 33 | q12.2 | CT | 0.15 | 2.262 | 8.74E-08 |
| 3 | rs2245473 | 102098826 | ABI3BP | intron 31 | q12.2 | AG | 0.8506 | 0.441 | 8.21E-08 |
| 3 | rs13060137 | 102130617 | ABI3BP | intron 34 | q12.2 | AG | 0.8501 | 0.442 | 8.96E-08 |
| 3 | rs13077353 | 102132997 | ABI3BP | intron 34 | q12.2 | GT | 0.1499 | 2.26 | 9.04E-08 |
| 3 | rs2245556 | 102098240 | ABI3BP | intron 31 | q12.2 | CT | 0.8506 | 0.441 | 8.31E-08 |
| 3 | rs2576382 | 102150519 | ABI3BP | intron 34 | q12.2 | AT | 0.8502 | 0.445 | 1.10E-07 |
| 3 | rs2595894 | 102160572 | ABI3BP | intron 34 | q12.2 | CG | 0.8506 | 0.452 | 1.54E-07 |
| 3 | rs10511181 | 102172552 | ABI3BP | intron 34 | q12.2 | GT | 0.1493 | 2.211 | 1.53E-07 |
| 3 | rs2576391 | 102159700 | ABI3BP | intron 34 | q12.2 | CG | 0.1494 | 2.211 | 1.56E-07 |
| 3 | rs17398684 | 102178032 | ABI3BP | intron 34 | q12.2 | AG | 0.1493 | 2.21 | 1.53E-07 |
| 3 | rs13088524 | 102170772 | ABI3BP | intron 34 | q12.2 | AC | 0.8507 | 0.452 | 1.53E-07 |
| 3 | rs17398421 | 102155597 | ABI3BP | intron 34 | q12.2 | GT | 0.1494 | 2.211 | 1.56E-07 |
| 3 | rs2595893 | 102160532 | ABI3BP | intron 34 | q12.2 | CT | 0.1494 | 2.211 | 1.55E-07 |
| 3 | rs13074729 | 102248274 | ABI3BP | 53270 base downstream | q12.2 | GT | 0.8522 | 0.457 | 2.64E-07 |
| 3 | rs17399603 | 102218829 | ABI3BP | 23825 base downstream | q12.2 | AG | 0.8513 | 0.461 | 2.71E-07 |
| 3 | rs13099753 | 102252014 | ABI3BP | 57010 base downstream | q12.2 | CG | 0.8138 | 0.483 | 4.19E-07 |
| 3 | rs16843216 | 102279569 | ABI3BP | 84565 base downstream | q12.2 | CT | 0.8646 | 0.462 | 8.54E-07 |
| 3 | rs1375513 | 102253981 | ABI3BP | 58977 base downstream | q12.2 | GT | 0.1886 | 2.031 | 1.13E-06 |
| 3 | rs16843229 | 102284910 | ABI3BP | 89906 base downstream | q12.2 | AG | 0.1333 | 2.211 | 7.44E-07 |
| 3 | rs13081830 | 102273952 | ABI3BP | 78948 base downstream | q12.2 | AG | 0.1353 | 2.159 | 9.15E-07 |
| 3 | rs16843225 | 102283947 | ABI3BP | 88943 base downstream | q12.2 | GT | 0.1355 | 2.17 | 7.81E-07 |
| 3 | rs17219986 | 102282360 | ABI3BP | 87356 base downstream | q12.2 | AG | 0.1354 | 2.168 | 8.03E-07 |

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|----|------------|-----------|-----------|-----------------------|--------|----|--------|-------|-----------|
| 2 | rs13390174 | 5606908 | SOX11 | 143341 base upstream | p25.2 | CT | 0.5146 | 0.639 | 0.0002307 |
| 2 | rs10929647 | 5605816 | SOX11 | 144433 base upstream | p25.2 | AC | 0.515 | 0.638 | 0.0002297 |
| 3 | rs13060849 | 102256173 | ABI3BP | 61169 base downstream | q12.2 | AC | 0.8649 | 0.472 | 1.85E-06 |
| 2 | rs2882274 | 5606432 | SOX11 | 143817 base upstream | p25.2 | CT | 0.5149 | 0.638 | 0.0002304 |
| 3 | rs13065684 | 102256428 | ABI3BP | 61424 base downstream | q12.2 | CT | 0.1351 | 2.12 | 1.81E-06 |
| 3 | rs16843198 | 102265765 | ABI3BP | 70761 base downstream | q12.2 | GT | 0.8649 | 0.47 | 1.66E-06 |
| 3 | rs10511182 | 102255525 | ABI3BP | 60521 base downstream | q12.2 | CG | 0.8649 | 0.473 | 1.93E-06 |
| 3 | rs13096071 | 102284333 | ABI3BP | 89329 base downstream | q12.2 | CT | 0.0826 | 1.899 | 0.0004443 |
| 4 | rs2602098 | 72354319 | SLC4A4 | intron 3 | q13.3 | GT | 0.2061 | 1.96 | 8.80E-07 |
| 21 | rs2245338 | 29929217 | GRIK1 | intron 9 | q21.3 | CT | 0.8804 | 0.552 | 0.0002493 |
| 18 | rs1785416 | 5589104 | EPB41L3 | 55118 base downstream | p11.31 | CT | 0.4914 | 0.658 | 0.0004779 |
| 20 | rs6039433 | 927720 | RSPO4 | intron 4 | p13 | CT | 0.1326 | 1.73 | 0.0004918 |
| 18 | rs1785414 | 5587676 | EPB41L3 | 53690 base downstream | p11.31 | GT | 0.4954 | 0.66 | 0.0005065 |
| 18 | rs2703167 | 37290341 | PIK3C3 | 498855 base upstream | q12.3 | AC | 0.1075 | 0.404 | 0.0008151 |
| 18 | rs1539811 | 5585958 | EPB41L3 | 51972 base downstream | p11.31 | CT | 0.5134 | 1.56 | 0.0004098 |
| 18 | rs1719983 | 5586822 | EPB41L3 | 52836 base downstream | p11.31 | CT | 0.5086 | 1.513 | 0.000484 |
| 18 | rs1785413 | 5586929 | EPB41L3 | 52943 base downstream | p11.31 | AG | 0.5086 | 1.513 | 0.0004847 |
| 20 | rs6100397 | 57284330 | C20orf174 | 16768 base downstream | q13.32 | GT | 0.034 | 2.455 | 0.0006701 |
| 18 | rs1785415 | 5588976 | EPB41L3 | 54990 base downstream | p11.31 | AG | 0.4915 | 0.661 | 0.0004889 |
| 18 | rs1785410 | 5584917 | EPB41L3 | 50931 base downstream | p11.31 | CT | 0.5088 | 1.514 | 0.000481 |
| 5 | rs11958887 | 178229183 | ZNF354B | intron 4 | q35.3 | CT | 0.8809 | 0.574 | 0.0005138 |
| 5 | rs6870926 | 178232797 | ZNF354B | intron 4 | q35.3 | CT | 0.1193 | 1.732 | 0.0005319 |
| 18 | rs1539812 | 5586091 | EPB41L3 | 52105 base downstream | p11.31 | CT | 0.4913 | 0.661 | 0.0004821 |
| 18 | rs1719944 | 5586603 | EPB41L3 | 52617 base downstream | p11.31 | CT | 0.4913 | 0.661 | 0.0004824 |
| 5 | rs6883566 | 178239195 | ZNF354B | intron 4 | q35.3 | AG | 0.8806 | 0.578 | 0.0005466 |
| 18 | rs948271 | 13793024 | MC5R | 22740 base upstream | p11.21 | CT | 0.0999 | 1.8 | 0.0009326 |
| 5 | rs6862829 | 178239194 | ZNF354B | intron 4 | q35.3 | CT | 0.8806 | 0.578 | 0.0005452 |
| 5 | rs11949180 | 178229142 | ZNF354B | intron 4 | q35.3 | AG | 0.881 | 0.573 | 0.000511 |
| 5 | rs11954382 | 178253452 | ZFP2 | 2069 base upstream | q35.3 | CT | 0.8805 | 0.58 | 0.0005934 |
| 5 | rs6894878 | 178244599 | ZNF354B | 578 base downstream | q35.3 | AG | 0.1194 | 1.73 | 0.0005491 |
| 5 | rs11949892 | 178229129 | ZNF354B | intron 4 | q35.3 | CT | 0.1189 | 1.745 | 0.0005082 |
| 15 | rs17303111 | 58797094 | RORA | intron 10 | q22.2 | CT | 0.2566 | 0.566 | 0.0001731 |
| 5 | rs11948175 | 178227589 | ZNF354B | intron 4 | q35.3 | AC | 0.8811 | 0.572 | 0.0005041 |
| 18 | rs9949908 | 13790956 | MC5R | 24808 base upstream | p11.21 | GT | 0.8999 | 0.556 | 0.0009336 |
| 5 | rs6895371 | 178257390 | ZFP2 | intron 1 | q35.3 | CT | 0.8805 | 0.58 | 0.0005966 |
| 18 | rs1785427 | 5569427 | EPB41L3 | 35441 base downstream | p11.31 | AG | 0.5105 | 1.501 | 0.0005511 |
| 8 | rs971555 | 4095738 | CSMD1 | intron 67 | p23.2 | AG | 0.9399 | 0.403 | 1.93E-05 |

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|----|------------|-----------|----------|-----------------------|--------|----|--------|-------|-----------|
| 8 | rs6998882 | 4095458 | CSMD1 | intron 67 | p23.2 | AC | 0.9399 | 0.403 | 1.93E-05 |
| 3 | rs7621961 | 18374868 | SATB1 | intron 2 | p24.3 | AG | 0.0375 | 2.802 | 2.83E-05 |
| 18 | rs1719939 | 5582779 | EPB41L3 | 48793 base downstream | p11.31 | CT | 0.4911 | 0.66 | 0.0004796 |
| 5 | rs11958941 | 178229382 | ZNF354B | intron 4 | q35.3 | CT | 0.8809 | 0.575 | 0.0005155 |
| 15 | rs2414680 | 58798563 | RORA | intron 10 | q22.2 | AG | 0.7428 | 1.817 | 0.0001427 |
| 18 | rs1719933 | 5570911 | EPB41L3 | 36925 base downstream | p11.31 | CT | 0.4896 | 0.666 | 0.0005461 |
| 5 | rs11948690 | 178226479 | ZNF354B | intron 3 | q35.3 | CG | 0.8812 | 0.571 | 0.000499 |
| 11 | rs17141842 | 80656128 | MGC33846 | 1464570 base upstream | q14.1 | CT | 0.9459 | 0.441 | 5.14E-05 |
| 2 | rs6752812 | 172559748 | HAT1 | 2903 base downstream | q31.1 | AC | 0.3181 | 1.513 | 0.0007443 |
| 2 | rs6737169 | 38431205 | ARL6IP2 | intron 12 | p22.1 | CT | 0.2691 | 0.515 | 8.86E-06 |
| 18 | rs1785407 | 5584350 | EPB41L3 | 50364 base downstream | p11.31 | AG | 0.5089 | 1.514 | 0.0004798 |
| 18 | rs1785408 | 5584648 | EPB41L3 | 50662 base downstream | p11.31 | AG | 0.5089 | 1.514 | 0.0004804 |
| 18 | rs1719943 | 5584667 | EPB41L3 | 50681 base downstream | p11.31 | CT | 0.5088 | 1.514 | 0.0004798 |
| 18 | rs1785409 | 5584739 | EPB41L3 | 50753 base downstream | p11.31 | CT | 0.4912 | 0.661 | 0.0004805 |
| 3 | rs11927883 | 18376571 | SATB1 | intron 2 | p24.3 | AG | 0.9627 | 0.357 | 2.71E-05 |
| 3 | rs3922895 | 18377595 | SATB1 | intron 2 | p24.3 | AT | 0.0372 | 2.79 | 2.68E-05 |
| 8 | rs1504769 | 4089356 | CSMD1 | intron 67 | p23.2 | CT | 0.957 | 0.382 | 3.28E-05 |
| 2 | rs10198323 | 38424759 | ARL6IP2 | intron 12 | p22.1 | CT | 0.2694 | 0.515 | 8.87E-06 |
| 2 | rs6716350 | 38439578 | ARL6IP2 | intron 12 | p22.1 | CT | 0.7256 | 1.928 | 8.99E-06 |
| 8 | rs2407941 | 4097308 | CSMD1 | intron 67 | p23.2 | CT | 0.0675 | 2.305 | 2.92E-05 |
| 4 | rs3907208 | 72328528 | SLC4A4 | intron 2 | q13.3 | AT | 0.1334 | 1.936 | 5.75E-06 |
| 4 | rs12506660 | 72327457 | SLC4A4 | intron 2 | q13.3 | CT | 0.1335 | 1.935 | 5.84E-06 |
| 18 | rs1719985 | 5588554 | EPB41L3 | 54568 base downstream | p11.31 | CT | 0.5199 | 1.506 | 0.0005406 |
| 4 | rs2045012 | 72332316 | SLC4A4 | intron 2 | q13.3 | GT | 0.1332 | 1.939 | 5.42E-06 |
| 1 | rs6719 | 152446303 | C1orf43 | EXON 1 | q21.3 | CT | 0.4442 | 0.606 | 3.95E-05 |
| 4 | rs9790757 | 72333961 | SLC4A4 | intron 2 | q13.3 | CT | 0.1166 | 2.013 | 5.02E-06 |
| 8 | rs7838274 | 4089879 | CSMD1 | intron 67 | p23.2 | AT | 0.9573 | 0.381 | 2.98E-05 |
| 11 | rs10891069 | 109525001 | ZC3H12C | intron 2 | q22.3 | CT | 0.757 | 0.605 | 9.13E-05 |
| 1 | rs2340473 | 152491968 | UBAP2L | intron 13 | q21.3 | CT | 0.4444 | 0.608 | 4.03E-05 |
| 1 | rs2879788 | 152470934 | UBAP2L | intron 3 | q21.3 | AT | 0.5562 | 1.644 | 4.19E-05 |
| 1 | rs6427509 | 152486342 | UBAP2L | intron 10 | q21.3 | CT | 0.5557 | 1.644 | 4.03E-05 |
| 1 | rs10158820 | 152484387 | UBAP2L | intron 9 | q21.3 | CT | 0.5558 | 1.644 | 4.05E-05 |
| 2 | rs11687878 | 38443251 | ARL6IP2 | intron 12 | p22.1 | GT | 0.7624 | 1.925 | 2.92E-05 |
| 1 | rs12062977 | 152478140 | UBAP2L | intron 7 | q21.3 | CT | 0.5558 | 1.644 | 4.06E-05 |
| 2 | rs11900967 | 38441642 | ARL6IP2 | intron 12 | p22.1 | AT | 0.2378 | 0.519 | 2.91E-05 |
| 1 | rs9803857 | 152458415 | C1orf43 | intron 4 | q21.3 | AG | 0.4436 | 0.609 | 4.30E-05 |
| 4 | rs7655668 | 72311240 | SLC4A4 | intron 1 | q13.3 | CG | 0.8876 | 0.476 | 4.17E-06 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs11687138 | 38427194 | ARL6IP2 | intron 12 | p22.1 | AG | 0.2395 | 0.519 | 2.87E-05 |
| 11 | rs10891068 | 109524916 | ZC3H12C | intron 2 | q22.3 | AG | 0.2419 | 1.65 | 9.77E-05 |
| 4 | rs1563045 | 72334532 | SLC4A4 | intron 2 | q13.3 | CT | 0.8681 | 0.52 | 8.13E-06 |
| 1 | rs10493528 | 74185240 | LRRC44 | 79049 base upstream | p31.1 | AT | 0.3731 | 1.726 | 3.52E-06 |
| 7 | rs10238136 | 6389871 | RAC1 | intron 1 | p22.1 | AT | 0.9655 | 0.396 | 0.0002442 |
| 1 | rs7544238 | 74191995 | LRRC44 | 72294 base upstream | p31.1 | AC | 0.3737 | 1.732 | 3.18E-06 |
| 1 | rs1417259 | 74191025 | LRRC44 | 73264 base upstream | p31.1 | GT | 0.3737 | 1.732 | 3.17E-06 |
| 4 | rs1319630 | 72334992 | SLC4A4 | intron 2 | q13.3 | CT | 0.1319 | 1.923 | 8.14E-06 |
| 4 | rs7689609 | 72302238 | SLC4A4 | intron 1 | q13.3 | CT | 0.128 | 1.976 | 8.69E-06 |
| 1 | rs12081389 | 74168149 | LRRC44 | 96140 base upstream | p31.1 | AT | 0.3735 | 1.72 | 4.19E-06 |
| 4 | rs2060903 | 72336555 | SLC4A4 | intron 2 | q13.3 | AG | 0.8686 | 0.521 | 9.41E-06 |
| 1 | rs7533599 | 74165700 | LRRC44 | 98589 base upstream | p31.1 | AG | 0.3735 | 1.72 | 4.21E-06 |
| 1 | rs11210377 | 74195971 | LRRC44 | 68318 base upstream | p31.1 | GT | 0.6255 | 0.579 | 3.43E-06 |
| 1 | rs12116914 | 74196206 | LRRC44 | 68083 base upstream | p31.1 | GT | 0.3745 | 1.727 | 3.44E-06 |
| 1 | rs12082647 | 74170715 | LRRC44 | 93574 base upstream | p31.1 | AC | 0.6276 | 0.58 | 3.52E-06 |
| 1 | rs11210368 | 74153059 | LRRC44 | 111230 base upstream | p31.1 | AG | 0.3741 | 1.718 | 4.60E-06 |
| 1 | rs12062996 | 74150383 | LRRC44 | 113906 base upstream | p31.1 | CT | 0.3742 | 1.717 | 4.66E-06 |
| 1 | rs7550937 | 74151900 | LRRC44 | 112389 base upstream | p31.1 | AG | 0.3741 | 1.718 | 4.63E-06 |
| 2 | rs10202823 | 172488378 | HAT1 | intron 1 | q31.1 | CT | 0.3177 | 1.516 | 0.0007101 |
| 1 | rs1768649 | 74152537 | LRRC44 | 111752 base upstream | p31.1 | AG | 0.3741 | 1.718 | 4.62E-06 |
| 18 | rs1785382 | 5580926 | EPB41L3 | 46940 base downstream | p11.31 | CT | 0.5204 | 1.512 | 0.0005066 |
| 2 | rs6727017 | 172475093 | HAT1 | 12110 base upstream | q31.1 | AT | 0.3129 | 1.511 | 0.0009258 |
| 1 | rs7544252 | 74149450 | LRRC44 | 114839 base upstream | p31.1 | CG | 0.3742 | 1.717 | 4.69E-06 |
| 18 | rs1719934 | 5575158 | EPB41L3 | 41172 base downstream | p11.31 | AG | 0.5376 | 1.529 | 0.0007239 |
| 18 | rs1785378 | 5577094 | EPB41L3 | 43108 base downstream | p11.31 | AG | 0.4626 | 0.654 | 0.0007177 |
| 18 | rs1785418 | 5591403 | EPB41L3 | 57417 base downstream | p11.31 | AG | 0.4836 | 0.656 | 0.0005431 |
| 1 | rs2733260 | 74159865 | LRRC44 | 104424 base upstream | p31.1 | CT | 0.626 | 0.582 | 4.53E-06 |
| 5 | rs11950641 | 178229512 | ZNF354B | intron 4 | q35.3 | CT | 0.1224 | 1.73 | 0.00079 |
| 1 | rs6600426 | 38656605 | POU3F1 | 371568 base downstream | p34.3 | AG | 0.1744 | 1.623 | 0.0006588 |
| 1 | rs12064998 | 74202690 | LRRC44 | 61599 base upstream | p31.1 | AG | 0.6253 | 0.579 | 3.51E-06 |
| 1 | rs12064944 | 74202532 | LRRC44 | 61757 base upstream | p31.1 | AG | 0.6254 | 0.579 | 3.48E-06 |
| 5 | rs6865216 | 178252143 | ZFP2 | 3378 base upstream | q35.3 | AG | 0.1304 | 1.803 | 0.0004031 |
| 4 | rs10470737 | 72337409 | SLC4A4 | intron 2 | q13.3 | AG | 0.8688 | 0.522 | 1.03E-05 |
| 18 | rs1785381 | 5579721 | EPB41L3 | 45735 base downstream | p11.31 | CT | 0.5257 | 1.545 | 0.0007352 |
| 5 | rs32972 | 115858991 | SEMA6A | intron 13 | q23.1 | CT | 0.5146 | 1.704 | 2.13E-05 |
| 18 | rs1719937 | 5577607 | EPB41L3 | 43621 base downstream | p11.31 | AG | 0.5298 | 1.542 | 0.000701 |
| 7 | rs10234438 | 6389325 | RAC1 | intron 1 | p22.1 | AG | 0.9655 | 0.397 | 0.0002445 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 8 | rs12675002 | 4101682 | CSMD1 | intron 67 | p23.2 | AG | 0.0676 | 2.204 | 5.40E-05 |
| 4 | rs17051173 | 132424433 | PCDH10 | 1865486 base upstream | q28.3 | CT | 0.0285 | 2.816 | 0.0001177 |
| 2 | rs312924 | 172272267 | DYNC1I2 | intron 5 | q31.1 | AT | 0.7163 | 0.637 | 0.0002489 |
| 10 | rs6482660 | 129849048 | MKI67 | 34403 base downstream | q26.2 | AG | 0.3201 | 1.6 | 0.0001477 |
| 4 | rs2861393 | 132426397 | PCDH10 | 1863522 base upstream | q28.3 | AG | 0.0285 | 2.816 | 0.0001172 |
| 4 | rs11941498 | 132422269 | PCDH10 | 1867650 base upstream | q28.3 | CT | 0.0287 | 2.811 | 0.0001245 |
| 18 | rs1785380 | 5579629 | EPB41L3 | 45643 base downstream | p11.31 | AC | 0.5221 | 1.528 | 0.0008792 |
| 11 | rs12362273 | 109527367 | ZC3H12C | intron 2 | q22.3 | AC | 0.7582 | 0.606 | 9.89E-05 |
| 1 | rs1340434 | 74138234 | LRRC44 | 126055 base upstream | p31.1 | CT | 0.3745 | 1.715 | 4.97E-06 |
| 1 | rs1361463 | 74194799 | LRRC44 | 69490 base upstream | p31.1 | AT | 0.3744 | 1.728 | 3.41E-06 |
| 4 | rs2861394 | 132429544 | PCDH10 | 1860375 base upstream | q28.3 | AG | 0.0285 | 2.817 | 0.0001165 |
| 1 | rs12138557 | 74215111 | LRRC44 | 49178 base upstream | p31.1 | AC | 0.3751 | 1.724 | 3.71E-06 |
| 1 | rs10890094 | 74175476 | LRRC44 | 88813 base upstream | p31.1 | AG | 0.6273 | 0.58 | 3.51E-06 |
| 13 | rs9597010 | 54051478 | OLFM4 | 1527291 base downstream | q21.1 | AT | 0.1705 | 0.473 | 0.0002237 |
| 1 | rs10890093 | 74175413 | LRRC44 | 88876 base upstream | p31.1 | GT | 0.6274 | 0.58 | 3.51E-06 |
| 7 | rs1541363 | 24845137 | OSBPL3 | intron 9 | p15.3 | CT | 0.8888 | 2.302 | 0.0008451 |
| 4 | rs10006868 | 132421378 | PCDH10 | 1868541 base upstream | q28.3 | CG | 0.9707 | 0.358 | 0.00015 |
| 7 | rs2286192 | 84542645 | SEMA3D | intron 14 | q21.11 | CT | 0.1324 | 1.846 | 0.0001791 |
| 2 | rs11884107 | 38418894 | ARL6IP2 | intron 11 | p22.1 | CT | 0.7517 | 1.878 | 3.75E-05 |
| 7 | rs6957484 | 84540088 | SEMA3D | intron 13 | q21.11 | GT | 0.8682 | 0.544 | 0.0001835 |
| 7 | rs6966472 | 84537323 | SEMA3D | intron 13 | q21.11 | CT | 0.1316 | 1.834 | 0.0001854 |
| 7 | rs16887821 | 84534250 | SEMA3D | intron 12 | q21.11 | CG | 0.1315 | 1.831 | 0.0001874 |
| 4 | rs17051172 | 132412892 | PCDH10 | 1877027 base upstream | q28.3 | CT | 0.0294 | 2.786 | 0.0001558 |
| 4 | rs17051170 | 132412751 | PCDH10 | 1877168 base upstream | q28.3 | AC | 0.0295 | 2.784 | 0.000161 |
| 1 | rs11210383 | 74208096 | LRRC44 | 56193 base upstream | p31.1 | AC | 0.3748 | 1.725 | 3.58E-06 |
| 3 | rs9869809 | 176304233 | NAALADL2 | intron 2 | q26.31 | AT | 0.4775 | 0.615 | 4.07E-05 |
| 4 | rs10008591 | 132437567 | PCDH10 | 1852352 base upstream | q28.3 | CT | 0.9712 | 0.345 | 6.77E-05 |
| 8 | rs16894295 | 97172072 | GDF6 | 51665 base upstream | q22.1 | AG | 0.0573 | 2.416 | 0.0001202 |
| 4 | rs4624669 | 132434465 | PCDH10 | 1855454 base upstream | q28.3 | AG | 0.9712 | 0.345 | 6.80E-05 |
| 2 | rs312918 | 172277833 | DYNC1I2 | intron 6 | q31.1 | CG | 0.2838 | 1.569 | 0.0002508 |
| 18 | rs2703175 | 37303085 | PIK3C3 | 486111 base upstream | q12.3 | AG | 0.1099 | 0.415 | 0.0008618 |
| 1 | rs12076161 | 74161472 | LRRC44 | 102817 base upstream | p31.1 | AC | 0.625 | 0.584 | 5.11E-06 |
| 4 | rs12504073 | 182937652 | ODZ3 | 544478 base upstream | q35.1 | AC | 0.532 | 0.664 | 0.0009087 |
| 2 | rs7597387 | 172285362 | DYNC1I2 | intron 7 | q31.1 | CT | 0.2835 | 1.567 | 0.0002664 |
| 11 | rs600421 | 109526092 | ZC3H12C | intron 2 | q22.3 | GT | 0.2508 | 1.609 | 0.0001717 |
| 1 | rs12077198 | 74161523 | LRRC44 | 102766 base upstream | p31.1 | AG | 0.625 | 0.584 | 5.09E-06 |
| 4 | rs12641606 | 132409675 | PCDH10 | 1880244 base upstream | q28.3 | CT | 0.0296 | 2.781 | 0.000173 |

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|----|------------|-----------|---------|-----------------------|--------|----|--------|-------|-----------|
| 4 | rs11947432 | 132410530 | PCDH10 | 1879389 base upstream | q28.3 | AG | 0.0295 | 2.783 | 0.0001699 |
| 2 | rs10206062 | 172285522 | DYNC1I2 | intron 7 | q31.1 | AT | 0.7165 | 0.638 | 0.0002678 |
| 6 | rs9384957 | 116166045 | FRK | 203341 base upstream | q22.1 | CT | 0.1769 | 1.621 | 0.0005427 |
| 7 | rs7809347 | 84545533 | SEMA3D | intron 14 | q21.11 | AG | 0.8633 | 0.54 | 0.0001931 |
| 2 | rs12185567 | 172268975 | DYNC1I2 | intron 3 | q31.1 | AC | 0.2835 | 1.57 | 0.0002489 |
| 2 | rs13431831 | 38418548 | ARL6IP2 | intron 11 | p22.1 | CG | 0.2484 | 0.533 | 3.78E-05 |
| 1 | rs9662322 | 74224911 | LRRC44 | 39378 base upstream | p31.1 | GT | 0.5953 | 0.567 | 4.84E-06 |
| 2 | rs973889 | 172288200 | DYNC1I2 | intron 7 | q31.1 | AG | 0.7167 | 0.639 | 0.0002741 |
| 2 | rs10177042 | 38417031 | ARL6IP2 | intron 11 | p22.1 | CG | 0.7163 | 1.877 | 1.26E-05 |
| 11 | rs2846615 | 109527801 | ZC3H12C | intron 2 | q22.3 | CT | 0.7493 | 0.622 | 0.0001786 |
| 1 | rs11265251 | 152423714 | TPM3 | intron 8 | q21.3 | CT | 0.4245 | 0.614 | 9.84E-05 |
| 2 | rs312925 | 172272168 | DYNC1I2 | intron 5 | q31.1 | AG | 0.2836 | 1.57 | 0.0002489 |
| 2 | rs10207085 | 172294131 | DYNC1I2 | intron 14 | q31.1 | GT | 0.2833 | 1.565 | 0.0002758 |
| 1 | rs10493526 | 74158268 | LRRC44 | 106021 base upstream | p31.1 | CT | 0.3754 | 1.71 | 5.38E-06 |
| 11 | rs665013 | 109528838 | ZC3H12C | intron 2 | q22.3 | CT | 0.2505 | 1.603 | 0.0001968 |
| 11 | rs1675981 | 109527878 | ZC3H12C | intron 2 | q22.3 | GT | 0.7493 | 0.622 | 0.0001808 |
| 11 | rs667625 | 109528270 | ZC3H12C | intron 2 | q22.3 | GT | 0.7494 | 0.623 | 0.0001862 |
| 7 | rs13222785 | 84546498 | SEMA3D | intron 14 | q21.11 | AG | 0.1367 | 1.853 | 0.0001926 |
| 11 | rs581464 | 109527592 | ZC3H12C | intron 2 | q22.3 | GT | 0.7493 | 0.622 | 0.0001756 |
| 6 | rs6901833 | 40745631 | LRFN2 | 82527 base downstream | p21.1 | AG | 0.2165 | 1.613 | 0.0008813 |
| 4 | rs10938138 | 72339473 | SLC4A4 | intron 2 | q13.3 | CG | 0.1148 | 1.98 | 9.33E-06 |
| 4 | rs12650549 | 72340320 | SLC4A4 | intron 3 | q13.3 | GT | 0.8855 | 0.506 | 9.84E-06 |
| 11 | rs622822 | 109528374 | ZC3H12C | intron 2 | q22.3 | GT | 0.2506 | 1.604 | 0.0001896 |
| 11 | rs649847 | 109529837 | ZC3H12C | intron 3 | q22.3 | CG | 0.2504 | 1.6 | 0.0002058 |
| 4 | rs4694388 | 72340027 | SLC4A4 | intron 3 | q13.3 | AG | 0.8855 | 0.506 | 9.76E-06 |
| 11 | rs683593 | 109526143 | ZC3H12C | intron 2 | q22.3 | AC | 0.7492 | 0.621 | 0.0001717 |
| 4 | rs10518587 | 132410710 | PCDH10 | 1879209 base upstream | q28.3 | GT | 0.0295 | 2.783 | 0.0001663 |
| 4 | rs2363717 | 72342980 | SLC4A4 | intron 3 | q13.3 | GT | 0.1141 | 1.973 | 1.07E-05 |
| 11 | rs694974 | 109524562 | ZC3H12C | intron 2 | q22.3 | CT | 0.7491 | 0.621 | 0.0001668 |
| 7 | rs7804456 | 148246576 | EZH2 | 34229 base downstream | q36.1 | CT | 0.2142 | 1.595 | 0.0005006 |
| 8 | rs10503418 | 11156393 | MTMR9 | 23016 base upstream | p23.1 | CT | 0.4227 | 1.462 | 0.0009047 |
| 2 | rs6757773 | 172257876 | DYNC1I2 | intron 3 | q31.1 | AT | 0.7167 | 0.636 | 0.0002495 |
| 4 | rs9992638 | 132404922 | PCDH10 | 1884997 base upstream | q28.3 | AT | 0.9703 | 0.36 | 0.0001852 |
| 11 | rs679264 | 109531670 | ZC3H12C | intron 3 | q22.3 | AG | 0.7498 | 0.627 | 0.0002258 |
| 2 | rs6721680 | 172252159 | DYNC1I2 | 68 base upstream | q31.1 | GT | 0.283 | 1.572 | 0.0002511 |
| 11 | rs17110877 | 109532396 | ZC3H12C | intron 3 | q22.3 | AG | 0.7499 | 0.628 | 0.0002353 |
| 1 | rs2789708 | 74129798 | LRRC44 | 134491 base upstream | p31.1 | AT | 0.4293 | 1.669 | 1.37E-05 |

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|----|------------|-----------|----------|-----------------------|--------|----|--------|-------|-----------|
| 2 | rs6725388 | 172438261 | SLC25A12 | intron 16 | q31.1 | CG | 0.3196 | 1.505 | 0.0008992 |
| 2 | rs11678984 | 172244094 | DYNC1I2 | 8133 base upstream | q31.1 | GT | 0.7174 | 0.637 | 0.0002661 |
| 1 | rs2792075 | 74129950 | LRRC44 | 134339 base upstream | p31.1 | CT | 0.5708 | 0.599 | 1.39E-05 |
| 11 | rs585334 | 109530847 | ZC3H12C | intron 3 | q22.3 | AG | 0.2503 | 1.598 | 0.0002168 |
| 11 | rs678835 | 109531787 | ZC3H12C | intron 3 | q22.3 | CT | 0.2502 | 1.594 | 0.0002321 |
| 7 | rs17153906 | 26553081 | SCAP2 | 120133 base upstream | p15.2 | CT | 0.7902 | 0.602 | 0.0001139 |
| 11 | rs3017769 | 109533247 | ZC3H12C | intron 3 | q22.3 | AG | 0.25 | 1.59 | 0.000249 |
| 4 | rs2016353 | 72341689 | SLC4A4 | intron 3 | q13.3 | AG | 0.1142 | 1.974 | 1.06E-05 |
| 2 | rs2292815 | 172294897 | DYNC1I2 | intron 15 | q31.1 | CG | 0.7168 | 0.639 | 0.0002803 |
| 1 | rs6660710 | 74233724 | LRRC44 | 30565 base upstream | p31.1 | AG | 0.5997 | 0.571 | 7.88E-06 |
| 1 | rs6663201 | 74233585 | LRRC44 | 30704 base upstream | p31.1 | CT | 0.4001 | 1.75 | 7.90E-06 |
| 2 | rs2138348 | 172266418 | DYNC1I2 | intron 3 | q31.1 | GT | 0.7166 | 0.637 | 0.0002489 |
| 11 | rs622192 | 109538447 | ZC3H12C | intron 4 | q22.3 | AT | 0.25 | 1.589 | 0.0002562 |
| 1 | rs2104861 | 225275244 | CDC42BPA | intron 5 | q42.13 | CT | 0.35 | 0.639 | 0.0006271 |
| 8 | rs542253 | 97177903 | GDF6 | 45834 base upstream | q22.1 | AG | 0.0571 | 2.423 | 0.0001162 |
| 2 | rs4667694 | 172313645 | DYNC1I2 | 480 base downstream | q31.1 | AG | 0.2831 | 1.563 | 0.0002908 |
| 8 | rs546474 | 97181208 | GDF6 | 42529 base upstream | q22.1 | AG | 0.9429 | 0.411 | 0.0001127 |
| 2 | rs10166005 | 172315540 | DYNC1I2 | 2375 base downstream | q31.1 | CT | 0.717 | 0.64 | 0.0002933 |
| 2 | rs4668412 | 172328016 | DYNC1I2 | 14851 base downstream | q31.1 | AG | 0.717 | 0.64 | 0.0002985 |
| 2 | rs10184866 | 172317202 | DYNC1I2 | 4037 base downstream | q31.1 | GT | 0.283 | 1.562 | 0.0002946 |
| 10 | rs11597105 | 6552587 | PRKCQ | intron 6 | p15.1 | AG | 0.1446 | 0.499 | 0.0009471 |
| 11 | rs621672 | 109538856 | ZC3H12C | intron 4 | q22.3 | CT | 0.7501 | 0.629 | 0.0002503 |
| 2 | rs6745929 | 38406957 | ARL6IP2 | intron 11 | p22.1 | CT | 0.7334 | 1.958 | 1.06E-05 |
| 2 | rs1554166 | 172249855 | DYNC1I2 | 2372 base upstream | q31.1 | GT | 0.7174 | 0.636 | 0.0002546 |
| 5 | rs1435195 | 105490206 | EFNA5 | 1254043 base upstream | q21.3 | CG | 0.1604 | 1.783 | 4.35E-05 |
| 1 | rs2343196 | 74235010 | LRRC44 | 29279 base upstream | p31.1 | CT | 0.4007 | 1.754 | 7.91E-06 |
| 4 | rs2579331 | 72345306 | SLC4A4 | intron 3 | q13.3 | AG | 0.1302 | 1.87 | 2.37E-05 |
| 10 | rs11199590 | 122593274 | BRWD2 | 7410 base upstream | q26.12 | CT | 0.02 | 3.592 | 5.76E-05 |
| 11 | rs602189 | 109525740 | ZC3H12C | intron 2 | q22.3 | AG | 0.2344 | 1.624 | 0.0002395 |
| 2 | rs10194102 | 172334389 | SLC25A12 | 14737 base upstream | q31.1 | CG | 0.2829 | 1.561 | 0.0003037 |
| 7 | rs6946693 | 69791004 | AUTS2 | intron 5 | q11.22 | GT | 0.3054 | 1.496 | 0.0008562 |
| 4 | rs2063658 | 21477856 | KCNIP4 | intron 8 | p15.31 | AT | 0.5138 | 0.654 | 0.0003271 |
| 11 | rs633410 | 109529896 | ZC3H12C | intron 3 | q22.3 | CT | 0.2503 | 1.599 | 0.0002126 |
| 2 | rs6722757 | 172300209 | DYNC1I2 | intron 15 | q31.1 | AG | 0.7139 | 0.639 | 0.0002964 |
| 4 | rs9995748 | 132454388 | PCDH10 | 1835531 base upstream | q28.3 | CT | 0.033 | 2.789 | 0.0001127 |
| 11 | rs1026608 | 109540472 | ZC3H12C | EXON 6 | q22.3 | AG | 0.7509 | 0.625 | 0.0002148 |
| 11 | rs1026607 | 109540511 | ZC3H12C | EXON 6 | q22.3 | AG | 0.7509 | 0.625 | 0.0002153 |

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|----|------------|-----------|----------|-----------------------|--------|----|--------|-------|-----------|
| 2 | rs11904009 | 172335589 | SLC25A12 | 13537 base upstream | q31.1 | GT | 0.2828 | 1.56 | 0.0003092 |
| 11 | rs653992 | 109524141 | ZC3H12C | intron 2 | q22.3 | CT | 0.7493 | 0.621 | 0.0001706 |
| 3 | rs9290531 | 176306423 | NAALADL2 | intron 2 | q26.31 | AG | 0.5298 | 1.593 | 8.07E-05 |
| 7 | rs4461846 | 84530345 | SEMA3D | intron 11 | q21.11 | CT | 0.864 | 0.583 | 0.0004403 |
| 4 | rs12641430 | 132449990 | PCDH10 | 1839929 base upstream | q28.3 | CT | 0.0329 | 2.799 | 0.0001067 |
| 8 | rs17069688 | 4084387 | CSMD1 | intron 67 | p23.2 | CG | 0.0446 | 2.771 | 1.39E-05 |
| 7 | rs2240394 | 84530877 | SEMA3D | intron 11 | q21.11 | CT | 0.1361 | 1.718 | 0.0004363 |
| 2 | rs10174525 | 172343943 | SLC25A12 | 5183 base upstream | q31.1 | CT | 0.2828 | 1.559 | 0.0003127 |
| 7 | rs2347338 | 6384803 | RAC1 | intron 1 | p22.1 | CT | 0.9649 | 0.392 | 0.0002421 |
| 2 | rs6705200 | 172345846 | SLC25A12 | 3280 base upstream | q31.1 | AG | 0.7173 | 0.642 | 0.0003148 |
| 2 | rs10803863 | 172243583 | DYNC1I2 | 8644 base upstream | q31.1 | CT | 0.7173 | 0.637 | 0.000274 |
| 4 | rs12641562 | 132446415 | PCDH10 | 1843504 base upstream | q28.3 | AC | 0.9672 | 0.354 | 8.97E-05 |
| 2 | rs10497374 | 172348869 | SLC25A12 | 257 base upstream | q31.1 | AG | 0.7173 | 0.642 | 0.0003161 |
| 15 | rs4420510 | 89947230 | SLCO3A1 | 250719 base upstream | q26.1 | AG | 0.3302 | 0.6 | 0.0001749 |
| 7 | rs16887818 | 84529379 | SEMA3D | intron 11 | q21.11 | CG | 0.8641 | 0.583 | 0.0004441 |
| 6 | rs1415699 | 130357104 | L3MBTL3 | 24322 base upstream | q22.33 | AG | 0.0848 | 0.263 | 6.63E-05 |
| 4 | rs12641624 | 132453787 | PCDH10 | 1836132 base upstream | q28.3 | CT | 0.967 | 0.358 | 0.000111 |
| 4 | rs2063656 | 21478155 | KCNIP4 | intron 8 | p15.31 | AC | 0.4729 | 1.492 | 0.0005537 |
| 5 | rs10479364 | 105631852 | EFNA5 | 1112397 base upstream | q21.3 | CT | 0.8364 | 0.542 | 1.94E-05 |
| 4 | rs10018289 | 132440597 | PCDH10 | 1849322 base upstream | q28.3 | AG | 0.0288 | 2.899 | 6.69E-05 |
| 3 | rs936475 | 176304842 | NAALADL2 | intron 2 | q26.31 | GT | 0.5661 | 0.632 | 5.22E-05 |
| 2 | rs908671 | 172398511 | SLC25A12 | intron 10 | q31.1 | CG | 0.7068 | 0.642 | 0.0003738 |
| 4 | rs12647579 | 132453477 | PCDH10 | 1836442 base upstream | q28.3 | AT | 0.967 | 0.358 | 0.0001103 |
| 2 | rs6710698 | 172304324 | DYNC1I2 | intron 15 | q31.1 | CG | 0.2987 | 1.549 | 0.0004992 |
| 8 | rs17069682 | 4083982 | CSMD1 | intron 67 | p23.2 | AC | 0.0445 | 2.767 | 1.48E-05 |
| 4 | rs11946051 | 132450305 | PCDH10 | 1839614 base upstream | q28.3 | GT | 0.9671 | 0.358 | 0.0001082 |
| 3 | rs17338506 | 102089971 | ABI3BP | intron 31 | q12.2 | CT | 0.1436 | 1.836 | 0.0001612 |
| 5 | rs13154869 | 105619351 | EFNA5 | 1124898 base upstream | q21.3 | GT | 0.8365 | 0.542 | 1.94E-05 |
| 4 | rs2063657 | 21478058 | KCNIP4 | intron 8 | p15.31 | AG | 0.527 | 0.67 | 0.0005567 |
| 2 | rs7608403 | 172355011 | SLC25A12 | intron 3 | q31.1 | AC | 0.7169 | 0.645 | 0.0003633 |
| 2 | rs11757 | 172349291 | SLC25A12 | EXON 1 | q31.1 | CG | 0.7173 | 0.642 | 0.0003206 |
| 8 | rs17069679 | 4081661 | CSMD1 | intron 67 | p23.2 | AG | 0.0441 | 2.715 | 2.74E-05 |
| 2 | rs6754817 | 172371640 | SLC25A12 | intron 5 | q31.1 | CT | 0.7169 | 0.645 | 0.0003647 |
| 4 | rs12512316 | 21480772 | KCNIP4 | intron 8 | p15.31 | AG | 0.5265 | 0.675 | 0.0006364 |
| 12 | rs1504558 | 97093097 | TMPO | 340442 base upstream | q23.1 | CG | 0.6549 | 1.668 | 0.0004899 |
| 4 | rs12650292 | 132449623 | PCDH10 | 1840296 base upstream | q28.3 | AG | 0.0328 | 2.827 | 9.05E-05 |
| 2 | rs908670 | 172398426 | SLC25A12 | intron 10 | q31.1 | CT | 0.2932 | 1.557 | 0.0003731 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 11 | rs584008 | 109531136 | ZC3H12C | intron 3 | q22.3 | CT | 0.7444 | 0.61 | 0.0002356 |
| 5 | rs10040995 | 105596450 | EFNA5 | 1147799 base upstream | q21.3 | CT | 0.8284 | 0.552 | 3.12E-05 |
| 13 | rs9555926 | 89090532 | GPC5 | 1758355 base upstream | q31.3 | AG | 0.0266 | 2.8 | 0.0001766 |
| 2 | rs10167419 | 172358072 | SLC25A12 | intron 4 | q31.1 | AG | 0.7166 | 0.646 | 0.0003851 |
| 4 | rs980363 | 72358121 | SLC4A4 | intron 3 | q13.3 | AG | 0.7504 | 0.59 | 2.86E-05 |
| 4 | rs1316758 | 132492216 | PCDH10 | 1797703 base upstream | q28.3 | CT | 0.0335 | 2.498 | 0.0003831 |
| 2 | rs4953868 | 133486143 | NAP5 | intron 12 | q21.2 | AG | 0.4372 | 0.647 | 0.0005784 |
| 2 | rs6759575 | 172397314 | SLC25A12 | intron 10 | q31.1 | CT | 0.7169 | 0.645 | 0.000364 |
| 2 | rs12692973 | 172350303 | SLC25A12 | intron 1 | q31.1 | CT | 0.7174 | 0.642 | 0.0003265 |
| 2 | rs3770445 | 172417165 | SLC25A12 | intron 14 | q31.1 | CT | 0.2934 | 1.556 | 0.0003811 |
| 16 | rs9935841 | 45096893 | SHCBP1 | 75074 base upstream | q11.2 | AG | 0.1525 | 1.658 | 0.0005619 |
| 2 | rs12692978 | 172434227 | SLC25A12 | intron 16 | q31.1 | CT | 0.7256 | 0.64 | 0.0003887 |
| 15 | rs11637543 | 89900920 | SV2B | 261268 base downstream | q26.1 | CT | 0.2938 | 0.593 | 0.0001648 |
| 2 | rs2316431 | 236072455 | CENTG2 | intron 1 | q37.2 | CT | 0.8295 | 0.614 | 0.0007769 |
| 6 | rs2876066 | 130363872 | L3MBTL3 | 17554 base upstream | q22.33 | AC | 0.0838 | 0.261 | 7.74E-05 |
| 4 | rs12504827 | 21481084 | KCNIP4 | intron 8 | p15.31 | AG | 0.4732 | 1.476 | 0.0007111 |
| 4 | rs11931096 | 132488079 | PCDH10 | 1801840 base upstream | q28.3 | CT | 0.9664 | 0.397 | 0.0003622 |
| 6 | rs945889 | 130362937 | L3MBTL3 | 18489 base upstream | q22.33 | CT | 0.0847 | 0.266 | 7.57E-05 |
| 4 | rs17051178 | 132486892 | PCDH10 | 1803027 base upstream | q28.3 | GT | 0.0336 | 2.519 | 0.00036 |
| 2 | rs3770451 | 172376961 | SLC25A12 | intron 7 | q31.1 | GT | 0.283 | 1.551 | 0.0003581 |
| 2 | rs3770452 | 172376928 | SLC25A12 | intron 7 | q31.1 | AG | 0.7171 | 0.645 | 0.0003577 |
| 2 | rs7586207 | 172379340 | SLC25A12 | intron 8 | q31.1 | AG | 0.717 | 0.645 | 0.0003595 |
| 2 | rs4668414 | 172412537 | SLC25A12 | intron 14 | q31.1 | AC | 0.7166 | 0.645 | 0.0003735 |
| 2 | rs6758704 | 172363343 | SLC25A12 | intron 5 | q31.1 | CT | 0.2834 | 1.547 | 0.0003875 |
| 9 | rs10815714 | 7904008 | C9orf123 | 114209 base downstream | p24.1 | CT | 0.1056 | 1.752 | 0.0008156 |
| 5 | rs974073 | 105493632 | EFNA5 | 1250617 base upstream | q21.3 | GT | 0.1438 | 1.748 | 0.0001046 |
| 2 | rs1865951 | 236080078 | CENTG2 | intron 1 | q37.2 | AG | 0.8291 | 0.62 | 0.000827 |
| 5 | rs10520944 | 28874857 | CDH9 | 1800411 base downstream | p14.1 | AC | 0.7684 | 0.633 | 0.000731 |
| 3 | rs17588879 | 176306452 | NAALADL2 | intron 2 | q26.31 | AT | 0.4342 | 1.583 | 5.14E-05 |
| 5 | rs7705866 | 105596842 | EFNA5 | 1147407 base upstream | q21.3 | CT | 0.1717 | 1.812 | 3.11E-05 |
| 16 | rs246240 | 16026525 | ABCC1 | intron 5 | p13.11 | AG | 0.8452 | 2.111 | 0.0001886 |
| 21 | rs363529 | 29936192 | GRIK1 | intron 9 | q21.3 | CG | 0.8489 | 0.594 | 0.0003994 |
| 5 | rs17616969 | 28895838 | CDH9 | 1821392 base downstream | p14.1 | AG | 0.7685 | 0.633 | 0.0007268 |
| 4 | rs1709257 | 71017595 | LOC401137 | 36897 base upstream | q13.3 | AC | 0.0381 | 2.487 | 0.000442 |
| 5 | rs16898178 | 28851719 | CDH9 | 1777273 base downstream | p14.1 | AC | 0.7682 | 0.634 | 0.0007811 |
| 21 | rs16998436 | 40067833 | LOC150084 | intron 4 | q22.2 | CT | 0.0871 | 1.936 | 0.0003793 |
| 4 | rs4585325 | 132501459 | PCDH10 | 1788460 base upstream | q28.3 | CT | 0.9665 | 0.4 | 0.0003838 |

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|----|------------|-----------|-----------|-----------------------|--------|----|--------|-------|-----------|
| 8 | rs17329730 | 53656739 | UNQ9433 | 16174 base downstream | q11.23 | AT | 0.4365 | 1.497 | 0.0009241 |
| 4 | rs17051177 | 132486687 | PCDH10 | 1803232 base upstream | q28.3 | AG | 0.0336 | 2.52 | 0.0003594 |
| 4 | rs1991316 | 95487295 | PGDS | 4245 base downstream | q22.3 | GT | 0.3718 | 1.499 | 0.0006844 |
| 4 | rs1040036 | 21465676 | KCNIP4 | intron 8 | p15.31 | GT | 0.5249 | 0.677 | 0.0009154 |
| 2 | rs6724337 | 172443575 | SLC25A12 | intron 16 | q31.1 | CT | 0.7166 | 0.645 | 0.0003724 |
| 4 | rs11940669 | 132476044 | PCDH10 | 1813875 base upstream | q28.3 | CT | 0.9664 | 0.396 | 0.0003523 |
| 2 | rs7599284 | 236075691 | CENTG2 | intron 1 | q37.2 | AG | 0.8291 | 0.62 | 0.0008281 |
| 4 | rs8180150 | 132508352 | PCDH10 | 1781567 base upstream | q28.3 | AC | 0.0334 | 2.481 | 0.0004032 |
| 16 | rs3814883 | 29902423 | TAOK2 | EXON 13 | p11.2 | CT | 0.517 | 0.623 | 0.0001385 |
| 4 | rs2865353 | 95489901 | PGDS | 6851 base downstream | q22.3 | CT | 0.6283 | 0.667 | 0.0006833 |
| 4 | rs7438414 | 95484845 | PGDS | 1795 base downstream | q22.3 | CT | 0.6282 | 0.667 | 0.0006842 |
| 5 | rs972529 | 105495362 | EFNA5 | 1248887 base upstream | q21.3 | AC | 0.8562 | 0.572 | 0.0001046 |
| 4 | rs17051181 | 132509434 | PCDH10 | 1780485 base upstream | q28.3 | CT | 0.0334 | 2.481 | 0.0004022 |
| 21 | rs2837204 | 40067939 | LOC150084 | intron 4 | q22.2 | CT | 0.095 | 1.908 | 0.0002721 |
| 4 | rs4282187 | 95492168 | PGDS | 9118 base downstream | q22.3 | CT | 0.6283 | 0.667 | 0.0006838 |
| 16 | rs246214 | 16022393 | ABCC1 | intron 5 | p13.11 | CT | 0.845 | 2.107 | 0.0001895 |
| 3 | rs17588796 | 176306392 | NAALADL2 | intron 2 | q26.31 | AG | 0.4341 | 1.582 | 5.25E-05 |
| 4 | rs11727030 | 95481688 | PGDS | intron 5 | q22.3 | AG | 0.3719 | 1.499 | 0.0006851 |
| 21 | rs16998444 | 40068571 | LOC150084 | intron 4 | q22.2 | AG | 0.0872 | 1.935 | 0.0003835 |
| 5 | rs10063657 | 105638139 | EFNA5 | 1106110 base upstream | q21.3 | CT | 0.172 | 1.819 | 2.96E-05 |
| 3 | rs936474 | 176305423 | NAALADL2 | intron 2 | q26.31 | AG | 0.5661 | 0.632 | 5.22E-05 |
| 1 | rs4650237 | 74232437 | LRRC44 | 31852 base upstream | p31.1 | GT | 0.5595 | 0.592 | 2.62E-05 |
| 5 | rs1991970 | 105458740 | EFNA5 | 1285509 base upstream | q21.3 | AC | 0.1437 | 1.749 | 0.0001017 |
| 4 | rs8180189 | 132509387 | PCDH10 | 1780532 base upstream | q28.3 | CT | 0.9666 | 0.403 | 0.0004026 |
| 18 | rs2635509 | 44768190 | SMAD7 | 37111 base downstream | q21.1 | AG | 0.4226 | 1.618 | 6.37E-05 |
| 10 | rs11199677 | 122705142 | BRWD2 | 46117 base downstream | q26.12 | AC | 0.0208 | 3.753 | 4.75E-05 |
| 4 | rs724260 | 95479708 | PGDS | intron 5 | q22.3 | AG | 0.3719 | 1.499 | 0.0006853 |
| 4 | rs6840479 | 95494865 | PGDS | 11815 base downstream | q22.3 | AG | 0.3708 | 1.5 | 0.0007004 |
| 6 | rs9396812 | 17953140 | KIF13A | intron 29 | p22.3 | AG | 0.5858 | 0.678 | 0.0006775 |
| 4 | rs1343670 | 132503523 | PCDH10 | 1786396 base upstream | q28.3 | CT | 0.0334 | 2.48 | 0.0004043 |
| 6 | rs7759444 | 40754017 | LRFN2 | 90913 base downstream | p21.1 | AG | 0.2005 | 1.608 | 0.0004671 |
| 5 | rs12719550 | 105507616 | EFNA5 | 1236633 base upstream | q21.3 | AT | 0.8561 | 0.572 | 0.0001057 |
| 7 | rs7800255 | 84532070 | SEMA3D | intron 11 | q21.11 | AT | 0.1327 | 1.758 | 0.0007137 |
| 8 | rs10903331 | 10769957 | XKR6 | 21109 base upstream | p23.1 | CG | 0.1939 | 0.449 | 1.68E-05 |
| 8 | rs2919390 | 32646497 | NRG1 | intron 3 | p12 | AC | 0.6049 | 1.606 | 0.0002093 |
| 1 | rs11210390 | 74227364 | LRRC44 | 36925 base upstream | p31.1 | CT | 0.4403 | 1.686 | 2.63E-05 |
| 2 | rs938675 | 236087152 | CENTG2 | intron 1 | q37.2 | CT | 0.8289 | 0.625 | 0.0009575 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 3 | rs17059208 | 41611668 | ULK4 | intron 6 | p22.1 | CG | 0.9443 | 0.422 | 0.0001236 |
| 3 | rs9848123 | 176299863 | NAALADL2 | intron 2 | q26.31 | AG | 0.4047 | 0.627 | 0.0001476 |
| 16 | rs12325539 | 29941134 | FLJ25404 | 1021 base upstream | p11.2 | CT | 0.4039 | 1.663 | 0.0001161 |
| 16 | rs11150581 | 29938200 | FLJ25404 | 3955 base upstream | p11.2 | CT | 0.4037 | 1.657 | 0.0001145 |
| 10 | rs11199603 | 122607331 | BRWD2 | intron 2 | q26.12 | AG | 0.9812 | 0.284 | 8.31E-05 |
| 16 | rs11642612 | 29937696 | FLJ25404 | 4459 base upstream | p11.2 | AC | 0.5964 | 0.604 | 0.0001144 |
| 4 | rs4146422 | 132508470 | PCDH10 | 1781449 base upstream | q28.3 | CT | 0.9666 | 0.403 | 0.0004032 |
| 9 | rs1322303 | 10639309 | PTPRD | 36800 base downstream | p23 | AG | 0.7631 | 0.618 | 0.0001344 |
| 10 | rs11199612 | 122621095 | BRWD2 | intron 10 | q26.12 | CT | 0.9813 | 0.285 | 8.72E-05 |
| 2 | rs4663602 | 236091352 | CENTG2 | intron 1 | q37.2 | AG | 0.1712 | 1.6 | 0.0009678 |
| 15 | rs4775230 | 58091041 | FOXB1 | 5607 base downstream | q22.2 | CT | 0.1623 | 1.683 | 0.0005146 |
| 5 | rs10073985 | 105575000 | EFNA5 | 1169249 base upstream | q21.3 | CT | 0.8546 | 0.558 | 5.50E-05 |
| 10 | rs11199613 | 122622408 | BRWD2 | intron 10 | q26.12 | CT | 0.0187 | 3.508 | 8.75E-05 |
| 10 | rs12355961 | 122624977 | BRWD2 | intron 11 | q26.12 | AG | 0.0186 | 3.505 | 8.87E-05 |
| 15 | rs9920841 | 58089832 | FOXB1 | 4398 base downstream | q22.2 | AG | 0.8377 | 0.594 | 0.0005162 |
| 10 | rs12355108 | 122623411 | BRWD2 | EXON 11 | q26.12 | CT | 0.9813 | 0.285 | 8.78E-05 |
| 2 | rs2316435 | 236090677 | CENTG2 | intron 1 | q37.2 | AT | 0.8288 | 0.625 | 0.0009674 |
| 9 | rs1923439 | 10638898 | PTPRD | 36389 base downstream | p23 | GT | 0.237 | 1.619 | 0.0001367 |
| 2 | rs4663604 | 236094249 | CENTG2 | intron 1 | q37.2 | AG | 0.1712 | 1.6 | 0.0009712 |
| 5 | rs1423298 | 28807655 | CDH9 | 1733209 base downstream | p14.1 | CT | 0.2314 | 1.578 | 0.0007495 |
| 3 | rs7646135 | 176312988 | NAALADL2 | intron 2 | q26.31 | AT | 0.4385 | 1.57 | 8.47E-05 |
| 2 | rs6753473 | 26379923 | GPR113 | 4621 base upstream | p23.3 | GT | 0.0235 | 2.87 | 0.0002956 |
| 2 | rs10460276 | 236094532 | CENTG2 | intron 1 | q37.2 | CT | 0.8288 | 0.625 | 0.0009762 |
| 4 | rs6821156 | 154491352 | MND1 | intron 2 | q31.3 | AT | 0.5646 | 0.612 | 9.20E-05 |
| 5 | rs17583873 | 28990579 | CDH9 | 1916133 base downstream | p14.1 | CT | 0.232 | 1.578 | 0.0007753 |
| 2 | rs6731720 | 236095585 | CENTG2 | intron 1 | q37.2 | GT | 0.1712 | 1.6 | 0.0009782 |
| 5 | rs11742039 | 6574824 | NSUN2 | 77530 base upstream | p15.31 | GT | 0.2049 | 1.717 | 0.0002294 |
| 15 | rs7495265 | 89951919 | SLCO3A1 | 246030 base upstream | q26.1 | CT | 0.2946 | 0.564 | 0.0001157 |
| 1 | rs12593 | 225238913 | CABC1 | EXON 12 | q42.13 | CT | 0.5255 | 0.658 | 0.0002853 |
| 1 | rs11210389 | 74227289 | LRRC44 | 37000 base upstream | p31.1 | AC | 0.4398 | 1.681 | 2.64E-05 |
| 7 | rs10259316 | 17412231 | AHR | 59934 base downstream | p21.1 | GT | 0.3895 | 0.615 | 0.0004296 |
| 10 | rs12360470 | 122586221 | BRWD2 | 14463 base upstream | q26.12 | AG | 0.0215 | 3.504 | 5.25E-05 |
| 3 | rs1381130 | 176299621 | NAALADL2 | intron 2 | q26.31 | CT | 0.4047 | 0.627 | 0.0001481 |
| 6 | rs11962303 | 40752262 | LRFN2 | 89158 base downstream | p21.1 | AC | 0.2011 | 1.591 | 0.0005956 |
| 8 | rs3898733 | 124803982 | ANXA13 | intron 10 | q24.13 | CT | 0.6952 | 1.623 | 0.0009095 |
| 16 | rs17291845 | 53802538 | IRX6 | 113433 base upstream | q12.2 | AG | 0.1336 | 1.671 | 0.0009338 |
| 4 | rs4694387 | 72339718 | SLC4A4 | intron 2 | q13.3 | AC | 0.1146 | 1.979 | 9.57E-06 |

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|----|------------|-----------|-----------|-----------------------|--------|----|--------|-------|-----------|
| 8 | rs17069674 | 4081435 | CSMD1 | intron 67 | p23.2 | CT | 0.0425 | 2.655 | 5.69E-05 |
| 10 | rs11199632 | 122645462 | BRWD2 | intron 19 | q26.12 | CT | 0.9815 | 0.286 | 9.51E-05 |
| 18 | rs4800580 | 20402119 | HRH4 | 88201 base downstream | q11.2 | AG | 0.3361 | 0.644 | 0.0009324 |
| 10 | rs12355611 | 122646633 | BRWD2 | intron 19 | q26.12 | AC | 0.9815 | 0.287 | 9.66E-05 |
| 10 | rs12355703 | 122589381 | BRWD2 | 11303 base upstream | q26.12 | CG | 0.0214 | 3.521 | 5.22E-05 |
| 9 | rs4380991 | 10655668 | PTPRD | 53159 base downstream | p23 | AT | 0.1457 | 1.891 | 4.95E-05 |
| 1 | rs6665290 | 225267729 | CDC42BPA | intron 3 | q42.13 | CT | 0.5203 | 0.655 | 0.0003034 |
| 5 | rs11134164 | 6575043 | NSUN2 | 77311 base upstream | p15.31 | AG | 0.7942 | 0.586 | 0.0002638 |
| 1 | rs11165870 | 97668350 | DPYD | intron 9 | p21.3 | CT | 0.4468 | 0.614 | 7.16E-05 |
| 3 | rs4505709 | 176311011 | NAALADL2 | intron 2 | q26.31 | AG | 0.4396 | 1.564 | 9.40E-05 |
| 3 | rs9859106 | 176302128 | NAALADL2 | intron 2 | q26.31 | AT | 0.3972 | 0.638 | 0.0002635 |
| 3 | rs6782155 | 176310488 | NAALADL2 | intron 2 | q26.31 | AG | 0.4394 | 1.563 | 9.46E-05 |
| 18 | rs9304467 | 20403162 | HRH4 | 89244 base downstream | q11.2 | AG | 0.3365 | 0.645 | 0.0009399 |
| 4 | rs16849331 | 74496772 | ALB | intron 7 | q13.3 | GT | 0.971 | 0.359 | 0.0002017 |
| 18 | rs9950310 | 20403739 | HRH4 | 89821 base downstream | q11.2 | CT | 0.3367 | 0.645 | 0.0009435 |
| 1 | rs6693140 | 107983470 | VAV3 | intron 7 | p13.3 | CT | 0.19 | 1.624 | 0.0002826 |
| 3 | rs6796537 | 176315077 | NAALADL2 | intron 2 | q26.31 | CT | 0.4428 | 0.635 | 0.0001379 |
| 3 | rs6797510 | 176309960 | NAALADL2 | intron 2 | q26.31 | AG | 0.4393 | 1.562 | 9.60E-05 |
| 18 | rs4800186 | 20407884 | HRH4 | 93966 base downstream | q11.2 | AT | 0.6625 | 1.549 | 0.0009676 |
| 3 | rs6797428 | 176309927 | NAALADL2 | intron 2 | q26.31 | AG | 0.4392 | 1.562 | 9.64E-05 |
| 6 | rs1471546 | 136513493 | PDE7B | intron 5 | q23.3 | CT | 0.4191 | 1.601 | 6.28E-05 |
| 9 | rs10809144 | 10637333 | PTPRD | 34824 base downstream | p23 | CT | 0.2374 | 1.615 | 0.0001459 |
| 3 | rs6809009 | 176315114 | NAALADL2 | intron 2 | q26.31 | GT | 0.5573 | 1.576 | 0.0001378 |
| 3 | rs6774509 | 176315311 | NAALADL2 | intron 2 | q26.31 | AT | 0.4427 | 0.635 | 0.0001378 |
| 6 | rs1038214 | 136520887 | PDE7B | intron 8 | q23.3 | AG | 0.5753 | 0.633 | 8.60E-05 |
| 3 | rs6774272 | 176319087 | NAALADL2 | intron 2 | q26.31 | CT | 0.5571 | 1.583 | 0.0001361 |
| 3 | rs6773961 | 176318751 | NAALADL2 | intron 2 | q26.31 | AT | 0.5573 | 1.576 | 0.0001377 |
| 3 | rs11710345 | 176309283 | NAALADL2 | intron 2 | q26.31 | AG | 0.4392 | 1.562 | 9.66E-05 |
| 2 | rs1712005 | 115906362 | DPP10 | intron 3 | q14.1 | AG | 0.0912 | 1.912 | 0.0001381 |
| 3 | rs6809556 | 176318826 | NAALADL2 | intron 2 | q26.31 | CT | 0.4427 | 0.635 | 0.0001376 |
| 3 | rs2862042 | 176319542 | NAALADL2 | intron 2 | q26.31 | CT | 0.4431 | 0.629 | 0.0001351 |
| 19 | rs12976005 | 37368143 | ZNF507 | 160249 base upstream | q13.11 | CG | 0.4801 | 1.568 | 0.0001498 |
| 3 | rs4355289 | 176311154 | NAALADL2 | intron 2 | q26.31 | AG | 0.5571 | 1.575 | 0.0001398 |
| 3 | rs9877212 | 176314128 | NAALADL2 | intron 2 | q26.31 | CT | 0.5572 | 1.575 | 0.0001381 |
| 21 | rs16998556 | 40093555 | LOC150084 | intron 8 | q22.2 | GT | 0.9133 | 0.512 | 0.0003171 |
| 4 | rs11099102 | 132536774 | PCDH10 | 1753145 base upstream | q28.3 | CT | 0.0324 | 2.453 | 0.0006265 |
| 13 | rs9555925 | 89090502 | GPC5 | 1758385 base upstream | q31.3 | CT | 0.0266 | 2.8 | 0.0001769 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs11679270 | 38422312 | ARL6IP2 | intron 11 | p22.1 | AC | 0.319 | 0.561 | 2.32E-05 |
| 18 | rs9304466 | 20402971 | HRH4 | 89053 base downstream | q11.2 | CG | 0.6638 | 1.552 | 0.0009341 |
| 2 | rs11679271 | 38422331 | ARL6IP2 | intron 11 | p22.1 | CT | 0.6811 | 1.784 | 2.31E-05 |
| 21 | rs16998519 | 40087119 | LOC150084 | intron 7 | q22.2 | GT | 0.0863 | 1.967 | 0.0002768 |
| 16 | rs12935507 | 53798452 | IRX6 | 117519 base upstream | q12.2 | AT | 0.8662 | 0.595 | 0.0009672 |
| 3 | rs9847129 | 176312381 | NAALADL2 | intron 2 | q26.31 | CT | 0.4429 | 0.635 | 0.0001395 |
| 4 | rs11936773 | 132537559 | PCDH10 | 1752360 base upstream | q28.3 | GT | 0.9677 | 0.408 | 0.0006234 |
| 9 | rs4131202 | 10643484 | PTPRD | 40975 base downstream | p23 | CT | 0.7793 | 0.59 | 7.16E-05 |
| 16 | rs2647972 | 50225696 | SALL1 | 483012 base downstream | q12.1 | CT | 0.4858 | 1.541 | 0.0004213 |
| 1 | rs12354219 | 97693544 | DPYD | intron 10 | p21.3 | CT | 0.4422 | 0.61 | 6.32E-05 |
| 4 | rs12648650 | 132565936 | PCDH10 | 1723983 base upstream | q28.3 | AC | 0.9678 | 0.406 | 0.0005888 |
| 5 | rs9327956 | 105488872 | EFNA5 | 1255377 base upstream | q21.3 | CT | 0.1438 | 1.748 | 0.0001039 |
| 6 | rs4896202 | 136514189 | PDE7B | intron 6 | q23.3 | GT | 0.4192 | 1.6 | 6.18E-05 |
| 6 | rs9320545 | 116106532 | FRK | 262854 base upstream | q22.1 | CT | 0.7825 | 0.632 | 0.000523 |
| 12 | rs1847534 | 97094264 | TMPO | 339275 base upstream | q23.1 | AC | 0.323 | 0.604 | 0.0007308 |
| 4 | rs6532482 | 95496437 | PGDS | 13387 base downstream | q22.3 | AG | 0.3647 | 1.51 | 0.0004858 |
| 5 | rs4702359 | 6574202 | NSUN2 | 78152 base upstream | p15.31 | AG | 0.7625 | 0.586 | 0.0001128 |
| 10 | rs11199530 | 122502220 | BRWD2 | 98464 base upstream | q26.12 | AG | 0.9762 | 0.294 | 9.65E-05 |
| 15 | rs729978 | 58974308 | RORA | intron 10 | q22.2 | CT | 0.3038 | 0.606 | 0.0006601 |
| 4 | rs11945624 | 132550197 | PCDH10 | 1739722 base upstream | q28.3 | AG | 0.0323 | 2.457 | 0.0006124 |
| 4 | rs6532481 | 95496334 | PGDS | 13284 base downstream | q22.3 | GT | 0.6352 | 0.662 | 0.0004826 |
| 6 | rs1471545 | 136513400 | PDE7B | intron 5 | q23.3 | CT | 0.419 | 1.601 | 6.27E-05 |
| 16 | rs7204626 | 50235764 | SALL1 | 493080 base downstream | q12.1 | CT | 0.2801 | 1.59 | 0.0001191 |
| 4 | rs1911882 | 132482173 | PCDH10 | 1807746 base upstream | q28.3 | CT | 0.0336 | 2.524 | 0.0003539 |
| 1 | rs4949953 | 97677368 | DPYD | intron 9 | p21.3 | CT | 0.4463 | 0.613 | 7.03E-05 |
| 1 | rs6659424 | 225264498 | CDC42BPA | intron 3 | q42.13 | AG | 0.5173 | 0.661 | 0.000331 |
| 9 | rs13299260 | 123780890 | TTLL11 | 10122 base upstream | q33.2 | CT | 0.5053 | 1.499 | 0.0005451 |
| 18 | rs12607480 | 41955585 | CCDC5 | intron 4 | q21.1 | AG | 0.1424 | 0.479 | 0.0007334 |
| 1 | rs12129397 | 97673140 | DPYD | intron 9 | p21.3 | AT | 0.5535 | 1.63 | 7.07E-05 |
| 1 | rs11165873 | 97675378 | DPYD | intron 9 | p21.3 | AT | 0.5536 | 1.63 | 7.05E-05 |
| 3 | rs212039 | 60013621 | FHIT | intron 5 | p14.2 | CT | 0.9085 | 0.537 | 0.0003842 |
| 4 | rs1593554 | 95497524 | PGDS | 14474 base downstream | q22.3 | CT | 0.3648 | 1.511 | 0.0004852 |
| 15 | rs729977 | 58974360 | RORA | intron 10 | q22.2 | CT | 0.6959 | 1.641 | 0.0006717 |
| 1 | rs1929862 | 225266341 | CDC42BPA | intron 3 | q42.13 | AG | 0.4828 | 1.513 | 0.0003301 |
| 1 | rs12403236 | 225263125 | CDC42BPA | intron 3 | q42.13 | CG | 0.5165 | 0.663 | 0.0003738 |
| 8 | rs12541855 | 32647451 | NRG1 | intron 3 | p12 | CT | 0.6371 | 1.588 | 0.0003957 |
| 16 | rs3814881 | 29908402 | TAOK2 | intron 16 | p11.2 | AG | 0.4525 | 1.544 | 0.0002381 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 4 | rs16849372 | 74514655 | AFP | 6141 base upstream | q13.3 | AT | 0.0291 | 2.781 | 0.0002026 |
| 3 | rs212041 | 60013318 | FHIT | intron 5 | p14.2 | GT | 0.9086 | 0.537 | 0.0003937 |
| 2 | rs11902679 | 26381302 | GPR113 | 3242 base upstream | p23.3 | CT | 0.9765 | 0.348 | 0.0002974 |
| 16 | rs2647971 | 50225366 | SALL1 | 482682 base downstream | q12.1 | CT | 0.4857 | 1.538 | 0.0004312 |
| 1 | rs12409755 | 225263572 | CDC42BPA | intron 3 | q42.13 | AT | 0.5166 | 0.663 | 0.0003658 |
| 4 | rs9997915 | 95497050 | PGDS | 14000 base downstream | q22.3 | CT | 0.3648 | 1.511 | 0.0004854 |
| 1 | rs6704144 | 225267653 | CDC42BPA | intron 3 | q42.13 | CG | 0.4828 | 1.514 | 0.0003287 |
| 4 | rs6535584 | 149309538 | NR3C2 | intron 5 | q31.23 | CT | 0.5913 | 1.528 | 0.0004436 |
| 1 | rs3897854 | 97690894 | DPYD | intron 10 | p21.3 | CT | 0.5578 | 1.64 | 6.33E-05 |
| 4 | rs6839224 | 95498237 | PGDS | 15187 base downstream | q22.3 | GT | 0.6352 | 0.662 | 0.0004851 |
| 16 | rs3935873 | 29926001 | DOC2A | EXON 6 | p11.2 | CT | 0.5481 | 0.645 | 0.0002116 |
| 16 | rs2346943 | 7435187 | A2BP1 | intron 4 | p13.2 | GT | 0.4305 | 0.657 | 0.000534 |
| 1 | rs7550959 | 97699427 | DPYD | intron 10 | p21.3 | AG | 0.4364 | 0.614 | 9.59E-05 |
| 1 | rs2149186 | 89277631 | GBP1 | 12943 base upstream | p22.2 | GT | 0.1644 | 0.487 | 0.000389 |
| 16 | rs9933246 | 7437703 | A2BP1 | intron 4 | p13.2 | CT | 0.4304 | 0.659 | 0.0005856 |
| 1 | rs6426559 | 225262499 | CDC42BPA | intron 3 | q42.13 | CT | 0.4835 | 1.508 | 0.0003713 |
| 2 | rs1375010 | 38411164 | ARL6IP2 | intron 11 | p22.1 | AG | 0.3228 | 0.567 | 2.62E-05 |
| 2 | rs10496652 | 126453217 | GYPC | 676936 base upstream | q14.3 | AG | 0.2699 | 0.594 | 0.000593 |
| 4 | rs6844516 | 74453060 | ALB | 35809 base upstream | q13.3 | AT | 0.0289 | 2.801 | 0.0002008 |
| 21 | rs16998521 | 40087288 | LOC150084 | intron 7 | q22.2 | AG | 0.0863 | 1.967 | 0.0002769 |
| 2 | rs1717054 | 115906019 | DPP10 | intron 3 | q14.1 | CT | 0.9088 | 0.523 | 0.0001365 |
| 2 | rs1437896 | 133485247 | NAP5 | intron 12 | q21.2 | CT | 0.413 | 0.657 | 0.0009846 |
| 13 | rs994066 | 89081759 | GPC5 | 1767128 base upstream | q31.3 | CG | 0.0267 | 2.801 | 0.0001865 |
| 16 | rs3814880 | 29925396 | DOC2A | intron 2 | p11.2 | CT | 0.4519 | 1.55 | 0.0002136 |
| 4 | rs12649130 | 132578708 | PCDH10 | 1711211 base upstream | q28.3 | CG | 0.9678 | 0.406 | 0.0005891 |
| 1 | rs1045252 | 225248178 | CDC42BPA | EXON 1 | q42.13 | AG | 0.5168 | 0.663 | 0.0003577 |
| 13 | rs2325129 | 43897258 | TSC22D1 | 8402 base upstream | q14.11 | CT | 0.4206 | 0.626 | 0.0001984 |
| 1 | rs11588904 | 225262834 | CDC42BPA | intron 3 | q42.13 | CT | 0.4835 | 1.508 | 0.0003723 |
| 1 | rs1062908 | 225248177 | CDC42BPA | EXON 1 | q42.13 | CG | 0.5169 | 0.663 | 0.000357 |
| 18 | rs8083916 | 41948674 | CCDC5 | intron 2 | q21.1 | AC | 0.1418 | 0.487 | 0.0008544 |
| 1 | rs3795451 | 225248546 | CDC42BPA | EXON 1 | q42.13 | CT | 0.5168 | 0.663 | 0.0003591 |
| 1 | rs1045287 | 225245585 | CDC42BPA | EXON 1 | q42.13 | CT | 0.4831 | 1.509 | 0.000356 |
| 1 | rs3795449 | 225248461 | CDC42BPA | EXON 1 | q42.13 | GT | 0.4832 | 1.509 | 0.0003584 |
| 1 | rs7541033 | 225254994 | CDC42BPA | intron 2 | q42.13 | AC | 0.4829 | 1.51 | 0.0003479 |
| 1 | rs1186 | 225244354 | CDC42BPA | EXON 1 | q42.13 | AT | 0.5169 | 0.662 | 0.0003554 |
| 8 | rs2406453 | 3078201 | CSMD1 | intron 44 | p23.2 | CG | 0.0453 | 2.176 | 0.0008694 |
| 1 | rs1045290 | 225245323 | CDC42BPA | EXON 1 | q42.13 | AG | 0.5169 | 0.663 | 0.0003557 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 18 | rs4243278 | 41961878 | CCDC5 | intron 8 | q21.1 | AG | 0.8575 | 2.096 | 0.0007127 |
| 1 | rs3768425 | 225244750 | CDC42BPA | EXON 1 | q42.13 | AG | 0.5169 | 0.662 | 0.0003555 |
| 1 | rs1343743 | 225249748 | CDC42BPA | intron 2 | q42.13 | CT | 0.5166 | 0.663 | 0.0003645 |
| 1 | rs1045289 | 225245336 | CDC42BPA | EXON 1 | q42.13 | CT | 0.5169 | 0.663 | 0.0003558 |
| 1 | rs2297418 | 225259202 | CDC42BPA | intron 2 | q42.13 | AC | 0.5161 | 0.663 | 0.0003802 |
| 1 | rs11587443 | 225254519 | CDC42BPA | intron 2 | q42.13 | CT | 0.4835 | 1.508 | 0.0003684 |
| 18 | rs12185417 | 20409016 | HRH4 | 95098 base downstream | q11.2 | AC | 0.3337 | 0.636 | 0.0007598 |
| 6 | rs9494457 | 136516487 | PDE7B | intron 6 | q23.3 | AT | 0.3987 | 1.606 | 7.09E-05 |
| 2 | rs843385 | 115894049 | DPP10 | intron 3 | q14.1 | CT | 0.0911 | 1.921 | 0.0001201 |
| 1 | rs10916075 | 225250697 | CDC42BPA | intron 2 | q42.13 | AG | 0.4835 | 1.509 | 0.0003665 |
| 18 | rs1945153 | 20409841 | HRH4 | 95923 base downstream | q11.2 | AG | 0.6619 | 1.547 | 0.0009862 |
| 2 | rs17650774 | 6830471 | LOC129607 | 75432 base upstream | p25.2 | AG | 0.74 | 0.636 | 0.0002943 |
| 1 | rs1045285 | 225245677 | CDC42BPA | EXON 1 | q42.13 | AG | 0.4831 | 1.509 | 0.0003562 |
| 5 | rs931062 | 6573684 | NSUN2 | 78670 base upstream | p15.31 | CT | 0.2056 | 1.702 | 0.0002619 |
| 9 | rs11794075 | 120842902 | DBC1 | 125826 base upstream | q33.1 | AG | 0.9087 | 0.501 | 6.98E-05 |
| 6 | rs4896198 | 136507126 | PDE7B | intron 3 | q23.3 | CT | 0.4034 | 1.601 | 8.28E-05 |
| 6 | rs12662330 | 136508312 | PDE7B | intron 3 | q23.3 | AC | 0.5964 | 0.624 | 7.98E-05 |
| 13 | rs9560407 | 89086817 | GPC5 | 1762070 base upstream | q31.3 | AG | 0.9734 | 0.357 | 0.0001788 |
| 6 | rs9449500 | 83338480 | TPBG | 205147 base downstream | q14.1 | GT | 0.032 | 2.519 | 0.0005234 |
| 13 | rs11619041 | 43927733 | TSC22D1 | intron 2 | q14.11 | AG | 0.5758 | 1.557 | 0.0003174 |
| 1 | rs17536161 | 115171509 | SYCP1 | 27468 base upstream | p13.2 | AG | 0.0433 | 2.366 | 0.0009034 |
| 9 | rs16909038 | 2668958 | VLDLR | 24473 base downstream | p24.2 | CG | 0.9267 | 0.502 | 0.0003008 |
| 1 | rs10495273 | 225249982 | CDC42BPA | intron 2 | q42.13 | GT | 0.4834 | 1.509 | 0.0003652 |
| 1 | rs6684821 | 225256856 | CDC42BPA | intron 2 | q42.13 | AG | 0.4837 | 1.508 | 0.0003736 |
| 3 | rs13091963 | 102220701 | ABI3BP | 25697 base downstream | q12.2 | AG | 0.2905 | 1.621 | 8.21E-05 |
| 16 | rs9924686 | 29910577 | TAOK2 | EXON 19 | p11.2 | AG | 0.4524 | 1.544 | 0.0002353 |
| 15 | rs12592999 | 58975113 | RORA | intron 10 | q22.2 | AG | 0.2977 | 0.611 | 0.0006927 |
| 1 | rs12409428 | 225256592 | CDC42BPA | intron 2 | q42.13 | CT | 0.4836 | 1.508 | 0.0003723 |
| 3 | rs1546060 | 56410435 | CAST1 | intron 15 | p14.3 | AC | 0.6225 | 0.677 | 0.0009996 |
| 21 | rs16998550 | 40092123 | LOC150084 | intron 8 | q22.2 | CT | 0.0867 | 1.957 | 0.0003094 |
| 3 | rs9851360 | 56410015 | CAST1 | intron 15 | p14.3 | CT | 0.6236 | 0.674 | 0.0008676 |
| 9 | rs6475926 | 2668059 | VLDLR | 23574 base downstream | p24.2 | CT | 0.0734 | 1.993 | 0.000299 |
| 6 | rs4714357 | 40749271 | LRFN2 | 86167 base downstream | p21.1 | AG | 0.7984 | 0.629 | 0.0006491 |
| 2 | rs843394 | 115904553 | DPP10 | intron 3 | q14.1 | GT | 0.0913 | 1.914 | 0.0001338 |
| 9 | rs1542358 | 2663393 | VLDLR | 18908 base downstream | p24.2 | CT | 0.9284 | 0.48 | 0.0002079 |
| 9 | rs7046015 | 2667787 | VLDLR | 23302 base downstream | p24.2 | AG | 0.9266 | 0.502 | 0.0002981 |
| 2 | rs4589732 | 38409334 | ARL6IP2 | intron 11 | p22.1 | CG | 0.6771 | 1.762 | 2.64E-05 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 13 | rs12873354 | 39474064 | COG6 | 249432 base downstream | q13.3 | CT | 0.6402 | 0.641 | 0.0001497 |
| 6 | rs16893894 | 40749486 | LRFN2 | 86382 base downstream | p21.1 | CT | 0.2016 | 1.589 | 0.0006503 |
| 3 | rs6805882 | 56414093 | CAST1 | intron 15 | p14.3 | CT | 0.3785 | 1.481 | 0.0009577 |
| 9 | rs7847455 | 2668427 | VLDLR | 23942 base downstream | p24.2 | AT | 0.9266 | 0.502 | 0.0002995 |
| 4 | rs7675336 | 74455492 | ALB | 33377 base upstream | q13.3 | AG | 0.9711 | 0.357 | 0.0002009 |
| 6 | rs1600619 | 136507868 | PDE7B | intron 3 | q23.3 | AT | 0.4036 | 1.602 | 7.99E-05 |
| 3 | rs1491158 | 56411201 | CAST1 | intron 15 | p14.3 | AG | 0.3765 | 1.487 | 0.0008208 |
| 13 | rs7339164 | 39470053 | COG6 | 245421 base downstream | q13.3 | AG | 0.3602 | 1.567 | 0.000129 |
| 4 | rs16849293 | 74460813 | ALB | 28056 base upstream | q13.3 | AG | 0.9711 | 0.357 | 0.000201 |
| 8 | rs2701438 | 73175792 | TRPA1 | 25419 base downstream | q13.3 | GT | 0.1938 | 1.617 | 0.0003257 |
| 9 | rs10756080 | 10647559 | PTPRD | 45050 base downstream | p23 | CT | 0.136 | 1.833 | 4.93E-05 |
| 6 | rs4896199 | 136507265 | PDE7B | intron 3 | q23.3 | AC | 0.5966 | 0.625 | 8.28E-05 |
| 6 | rs4714358 | 40749374 | LRFN2 | 86270 base downstream | p21.1 | AC | 0.2016 | 1.589 | 0.0006493 |
| 1 | rs10912878 | 173301266 | TNN | 2350 base upstream | q25.1 | AT | 0.729 | 0.579 | 1.77E-05 |
| 19 | rs10411220 | 37367247 | ZNF507 | 161145 base upstream | q13.11 | AG | 0.3424 | 1.529 | 0.0002541 |
| 1 | rs12409660 | 173288830 | TNN | 14786 base upstream | q25.1 | CG | 0.2711 | 1.728 | 1.79E-05 |
| 19 | rs7260436 | 37368934 | ZNF507 | 159458 base upstream | q13.11 | AC | 0.4834 | 1.551 | 0.0002469 |
| 14 | rs1698517 | 42258722 | LRFN5 | 815224 base downstream | q21.2 | CT | 0.0669 | 2.157 | 0.0002147 |
| 6 | rs7748159 | 136506228 | PDE7B | intron 3 | q23.3 | GT | 0.4033 | 1.601 | 8.42E-05 |
| 1 | rs3856106 | 180321600 | ZNF648 | 24130 base downstream | q25.3 | CT | 0.6199 | 1.713 | 0.000138 |
| 15 | rs12917513 | 52109020 | UNC13C | intron 1 | q21.3 | AT | 0.8285 | 0.553 | 0.0001766 |
| 2 | rs843390 | 115891622 | DPP10 | intron 3 | q14.1 | CG | 0.0911 | 1.923 | 0.000116 |
| 9 | rs6475927 | 2668077 | VLDLR | 23592 base downstream | p24.2 | AG | 0.0734 | 1.993 | 0.0002995 |
| 4 | rs10020236 | 95497016 | PGDS | 13966 base downstream | q22.3 | AG | 0.3679 | 1.521 | 0.0005544 |
| 2 | rs843393 | 115890266 | DPP10 | intron 3 | q14.1 | AG | 0.091 | 1.924 | 0.0001166 |
| 9 | rs7859818 | 2664110 | VLDLR | 19625 base downstream | p24.2 | AG | 0.9266 | 0.499 | 0.0002721 |
| 15 | rs12595222 | 58093606 | FOXB1 | 8172 base downstream | q22.2 | AG | 0.159 | 1.68 | 0.0004862 |
| 8 | rs2701437 | 73179080 | TRPA1 | 28707 base downstream | q13.3 | AG | 0.8059 | 0.619 | 0.0003302 |
| 3 | rs11130518 | 56412896 | CAST1 | intron 15 | p14.3 | CT | 0.3782 | 1.48 | 0.0009687 |
| 9 | rs7874073 | 2664864 | VLDLR | 20379 base downstream | p24.2 | AG | 0.0735 | 1.999 | 0.0002799 |
| 6 | rs1600620 | 136507734 | PDE7B | intron 3 | q23.3 | AT | 0.5965 | 0.624 | 8.17E-05 |
| 3 | rs1463524 | 176290623 | NAALADL2 | intron 1 | q26.31 | CT | 0.5775 | 1.493 | 0.0009639 |
| 1 | rs8179259 | 180318899 | ZNF648 | 21429 base downstream | q25.3 | CG | 0.6206 | 1.717 | 0.0001487 |
| 1 | rs11586346 | 95633790 | RWDD3 | 148421 base downstream | p21.3 | AC | 0.9131 | 0.521 | 0.0001899 |
| 3 | rs2713775 | 102221017 | ABI3BP | 26013 base downstream | q12.2 | AT | 0.7095 | 0.617 | 8.30E-05 |
| 8 | rs4076071 | 26559908 | DPYSL2 | intron 10 | p21.2 | CT | 0.8764 | 2.2 | 0.0007815 |
| 3 | rs6445788 | 56418235 | CAST1 | intron 15 | p14.3 | CG | 0.3564 | 1.49 | 0.0009352 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs12743570 | 75106090 | C1orf171 | 102194 base downstream | p31.1 | CG | 0.2578 | 1.587 | 0.0003734 |
| 14 | rs11159275 | 77087999 | SPTLC2 | intron 3 | q24.3 | CT | 0.4608 | 1.566 | 0.0006741 |
| 15 | rs17237465 | 58977303 | RORA | intron 10 | q22.2 | CT | 0.3022 | 0.62 | 0.0007618 |
| 6 | rs2170231 | 136508827 | PDE7B | intron 3 | q23.3 | CT | 0.6015 | 0.623 | 7.40E-05 |
| 9 | rs4641116 | 10649290 | PTPRD | 46781 base downstream | p23 | CT | 0.864 | 0.546 | 4.95E-05 |
| 9 | rs10756088 | 10651370 | PTPRD | 48861 base downstream | p23 | AG | 0.8634 | 0.541 | 5.17E-05 |
| 13 | rs9546775 | 84064321 | SLITRK1 | 709792 base downstream | q31.1 | GT | 0.1306 | 1.648 | 0.0009609 |
| 9 | rs11793970 | 2665728 | VLDLR | 21243 base downstream | p24.2 | CG | 0.0735 | 1.996 | 0.0002901 |
| 1 | rs7552148 | 75112763 | C1orf171 | 108867 base downstream | p31.1 | CT | 0.742 | 0.631 | 0.0003738 |
| 9 | rs7030381 | 10651622 | PTPRD | 49113 base downstream | p23 | AG | 0.1367 | 1.849 | 5.19E-05 |
| 16 | rs4583255 | 29896442 | TAOK2 | intron 1 | p11.2 | AG | 0.5461 | 0.651 | 0.0002902 |
| 3 | rs1546061 | 56410482 | CAST1 | intron 15 | p14.3 | CG | 0.3777 | 1.478 | 0.0009881 |
| 9 | rs7030672 | 10651798 | PTPRD | 49289 base downstream | p23 | CG | 0.1369 | 1.853 | 5.28E-05 |
| 8 | rs1544980 | 10715391 | PINX1 | intron 2 | p23.1 | CT | 0.2004 | 0.546 | 0.0003709 |
| 2 | rs1402446 | 115885861 | DPP10 | intron 3 | q14.1 | AG | 0.9096 | 0.518 | 0.0001358 |
| 10 | rs11002926 | 80752296 | RAI17 | 6017 base downstream | q22.3 | AC | 0.7334 | 1.744 | 0.0003935 |
| 9 | rs4587381 | 10647075 | PTPRD | 44566 base downstream | p23 | GT | 0.1361 | 1.831 | 5.09E-05 |
| 13 | rs9575636 | 84142066 | SLITRK1 | 787537 base downstream | q31.1 | AG | 0.119 | 1.686 | 0.0007148 |
| 9 | rs7034568 | 10652358 | PTPRD | 49849 base downstream | p23 | CT | 0.1373 | 1.861 | 5.44E-05 |
| 2 | rs1717040 | 115885270 | DPP10 | intron 3 | q14.1 | CT | 0.0904 | 1.93 | 0.0001371 |
| 3 | rs6763636 | 56415469 | CAST1 | intron 15 | p14.3 | GT | 0.381 | 1.489 | 0.0008714 |
| 4 | rs6535914 | 154482001 | TRIM2 | 2083 base downstream | q31.3 | CT | 0.3633 | 1.662 | 0.0001162 |
| 8 | rs1469557 | 10744211 | PINX1 | 9502 base downstream | p23.1 | CT | 0.7945 | 1.915 | 0.0001281 |
| 13 | rs7319590 | 84181912 | SLITRK1 | 827383 base downstream | q31.1 | CT | 0.1147 | 1.737 | 0.0004612 |
| 1 | rs6693535 | 225264308 | CDC42BPA | intron 3 | q42.13 | AG | 0.491 | 1.517 | 0.0003494 |
| 9 | rs7029311 | 2667743 | VLDLR | 23258 base downstream | p24.2 | AG | 0.0734 | 1.994 | 0.0002973 |
| 3 | rs11130520 | 56416159 | CAST1 | intron 15 | p14.3 | GT | 0.3812 | 1.49 | 0.0008646 |
| 9 | rs2890924 | 10622596 | PTPRD | 20087 base downstream | p23 | GT | 0.8541 | 0.567 | 0.0001375 |
| 9 | rs7019756 | 10652166 | PTPRD | 49657 base downstream | p23 | CT | 0.8628 | 0.538 | 5.42E-05 |
| 13 | rs9514322 | 104282823 | DAOA | 633541 base upstream | q33.2 | CT | 0.6023 | 0.649 | 0.0003615 |
| 15 | rs3803487 | 58976901 | RORA | intron 10 | q22.2 | AG | 0.3022 | 0.62 | 0.0007589 |
| 4 | rs13110782 | 187045575 | SORBS2 | intron 20 | q35.1 | AG | 0.4215 | 0.657 | 0.0008475 |
| 1 | rs10890086 | 74134374 | LRRC44 | 129915 base upstream | p31.1 | AC | 0.5271 | 0.635 | 0.0001216 |
| 5 | rs10068181 | 105642920 | EFNA5 | 1101329 base upstream | q21.3 | AG | 0.1559 | 1.784 | 7.69E-05 |
| 14 | rs1712699 | 42258562 | LRFN5 | 815064 base downstream | q21.2 | AC | 0.9267 | 0.492 | 0.0002635 |
| 9 | rs4262363 | 10654367 | PTPRD | 51858 base downstream | p23 | AG | 0.1377 | 1.87 | 5.63E-05 |
| 1 | rs1194596 | 152505007 | UBAP2L | intron 23 | q21.3 | AG | 0.4704 | 0.671 | 0.0008161 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 9 | rs4578000 | 10647332 | PTPRD | 44823 base downstream | p23 | AG | 0.8639 | 0.546 | 5.06E-05 |
| 15 | rs12592976 | 81227450 | FSD2 | intron 1 | q25.2 | CT | 0.1178 | 0.467 | 0.0009505 |
| 1 | rs17113478 | 95634310 | RWDD3 | 148941 base downstream | p21.3 | CG | 0.9131 | 0.522 | 0.0001912 |
| 4 | rs7659326 | 92459702 | TMSL3 | 480410 base downstream | q22.1 | AT | 0.2572 | 0.528 | 8.29E-05 |
| 9 | rs7045753 | 10658198 | PTPRD | 55689 base downstream | p23 | CT | 0.8612 | 0.528 | 6.30E-05 |
| 9 | rs10756079 | 10646211 | PTPRD | 43702 base downstream | p23 | CT | 0.1364 | 1.828 | 5.34E-05 |
| 9 | rs7029840 | 2667429 | VLDLR | 22944 base downstream | p24.2 | AC | 0.0734 | 1.994 | 0.0002965 |
| 8 | rs11986722 | 127597922 | FAM84B | 35946 base upstream | q24.21 | CG | 0.893 | 0.569 | 0.0006072 |
| 9 | rs4272438 | 10655040 | PTPRD | 52531 base downstream | p23 | AT | 0.8619 | 0.532 | 5.84E-05 |
| 5 | rs13185419 | 105650965 | EFNA5 | 1093284 base upstream | q21.3 | AC | 0.8437 | 0.559 | 7.68E-05 |
| 1 | rs11210366 | 74140143 | LRRC44 | 124146 base upstream | p31.1 | CT | 0.5575 | 0.613 | 7.11E-05 |
| 16 | rs4788209 | 29920767 | FLJ90652 | intron 6 | p11.2 | CT | 0.5542 | 0.649 | 0.0002986 |
| 9 | rs10756092 | 10654583 | PTPRD | 52074 base downstream | p23 | AC | 0.862 | 0.532 | 5.85E-05 |
| 13 | rs12561049 | 89050456 | GPC5 | 1798431 base upstream | q31.3 | AG | 0.0267 | 2.81 | 0.0002557 |
| 8 | rs2587578 | 73172159 | TRPA1 | 21786 base downstream | q13.3 | AG | 0.1919 | 1.615 | 0.0003183 |
| 16 | rs4788204 | 29902719 | TAOK2 | intron 13 | p11.2 | AG | 0.4539 | 1.536 | 0.0002877 |
| 1 | rs10890092 | 74174906 | LRRC44 | 89383 base upstream | p31.1 | CT | 0.4719 | 1.578 | 0.0001092 |
| 1 | rs12121720 | 75159525 | C1orf171 | 155629 base downstream | p31.1 | AG | 0.2694 | 1.541 | 0.0005993 |
| 3 | rs9880091 | 56416835 | CAST1 | intron 15 | p14.3 | CT | 0.3554 | 1.488 | 0.0009532 |
| 5 | rs13185392 | 105650703 | EFNA5 | 1093546 base upstream | q21.3 | CT | 0.1563 | 1.788 | 7.63E-05 |
| 5 | rs6452297 | 25914456 | CDH9 | 1002009 base upstream | p14.1 | CT | 0.3411 | 1.596 | 0.0001491 |
| 13 | rs9634611 | 89054175 | GPC5 | 1794712 base upstream | q31.3 | GT | 0.9733 | 0.356 | 0.0002507 |
| 18 | rs12960420 | 20409134 | HRH4 | 95216 base downstream | q11.2 | CT | 0.6619 | 1.547 | 0.000984 |
| 9 | rs10756076 | 10645642 | PTPRD | 43133 base downstream | p23 | AG | 0.1365 | 1.827 | 5.42E-05 |
| 6 | rs210051 | 90708821 | BACH2 | intron 2 | q15 | AG | 0.6803 | 1.618 | 0.0003449 |
| 10 | rs11593579 | 36687776 | FZD8 | 717408 base downstream | p11.21 | AG | 0.1146 | 1.806 | 0.0001818 |
| 1 | rs11165434 | 95758927 | RWDD3 | 273558 base downstream | p21.3 | GT | 0.9131 | 0.537 | 0.000404 |
| 20 | rs6056491 | 925164 | RSPO4 | intron 4 | p13 | AG | 0.9386 | 0.456 | 0.0001557 |
| 7 | rs760226 | 152433153 | ACTR3B | 249757 base downstream | q36.2 | AG | 0.6543 | 1.654 | 0.000196 |
| 16 | rs4787489 | 29903381 | TAOK2 | intron 13 | p11.2 | AG | 0.4538 | 1.536 | 0.0002864 |
| 1 | rs12135050 | 95765051 | RWDD3 | 279682 base downstream | p21.3 | AG | 0.0868 | 1.877 | 0.0004256 |
| 1 | rs12118601 | 88293965 | PKN2 | 628544 base upstream | p22.2 | CT | 0.6626 | 1.681 | 0.0001243 |
| 3 | rs9817231 | 56416017 | CAST1 | intron 15 | p14.3 | AT | 0.6189 | 0.671 | 0.0008671 |
| 20 | rs6055881 | 8455713 | PLCB1 | intron 3 | p12.3 | CT | 0.6108 | 1.666 | 8.80E-05 |
| 9 | rs10809147 | 10645366 | PTPRD | 42857 base downstream | p23 | CT | 0.8633 | 0.548 | 5.62E-05 |
| 1 | rs17600725 | 225270854 | CDC42BPA | intron 4 | q42.13 | AG | 0.5191 | 0.674 | 0.0006899 |
| 2 | rs7581748 | 115905074 | DPP10 | intron 3 | q14.1 | AT | 0.9055 | 0.533 | 0.000206 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 8 | rs1896238 | 112148387 | KCNV1 | 1092252 base downstream | q23.2 | AG | 0.2755 | 0.583 | 0.0003723 |
| 6 | rs9387353 | 116094037 | FRK | 275349 base upstream | q22.1 | CT | 0.7847 | 0.627 | 0.000484 |
| 5 | rs7728507 | 153738544 | GALNT10 | intron 5 | q33.2 | CT | 0.7111 | 1.8 | 7.50E-05 |
| 5 | rs1422665 | 153737245 | GALNT10 | intron 5 | q33.2 | CT | 0.7089 | 1.801 | 7.61E-05 |
| 5 | rs1428660 | 25917816 | CDH9 | 998649 base upstream | p14.1 | CT | 0.6592 | 0.629 | 0.0001548 |
| 13 | rs9575638 | 84147159 | SLITRK1 | 792630 base downstream | q31.1 | GT | 0.8807 | 0.594 | 0.000705 |
| 2 | rs875653 | 38366026 | ARL6IP2 | 10601 base upstream | p22.2 | CT | 0.8352 | 2.018 | 0.0002985 |
| 1 | rs4650235 | 74143228 | LRRC44 | 121061 base upstream | p31.1 | AG | 0.4815 | 1.602 | 9.50E-05 |
| 4 | rs2319750 | 52565714 | LOC339977 | intron 3 | q12 | CT | 0.1497 | 0.513 | 0.0007543 |
| 9 | rs10809145 | 10645189 | PTPRD | 42680 base downstream | p23 | AG | 0.1367 | 1.825 | 5.66E-05 |
| 1 | rs6664850 | 75124915 | C1orf171 | 121019 base downstream | p31.1 | AG | 0.2674 | 1.539 | 0.0006167 |
| 8 | rs4733048 | 26555006 | DPYSL2 | intron 8 | p21.2 | CT | 0.1228 | 0.457 | 0.000829 |
| 4 | rs4336191 | 74419872 | ALB | 68997 base upstream | q13.3 | CT | 0.0276 | 2.737 | 0.0003229 |
| 3 | rs7627996 | 176301721 | NAALADL2 | intron 2 | q26.31 | CT | 0.6069 | 1.532 | 0.0005387 |
| 16 | rs4283241 | 29895850 | TAOK2 | intron 1 | p11.2 | AG | 0.4539 | 1.536 | 0.0002908 |
| 13 | rs9319065 | 84157238 | SLITRK1 | 802709 base downstream | q31.1 | AG | 0.8807 | 0.594 | 0.0007027 |
| 5 | rs17116042 | 153740522 | GALNT10 | intron 6 | q33.2 | CT | 0.2906 | 0.555 | 7.24E-05 |
| 13 | rs12100200 | 84143232 | SLITRK1 | 788703 base downstream | q31.1 | AG | 0.1193 | 1.682 | 0.000725 |
| 1 | rs1760802 | 152525899 | HAX1 | 10926 base downstream | q21.3 | CG | 0.4701 | 0.665 | 0.0007681 |
| 14 | rs17633001 | 42261110 | LRFN5 | 817612 base downstream | q21.2 | AG | 0.929 | 0.476 | 0.000336 |
| 1 | rs17600669 | 225268494 | CDC42BPA | intron 3 | q42.13 | AG | 0.519 | 0.673 | 0.000655 |
| 1 | rs1044013 | 152509739 | UBAP2L | EXON 26 | q21.3 | CT | 0.4703 | 0.668 | 0.0007783 |
| 4 | rs13123243 | 116420192 | NDST4 | 165711 base downstream | q26 | AT | 0.3902 | 1.594 | 7.39E-05 |
| 1 | rs1194593 | 152512136 | HAX1 | intron 1 | q21.3 | AG | 0.4702 | 0.666 | 0.0007677 |
| 16 | rs2075157 | 45321875 | MLCK | intron 8 | q11.2 | CT | 0.8581 | 0.58 | 0.0004669 |
| 13 | rs7994475 | 89055707 | GPC5 | 1793180 base upstream | q31.3 | AG | 0.0267 | 2.806 | 0.0002488 |
| 1 | rs10798331 | 173301060 | TNN | 2556 base upstream | q25.1 | AG | 0.3457 | 1.63 | 4.63E-05 |
| 4 | rs6816636 | 92459915 | TMSL3 | 480623 base downstream | q22.1 | AC | 0.7424 | 1.887 | 8.27E-05 |
| 13 | rs1326452 | 104282736 | DAOA | 633628 base upstream | q33.2 | AG | 0.4146 | 1.546 | 0.0002203 |
| 12 | rs1354486 | 97094459 | TMPO | 339080 base upstream | q23.1 | AG | 0.3016 | 0.6 | 0.0008662 |
| 16 | rs9925915 | 29901187 | TAOK2 | intron 10 | p11.2 | CG | 0.4539 | 1.536 | 0.0002893 |
| 4 | rs6813599 | 116426743 | NDST4 | 172262 base downstream | q26 | AT | 0.6098 | 0.629 | 7.62E-05 |
| 7 | rs12672384 | 26559015 | SCAP2 | 114199 base upstream | p15.2 | CT | 0.2133 | 1.618 | 0.0002368 |
| 1 | rs1340447 | 74176368 | LRRC44 | 87921 base upstream | p31.1 | AC | 0.5278 | 0.634 | 0.0001087 |
| 6 | rs3846739 | 80193185 | C6orf152 | 58242 base upstream | q14.1 | AG | 0.1231 | 1.716 | 0.0004084 |
| 7 | rs13224424 | 97318328 | ASNS | 1048 base upstream | q21.3 | CT | 0.132 | 1.732 | 0.0002415 |
| 13 | rs9565956 | 84121490 | SLITRK1 | 766961 base downstream | q31.1 | CT | 0.1118 | 1.723 | 0.0006758 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs6424568 | 74212970 | LRRC44 | 51319 base upstream | p31.1 | AG | 0.5172 | 0.617 | 6.52E-05 |
| 4 | rs7676815 | 116469038 | NDST4 | 214557 base downstream | q26 | CT | 0.3897 | 1.573 | 8.89E-05 |
| 4 | rs6533855 | 116473561 | NDST4 | 219080 base downstream | q26 | AG | 0.3897 | 1.573 | 8.89E-05 |
| 1 | rs17562236 | 75146613 | C1orf171 | 142717 base downstream | p31.1 | AG | 0.7319 | 0.652 | 0.0006145 |
| 5 | rs6891526 | 105644816 | EFNA5 | 1099433 base upstream | q21.3 | AG | 0.1943 | 1.688 | 0.0001594 |
| 1 | rs12755578 | 75147442 | C1orf171 | 143546 base downstream | p31.1 | CG | 0.7319 | 0.651 | 0.000614 |
| 4 | rs7439118 | 116481902 | NDST4 | 227421 base downstream | q26 | CT | 0.3897 | 1.573 | 8.89E-05 |
| 16 | rs7204797 | 29875516 | LOC124446 | 5335 base upstream | p11.2 | CT | 0.5458 | 0.655 | 0.0003558 |
| 1 | rs2733267 | 74177642 | LRRC44 | 86647 base upstream | p31.1 | AG | 0.5277 | 0.633 | 0.0001086 |
| 4 | rs12503088 | 116491650 | NDST4 | 237169 base downstream | q26 | CG | 0.6104 | 0.636 | 8.88E-05 |
| 13 | rs7997861 | 104283297 | DAOA | 633067 base upstream | q33.2 | CT | 0.4149 | 1.547 | 0.0002269 |
| 8 | rs11990167 | 10741808 | PINX1 | 7099 base downstream | p23.1 | CT | 0.7967 | 1.881 | 0.000187 |
| 7 | rs10486010 | 97316254 | ASNS | 3122 base upstream | q21.3 | CT | 0.132 | 1.731 | 0.0002396 |
| 6 | rs12205135 | 116092185 | FRK | 277201 base upstream | q22.1 | CG | 0.215 | 1.596 | 0.0004907 |
| 1 | rs12127639 | 75167786 | C1orf171 | 163890 base downstream | p31.1 | CG | 0.7306 | 0.649 | 0.0006013 |
| 1 | rs2733262 | 74169484 | LRRC44 | 94805 base upstream | p31.1 | CT | 0.5275 | 0.638 | 0.0001358 |
| 8 | rs7010709 | 10739369 | PINX1 | 4660 base downstream | p23.1 | CT | 0.2032 | 0.534 | 0.0001974 |
| 7 | rs10486011 | 97319748 | ASNS | intron 1 | q21.3 | CT | 0.8682 | 0.577 | 0.0002448 |
| 4 | rs4349617 | 116465817 | NDST4 | 211336 base downstream | q26 | CT | 0.6103 | 0.636 | 8.88E-05 |
| 16 | rs11150577 | 29894026 | TAOK2 | intron 1 | p11.2 | AG | 0.454 | 1.534 | 0.0003047 |
| 4 | rs4694161 | 74413190 | ANKRD17 | 69824 base downstream | q13.3 | AG | 0.0275 | 2.721 | 0.0003445 |
| 11 | rs12222200 | 19040692 | MRGPRX2 | 1888 base downstream | p15.1 | CT | 0.6274 | 0.666 | 0.0009916 |
| 4 | rs4519812 | 116466112 | NDST4 | 211631 base downstream | q26 | AG | 0.6103 | 0.636 | 8.88E-05 |
| 9 | rs1322300 | 10625232 | PTPRD | 22723 base downstream | p23 | CT | 0.2401 | 1.57 | 0.0003158 |
| 4 | rs4274815 | 74418309 | ALB | 70560 base upstream | q13.3 | AT | 0.0276 | 2.73 | 0.0003319 |
| 9 | rs7031441 | 2673052 | VLDLR | 28567 base downstream | p24.2 | CG | 0.0991 | 1.908 | 0.000124 |
| 8 | rs17152571 | 10720187 | PINX1 | intron 2 | p23.1 | AG | 0.1311 | 0.418 | 0.0001039 |
| 11 | rs1714336 | 15201694 | INSC | intron 8 | p15.2 | CT | 0.5971 | 0.669 | 0.0005477 |
| 16 | rs4318227 | 29892340 | TAOK2 | 382 base upstream | p11.2 | CG | 0.546 | 0.652 | 0.0003076 |
| 1 | rs2733265 | 74175716 | LRRC44 | 88573 base upstream | p31.1 | CG | 0.5278 | 0.634 | 0.0001088 |
| 11 | rs4755236 | 44205402 | EXT2 | intron 12 | p11.2 | CG | 0.6341 | 0.667 | 0.0004737 |
| 16 | rs11247495 | 45361965 | MLCK | 22243 base downstream | q11.2 | CT | 0.8528 | 0.568 | 0.0003604 |
| 13 | rs7139884 | 104283684 | DAOA | 632680 base upstream | q33.2 | AC | 0.4151 | 1.549 | 0.0002328 |
| 4 | rs4345145 | 74420504 | ALB | 68365 base upstream | q13.3 | CT | 0.9722 | 0.363 | 0.0002957 |
| 10 | rs11199661 | 122679558 | BRWD2 | 20533 base downstream | q26.12 | AG | 0.0193 | 3.413 | 0.0001232 |
| 13 | rs7322623 | 39454803 | COG6 | 230171 base downstream | q13.3 | AC | 0.3539 | 1.568 | 0.0002029 |
| 8 | rs6990589 | 10739944 | PINX1 | 5235 base downstream | p23.1 | AG | 0.2029 | 0.534 | 0.0002027 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 10 | rs7897007 | 24661175 | KIAA1217 | intron 3 | p12.1 | AG | 0.8217 | 0.584 | 0.0001035 |
| 1 | rs10782637 | 75176175 | C1orf171 | 172279 base downstream | p31.1 | AC | 0.7307 | 0.649 | 0.0006105 |
| 7 | rs10486009 | 97316047 | ASNS | 3329 base upstream | q21.3 | CG | 0.8679 | 0.578 | 0.0002381 |
| 4 | rs6446922 | 74415477 | ANKRD17 | 72111 base downstream | q13.3 | AG | 0.9724 | 0.367 | 0.0003384 |
| 1 | rs881713 | 95757654 | RWDD3 | 272285 base downstream | p21.3 | AG | 0.0869 | 1.86 | 0.0004031 |
| 10 | rs12359177 | 122678184 | BRWD2 | 19159 base downstream | q26.12 | AG | 0.0193 | 3.42 | 0.000121 |
| 3 | rs1282931 | 113073512 | PHLDB2 | 11987 base upstream | q13.2 | AT | 0.3289 | 1.512 | 0.0009784 |
| 10 | rs12357022 | 122680429 | BRWD2 | 21404 base downstream | q26.12 | AG | 0.9807 | 0.293 | 0.0001246 |
| 10 | rs11199663 | 122682094 | BRWD2 | 23069 base downstream | q26.12 | AG | 0.0194 | 3.405 | 0.000126 |
| 4 | rs1948983 | 116464246 | NDST4 | 209765 base downstream | q26 | CG | 0.6103 | 0.636 | 8.88E-05 |
| 4 | rs4834466 | 116483034 | NDST4 | 228553 base downstream | q26 | CG | 0.3897 | 1.573 | 8.89E-05 |
| 10 | rs11199660 | 122679402 | BRWD2 | 20377 base downstream | q26.12 | AG | 0.0193 | 3.418 | 0.0001217 |
| 9 | rs10756072 | 10625939 | PTPRD | 23430 base downstream | p23 | AG | 0.7599 | 0.636 | 0.0003077 |
| 2 | rs10496495 | 115959914 | DPP10 | intron 3 | q14.1 | CT | 0.091 | 1.868 | 0.000242 |
| 13 | rs9602525 | 84114641 | SLITRK1 | 760112 base downstream | q31.1 | AT | 0.1102 | 1.719 | 0.0007262 |
| 1 | rs3795453 | 225271954 | CDC42BPA | intron 5 | q42.13 | CT | 0.4797 | 1.465 | 0.0009705 |
| 8 | rs2701444 | 73172073 | TRPA1 | 21700 base downstream | q13.3 | CT | 0.8081 | 0.619 | 0.0003189 |
| 6 | rs9405506 | 1653870 | GMDS | intron 2 | p25.3 | CT | 0.2307 | 1.648 | 0.0001819 |
| 4 | rs6446920 | 74412327 | ANKRD17 | 68961 base downstream | q13.3 | CT | 0.0275 | 2.724 | 0.0003474 |
| 18 | rs2587642 | 37343203 | PIK3C3 | 445993 base upstream | q12.3 | CT | 0.3696 | 1.555 | 0.000201 |
| 13 | rs9567450 | 44106744 | TSC22D1 | 58043 base downstream | q14.11 | CT | 0.639 | 1.581 | 0.0003355 |
| 10 | rs11199659 | 122678943 | BRWD2 | 19918 base downstream | q26.12 | AT | 0.0193 | 3.42 | 0.0001211 |
| 4 | rs6829587 | 116486031 | NDST4 | 231550 base downstream | q26 | CT | 0.3897 | 1.572 | 8.98E-05 |
| 8 | rs7819694 | 4080287 | CSMD1 | intron 67 | p23.2 | CT | 0.0411 | 2.534 | 0.0001302 |
| 13 | rs13378761 | 84112297 | SLITRK1 | 757768 base downstream | q31.1 | AC | 0.1101 | 1.719 | 0.0007311 |
| 10 | rs7092964 | 128737210 | DOCK1 | intron 21 | q26.2 | CT | 0.9159 | 0.556 | 0.0009566 |
| 4 | rs4408930 | 74419733 | ALB | 69136 base upstream | q13.3 | AG | 0.0276 | 2.735 | 0.0003258 |
| 1 | rs12747472 | 75084050 | C1orf171 | 80154 base downstream | p31.1 | CT | 0.2902 | 1.573 | 0.0005066 |
| 1 | rs17479604 | 108005170 | VAV3 | intron 8 | p13.3 | AC | 0.1372 | 1.654 | 0.0006977 |
| 10 | rs10741051 | 24662335 | KIAA1217 | intron 3 | p12.1 | AG | 0.1782 | 1.709 | 0.0001054 |
| 3 | rs1495693 | 41535096 | ULK4 | intron 5 | p22.1 | CT | 0.0609 | 1.977 | 0.0007539 |
| 7 | rs672366 | 152434353 | ACTR3B | 250957 base downstream | q36.2 | CG | 0.3148 | 0.593 | 0.0002327 |
| 19 | rs7260548 | 37369022 | ZNF507 | 159370 base upstream | q13.11 | CT | 0.5132 | 0.656 | 0.0004333 |
| 1 | rs4465211 | 219585205 | DUSP10 | 356183 base upstream | q41 | AG | 0.3607 | 1.524 | 0.0004758 |
| 1 | rs10863604 | 219588044 | DUSP10 | 353344 base upstream | q41 | CG | 0.3608 | 1.525 | 0.0004726 |
| 4 | rs13101335 | 116474793 | NDST4 | 220312 base downstream | q26 | GT | 0.3897 | 1.573 | 8.89E-05 |
| 8 | rs17152584 | 10723261 | PINX1 | intron 3 | p23.1 | AG | 0.1315 | 0.418 | 0.0001025 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 8 | rs6995541 | 10708670 | PINX1 | intron 1 | p23.1 | AG | 0.6961 | 1.606 | 0.0009987 |
| 20 | rs17782078 | 3489382 | ATRN | EXON 8 | p13 | CT | 0.0498 | 2.071 | 0.0009643 |
| 1 | rs7537211 | 180325179 | ZNF648 | 27709 base downstream | q25.3 | AG | 0.613 | 1.637 | 0.0002781 |
| 1 | rs12129191 | 75167915 | C1orf171 | 164019 base downstream | p31.1 | AG | 0.7306 | 0.649 | 0.0006025 |
| 7 | rs6966699 | 97314777 | ASNS | 4599 base upstream | q21.3 | CT | 0.8674 | 0.579 | 0.0002297 |
| 1 | rs12732265 | 75170858 | C1orf171 | 166962 base downstream | p31.1 | CT | 0.2694 | 1.541 | 0.0006031 |
| 1 | rs6671621 | 219584095 | DUSP10 | 357293 base upstream | q41 | CG | 0.3607 | 1.524 | 0.0004795 |
| 11 | rs12364403 | 106336866 | GUCY1A2 | intron 5 | q22.3 | CT | 0.2479 | 0.581 | 0.0007451 |
| 5 | rs6883970 | 105632419 | EFNA5 | 1111830 base upstream | q21.3 | CT | 0.807 | 0.598 | 0.000191 |
| 1 | rs6693646 | 75238998 | LHX8 | 127708 base upstream | p31.1 | GT | 0.2769 | 1.554 | 0.000425 |
| 8 | rs11250082 | 10741204 | PINX1 | 6495 base downstream | p23.1 | CT | 0.7971 | 1.872 | 0.0002038 |
| 10 | rs12355094 | 122688268 | BRWD2 | 29243 base downstream | q26.12 | CT | 0.9804 | 0.298 | 0.0001406 |
| 3 | rs1913494 | 113072652 | PHLDB2 | 12847 base upstream | q13.2 | AG | 0.6711 | 0.661 | 0.0009518 |
| 6 | rs182382 | 90704480 | BACH2 | intron 1 | q15 | CG | 0.6805 | 1.597 | 0.0004528 |
| 16 | rs4787486 | 29885063 | LOC124446 | intron 3 | p11.2 | AT | 0.5458 | 0.654 | 0.0003442 |
| 3 | rs17040733 | 15109324 | ZFYVE20 | intron 10 | p24.3 | CG | 0.9566 | 0.422 | 0.000111 |
| 1 | rs12136757 | 95769656 | RWDD3 | 284287 base downstream | p21.3 | CT | 0.0868 | 1.882 | 0.0004422 |
| 16 | rs6565173 | 29881668 | LOC124446 | intron 1 | p11.2 | AG | 0.4542 | 1.528 | 0.0003471 |
| 7 | rs498474 | 152436044 | ACTR3B | 252648 base downstream | q36.2 | AG | 0.3144 | 0.593 | 0.0002324 |
| 4 | rs6533852 | 116461695 | NDST4 | 207214 base downstream | q26 | GT | 0.6103 | 0.636 | 8.88E-05 |
| 16 | rs11901 | 29891571 | LOC124446 | intron 5 | p11.2 | CG | 0.5459 | 0.654 | 0.0003407 |
| 20 | rs17370440 | 19711787 | SLC24A3 | 60247 base downstream | p11.23 | AT | 0.1058 | 1.885 | 0.0001313 |
| 7 | rs496724 | 152435872 | ACTR3B | 252476 base downstream | q36.2 | AG | 0.6855 | 1.687 | 0.0002325 |
| 11 | rs1714337 | 15203462 | INSC | intron 8 | p15.2 | AG | 0.5972 | 0.669 | 0.0005645 |
| 8 | rs2701445 | 73171999 | TRPA1 | 21626 base downstream | q13.3 | GT | 0.1919 | 1.615 | 0.0003191 |
| 5 | rs2116732 | 159147091 | ADRA1B | 129226 base upstream | q33.3 | AG | 0.0135 | 3.438 | 0.0008476 |
| 13 | rs9519488 | 104284523 | DAOA | 631841 base upstream | q33.2 | AT | 0.5838 | 0.643 | 0.0002599 |
| 6 | rs292250 | 90703875 | BACH2 | intron 1 | q15 | AG | 0.6805 | 1.597 | 0.0004534 |
| 3 | rs1565960 | 41542696 | ULK4 | intron 5 | p22.1 | AG | 0.0608 | 1.977 | 0.0007479 |
| 6 | rs9357865 | 55494436 | HMGCLL1 | intron 6 | p12.1 | AG | 0.8803 | 0.55 | 0.0007631 |
| 13 | rs9560417 | 89159717 | GPC5 | 1689170 base upstream | q31.3 | AG | 0.9732 | 0.366 | 0.0002361 |
| 3 | rs931461 | 56421736 | CAST1 | intron 15 | p14.3 | GT | 0.3602 | 1.49 | 0.0009195 |
| 7 | rs594243 | 152436388 | ACTR3B | 252992 base downstream | q36.2 | CT | 0.6866 | 1.686 | 0.0002337 |
| 7 | rs593874 | 152436337 | ACTR3B | 252941 base downstream | q36.2 | AG | 0.6865 | 1.686 | 0.0002334 |
| 3 | rs13318013 | 15120491 | ZFYVE20 | 4832 base downstream | p24.3 | AG | 0.0453 | 2.298 | 0.0001806 |
| 6 | rs2046092 | 136500931 | PDE7B | intron 3 | q23.3 | AG | 0.6049 | 0.635 | 0.000171 |
| 1 | rs2346344 | 75219251 | LHX8 | 147455 base upstream | p31.1 | GT | 0.7231 | 0.643 | 0.0004275 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 13 | rs1409470 | 104284951 | DAOA | 631413 base upstream | q33.2 | AG | 0.5837 | 0.643 | 0.0002629 |
| 7 | rs593793 | 152436277 | ACTR3B | 252881 base downstream | q36.2 | AG | 0.3135 | 0.593 | 0.000234 |
| 3 | rs1795312 | 41535386 | ULK4 | intron 5 | p22.1 | AT | 0.0609 | 1.977 | 0.0007529 |
| 1 | rs2789706 | 74186512 | LRRC44 | 77777 base upstream | p31.1 | CT | 0.5268 | 0.63 | 9.38E-05 |
| 1 | rs12565220 | 61295468 | NFIA | 25414 base upstream | p31.3 | CT | 0.8928 | 0.555 | 0.0009018 |
| 3 | rs13326820 | 15097982 | ZFYVE20 | intron 5 | p24.3 | AG | 0.9556 | 0.43 | 0.000147 |
| 11 | rs3925045 | 131494847 | HNT | intron 2 | q25 | CG | 0.8249 | 1.911 | 0.000433 |
| 6 | rs9374564 | 116121301 | FRK | 248085 base upstream | q22.1 | CT | 0.7799 | 0.643 | 0.000738 |
| 9 | rs10738172 | 10624079 | PTPRD | 21570 base downstream | p23 | AG | 0.2416 | 1.558 | 0.0003849 |
| 6 | rs292251 | 90702947 | BACH2 | intron 1 | q15 | AG | 0.6805 | 1.598 | 0.0004617 |
| 1 | rs1340424 | 74160464 | LRRC44 | 103825 base upstream | p31.1 | CG | 0.4741 | 1.561 | 0.0001561 |
| 6 | rs2046091 | 136500942 | PDE7B | intron 3 | q23.3 | AG | 0.6049 | 0.635 | 0.0001701 |
| 3 | rs9867224 | 15125801 | ZFYVE20 | 10142 base downstream | p24.3 | AG | 0.9546 | 0.438 | 0.0001965 |
| 1 | rs10863605 | 219590026 | DUSP10 | 351362 base upstream | q41 | AG | 0.3477 | 1.55 | 0.0004577 |
| 1 | rs12402756 | 61296851 | NFIA | 24031 base upstream | p31.3 | CT | 0.1072 | 1.802 | 0.000903 |
| 19 | rs12611033 | 61166048 | NALP8 | intron 4 | q13.42 | AG | 0.1607 | 0.468 | 0.0001767 |
| 4 | rs6821637 | 116484342 | NDST4 | 229861 base downstream | q26 | GT | 0.3897 | 1.573 | 8.91E-05 |
| 4 | rs4464590 | 116435600 | NDST4 | 181119 base downstream | q26 | CT | 0.3898 | 1.572 | 9.16E-05 |
| 9 | rs7851410 | 133647911 | RAPGEF1 | 45165 base downstream | q34.13 | CT | 0.2951 | 1.634 | 0.0001621 |
| 1 | rs10922574 | 89361971 | GBP2 | intron 10 | p22.2 | CT | 0.1825 | 0.544 | 0.0006533 |
| 1 | rs12141480 | 95771471 | RWDD3 | 286102 base downstream | p21.3 | CG | 0.0867 | 1.884 | 0.000442 |
| 18 | rs11874148 | 37292163 | PIK3C3 | 497033 base upstream | q12.3 | CT | 0.6192 | 0.639 | 0.0003716 |
| 3 | rs1629284 | 41561312 | ULK4 | intron 5 | p22.1 | CG | 0.0597 | 2.01 | 0.0004893 |
| 9 | rs7855045 | 123781479 | TTLL11 | 9533 base upstream | q33.2 | AG | 0.5336 | 1.498 | 0.0005978 |
| 20 | rs17298185 | 19708160 | SLC24A3 | 56620 base downstream | p11.23 | AG | 0.104 | 1.871 | 0.0001736 |
| 6 | rs4896201 | 136514132 | PDE7B | intron 6 | q23.3 | AG | 0.4138 | 1.574 | 0.0001287 |
| 3 | rs13071948 | 18167244 | SATB1 | 197194 base upstream | p24.3 | AG | 0.8547 | 0.584 | 0.0008792 |
| 1 | rs7522882 | 75215582 | LHX8 | 151124 base upstream | p31.1 | AT | 0.7231 | 0.643 | 0.0004163 |
| 9 | rs7870258 | 2671397 | VLDLR | 26912 base downstream | p24.2 | GT | 0.0992 | 1.915 | 0.0001168 |
| 3 | rs1631168 | 41534618 | ULK4 | intron 5 | p22.1 | AC | 0.0609 | 1.977 | 0.0007552 |
| 8 | rs2087688 | 127013476 | TRIB1 | 493652 base downstream | q24.13 | AG | 0.3789 | 1.564 | 0.0001628 |
| 5 | rs10066864 | 105465931 | EFNA5 | 1278318 base upstream | q21.3 | CT | 0.8674 | 0.598 | 0.0009395 |
| 4 | rs6821554 | 74411672 | ANKRD17 | 68306 base downstream | q13.3 | AG | 0.0241 | 2.816 | 0.0004364 |
| 11 | rs10890590 | 106171269 | GUCY1A2 | intron 3 | q22.3 | AG | 0.2503 | 0.573 | 0.0004604 |
| 8 | rs7819223 | 127015428 | TRIB1 | 495604 base downstream | q24.13 | CT | 0.621 | 0.639 | 0.0001644 |
| 7 | rs10486848 | 84575619 | SEMA3D | intron 16 | q21.11 | AG | 0.1861 | 1.716 | 0.0002007 |
| 7 | rs17131831 | 97313206 | ASNS | 6170 base upstream | q21.3 | AG | 0.8673 | 0.579 | 0.00023 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 4 | rs6841435 | 154494114 | MND1 | intron 2 | q31.3 | CT | 0.5646 | 0.621 | 0.0001165 |
| 8 | rs7005531 | 10719627 | PINX1 | intron 2 | p23.1 | AG | 0.2394 | 0.602 | 0.0009611 |
| 1 | rs511201 | 199815919 | NAV1 | 68153 base upstream | q32.1 | AG | 0.7466 | 0.641 | 0.0004701 |
| 9 | rs11243525 | 133646531 | RAPGEF1 | 43785 base downstream | q34.13 | AT | 0.7043 | 0.611 | 0.0001657 |
| 9 | rs10793897 | 133647188 | RAPGEF1 | 44442 base downstream | q34.13 | CT | 0.7044 | 0.612 | 0.0001653 |
| 8 | rs4568586 | 127018859 | TRIB1 | 499035 base downstream | q24.13 | AT | 0.6207 | 0.639 | 0.0001723 |
| 8 | rs1491474 | 127011528 | TRIB1 | 491704 base downstream | q24.13 | AC | 0.6211 | 0.635 | 0.0001353 |
| 1 | rs11162286 | 75199985 | LHX8 | 166721 base upstream | p31.1 | AG | 0.2768 | 1.56 | 0.0003942 |
| 4 | rs10516610 | 116460667 | NDST4 | 206186 base downstream | q26 | CT | 0.6103 | 0.636 | 8.88E-05 |
| 18 | rs4318293 | 37293712 | PIK3C3 | 495484 base upstream | q12.3 | AC | 0.3801 | 1.561 | 0.0003686 |
| 1 | rs6690986 | 219579859 | DUSP10 | 361529 base upstream | q41 | CT | 0.6393 | 0.657 | 0.0004847 |
| 8 | rs2271356 | 10721186 | PINX1 | intron 3 | p23.1 | AT | 0.2396 | 0.599 | 0.0008677 |
| 6 | rs9498719 | 102373779 | GRIK2 | intron 9 | q16.3 | CT | 0.9239 | 0.526 | 0.0005822 |
| 15 | rs12592703 | 52099177 | UNC13C | intron 1 | q21.3 | CT | 0.7878 | 0.616 | 0.0004098 |
| 1 | rs4313406 | 219578338 | DUSP10 | 363050 base upstream | q41 | CT | 0.6393 | 0.657 | 0.000486 |
| 8 | rs2409651 | 10717307 | PINX1 | intron 2 | p23.1 | CT | 0.7606 | 1.66 | 0.0009692 |
| 7 | rs6465629 | 97308426 | ASNS | 10950 base upstream | q21.3 | CT | 0.8674 | 0.58 | 0.0002354 |
| 11 | rs1792556 | 15201097 | INSC | intron 8 | p15.2 | GT | 0.4031 | 1.495 | 0.0005485 |
| 8 | rs9693235 | 4109411 | CSMD1 | intron 67 | p23.2 | AG | 0.0657 | 2.105 | 0.000209 |
| 9 | rs4741044 | 10629445 | PTPRD | 26936 base downstream | p23 | AG | 0.862 | 0.555 | 7.89E-05 |
| 7 | rs17561700 | 84580693 | SEMA3D | intron 16 | q21.11 | GT | 0.1865 | 1.701 | 0.0002313 |
| 7 | rs13223125 | 97309563 | ASNS | 9813 base upstream | q21.3 | AT | 0.8673 | 0.579 | 0.0002327 |
| 12 | rs1160327 | 97086002 | TMPO | 347537 base upstream | q23.1 | AG | 0.3762 | 0.647 | 0.0009877 |
| 4 | rs7434366 | 116535799 | NDST4 | 281318 base downstream | q26 | AT | 0.3655 | 1.585 | 9.89E-05 |
| 1 | rs3845358 | 75222180 | LHX8 | 144526 base upstream | p31.1 | AC | 0.2769 | 1.554 | 0.0004274 |
| 1 | rs10797093 | 159370069 | DEDD | 967 base downstream | q23.3 | GT | 0.3052 | 1.533 | 0.000322 |
| 11 | rs12223742 | 131489477 | HNT | intron 2 | q25 | CT | 0.1751 | 0.528 | 0.0004527 |
| 1 | rs678378 | 95781532 | RWDD3 | 296163 base downstream | p21.3 | AG | 0.0867 | 1.893 | 0.0004592 |
| 6 | rs12333317 | 102368610 | GRIK2 | intron 8 | q16.3 | AG | 0.0815 | 1.893 | 0.0006349 |
| 13 | rs1853979 | 104285669 | DAOA | 630695 base upstream | q33.2 | AG | 0.4174 | 1.56 | 0.0002964 |
| 1 | rs3912426 | 75235049 | LHX8 | 131657 base upstream | p31.1 | AG | 0.2769 | 1.554 | 0.0004259 |
| 5 | rs13361333 | 105649426 | EFNA5 | 1094823 base upstream | q21.3 | CT | 0.1621 | 1.78 | 9.53E-05 |
| 20 | rs6136836 | 19725525 | SLC24A3 | 73985 base downstream | p11.23 | CT | 0.1054 | 1.88 | 0.00014 |
| 11 | rs1532353 | 44191829 | EXT2 | intron 12 | p11.2 | CT | 0.3592 | 1.499 | 0.0005922 |
| 20 | rs6136840 | 19740762 | RIN2 | 77447 base upstream | p11.23 | CG | 0.9038 | 0.539 | 0.0001796 |
| 8 | rs2409667 | 10767033 | XKR6 | 24033 base upstream | p23.1 | AG | 0.8264 | 2.016 | 0.0001663 |
| 5 | rs11949195 | 25900953 | CDH9 | 1015512 base upstream | p14.1 | AT | 0.6164 | 0.608 | 0.0001894 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 20 | rs6035436 | 19705555 | SLC24A3 | 54015 base downstream | p11.23 | CG | 0.896 | 0.534 | 0.0001728 |
| 13 | rs9575613 | 84081505 | SLITRK1 | 726976 base downstream | q31.1 | AC | 0.8934 | 0.582 | 0.0007448 |
| 8 | rs2052963 | 10713033 | PINX1 | intron 1 | p23.1 | GT | 0.7611 | 1.655 | 0.0009989 |
| 11 | rs4755234 | 44189011 | EXT2 | intron 12 | p11.2 | CT | 0.641 | 0.667 | 0.0005962 |
| 8 | rs7824384 | 10720735 | PINX1 | intron 2 | p23.1 | AC | 0.7606 | 1.662 | 0.0009412 |
| 3 | rs1282932 | 113072462 | PHLDB2 | 13037 base upstream | q13.2 | AC | 0.6711 | 0.661 | 0.0009503 |
| 3 | rs9839660 | 15005549 | NR2C2 | intron 1 | p24.3 | AT | 0.0441 | 2.274 | 0.0002384 |
| 14 | rs10498375 | 42258065 | LRFN5 | 814567 base downstream | q21.2 | AC | 0.9266 | 0.492 | 0.0002622 |
| 15 | rs12593288 | 31695395 | RYR3 | intron 19 | q14 | CT | 0.79 | 1.793 | 0.0004028 |
| 8 | rs7840785 | 10720537 | PINX1 | intron 2 | p23.1 | CT | 0.7173 | 1.611 | 0.0008928 |
| 16 | rs3814884 | 29902237 | TAOK2 | intron 12 | p11.2 | AT | 0.4532 | 1.53 | 0.0004323 |
| 1 | rs6704485 | 219574484 | DUSP10 | 366904 base upstream | q41 | CG | 0.3607 | 1.521 | 0.0004937 |
| 1 | rs1355136 | 95792027 | RWDD3 | 306658 base downstream | p21.3 | CT | 0.9105 | 0.52 | 0.0005074 |
| 4 | rs7340984 | 154496631 | MND1 | intron 3 | q31.3 | CG | 0.5589 | 0.629 | 0.000127 |
| 3 | rs17040729 | 15104541 | ZFYVE20 | intron 9 | p24.3 | GT | 0.0446 | 2.335 | 0.0001339 |
| 13 | rs276420 | 39470070 | COG6 | 245438 base downstream | q13.3 | GT | 0.5443 | 0.666 | 0.0004339 |
| 5 | rs1366465 | 25905847 | CDH9 | 1010618 base upstream | p14.1 | CT | 0.3835 | 1.636 | 0.000192 |
| 8 | rs10109550 | 10722996 | PINX1 | intron 3 | p23.1 | GT | 0.7603 | 1.671 | 0.0008476 |
| 1 | rs10890101 | 74218172 | LRRC44 | 46117 base upstream | p31.1 | CT | 0.5113 | 0.628 | 0.0001671 |
| 5 | rs10056331 | 105416189 | EFNA5 | 1328060 base upstream | q21.3 | CT | 0.2986 | 1.556 | 0.0003101 |
| 12 | rs2364153 | 51736002 | TENC1 | intron 10 | q13.13 | CT | 0.6292 | 0.661 | 0.0004579 |
| 5 | rs11949113 | 25900515 | CDH9 | 1015950 base upstream | p14.1 | GT | 0.3836 | 1.645 | 0.0001893 |
| 5 | rs12658597 | 25906087 | CDH9 | 1010378 base upstream | p14.1 | CT | 0.6165 | 0.612 | 0.0001929 |
| 8 | rs16938030 | 73185849 | TRPA1 | 35476 base downstream | q13.3 | CT | 0.1978 | 1.584 | 0.000587 |
| 13 | rs9575621 | 84102404 | SLITRK1 | 747875 base downstream | q31.1 | AC | 0.1077 | 1.71 | 0.0008114 |
| 1 | rs6704281 | 219574269 | DUSP10 | 367119 base upstream | q41 | CT | 0.3607 | 1.521 | 0.0004939 |
| 15 | rs1897042 | 52090751 | UNC13C | 1641 base upstream | q21.3 | AT | 0.3478 | 1.563 | 0.0007924 |
| 6 | rs210052 | 90708506 | BACH2 | intron 2 | q15 | CT | 0.32 | 0.627 | 0.0004435 |
| 20 | rs2866743 | 39604287 | CHD6 | intron 35 | q12 | AG | 0.9827 | 0.331 | 0.00076 |
| 8 | rs6989846 | 10723495 | PINX1 | intron 3 | p23.1 | CT | 0.7603 | 1.673 | 0.0008297 |
| 18 | rs8089910 | 44764374 | SMAD7 | 33295 base downstream | q21.1 | CG | 0.3675 | 1.53 | 0.000268 |
| 7 | rs12670740 | 26560257 | SCAP2 | 112957 base upstream | p15.2 | CT | 0.7872 | 0.625 | 0.000338 |
| 1 | rs1267131 | 199813717 | NAV1 | 70355 base upstream | q32.1 | AC | 0.7462 | 0.639 | 0.0005089 |
| 20 | rs6136842 | 19742718 | RIN2 | 75491 base upstream | p11.23 | CG | 0.9033 | 0.542 | 0.0002028 |
| 5 | rs6878200 | 105608827 | EFNA5 | 1135422 base upstream | q21.3 | CT | 0.7987 | 0.609 | 0.0002889 |
| 1 | rs1509178 | 95774113 | RWDD3 | 288744 base downstream | p21.3 | CT | 0.0867 | 1.886 | 0.0004425 |
| 3 | rs13060927 | 18165497 | SATB1 | 198941 base upstream | p24.3 | AG | 0.1402 | 1.717 | 0.0008271 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs2893089 | 89403309 | GBP7 | intron 9 | p22.2 | GT | 0.8183 | 1.834 | 0.0006539 |
| 4 | rs11098294 | 116455651 | NDST4 | 201170 base downstream | q26 | CG | 0.6071 | 0.646 | 0.0001498 |
| 4 | rs1979975 | 116455401 | NDST4 | 200920 base downstream | q26 | AG | 0.6071 | 0.646 | 0.0001498 |
| 5 | rs347670 | 62562511 | LOC389293 | 453585 base downstream | q12.1 | CT | 0.1346 | 0.458 | 0.0006321 |
| 20 | rs16981125 | 19724391 | SLC24A3 | 72851 base downstream | p11.23 | AG | 0.8945 | 0.531 | 0.0001377 |
| 7 | rs4726247 | 152452942 | ACTR3B | 269546 base downstream | q36.2 | AG | 0.3295 | 0.622 | 0.0003716 |
| 4 | rs6851203 | 116459223 | NDST4 | 204742 base downstream | q26 | AG | 0.6071 | 0.646 | 0.0001499 |
| 4 | rs9999729 | 92459054 | TMSL3 | 479762 base downstream | q22.1 | CG | 0.2785 | 0.559 | 0.0001131 |
| 7 | rs17344459 | 97304570 | ASNS | 14806 base upstream | q21.3 | CT | 0.8693 | 0.578 | 0.000226 |
| 13 | rs276407 | 39479629 | COG6 | 254997 base downstream | q13.3 | AG | 0.5446 | 0.667 | 0.0004401 |
| 3 | rs9839836 | 15118432 | ZFYVE20 | 2773 base downstream | p24.3 | GT | 0.0453 | 2.302 | 0.0001773 |
| 13 | rs1446792 | 84089937 | SLITRK1 | 735408 base downstream | q31.1 | AG | 0.107 | 1.715 | 0.0007738 |
| 4 | rs9999885 | 92459103 | TMSL3 | 479811 base downstream | q22.1 | AG | 0.7213 | 1.787 | 0.0001133 |
| 5 | rs13154706 | 153749486 | GALNT10 | intron 7 | q33.2 | CT | 0.2926 | 0.573 | 0.0002054 |
| 7 | rs2732741 | 84685921 | SEMA3D | 96738 base downstream | q21.11 | AT | 0.2099 | 1.612 | 0.0006101 |
| 4 | rs17842205 | 89068576 | SPP1 | 47249 base upstream | q22.1 | AC | 0.0905 | 1.977 | 0.0001683 |
| 11 | rs7950006 | 80981836 | MGC33846 | 1138862 base upstream | q14.1 | AG | 0.5508 | 0.646 | 0.0001862 |
| 7 | rs760228 | 152433675 | ACTR3B | 250279 base downstream | q36.2 | CT | 0.6269 | 1.658 | 0.0002098 |
| 4 | rs1396064 | 116442250 | NDST4 | 187769 base downstream | q26 | GT | 0.3929 | 1.547 | 0.000153 |
| 4 | rs7653977 | 92459301 | TMSL3 | 480009 base downstream | q22.1 | AT | 0.2787 | 0.56 | 0.0001131 |
| 11 | rs7933268 | 80981521 | MGC33846 | 1139177 base upstream | q14.1 | GT | 0.5508 | 0.646 | 0.0001861 |
| 13 | rs9514325 | 104287517 | DAOA | 628847 base upstream | q33.2 | AG | 0.4185 | 1.564 | 0.0003311 |
| 21 | rs17000817 | 25543181 | MRPL39 | 336659 base upstream | q21.2 | CT | 0.0273 | 2.595 | 0.0009774 |
| 6 | rs1150711 | 28316514 | ZNF307 | 3954 base upstream | p22.1 | CT | 0.31 | 0.615 | 0.000479 |
| 4 | rs7698264 | 116450640 | NDST4 | 196159 base downstream | q26 | CT | 0.6071 | 0.646 | 0.0001507 |
| 20 | rs17370886 | 19731315 | SLC24A3 | 79775 base downstream | p11.23 | GT | 0.8948 | 0.536 | 0.0001668 |
| 4 | rs6533848 | 116448276 | NDST4 | 193795 base downstream | q26 | GT | 0.6071 | 0.646 | 0.0001516 |
| 12 | rs10860299 | 97075690 | TMPO | 357849 base upstream | q23.1 | AG | 0.3721 | 0.632 | 0.0008461 |
| 7 | rs12704945 | 97286690 | ASNS | 32686 base upstream | q21.3 | AT | 0.1303 | 1.745 | 0.0001951 |
| 19 | rs11084419 | 61182755 | NALP8 | intron 9 | q13.42 | CT | 0.8417 | 2.127 | 0.0001506 |
| 1 | rs1327098 | 75134581 | C1orf171 | 130685 base downstream | p31.1 | AG | 0.2541 | 1.543 | 0.0007072 |
| 5 | rs6870010 | 153745624 | GALNT10 | intron 6 | q33.2 | CT | 0.2761 | 0.573 | 0.0001233 |
| 13 | rs276402 | 39483845 | COG6 | 259213 base downstream | q13.3 | AC | 0.5445 | 0.668 | 0.0004482 |
| 7 | rs7808642 | 97288397 | ASNS | 30979 base upstream | q21.3 | GT | 0.8697 | 0.573 | 0.0001962 |
| 1 | rs11590181 | 95591184 | RWDD3 | 105815 base downstream | p21.3 | GT | 0.1303 | 1.721 | 0.0003174 |
| 15 | rs7174086 | 89915807 | SV2B | 276155 base downstream | q26.1 | CG | 0.3398 | 0.645 | 0.000765 |
| 8 | rs7460673 | 21342868 | GFRA2 | 250943 base upstream | p21.3 | CT | 0.7848 | 0.604 | 0.0001388 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 4 | rs6533850 | 116454363 | NDST4 | 199882 base downstream | q26 | AT | 0.6071 | 0.646 | 0.0001497 |
| 1 | rs4656002 | 88287316 | PKN2 | 635193 base upstream | p22.2 | CT | 0.6308 | 1.61 | 0.000194 |
| 1 | rs10923015 | 88287567 | PKN2 | 634942 base upstream | p22.2 | AT | 0.3692 | 0.621 | 0.0001925 |
| 1 | rs12750340 | 75241712 | LHX8 | 124994 base upstream | p31.1 | CT | 0.7243 | 0.645 | 0.0005205 |
| 3 | rs2306855 | 15094808 | ZFYVE20 | intron 4 | p24.3 | CT | 0.0432 | 2.319 | 0.0001695 |
| 1 | rs4656003 | 88288082 | PKN2 | 634427 base upstream | p22.2 | CT | 0.6308 | 1.611 | 0.0001917 |
| 1 | rs7511679 | 160514028 | NOS1AP | intron 2 | q23.3 | CT | 0.9068 | 2.706 | 0.0004909 |
| 1 | rs11800645 | 160514702 | NOS1AP | intron 2 | q23.3 | GT | 0.0933 | 0.37 | 0.0004887 |
| 7 | rs2078467 | 97297238 | ASNS | 22138 base upstream | q21.3 | CT | 0.1304 | 1.744 | 0.0001971 |
| 1 | rs4656001 | 88287018 | PKN2 | 635491 base upstream | p22.2 | AG | 0.6309 | 1.609 | 0.0001996 |
| 2 | rs11899039 | 6432676 | LOC129607 | 473227 base upstream | p25.2 | AT | 0.0874 | 1.845 | 0.0008742 |
| 7 | rs7786920 | 97274004 | ASNS | 45372 base upstream | q21.3 | CG | 0.8706 | 0.57 | 0.000195 |
| 7 | rs521309 | 152436269 | ACTR3B | 252873 base downstream | q36.2 | AG | 0.3022 | 0.596 | 0.0004058 |
| 7 | rs12668997 | 97303824 | ASNS | 15552 base upstream | q21.3 | CT | 0.8693 | 0.578 | 0.0002275 |
| 7 | rs12669324 | 97270302 | ASNS | 49074 base upstream | q21.3 | CT | 0.1292 | 1.756 | 0.0002006 |
| 20 | rs16981142 | 19738531 | RIN2 | 79678 base upstream | p11.23 | CG | 0.0952 | 1.847 | 0.0002017 |
| 1 | rs7528328 | 160514403 | NOS1AP | intron 2 | q23.3 | CT | 0.1664 | 0.519 | 0.0004705 |
| 11 | rs17125182 | 120728846 | SC5DL | 39517 base downstream | q24.1 | AG | 0.9687 | 0.401 | 0.0003826 |
| 16 | rs11150580 | 29922065 | FLJ90652 | intron 6 | p11.2 | CT | 0.5485 | 0.648 | 0.0003327 |
| 7 | rs2018083 | 152437650 | ACTR3B | 254254 base downstream | q36.2 | AG | 0.6697 | 1.608 | 0.0003726 |
| 13 | rs276422 | 39465395 | COG6 | 240763 base downstream | q13.3 | GT | 0.5487 | 0.669 | 0.0006076 |
| 18 | rs12962825 | 44767911 | SMAD7 | 36832 base downstream | q21.1 | AG | 0.6214 | 0.647 | 0.0002752 |
| 1 | rs625436 | 199828298 | NAV1 | 55774 base upstream | q32.1 | AG | 0.935 | 0.486 | 0.0003145 |
| 4 | rs6532289 | 92459825 | TMSL3 | 480533 base downstream | q22.1 | CT | 0.2788 | 0.56 | 0.0001132 |
| 3 | rs746665 | 15093737 | ZFYVE20 | intron 3 | p24.3 | AT | 0.9567 | 0.431 | 0.000168 |
| 6 | rs17456339 | 104872515 | HACE1 | 410145 base upstream | q21 | CT | 0.8265 | 0.612 | 0.0004882 |
| 9 | rs7030993 | 10616033 | PTPRD | 13524 base downstream | p23 | AG | 0.1402 | 1.731 | 0.0002219 |
| 5 | rs11957357 | 159163705 | ADRA1B | 112612 base upstream | q33.3 | AC | 0.9866 | 0.279 | 0.0006328 |
| 11 | rs16931216 | 15188429 | INSC | intron 7 | p15.2 | AG | 0.9629 | 0.412 | 0.000789 |
| 4 | rs12642075 | 135192004 | PABPC4L | 144934 base upstream | q28.3 | AG | 0.2387 | 0.6 | 0.0008446 |
| 3 | rs2306854 | 15094724 | ZFYVE20 | intron 4 | p24.3 | AC | 0.9568 | 0.431 | 0.0001695 |
| 3 | rs9851219 | 15090727 | ZFYVE20 | EXON 1 | p24.3 | CT | 0.0434 | 2.319 | 0.000168 |
| 1 | rs4655998 | 88286774 | PKN2 | 635735 base upstream | p22.2 | AC | 0.631 | 1.607 | 0.0002115 |
| 1 | rs4656000 | 88286988 | PKN2 | 635521 base upstream | p22.2 | AG | 0.3691 | 0.622 | 0.0002048 |
| 20 | rs17709518 | 3499637 | ATRNL | intron 11 | p13 | AG | 0.9495 | 0.484 | 0.0009304 |
| 9 | rs10733210 | 10614494 | PTPRD | 11985 base downstream | p23 | AC | 0.2403 | 1.546 | 0.000504 |
| 7 | rs459 | 97269283 | ASNS | 50093 base upstream | q21.3 | CT | 0.871 | 0.569 | 0.0002071 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs7525777 | 160514063 | NOS1AP | intron 2 | q23.3 | CT | 0.1664 | 0.519 | 0.0004711 |
| 4 | rs1565911 | 135194503 | PABPC4L | 142435 base upstream | q28.3 | GT | 0.7614 | 1.67 | 0.0008131 |
| 8 | rs17607798 | 21341257 | GFRA2 | 252554 base upstream | p21.3 | AC | 0.7718 | 0.606 | 0.0001017 |
| 1 | rs973886 | 48893107 | AGBL4 | intron 4 | p33 | GT | 0.0569 | 2.144 | 0.0002568 |
| 5 | rs1432711 | 159164640 | ADRA1B | 111677 base upstream | q33.3 | CT | 0.9867 | 0.279 | 0.0006454 |
| 8 | rs2587580 | 73173101 | TRPA1 | 22728 base downstream | q13.3 | CG | 0.7944 | 0.642 | 0.0008995 |
| 9 | rs2146089 | 10614748 | PTPRD | 12239 base downstream | p23 | AG | 0.8597 | 0.578 | 0.0002225 |
| 20 | rs17782347 | 3504956 | ATRN | intron 13 | p13 | CT | 0.0511 | 2.054 | 0.0009435 |
| 3 | rs9844449 | 151314149 | PFN2 | 142718 base downstream | q25.1 | CT | 0.8236 | 1.84 | 0.0009512 |
| 20 | rs17782370 | 3508191 | ATRN | intron 15 | p13 | CT | 0.9488 | 0.488 | 0.0009526 |
| 8 | rs2587579 | 73172373 | TRPA1 | 22000 base downstream | q13.3 | CT | 0.2055 | 1.556 | 0.0008991 |
| 8 | rs1491476 | 127007226 | TRIB1 | 487402 base downstream | q24.13 | AG | 0.6179 | 0.646 | 0.0002481 |
| 8 | rs4738207 | 73191306 | TRPA1 | 40933 base downstream | q13.3 | AG | 0.8028 | 0.633 | 0.0006747 |
| 8 | rs734364 | 21342815 | GFRA2 | 250996 base upstream | p21.3 | CT | 0.2282 | 1.651 | 0.0001002 |
| 9 | rs11788193 | 2682393 | KCNV2 | 25132 base upstream | p24.2 | AT | 0.0723 | 2.022 | 0.0004396 |
| 20 | rs17298654 | 19730288 | SLC24A3 | 78748 base downstream | p11.23 | GT | 0.1052 | 1.866 | 0.0001637 |
| 13 | rs276429 | 39454859 | COG6 | 230227 base downstream | q13.3 | AG | 0.5517 | 0.672 | 0.0007922 |
| 4 | rs6532292 | 92462703 | TMSL3 | 483411 base downstream | q22.1 | CT | 0.7197 | 1.756 | 0.0001165 |
| 5 | rs6862385 | 159173066 | ADRA1B | 103251 base upstream | q33.3 | AC | 0.9868 | 0.277 | 0.000626 |
| 13 | rs7338145 | 39443193 | COG6 | 218561 base downstream | q13.3 | AG | 0.6478 | 0.639 | 0.0002386 |
| 1 | rs7525955 | 160514456 | NOS1AP | intron 2 | q23.3 | AG | 0.8336 | 1.927 | 0.0004713 |
| 3 | rs3773478 | 15088046 | ZFYVE20 | EXON 1 | p24.3 | CT | 0.9565 | 0.432 | 0.0001739 |
| 5 | rs6884390 | 159168575 | ADRA1B | 107742 base upstream | q33.3 | CT | 0.9868 | 0.28 | 0.0006739 |
| 1 | rs617053 | 199814155 | NAV1 | 69917 base upstream | q32.1 | AG | 0.2488 | 1.56 | 0.0006441 |
| 4 | rs2421069 | 135195163 | PABPC4L | 141775 base upstream | q28.3 | CT | 0.761 | 1.672 | 0.0007692 |
| 6 | rs17516082 | 104874894 | HACE1 | 407766 base upstream | q21 | AG | 0.8268 | 0.612 | 0.0005067 |
| 7 | rs760229 | 152440071 | ACTR3B | 256675 base downstream | q36.2 | AG | 0.33 | 0.622 | 0.0003739 |
| 8 | rs2701439 | 73175604 | TRPA1 | 25231 base downstream | q13.3 | CG | 0.7942 | 0.642 | 0.0008994 |
| 7 | rs2286180 | 26562895 | SCAP2 | 110319 base upstream | p15.2 | CG | 0.2123 | 1.578 | 0.0004889 |
| 1 | rs7531138 | 97696087 | DPYD | intron 10 | p21.3 | AT | 0.4347 | 0.615 | 0.0001516 |
| 1 | rs585041 | 199817630 | NAV1 | 66442 base upstream | q32.1 | AT | 0.2491 | 1.567 | 0.0005677 |
| 11 | rs10890608 | 106217194 | GUCY1A2 | intron 4 | q22.3 | AT | 0.252 | 0.58 | 0.0004362 |
| 1 | rs12566140 | 48859991 | AGBL4 | intron 2 | p33 | AG | 0.0613 | 2.041 | 0.0007847 |
| 12 | rs11833072 | 104624341 | NUAK1 | 356913 base upstream | q23.3 | CT | 0.6987 | 0.635 | 0.0004645 |
| 6 | rs7770469 | 136506453 | PDE7B | intron 3 | q23.3 | AG | 0.39 | 1.579 | 0.0002057 |
| 8 | rs1394485 | 4107562 | CSMD1 | intron 67 | p23.2 | CT | 0.9266 | 0.481 | 0.0002696 |
| 5 | rs6883903 | 159168956 | ADRA1B | 107361 base upstream | q33.3 | AG | 0.0132 | 3.576 | 0.0006769 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 4 | rs11727958 | 116463016 | NDST4 | 208535 base downstream | q26 | CT | 0.3686 | 1.546 | 0.0001725 |
| 7 | rs13245026 | 97262856 | TAC1 | 55136 base downstream | q21.3 | AG | 0.8716 | 0.568 | 0.0002266 |
| 4 | rs1919227 | 92462591 | TMSL3 | 483299 base downstream | q22.1 | GT | 0.7197 | 1.757 | 0.0001159 |
| 13 | rs2296991 | 98300600 | DOCK9 | intron 21 | q32.3 | CT | 0.8463 | 0.59 | 0.0003028 |
| 18 | rs11662228 | 69451956 | FBXO15 | 439629 base upstream | q22.3 | CT | 0.561 | 1.532 | 0.000676 |
| 3 | rs9830744 | 15090482 | ZFYVE20 | EXON 1 | p24.3 | CT | 0.9554 | 0.439 | 0.0002219 |
| 4 | rs6532293 | 92463052 | TMSL3 | 483760 base downstream | q22.1 | AG | 0.7194 | 1.75 | 0.0001184 |
| 5 | rs4527577 | 105504488 | EFNA5 | 1239761 base upstream | q21.3 | CT | 0.1904 | 1.612 | 0.0004544 |
| 4 | rs1534556 | 92478508 | TMSL3 | 499216 base downstream | q22.1 | AG | 0.7194 | 1.748 | 0.0001312 |
| 4 | rs882733 | 40505735 | FLJ14001 | EXON 11 | p14 | AG | 0.1688 | 0.514 | 0.0003984 |
| 6 | rs4945639 | 104878861 | HACE1 | 403799 base upstream | q21 | CT | 0.8277 | 0.614 | 0.0005763 |
| 7 | rs2732743 | 84683866 | SEMA3D | 94683 base downstream | q21.11 | CT | 0.2113 | 1.592 | 0.0007572 |
| 15 | rs6496832 | 89910099 | SV2B | 270447 base downstream | q26.1 | AG | 0.66 | 1.548 | 0.0007989 |
| 1 | rs519693 | 95796000 | RWDD3 | 310631 base downstream | p21.3 | CT | 0.0865 | 1.918 | 0.000566 |
| 7 | rs993059 | 97262360 | TAC1 | 54640 base downstream | q21.3 | CT | 0.1282 | 1.761 | 0.0002327 |
| 13 | rs2324845 | 41467528 | KIAA0564 | 34307 base downstream | q14.11 | CT | 0.5428 | 1.534 | 0.0004405 |
| 9 | rs10966629 | 24988099 | TUSC1 | 678294 base upstream | p21.3 | AG | 0.3264 | 1.485 | 0.0007467 |
| 1 | rs10923014 | 88285953 | PKN2 | 636556 base upstream | p22.2 | CT | 0.631 | 1.605 | 0.000219 |
| 7 | rs2311855 | 152454874 | ACTR3B | 271478 base downstream | q36.2 | GT | 0.3701 | 0.632 | 0.0003354 |
| 13 | rs2031635 | 104286376 | DAOA | 629988 base upstream | q33.2 | AG | 0.4609 | 1.556 | 0.0007334 |
| 7 | rs2058106 | 97259519 | TAC1 | 51799 base downstream | q21.3 | AT | 0.1279 | 1.762 | 0.000244 |
| 1 | rs6674328 | 48894788 | AGBL4 | intron 4 | p33 | CT | 0.943 | 0.468 | 0.0002697 |
| 2 | rs17454262 | 116082577 | DPP10 | intron 5 | q14.1 | CT | 0.0861 | 2.028 | 0.0002852 |
| 1 | rs12117077 | 88284959 | PKN2 | 637550 base upstream | p22.2 | CT | 0.369 | 0.623 | 0.0002237 |
| 7 | rs11764340 | 97260570 | TAC1 | 52850 base downstream | q21.3 | AC | 0.8719 | 0.568 | 0.0002366 |
| 6 | rs1353588 | 99799997 | C6orf168 | 35261 base upstream | q16.2 | AC | 0.2139 | 1.57 | 0.0005752 |
| 7 | rs2732742 | 84684755 | SEMA3D | 95572 base downstream | q21.11 | AG | 0.7886 | 0.628 | 0.0007557 |
| 15 | rs4238566 | 31694920 | RYR3 | intron 19 | q14 | AC | 0.2562 | 0.594 | 0.0004663 |
| 1 | rs685982 | 199829227 | NAV1 | 54845 base upstream | q32.1 | AT | 0.2501 | 1.585 | 0.0005151 |
| 1 | rs677390 | 199818411 | NAV1 | 65661 base upstream | q32.1 | AG | 0.7509 | 0.638 | 0.0005671 |
| 13 | rs11619622 | 41468201 | KIAA0564 | 34980 base downstream | q14.11 | AG | 0.5765 | 0.675 | 0.0009514 |
| 18 | rs11876675 | 69453896 | FBXO15 | 437689 base upstream | q22.3 | AG | 0.4384 | 0.654 | 0.0007313 |
| 8 | rs4738208 | 73191692 | TRPA1 | 41319 base downstream | q13.3 | CT | 0.1971 | 1.578 | 0.0006935 |
| 7 | rs1525489 | 122420709 | TAS2R16 | 1285 base upstream | q31.32 | AG | 0.9368 | 0.472 | 0.0006167 |
| 6 | rs13197557 | 104880442 | HACE1 | 402218 base upstream | q21 | AG | 0.8279 | 0.614 | 0.000584 |
| 7 | rs2058105 | 97259532 | TAC1 | 51812 base downstream | q21.3 | AT | 0.872 | 0.568 | 0.0002422 |
| 9 | rs12347630 | 2663801 | VLDLR | 19316 base downstream | p24.2 | AG | 0.0759 | 2.014 | 0.0003564 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 16 | rs17698989 | 74938492 | CNTNAP4 | intron 2 | q23.1 | AG | 0.1959 | 1.598 | 0.0005257 |
| 3 | rs9868848 | 15090876 | ZFYVE20 | EXON 1 | p24.3 | AG | 0.9566 | 0.431 | 0.0001677 |
| 1 | rs608356 | 199826786 | NAV1 | 57286 base upstream | q32.1 | AG | 0.7504 | 0.634 | 0.0005397 |
| 3 | rs9831248 | 41524937 | ULK4 | intron 5 | p22.1 | CG | 0.0609 | 1.975 | 0.0007721 |
| 11 | rs16931218 | 15191628 | INSC | intron 7 | p15.2 | CT | 0.0368 | 2.408 | 0.000846 |
| 8 | rs17069790 | 4112508 | CSMD1 | intron 67 | p23.2 | AG | 0.074 | 2.086 | 0.0003973 |
| 1 | rs11589642 | 199367371 | TMEM9 | 3152 base upstream | q32.1 | AG | 0.2321 | 1.654 | 0.0002816 |
| 4 | rs6532291 | 92462653 | TMSL3 | 483361 base downstream | q22.1 | AG | 0.7017 | 1.754 | 0.000138 |
| 3 | rs1256396 | 41526055 | ULK4 | intron 5 | p22.1 | AT | 0.0609 | 1.975 | 0.0007703 |
| 12 | rs1962255 | 104624562 | NUAK1 | 356692 base upstream | q23.3 | AC | 0.3035 | 1.534 | 0.0007173 |
| 7 | rs2534851 | 84686087 | SEMA3D | 96904 base downstream | q21.11 | GT | 0.7882 | 0.627 | 0.0007483 |
| 6 | rs1997660 | 28377642 | PGBD1 | EXON 7 | p22.1 | AG | 0.687 | 1.594 | 0.0006861 |
| 8 | rs17069778 | 4108928 | CSMD1 | intron 67 | p23.2 | AT | 0.9266 | 0.484 | 0.0003111 |
| 8 | rs4614034 | 73197756 | TRPA1 | 47383 base downstream | q13.3 | CT | 0.8037 | 0.634 | 0.0007755 |
| 7 | rs2732744 | 84680820 | SEMA3D | 91637 base downstream | q21.11 | CT | 0.2114 | 1.59 | 0.0007827 |
| 7 | rs2732738 | 84686625 | SEMA3D | 97442 base downstream | q21.11 | AG | 0.7882 | 0.626 | 0.0007487 |
| 3 | rs17424938 | 113068623 | PHLDB2 | 16876 base upstream | q13.2 | AG | 0.8487 | 0.6 | 0.0009553 |
| 1 | rs17113368 | 95558817 | RWDD3 | 73448 base downstream | p21.3 | CT | 0.8844 | 0.545 | 0.0001781 |
| 6 | rs12193060 | 99797170 | C6orf168 | 38088 base upstream | q16.2 | AG | 0.7859 | 0.637 | 0.0005769 |
| 6 | rs4711122 | 26866458 | ZNF322A | 98516 base downstream | p22.1 | CT | 0.7597 | 0.64 | 0.0006981 |
| 1 | rs12143926 | 88276958 | PKN2 | 645551 base upstream | p22.2 | CT | 0.3689 | 0.624 | 0.0002387 |
| 1 | rs12145270 | 95798178 | RWDD3 | 312809 base downstream | p21.3 | AT | 0.0863 | 1.919 | 0.0007732 |
| 20 | rs16981148 | 19738602 | RIN2 | 79607 base upstream | p11.23 | AG | 0.1009 | 1.816 | 0.0002815 |
| 8 | rs4738209 | 73191724 | TRPA1 | 41351 base downstream | q13.3 | AC | 0.1968 | 1.576 | 0.0007461 |
| 1 | rs4912069 | 19518260 | PQLC2 | intron 2 | p36.13 | AG | 0.2764 | 1.568 | 0.0003977 |
| 3 | rs13085823 | 102219726 | ABI3BP | 24722 base downstream | q12.2 | GT | 0.674 | 0.658 | 0.0005352 |
| 4 | rs17513709 | 40496876 | FLJ14001 | intron 10 | p14 | GT | 0.1742 | 0.523 | 0.0005323 |
| 4 | rs6446921 | 74412384 | ANKRD17 | 69018 base downstream | q13.3 | AG | 0.0275 | 2.719 | 0.0003499 |
| 4 | rs1565912 | 135194459 | PABPC4L | 142479 base upstream | q28.3 | AG | 0.2387 | 0.599 | 0.0008198 |
| 1 | rs12566596 | 88279379 | PKN2 | 643130 base upstream | p22.2 | CG | 0.3462 | 0.598 | 0.0002687 |
| 3 | rs9834782 | 151306869 | PFN2 | 135438 base downstream | q25.1 | AC | 0.1465 | 0.467 | 0.0005598 |
| 3 | rs4258937 | 41519427 | ULK4 | intron 5 | p22.1 | AG | 0.9391 | 0.507 | 0.0007877 |
| 7 | rs2732737 | 84686884 | SEMA3D | 97701 base downstream | q21.11 | AG | 0.7879 | 0.625 | 0.0007427 |
| 20 | rs2423853 | 14862709 | C20orf133 | intron 5 | p12.1 | AT | 0.4246 | 0.642 | 0.0003372 |
| 1 | rs2296883 | 89290783 | GBP1 | EXON 1 | p22.2 | AG | 0.81 | 1.767 | 0.000907 |
| 7 | rs2159579 | 84683482 | SEMA3D | 94299 base downstream | q21.11 | GT | 0.7719 | 0.622 | 0.0004107 |
| 5 | rs6880807 | 26041000 | CDH9 | 875465 base upstream | p14.1 | GT | 0.3673 | 1.519 | 0.0006875 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 7 | rs10270627 | 69839751 | AUTS2 | intron 6 | q11.22 | GT | 0.3977 | 1.482 | 0.000855 |
| 19 | rs1560690 | 57270159 | ZNF432 | 26274 base downstream | q13.33 | AG | 0.7269 | 0.659 | 0.0008467 |
| 8 | rs4467976 | 73193049 | TRPA1 | 42676 base downstream | q13.3 | AG | 0.1967 | 1.575 | 0.0007591 |
| 3 | rs2017454 | 41530567 | ULK4 | intron 5 | p22.1 | AG | 0.0609 | 1.976 | 0.0007665 |
| 1 | rs10800760 | 199367062 | TMEM9 | 3461 base upstream | q32.1 | AG | 0.2318 | 1.652 | 0.0002819 |
| 11 | rs6254 | 13470839 | PTH | intron 1 | p15.2 | CT | 0.6624 | 0.663 | 0.0006841 |
| 7 | rs4129516 | 49051370 | ABCA13 | 393733 base downstream | p12.3 | CT | 0.2446 | 1.611 | 0.0003161 |
| 3 | rs17040623 | 15003482 | NR2C2 | intron 1 | p24.3 | AG | 0.9559 | 0.44 | 0.0002425 |
| 19 | rs11669439 | 57264112 | ZNF432 | 20227 base downstream | q13.33 | CT | 0.727 | 0.66 | 0.0008796 |
| 6 | rs270678 | 104891512 | HACE1 | 391148 base upstream | q21 | CT | 0.1705 | 1.645 | 0.0004536 |
| 4 | rs10021844 | 135184692 | PABPC4L | 152246 base upstream | q28.3 | AG | 0.2388 | 0.604 | 0.0009659 |
| 2 | rs10182455 | 38464515 | ARL6IP2 | 6596 base downstream | p22.1 | AG | 0.3842 | 0.639 | 0.0002799 |
| 17 | rs7213514 | 24561368 | CRYBA1 | 36632 base upstream | q11.2 | CT | 0.4822 | 0.635 | 0.0001623 |
| 8 | rs2701441 | 73174272 | TRPA1 | 23899 base downstream | q13.3 | AG | 0.7943 | 0.642 | 0.0008991 |
| 6 | rs7755721 | 26794868 | ZNF322A | 26926 base downstream | p22.1 | CT | 0.2377 | 1.561 | 0.0007264 |
| 1 | rs2064378 | 19517442 | PQLC2 | intron 2 | p36.13 | AG | 0.2752 | 1.577 | 0.0003698 |
| 16 | rs4788196 | 29874935 | LOC124446 | 5916 base upstream | p11.2 | AG | 0.5304 | 0.667 | 0.0008711 |
| 4 | rs17441923 | 40498127 | FLJ14001 | intron 10 | p14 | CT | 0.174 | 0.522 | 0.0005262 |
| 1 | rs17113374 | 95561952 | RWDD3 | 76583 base downstream | p21.3 | CT | 0.8845 | 0.545 | 0.0001778 |
| 19 | rs8101936 | 57268291 | ZNF432 | 24406 base downstream | q13.33 | AT | 0.2731 | 1.517 | 0.0008511 |
| 1 | rs12025414 | 199367119 | TMEM9 | 3404 base upstream | q32.1 | AG | 0.768 | 0.605 | 0.000282 |
| 1 | rs6427667 | 160510650 | NOS1AP | intron 2 | q23.3 | CG | 0.1626 | 0.514 | 0.0004974 |
| 4 | rs1840086 | 72354222 | SLC4A4 | intron 3 | q13.3 | AG | 0.1519 | 1.74 | 0.0002381 |
| 4 | rs4698460 | 13358506 | FAM44A | 120080 base downstream | p15.33 | GT | 0.2752 | 0.596 | 0.0007066 |
| 7 | rs12671326 | 26566825 | SCAP2 | 106389 base upstream | p15.2 | CT | 0.788 | 0.636 | 0.0005654 |
| 3 | rs9825022 | 15059018 | NR2C2 | intron 14 | p24.3 | CT | 0.955 | 0.445 | 0.0002893 |
| 4 | rs1528581 | 92461122 | TMSL3 | 481830 base downstream | q22.1 | CT | 0.724 | 1.758 | 0.0001407 |
| 9 | rs1322294 | 10616389 | PTPRD | 13880 base downstream | p23 | AG | 0.1533 | 1.689 | 0.0003902 |
| 4 | rs1565910 | 135194549 | PABPC4L | 142389 base upstream | q28.3 | AG | 0.7614 | 1.671 | 0.0007961 |
| 1 | rs10489284 | 170633685 | DNM3 | intron 20 | q24.3 | AG | 0.8353 | 1.914 | 0.0006193 |
| 7 | rs607348 | 152443576 | ACTR3B | 260180 base downstream | q36.2 | CT | 0.659 | 1.608 | 0.0004294 |
| 6 | rs12194369 | 99803170 | C6orf168 | 32088 base upstream | q16.2 | AG | 0.7871 | 0.634 | 0.0005198 |
| 1 | rs4471302 | 170633760 | DNM3 | intron 20 | q24.3 | CT | 0.1647 | 0.522 | 0.0006129 |
| 1 | rs2296882 | 89290761 | GBP1 | EXON 1 | p22.2 | AT | 0.81 | 1.767 | 0.0009069 |
| 1 | rs12125877 | 95798313 | RWDD3 | 312944 base downstream | p21.3 | CG | 0.9137 | 0.521 | 0.0007908 |
| 8 | rs12680834 | 140500127 | KCNK9 | 193858 base upstream | q24.3 | CT | 0.7901 | 0.618 | 0.0006363 |
| 2 | rs6726368 | 60183809 | BCL11A | 347996 base upstream | p16.1 | CG | 0.3314 | 1.527 | 0.0007336 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 5 | rs6888211 | 159144339 | ADRA1B | 131978 base upstream | q33.3 | CT | 0.9864 | 0.289 | 0.0008395 |
| 20 | rs2426960 | 58927301 | CDH4 | 333652 base upstream | q13.33 | AG | 0.4292 | 1.473 | 0.0006826 |
| 3 | rs9820676 | 15058788 | NR2C2 | intron 14 | p24.3 | CG | 0.955 | 0.446 | 0.0002919 |
| 13 | rs7333428 | 45873366 | C13orf18 | 13730 base downstream | q14.12 | CT | 0.1098 | 1.773 | 0.0008033 |
| 4 | rs6533889 | 116592228 | NDST4 | 337747 base downstream | q26 | GT | 0.615 | 0.65 | 0.0003581 |
| 8 | rs12541309 | 32664543 | NRG1 | intron 3 | p12 | AG | 0.1544 | 0.514 | 0.0007458 |
| 4 | rs3762827 | 92465367 | TMSL3 | 486075 base downstream | q22.1 | AG | 0.7218 | 1.73 | 0.0001681 |
| 13 | rs913560 | 98293824 | DOCK9 | intron 18 | q32.3 | AG | 0.5535 | 0.661 | 0.0003178 |
| 13 | rs9547416 | 85339936 | SLITRK6 | 68452 base downstream | q31.1 | AT | 0.5941 | 0.679 | 0.0009097 |
| 11 | rs10897779 | 80661868 | MGC33846 | 1458830 base upstream | q14.1 | GT | 0.7653 | 1.661 | 0.0009906 |
| 11 | rs1487892 | 106197626 | GUCY1A2 | intron 4 | q22.3 | AG | 0.2518 | 0.587 | 0.0005487 |
| 16 | rs3096190 | 24389161 | RBBP6 | 69247 base upstream | p12.1 | AC | 0.3646 | 1.505 | 0.0009158 |
| 7 | rs7341466 | 17140404 | AHR | 164427 base upstream | p21.1 | GT | 0.9345 | 0.501 | 0.0009508 |
| 7 | rs7777347 | 69842984 | AUTS2 | intron 6 | q11.22 | AG | 0.6028 | 0.67 | 0.0006992 |
| 4 | rs1528578 | 92466196 | TMSL3 | 486904 base downstream | q22.1 | CG | 0.7218 | 1.729 | 0.0001696 |
| 5 | rs16879856 | 51859304 | PELO | 260226 base upstream | q11.2 | CT | 0.9712 | 0.409 | 0.0009519 |
| 1 | rs12408132 | 89290506 | GBP1 | 68 base upstream | p22.2 | CT | 0.1976 | 0.562 | 0.0008712 |
| 6 | rs853683 | 28403018 | ZNF323 | intron 1 | p22.1 | AG | 0.6866 | 1.587 | 0.0007608 |
| 10 | rs17400327 | 6924140 | PRKCQ | 261896 base downstream | p14 | CT | 0.9671 | 0.378 | 0.0004228 |
| 7 | rs4718991 | 69844069 | AUTS2 | intron 6 | q11.22 | CG | 0.579 | 0.667 | 0.000626 |
| 13 | rs366300 | 39500866 | COG6 | 276234 base downstream | q14.11 | CT | 0.441 | 1.499 | 0.0005714 |
| 6 | rs707907 | 28399219 | ZNF323 | 1274 base upstream | p22.1 | AG | 0.6866 | 1.588 | 0.0007423 |
| 6 | rs17517558 | 104904271 | HACE1 | 378389 base upstream | q21 | AC | 0.8299 | 0.608 | 0.0004441 |
| 8 | rs1530402 | 73169428 | TRPA1 | 19055 base downstream | q13.3 | AG | 0.2057 | 1.557 | 0.0009114 |
| 12 | rs11176534 | 65691760 | CAND1 | 257655 base upstream | q14.3 | CT | 0.8966 | 0.53 | 0.000236 |
| 6 | rs156153 | 104904758 | HACE1 | 377902 base upstream | q21 | AG | 0.83 | 0.608 | 0.0004437 |
| 6 | rs155510 | 104912555 | HACE1 | 370105 base upstream | q21 | GT | 0.1698 | 1.642 | 0.0004541 |
| 10 | rs16937080 | 80764708 | PPIF | 12517 base upstream | q22.3 | AT | 0.2756 | 0.597 | 0.0004031 |
| 6 | rs156151 | 104905700 | HACE1 | 376960 base upstream | q21 | CG | 0.17 | 1.643 | 0.000446 |
| 3 | rs10510434 | 14995353 | NR2C2 | intron 1 | p24.3 | AG | 0.9558 | 0.442 | 0.0002568 |
| 14 | rs7157782 | 94397359 | GSC | 91107 base downstream | q32.13 | CT | 0.9369 | 0.503 | 0.0008033 |
| 7 | rs1107874 | 152455222 | ACTR3B | 271826 base downstream | q36.2 | AT | 0.3268 | 0.629 | 0.0005744 |
| 8 | rs17069640 | 4075094 | CSMD1 | intron 67 | p23.2 | GT | 0.0393 | 2.299 | 0.0005543 |
| 6 | rs13211684 | 51283445 | PKHD1 | 304658 base upstream | p12.2 | CT | 0.3792 | 0.649 | 0.0007549 |
| 7 | rs7806434 | 69846869 | AUTS2 | intron 6 | q11.22 | AG | 0.5791 | 0.666 | 0.0006104 |
| 3 | rs12485454 | 151327125 | PFN2 | 155694 base downstream | q25.1 | CT | 0.6711 | 1.564 | 0.0008133 |
| 12 | rs11176545 | 65709564 | CAND1 | 239851 base upstream | q14.3 | AT | 0.1292 | 1.759 | 0.000215 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 1 | rs10754315 | 88301956 | PKN2 | 620553 base upstream | p22.2 | CT | 0.3453 | 0.636 | 0.0005197 |
| 1 | rs1048848 | 89290653 | GBP1 | EXON 1 | p22.2 | CG | 0.1899 | 0.566 | 0.0009073 |
| 3 | rs2643977 | 41516991 | ULK4 | intron 5 | p22.1 | CT | 0.061 | 1.972 | 0.0007978 |
| 12 | rs10747658 | 51731549 | TENC1 | intron 1 | q13.13 | AG | 0.5859 | 0.656 | 0.0005021 |
| 1 | rs7556329 | 48896205 | AGBL4 | intron 4 | p33 | CG | 0.0572 | 2.119 | 0.000307 |
| 14 | rs1030124 | 78060216 | NRXN3 | intron 1 | q24.3 | GT | 0.6068 | 0.663 | 0.0004378 |
| 11 | rs7949287 | 80994506 | MGC33846 | 1126192 base upstream | q14.1 | AG | 0.5381 | 0.65 | 0.0002524 |
| 1 | rs6675866 | 89290398 | GBP1 | 176 base upstream | p22.2 | CT | 0.8101 | 1.769 | 0.0008996 |
| 7 | rs1107875 | 152454977 | ACTR3B | 271581 base downstream | q36.2 | AG | 0.6711 | 1.586 | 0.0005768 |
| 14 | rs4243660 | 78067940 | NRXN3 | intron 1 | q24.3 | CT | 0.3933 | 1.509 | 0.0004358 |
| 1 | rs967881 | 74116329 | LRRC44 | 147960 base upstream | p31.1 | AG | 0.6685 | 0.649 | 0.0003346 |
| 12 | rs11176539 | 65706599 | CAND1 | 242816 base upstream | q14.3 | CG | 0.1293 | 1.76 | 0.0002156 |
| 8 | rs2701449 | 73170538 | TRPA1 | 20165 base downstream | q13.3 | CT | 0.7945 | 0.643 | 0.0009055 |
| 14 | rs1030123 | 78060082 | NRXN3 | intron 1 | q24.3 | AG | 0.3932 | 1.508 | 0.0004372 |
| 12 | rs11176540 | 65708448 | CAND1 | 240967 base upstream | q14.3 | GT | 0.1293 | 1.76 | 0.0002156 |
| 7 | rs10258925 | 49031338 | ABCA13 | 373701 base downstream | p12.3 | AG | 0.2394 | 1.571 | 0.0005533 |
| 16 | rs2560922 | 24384824 | RBBP6 | 73584 base upstream | p12.1 | GT | 0.6387 | 0.661 | 0.0009667 |
| 13 | rs366815 | 85345072 | SLITRK6 | 73588 base downstream | q31.1 | AG | 0.5938 | 0.68 | 0.0009938 |
| 12 | rs6581729 | 65706048 | CAND1 | 243367 base upstream | q14.3 | AG | 0.1293 | 1.761 | 0.000216 |
| 14 | rs2193670 | 78085602 | NRXN3 | intron 1 | q24.3 | AG | 0.3931 | 1.513 | 0.0004287 |
| 12 | rs17103210 | 65705663 | CAND1 | 243752 base upstream | q14.3 | AT | 0.1293 | 1.761 | 0.0002154 |
| 1 | rs6672527 | 74111118 | LRRC44 | 153171 base upstream | p31.1 | CT | 0.6671 | 0.644 | 0.0003262 |
| 4 | rs1406316 | 92472949 | TMSL3 | 493657 base downstream | q22.1 | CT | 0.2776 | 0.581 | 0.000188 |
| 1 | rs11210363 | 74122434 | LRRC44 | 141855 base upstream | p31.1 | AG | 0.3312 | 1.546 | 0.0003158 |
| 12 | rs7955793 | 65718923 | CAND1 | 230492 base upstream | q14.3 | AG | 0.1289 | 1.754 | 0.0002084 |
| 1 | rs17579506 | 74117298 | LRRC44 | 146991 base upstream | p31.1 | CT | 0.3313 | 1.541 | 0.0003273 |
| 2 | rs4971622 | 49146315 | FSHR | intron 8 | p16.3 | AT | 0.9559 | 0.448 | 0.0008832 |
| 11 | rs547248 | 62420235 | SLC3A2 | 7307 base downstream | q12.3 | CT | 0.286 | 1.504 | 0.000882 |
| 12 | rs992738 | 65692893 | CAND1 | 256522 base upstream | q14.3 | CT | 0.8966 | 0.53 | 0.0002312 |
| 14 | rs7157079 | 94397102 | GSC | 90850 base downstream | q32.13 | AG | 0.9368 | 0.504 | 0.0007734 |
| 13 | rs10851281 | 89217299 | GPC5 | 1631588 base upstream | q31.3 | AG | 0.9681 | 0.375 | 0.0004084 |
| 1 | rs17520168 | 74117107 | LRRC44 | 147182 base upstream | p31.1 | CT | 0.3314 | 1.54 | 0.0003317 |
| 1 | rs12727614 | 159363865 | DEDD | intron 4 | q23.3 | AT | 0.2896 | 1.493 | 0.0009697 |
| 1 | rs12125905 | 95798397 | RWDD3 | 313028 base downstream | p21.3 | CG | 0.9137 | 0.521 | 0.0008384 |
| 13 | rs7984054 | 89221294 | GPC5 | 1627593 base upstream | q31.3 | AC | 0.0316 | 2.684 | 0.0004401 |
| 3 | rs1691983 | 41517346 | ULK4 | intron 5 | p22.1 | AG | 0.9391 | 0.507 | 0.0007945 |
| 4 | rs11944843 | 140857153 | MAML3 | EXON 1 | q31.1 | AG | 0.1798 | 1.611 | 0.0009609 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 3 | rs17315194 | 101331030 | C3orf26 | intron 1 | q12.1 | GT | 0.1172 | 1.713 | 0.0008636 |
| 1 | rs942703 | 199359602 | TMEM9 | 10921 base upstream | q32.1 | CT | 0.7656 | 0.626 | 0.0002938 |
| 6 | rs3757154 | 136476887 | PDE7B | intron 3 | q23.3 | CG | 0.6128 | 0.654 | 0.0004072 |
| 3 | rs2643976 | 41516845 | ULK4 | intron 5 | p22.1 | AG | 0.061 | 1.967 | 0.0008391 |
| 8 | rs1443942 | 73171160 | TRPA1 | 20787 base downstream | q13.3 | AC | 0.7945 | 0.643 | 0.0009024 |
| 1 | rs11210361 | 74112532 | LRRC44 | 151757 base upstream | p31.1 | CT | 0.3319 | 1.539 | 0.0003473 |
| 18 | rs2051413 | 69425930 | FBXO15 | 465655 base upstream | q22.3 | AG | 0.6272 | 1.538 | 0.0008833 |
| 12 | rs12369132 | 65699454 | CAND1 | 249961 base upstream | q14.3 | AG | 0.8701 | 0.566 | 0.0002335 |
| 11 | rs1945649 | 80986103 | MGC33846 | 1134595 base upstream | q14.1 | CT | 0.4619 | 1.54 | 0.0002489 |
| 1 | rs6685886 | 205560841 | CD55 | 598 base upstream | q32.2 | AC | 0.4243 | 1.486 | 0.0009032 |
| 12 | rs905699 | 65704574 | CAND1 | 244841 base upstream | q14.3 | CT | 0.8706 | 0.568 | 0.0002164 |
| 8 | rs2701440 | 73175388 | TRPA1 | 25015 base downstream | q13.3 | CT | 0.2058 | 1.557 | 0.0008995 |
| 8 | rs2701450 | 73168913 | TRPA1 | 18540 base downstream | q13.3 | AT | 0.7943 | 0.642 | 0.0009163 |
| 7 | rs7341406 | 17138564 | AHR | 166267 base upstream | p21.1 | CG | 0.9328 | 0.522 | 0.0009745 |
| 13 | rs7329978 | 89218832 | GPC5 | 1630055 base upstream | q31.3 | AG | 0.9682 | 0.374 | 0.0004194 |
| 11 | rs11608098 | 13516530 | PTH | 42387 base downstream | p15.2 | CT | 0.338 | 1.502 | 0.0007341 |
| 13 | rs7333687 | 98288560 | DOCK9 | intron 18 | q32.3 | AG | 0.555 | 0.666 | 0.0003827 |
| 13 | rs4772149 | 98305163 | DOCK9 | intron 22 | q32.3 | CT | 0.4235 | 1.509 | 0.0005135 |
| 13 | rs6492451 | 89220997 | GPC5 | 1627890 base upstream | q31.3 | CT | 0.0316 | 2.683 | 0.0004379 |
| 8 | rs1838285 | 73171725 | TRPA1 | 21352 base downstream | q13.3 | CT | 0.7945 | 0.643 | 0.0009028 |
| 12 | rs7953084 | 65700060 | CAND1 | 249355 base upstream | q14.3 | AC | 0.1299 | 1.766 | 0.0002332 |
| 14 | rs7156858 | 94396959 | GSC | 90707 base downstream | q32.13 | AC | 0.9368 | 0.504 | 0.0007754 |
| 14 | rs11629123 | 78053255 | NRXN3 | intron 1 | q24.3 | CT | 0.607 | 0.662 | 0.0004194 |
| 12 | rs11176528 | 65684056 | CAND1 | 265359 base upstream | q14.3 | CT | 0.1035 | 1.878 | 0.0002652 |
| 4 | rs6833290 | 92471115 | TMSL3 | 491823 base downstream | q22.1 | CT | 0.7224 | 1.722 | 0.0001876 |
| 13 | rs17591593 | 31563969 | FRY | intron 2 | q13.1 | CG | 0.3059 | 1.533 | 0.0008732 |
| 15 | rs12324460 | 89929416 | SLCO3A1 | 268533 base upstream | q26.1 | CT | 0.175 | 0.53 | 0.0008422 |
| 14 | rs2098518 | 78087589 | NRXN3 | intron 1 | q24.3 | CG | 0.607 | 0.661 | 0.000427 |
| 10 | rs1013250 | 6933270 | PRKCQ | 271026 base downstream | p14 | AG | 0.0334 | 2.722 | 0.0006818 |
| 4 | rs6532301 | 92491016 | TMSL3 | 511724 base downstream | q22.1 | AG | 0.2764 | 0.589 | 0.0002868 |
| 11 | rs10500784 | 13530401 | PTH | 56258 base downstream | p15.2 | AC | 0.6618 | 0.668 | 0.0007944 |
| 13 | rs7321357 | 98302606 | DOCK9 | intron 21 | q32.3 | CT | 0.8508 | 0.59 | 0.0004955 |
| 11 | rs10890611 | 106227169 | GUCY1A2 | intron 4 | q22.3 | CT | 0.2395 | 0.593 | 0.0008528 |
| 14 | rs1777077 | 42258660 | LRFN5 | 815162 base downstream | q21.2 | CT | 0.2364 | 1.628 | 0.0008463 |
| 7 | rs11762613 | 49076176 | ABCA13 | 418539 base downstream | p12.3 | AC | 0.2388 | 1.597 | 0.0004154 |
| 1 | rs4656008 | 88297128 | PKN2 | 625381 base upstream | p22.2 | GT | 0.6547 | 1.571 | 0.0005229 |
| 4 | rs1390026 | 135193417 | PABPC4L | 143521 base upstream | q28.3 | GT | 0.2387 | 0.6 | 0.0008298 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 18 | rs1943869 | 69430600 | FBXO15 | 460985 base upstream | q22.3 | CG | 0.6271 | 1.535 | 0.0008859 |
| 5 | rs17560965 | 125194811 | GRAMD3 | 592188 base upstream | q23.2 | AG | 0.0405 | 2.373 | 0.0009369 |
| 16 | rs11076229 | 56846460 | HSPC065 | intron 3 | q21 | AG | 0.1484 | 0.513 | 0.0008281 |
| 11 | rs11212007 | 106389222 | GUCY1A2 | intron 7 | q22.3 | AC | 0.2363 | 0.57 | 0.0007701 |
| 10 | rs11199656 | 122674538 | BRWD2 | 15513 base downstream | q26.12 | CT | 0.0385 | 2.34 | 0.0006159 |
| 2 | rs6760123 | 38456015 | ARL6IP2 | intron 12 | p22.1 | CT | 0.6155 | 1.566 | 0.0002906 |
| 11 | rs10792479 | 79787547 | ODZ4 | 1586714 base downstream | q14.1 | CT | 0.2582 | 1.572 | 0.0006423 |
| 3 | rs9835136 | 45011179 | EXOSC7 | intron 3 | p21.31 | AG | 0.5314 | 1.486 | 0.0009251 |
| 18 | rs4892117 | 69429890 | FBXO15 | 461695 base upstream | q22.3 | CT | 0.3727 | 0.652 | 0.0009108 |
| 3 | rs4894477 | 176307233 | NAALADL2 | intron 2 | q26.31 | AG | 0.3748 | 1.524 | 0.0003366 |
| 13 | rs9300518 | 98286664 | DOCK9 | intron 17 | q32.3 | CT | 0.4437 | 1.502 | 0.0003835 |
| 2 | rs3806551 | 38459723 | ARL6IP2 | 1804 base downstream | p22.1 | CG | 0.3896 | 0.637 | 0.0002793 |
| 6 | rs853693 | 28390627 | ZNF323 | 9866 base upstream | p22.1 | AG | 0.3135 | 0.628 | 0.0007056 |
| 16 | rs16959980 | 56847308 | HSPC065 | intron 3 | q21 | CT | 0.1486 | 0.512 | 0.000807 |
| 7 | rs2215361 | 48944124 | ABCA13 | 286487 base downstream | p12.3 | AG | 0.7583 | 0.653 | 0.0009407 |
| 11 | rs1903102 | 13531228 | PTH | 57085 base downstream | p15.2 | AC | 0.3382 | 1.498 | 0.0007936 |
| 11 | rs2037194 | 83252000 | DLG2 | intron 12 | q14.1 | AG | 0.9686 | 0.365 | 0.0004335 |
| 16 | rs11647205 | 53289736 | IRX5 | 232875 base upstream | q12.2 | AG | 0.3598 | 1.51 | 0.0005251 |
| 16 | rs8044591 | 53292008 | IRX5 | 230603 base upstream | q12.2 | AC | 0.3578 | 1.522 | 0.0005324 |
| 6 | rs2465043 | 51288724 | PKHD1 | 299379 base upstream | p12.2 | AG | 0.3535 | 1.521 | 0.0008637 |
| 3 | rs11919885 | 41516460 | ULK4 | intron 5 | p22.1 | CT | 0.9388 | 0.512 | 0.0009609 |
| 3 | rs1440524 | 29735511 | RBMS3 | intron 4 | p24.1 | CT | 0.3517 | 1.489 | 0.0005483 |
| 3 | rs4683016 | 45005286 | EXOSC7 | intron 1 | p21.31 | AG | 0.4684 | 0.673 | 0.0009401 |
| 4 | rs1348188 | 29184029 | PCDH7 | 1147105 base upstream | p15.1 | CT | 0.5955 | 0.661 | 0.0004234 |
| 6 | rs2504586 | 26862629 | ZNF322A | 94687 base downstream | p22.1 | CG | 0.2269 | 1.569 | 0.00088 |
| 4 | rs6854632 | 116559642 | NDST4 | 305161 base downstream | q26 | AG | 0.6409 | 0.657 | 0.0003162 |
| 4 | rs6849851 | 92645841 | TMSL3 | 666549 base downstream | q22.1 | AG | 0.4016 | 1.547 | 0.0004122 |
| 4 | rs6847471 | 116558804 | NDST4 | 304323 base downstream | q26 | AG | 0.3591 | 1.522 | 0.0003149 |
| 6 | rs1417665 | 104923637 | HACE1 | 359023 base upstream | q21 | CT | 0.168 | 1.635 | 0.0005055 |
| 11 | rs10890604 | 106210532 | GUCY1A2 | intron 4 | q22.3 | AG | 0.2458 | 0.598 | 0.00089 |
| 13 | rs2875552 | 43902494 | TSC22D1 | 3166 base upstream | q14.11 | CT | 0.6021 | 1.542 | 0.0005232 |
| 16 | rs12596498 | 56846678 | HSPC065 | intron 3 | q21 | CT | 0.8515 | 1.952 | 0.0008168 |
| 1 | rs17113360 | 95555047 | RWDD3 | 69678 base downstream | p21.3 | CT | 0.1175 | 1.765 | 0.0003163 |
| 3 | rs6441875 | 44998914 | EXOSC7 | intron 1 | p21.31 | CT | 0.5317 | 1.485 | 0.000952 |
| 11 | rs7941624 | 80658536 | MGC33846 | 1462162 base upstream | q14.1 | AG | 0.7895 | 1.83 | 0.0007665 |
| 6 | rs17459015 | 104924468 | HACE1 | 358192 base upstream | q21 | CT | 0.1681 | 1.636 | 0.0005074 |
| 6 | rs9374562 | 116111190 | FRK | 258196 base upstream | q22.1 | CT | 0.7303 | 0.648 | 0.0005912 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 4 | rs4833478 | 116549189 | NDST4 | 294708 base downstream | q26 | AG | 0.3591 | 1.523 | 0.0003117 |
| 1 | rs12120668 | 75093605 | C1orf171 | 89709 base downstream | p31.1 | CG | 0.4141 | 1.526 | 0.0008122 |
| 16 | rs1974876 | 56842704 | HSPC065 | intron 1 | q21 | CT | 0.8516 | 1.948 | 0.0008337 |
| 2 | rs3806552 | 38458897 | ARL6IP2 | 978 base downstream | p22.1 | AC | 0.6122 | 1.564 | 0.0003282 |
| 5 | rs327807 | 98306052 | CHD1 | 15914 base downstream | q21.1 | AG | 0.3301 | 1.513 | 0.0008027 |
| 4 | rs12233647 | 116540808 | NDST4 | 286327 base downstream | q26 | AG | 0.3591 | 1.523 | 0.0003117 |
| 4 | rs7687193 | 116540440 | NDST4 | 285959 base downstream | q26 | AG | 0.6409 | 0.657 | 0.0003117 |
| 20 | rs2024676 | 58926954 | CDH4 | 333999 base upstream | q13.33 | AG | 0.4294 | 1.472 | 0.0007014 |
| 11 | rs1954864 | 106222728 | GUCY1A2 | intron 4 | q22.3 | GT | 0.2465 | 0.592 | 0.0008942 |
| 4 | rs6836582 | 116552171 | NDST4 | 297690 base downstream | q26 | AG | 0.3585 | 1.522 | 0.0003177 |
| 4 | rs11947264 | 116548085 | NDST4 | 293604 base downstream | q26 | CT | 0.6409 | 0.657 | 0.0003117 |
| 3 | rs12639280 | 41515056 | ULK4 | intron 5 | p22.1 | CT | 0.0612 | 1.952 | 0.0009649 |
| 4 | rs11933617 | 116542863 | NDST4 | 288382 base downstream | q26 | AG | 0.3591 | 1.523 | 0.0003117 |
| 2 | rs13022199 | 115870472 | DPP10 | intron 3 | q14.1 | AG | 0.1239 | 1.698 | 0.0008936 |
| 16 | rs11076230 | 56846486 | HSPC065 | intron 3 | q21 | GT | 0.1484 | 0.513 | 0.0008243 |
| 11 | rs2097171 | 81001119 | MGC33846 | 1119579 base upstream | q14.1 | CT | 0.4608 | 1.523 | 0.0003378 |
| 4 | rs7440324 | 116554439 | NDST4 | 299958 base downstream | q26 | AT | 0.6409 | 0.657 | 0.0003117 |
| 1 | rs7556311 | 48896154 | AGBL4 | intron 4 | p33 | AG | 0.0572 | 2.12 | 0.0003055 |
| 5 | rs10054300 | 51883415 | PELO | 236115 base upstream | q11.2 | AG | 0.0287 | 2.47 | 0.0008679 |
| 6 | rs9342293 | 92328542 | MAP3K7 | 974914 base downstream | q16.1 | AT | 0.7814 | 1.72 | 0.0006304 |
| 11 | rs2448273 | 79783016 | ODZ4 | 1582183 base downstream | q14.1 | AC | 0.2569 | 1.56 | 0.0007651 |
| 4 | rs6814621 | 116548408 | NDST4 | 293927 base downstream | q26 | AC | 0.6409 | 0.657 | 0.0003117 |
| 13 | rs9595128 | 43934565 | TSC22D1 | intron 2 | q14.11 | AG | 0.5991 | 1.534 | 0.0005893 |
| 1 | rs7547762 | 199354868 | CACNA1S | 6551 base downstream | q32.1 | AG | 0.7664 | 0.628 | 0.0002989 |
| 4 | rs6533870 | 116537368 | NDST4 | 282887 base downstream | q26 | AG | 0.3591 | 1.523 | 0.0003119 |
| 2 | rs17453131 | 115868314 | DPP10 | intron 3 | q14.1 | AG | 0.8762 | 0.59 | 0.0009339 |
| 7 | rs10238315 | 78880949 | MAGI2 | intron 21 | q21.11 | GT | 0.7152 | 0.653 | 0.000411 |
| 3 | rs4683017 | 45009415 | EXOSC7 | intron 3 | p21.31 | CT | 0.4685 | 0.673 | 0.0009292 |
| 8 | rs3817664 | 17545472 | MTUS1 | 111 base upstream | p22 | GT | 0.3837 | 1.492 | 0.0008093 |
| 2 | rs1863704 | 219270919 | STK36 | EXON 25 | q35 | AG | 0.3753 | 0.629 | 0.0003006 |
| 1 | rs12568661 | 88292306 | PKN2 | 630203 base upstream | p22.2 | AG | 0.3455 | 0.64 | 0.000564 |
| 7 | rs17561679 | 84577029 | SEMA3D | intron 16 | q21.11 | CT | 0.2279 | 1.587 | 0.0005514 |
| 7 | rs1029563 | 84576431 | SEMA3D | intron 16 | q21.11 | GT | 0.2281 | 1.59 | 0.0005359 |
| 11 | rs7125479 | 107990612 | EXPH5 | 21042 base downstream | q22.3 | AC | 0.4647 | 0.669 | 0.0007634 |
| 13 | rs4943722 | 39493988 | COG6 | 269356 base downstream | q13.3 | AG | 0.3667 | 1.475 | 0.0008047 |
| 6 | rs271880 | 104920459 | HACE1 | 362201 base upstream | q21 | AG | 0.1699 | 1.644 | 0.0004812 |
| 7 | rs7796330 | 49098405 | ABCA13 | 440768 base downstream | p12.3 | CT | 0.7647 | 0.614 | 0.0005654 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 7 | rs1029564 | 84577791 | SEMA3D | intron 16 | q21.11 | GT | 0.2284 | 1.587 | 0.0005549 |
| 5 | rs7730948 | 51877283 | PELO | 242247 base upstream | q11.2 | CT | 0.0287 | 2.465 | 0.0008839 |
| 7 | rs9655226 | 22565267 | IL6 | 168075 base upstream | p15.3 | CT | 0.3705 | 0.656 | 0.0009557 |
| 19 | rs17685204 | 33606816 | UQCRFS1 | 783190 base upstream | q12 | CT | 0.0981 | 1.803 | 0.0005935 |
| 1 | rs2145408 | 46634494 | FAAH | intron 1 | p33 | AG | 0.2472 | 1.544 | 0.0007961 |
| 21 | rs2835491 | 37142992 | HLCS | intron 5 | q22.13 | GT | 0.0416 | 2.216 | 0.000961 |
| 11 | rs7943773 | 83240882 | DLG2 | intron 12 | q14.1 | CT | 0.0313 | 2.606 | 0.0004762 |
| 13 | rs9595132 | 43946832 | TSC22D1 | intron 2 | q14.11 | AG | 0.5985 | 1.536 | 0.0005852 |
| 6 | rs156123 | 104918438 | HACE1 | 364222 base upstream | q21 | AG | 0.8317 | 0.613 | 0.000538 |
| 8 | rs10101487 | 60881049 | CA8 | 382927 base upstream | q12.1 | AG | 0.3209 | 0.63 | 0.0007774 |
| 11 | rs10832047 | 13480447 | PTH | 6304 base downstream | p15.2 | AT | 0.6443 | 0.666 | 0.0009094 |
| 4 | rs1441670 | 29199244 | PCDH7 | 1131890 base upstream | p15.1 | AG | 0.4048 | 1.509 | 0.0004467 |
| 8 | rs2725673 | 5526530 | CSMD1 | 686794 base downstream | p23.2 | AG | 0.7958 | 0.634 | 0.0007277 |
| 6 | rs13219556 | 104917442 | HACE1 | 365218 base upstream | q21 | CT | 0.8317 | 0.612 | 0.0005331 |
| 4 | rs6847969 | 116558768 | NDST4 | 304287 base downstream | q26 | AG | 0.6409 | 0.657 | 0.0003117 |
| 11 | rs7944123 | 106221180 | GUCY1A2 | intron 4 | q22.3 | AG | 0.7603 | 1.69 | 0.0008165 |
| 2 | rs12232909 | 83399672 | SUCLG1 | 1104492 base upstream | p12 | AG | 0.5972 | 0.663 | 0.0004329 |
| 6 | rs17458588 | 104920190 | HACE1 | 362470 base upstream | q21 | CT | 0.1681 | 1.631 | 0.0005445 |
| 14 | rs2273154 | 34502938 | SRP54 | 19043 base upstream | q13.2 | CT | 0.8082 | 1.819 | 0.0007798 |
| 7 | rs2691810 | 12650865 | SCIN | intron 13 | p21.3 | CT | 0.1196 | 1.787 | 0.0003403 |
| 13 | rs9549041 | 39501308 | COG6 | 276676 base downstream | q14.11 | CT | 0.6399 | 0.681 | 0.0009546 |
| 3 | rs11128731 | 15034334 | NR2C2 | intron 5 | p24.3 | CT | 0.045 | 2.234 | 0.0003184 |
| 1 | rs12562662 | 48877073 | AGBL4 | intron 3 | p33 | CT | 0.0606 | 2.019 | 0.0007331 |
| 13 | rs12583155 | 43922370 | TSC22D1 | intron 2 | q14.11 | CT | 0.399 | 0.654 | 0.0006002 |
| 16 | rs7206354 | 53288365 | IRX5 | 234246 base upstream | q12.2 | AC | 0.6401 | 0.663 | 0.0005249 |
| 10 | rs1246758 | 30254709 | KIAA1462 | 88680 base upstream | p11.23 | AC | 0.2469 | 0.581 | 0.0005423 |
| 2 | rs17362720 | 115970570 | DPP10 | intron 3 | q14.1 | AG | 0.1116 | 1.777 | 0.0006202 |
| 21 | rs17192962 | 37142961 | HLCS | intron 5 | q22.13 | AG | 0.9584 | 0.451 | 0.0009591 |
| 4 | rs7436806 | 72354592 | SLC4A4 | intron 3 | q13.3 | AG | 0.0947 | 1.966 | 0.0002319 |
| 5 | rs13361153 | 118636074 | TNFAIP8 | intron 1 | q23.1 | AG | 0.7445 | 1.774 | 0.0004075 |
| 4 | rs4834470 | 116523298 | NDST4 | 268817 base downstream | q26 | CT | 0.3589 | 1.515 | 0.0003703 |
| 21 | rs8134687 | 37142296 | HLCS | intron 5 | q22.13 | CT | 0.0416 | 2.216 | 0.0009579 |
| 4 | rs7663921 | 116518282 | NDST4 | 263801 base downstream | q26 | CT | 0.6411 | 0.66 | 0.0003728 |
| 4 | rs11935578 | 115536217 | UGT8 | 226754 base upstream | q26 | GT | 0.6359 | 0.656 | 0.0003435 |
| 11 | rs540225 | 125258570 | HYLS1 | 148 base upstream | q24.2 | CT | 0.3129 | 1.537 | 0.0003892 |
| 7 | rs2190179 | 78883432 | MAGI2 | intron 21 | q21.11 | AC | 0.2854 | 1.528 | 0.0004328 |
| 20 | rs6071442 | 58941909 | CDH4 | 319044 base upstream | q13.33 | CT | 0.5707 | 0.683 | 0.0007853 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 14 | rs1122840 | 78035507 | NRXN3 | intron 1 | q24.3 | AG | 0.3924 | 1.496 | 0.0005471 |
| 3 | rs1866774 | 29756855 | RBMS3 | intron 5 | p24.1 | AG | 0.4941 | 1.466 | 0.0009942 |
| 6 | rs9345152 | 92326845 | MAP3K7 | 973217 base downstream | q16.1 | AG | 0.2186 | 0.582 | 0.0006474 |
| 7 | rs4140898 | 26555282 | SCAP2 | 117932 base upstream | p15.2 | AG | 0.2662 | 1.521 | 0.0009253 |
| 6 | rs156126 | 104916776 | HACE1 | 365884 base upstream | q21 | CT | 0.8289 | 0.608 | 0.0004893 |
| 11 | rs17141854 | 80661677 | MGC33846 | 1459021 base upstream | q14.1 | AG | 0.9576 | 0.432 | 0.0007204 |
| 11 | rs2852205 | 107987483 | EXPH5 | 17913 base downstream | q22.3 | AG | 0.5344 | 1.494 | 0.0007968 |
| 20 | rs725475 | 58938883 | CDH4 | 322070 base upstream | q13.33 | CT | 0.4294 | 1.465 | 0.0007874 |
| 11 | rs7934388 | 107991327 | EXPH5 | 21757 base downstream | q22.3 | AT | 0.5353 | 1.494 | 0.0007967 |
| 2 | rs6712054 | 115974128 | DPP10 | intron 4 | q14.1 | CT | 0.8884 | 0.563 | 0.0006224 |
| 13 | rs9603665 | 39500347 | COG6 | 275715 base downstream | q14.11 | CT | 0.6394 | 0.68 | 0.0009091 |
| 16 | rs13338826 | 50054960 | SALL1 | 312276 base downstream | q12.1 | CG | 0.8094 | 0.629 | 0.0006423 |
| 5 | rs16879891 | 51871156 | PELO | 248374 base upstream | q11.2 | GT | 0.9713 | 0.408 | 0.0009222 |
| 2 | rs12712583 | 38396077 | ARL6IP2 | intron 9 | p22.2 | CT | 0.4012 | 0.645 | 0.0003296 |
| 7 | rs2159575 | 84598360 | SEMA3D | 9177 base downstream | q21.11 | CT | 0.763 | 0.627 | 0.0005528 |
| 2 | rs7604319 | 219247043 | STK36 | intron 4 | q35 | AC | 0.6246 | 1.578 | 0.0003829 |
| 13 | rs7997862 | 41469136 | KIAA0564 | 35915 base downstream | q14.11 | AG | 0.5576 | 1.507 | 0.0007322 |
| 6 | rs12195114 | 26816186 | ZNF322A | 48244 base downstream | p22.1 | AG | 0.758 | 0.643 | 0.0007752 |
| 6 | rs9467847 | 26817570 | ZNF322A | 49628 base downstream | p22.1 | CT | 0.2421 | 1.554 | 0.0007769 |
| 4 | rs2135965 | 116428916 | NDST4 | 174435 base downstream | q26 | AG | 0.6807 | 0.653 | 0.0004115 |
| 3 | rs6782183 | 176310661 | NAALADL2 | intron 2 | q26.31 | CT | 0.601 | 0.676 | 0.0006005 |
| 2 | rs2241527 | 219245468 | STK36 | intron 1 | q35 | AG | 0.3754 | 0.635 | 0.0004098 |
| 11 | rs11022897 | 13577497 | MLSTD2 | 69349 base upstream | p15.2 | CT | 0.6575 | 0.659 | 0.0006406 |
| 2 | rs2305245 | 38391130 | ARL6IP2 | intron 6 | p22.2 | AC | 0.6012 | 1.551 | 0.0003417 |
| 13 | rs4942331 | 43928799 | TSC22D1 | intron 2 | q14.11 | CT | 0.6007 | 1.53 | 0.0005964 |
| 17 | rs12953287 | 9717196 | GLP2R | intron 10 | p13.1 | CT | 0.8463 | 0.601 | 0.0008705 |
| 2 | rs1022076 | 38397553 | ARL6IP2 | intron 9 | p22.2 | CT | 0.5988 | 1.551 | 0.000329 |
| 1 | rs7516699 | 48870913 | AGBL4 | intron 2 | p33 | AG | 0.9185 | 0.543 | 0.0009731 |
| 9 | rs1826415 | 104678314 | CYLC2 | 119169 base upstream | q31.1 | CT | 0.7689 | 0.637 | 0.0009647 |
| 6 | rs12202849 | 26812951 | ZNF322A | 45009 base downstream | p22.1 | AG | 0.242 | 1.554 | 0.000774 |
| 2 | rs6745924 | 83404583 | SUCLG1 | 1099581 base upstream | p12 | CG | 0.4029 | 1.51 | 0.000431 |
| 14 | rs1990531 | 78016834 | NRXN3 | intron 1 | q24.3 | AG | 0.3828 | 1.521 | 0.0004084 |
| 8 | rs10100498 | 5510132 | CSMD1 | 670396 base downstream | p23.2 | AC | 0.7512 | 0.642 | 0.0005539 |
| 4 | rs6820042 | 127239590 | FAT4 | 606053 base downstream | q28.1 | AG | 0.1393 | 1.678 | 0.0005336 |
| 11 | rs7946763 | 81005829 | MGC33846 | 1114869 base upstream | q14.1 | AC | 0.4512 | 1.515 | 0.0004144 |
| 12 | rs11176527 | 65682486 | CAND1 | 266929 base upstream | q14.3 | AG | 0.1037 | 1.852 | 0.000375 |
| 1 | rs6429600 | 46637098 | FAAH | intron 1 | p33 | AG | 0.7529 | 0.648 | 0.000806 |

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|----|------------|-----------|----------|-------------------------|--------|----|--------|-------|-----------|
| 1 | rs4556311 | 74234416 | LRRC44 | 29873 base upstream | p31.1 | AG | 0.4662 | 0.631 | 0.0003524 |
| 17 | rs9900880 | 24573932 | CRYBA1 | 24068 base upstream | q11.2 | AG | 0.3953 | 0.62 | 0.0003777 |
| 6 | rs9362888 | 92321886 | MAP3K7 | 968258 base downstream | q16.1 | AG | 0.7815 | 1.711 | 0.0007016 |
| 4 | rs13120921 | 13326569 | FAM44A | 88143 base downstream | p15.33 | CT | 0.6042 | 1.536 | 0.0004702 |
| 4 | rs1554850 | 92515582 | TMSL3 | 536290 base downstream | q22.1 | AC | 0.73 | 1.704 | 0.0005529 |
| 3 | rs4683014 | 44994064 | EXOSC7 | intron 1 | p21.31 | AG | 0.4682 | 0.674 | 0.0009763 |
| 11 | rs17142764 | 81054378 | MGC33846 | 1066320 base upstream | q14.1 | CG | 0.777 | 0.642 | 0.0008483 |
| 8 | rs1043883 | 17547711 | MTUS1 | EXON 1 | p22 | CG | 0.6194 | 0.669 | 0.0006589 |
| 1 | rs2008873 | 115298685 | SYCP1 | intron 27 | p13.2 | AT | 0.1225 | 1.703 | 0.0006426 |
| 17 | rs727999 | 24570756 | CRYBA1 | 27244 base upstream | q11.2 | AG | 0.3953 | 0.62 | 0.0003774 |
| 4 | rs7672780 | 92514491 | TMSL3 | 535199 base downstream | q22.1 | AG | 0.7007 | 1.659 | 0.0003579 |
| 4 | rs7685112 | 116508739 | NDST4 | 254258 base downstream | q26 | CT | 0.641 | 0.661 | 0.0003795 |
| 6 | rs9345149 | 92320478 | MAP3K7 | 966850 base downstream | q16.1 | AT | 0.2185 | 0.585 | 0.000717 |
| 18 | rs2960028 | 26046673 | DSC3 | 777376 base upstream | q12.1 | AT | 0.5564 | 1.507 | 0.0008251 |
| 2 | rs10181140 | 37367267 | PRKD3 | intron 14 | p22.2 | GT | 0.2238 | 1.564 | 0.0007586 |
| 10 | rs2776630 | 30256403 | KIAA1462 | 86986 base upstream | p11.23 | CT | 0.2395 | 0.59 | 0.0007324 |
| 4 | rs7436414 | 116514942 | NDST4 | 260461 base downstream | q26 | AG | 0.6411 | 0.661 | 0.0003766 |
| 7 | rs7810943 | 152475034 | ACTR3B | 291638 base downstream | q36.2 | AG | 0.6271 | 1.552 | 0.0004964 |
| 11 | rs10897849 | 81004683 | MGC33846 | 1116015 base upstream | q14.1 | AG | 0.5487 | 0.661 | 0.0004244 |
| 1 | rs6604543 | 215519038 | GPATCH2 | 151418 base upstream | q41 | AG | 0.5353 | 0.683 | 0.0008434 |
| 17 | rs8080958 | 24532830 | CRYBA1 | 65170 base upstream | q11.2 | AT | 0.5532 | 1.543 | 0.0003081 |
| 5 | rs952663 | 93824426 | MGC34713 | 56493 base upstream | q15 | AG | 0.4694 | 1.483 | 0.000618 |
| 6 | rs9342290 | 92320349 | MAP3K7 | 966721 base downstream | q16.1 | CT | 0.2185 | 0.585 | 0.0007201 |
| 12 | rs11043491 | 17575942 | FLJ22655 | 549127 base upstream | p12.3 | GT | 0.1868 | 0.53 | 0.0002866 |
| 12 | rs11178026 | 68680548 | RAB3IP | 177299 base downstream | q15 | CT | 0.2607 | 0.591 | 0.0004324 |
| 14 | rs3861665 | 94460547 | GSC | 154295 base downstream | q32.13 | AG | 0.8272 | 1.973 | 0.0004057 |
| 17 | rs4965978 | 24548368 | CRYBA1 | 49632 base upstream | q11.2 | CT | 0.553 | 1.546 | 0.0002971 |
| 1 | rs633696 | 199813623 | NAV1 | 70449 base upstream | q32.1 | CT | 0.0591 | 2.045 | 0.0008842 |
| 8 | rs9324508 | 140497987 | KCNK9 | 195998 base upstream | q24.3 | AG | 0.2428 | 1.559 | 0.0006541 |
| 1 | rs2343194 | 74229988 | LRRC44 | 34301 base upstream | p31.1 | AG | 0.4695 | 0.634 | 0.0004293 |
| 11 | rs2448274 | 79784289 | ODZ4 | 1583456 base downstream | q14.1 | CG | 0.7494 | 0.643 | 0.0009398 |
| 14 | rs11622766 | 78027611 | NRXN3 | intron 1 | q24.3 | AG | 0.6178 | 0.656 | 0.0003683 |
| 11 | rs7482266 | 79783565 | ODZ4 | 1582732 base downstream | q14.1 | CT | 0.7494 | 0.643 | 0.0009388 |
| 4 | rs7437909 | 116501880 | NDST4 | 247399 base downstream | q26 | CT | 0.6406 | 0.661 | 0.0003939 |
| 1 | rs7535727 | 48878877 | AGBL4 | intron 3 | p33 | GT | 0.9188 | 0.541 | 0.0008738 |
| 4 | rs6844256 | 92524147 | TMSL3 | 544855 base downstream | q22.1 | CG | 0.2995 | 0.602 | 0.0003474 |
| 4 | rs17010704 | 127248513 | FAT4 | 614976 base downstream | q28.1 | AT | 0.1393 | 1.681 | 0.0005095 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 19 | rs4334417 | 37368199 | ZNF507 | 160193 base upstream | q13.11 | AG | 0.4813 | 0.657 | 0.0008017 |
| 4 | rs1528564 | 92477494 | TMSL3 | 498202 base downstream | q22.1 | CT | 0.2912 | 0.597 | 0.0003137 |
| 4 | rs2178221 | 92521289 | TMSL3 | 541997 base downstream | q22.1 | CT | 0.2995 | 0.602 | 0.0003501 |
| 13 | rs2026026 | 98301534 | DOCK9 | intron 21 | q32.3 | CT | 0.1652 | 1.634 | 0.0005855 |
| 11 | rs7929262 | 125183381 | C11orf38 | 29457 base downstream | q24.2 | AT | 0.6869 | 0.655 | 0.0004373 |
| 13 | rs9603660 | 39493139 | COG6 | 268507 base downstream | q13.3 | CT | 0.6374 | 0.678 | 0.0007457 |
| 17 | rs9895410 | 45486194 | ITGA3 | 2535 base upstream | q21.33 | CT | 0.1189 | 1.793 | 0.0002947 |
| 11 | rs1945662 | 81005553 | MGC33846 | 1115145 base upstream | q14.1 | CT | 0.5487 | 0.66 | 0.0004211 |
| 3 | rs6763592 | 176315642 | NAALADL2 | intron 2 | q26.31 | GT | 0.3997 | 1.484 | 0.0005766 |
| 1 | rs11120691 | 205553098 | CD55 | 8341 base upstream | q32.2 | GT | 0.4399 | 1.468 | 0.0009389 |
| 4 | rs10000358 | 116502459 | NDST4 | 247978 base downstream | q26 | AG | 0.3593 | 1.513 | 0.0003897 |
| 4 | rs17010686 | 127243008 | FAT4 | 609471 base downstream | q28.1 | AG | 0.8607 | 0.595 | 0.0005093 |
| 4 | rs7668527 | 92527407 | TMSL3 | 548115 base downstream | q22.1 | AT | 0.7011 | 1.665 | 0.0003319 |
| 4 | rs1678305 | 8400638 | ACOX3 | 18270 base upstream | p16.1 | CT | 0.5887 | 1.597 | 0.0003165 |
| 4 | rs6837355 | 92523247 | TMSL3 | 543955 base downstream | q22.1 | AG | 0.2995 | 0.602 | 0.0003484 |
| 5 | rs7728878 | 93827557 | MGC34713 | 53362 base upstream | q15 | CT | 0.5253 | 0.675 | 0.0007419 |
| 3 | rs17550007 | 29734340 | RBMS3 | intron 4 | p24.1 | GT | 0.6586 | 0.675 | 0.0008584 |
| 20 | rs6128962 | 58942206 | CDH4 | 318747 base upstream | q13.33 | AG | 0.5709 | 0.683 | 0.0008165 |
| 2 | rs7606701 | 38403351 | ARL6IP2 | intron 11 | p22.1 | AC | 0.6045 | 1.551 | 0.0003361 |
| 5 | rs9314112 | 93821414 | MGC34713 | 59505 base upstream | q15 | AG | 0.469 | 1.485 | 0.0006204 |
| 1 | rs841329 | 94942350 | SLC44A3 | 116138 base upstream | p21.3 | AG | 0.444 | 1.504 | 0.0008246 |
| 7 | rs7776954 | 124677258 | POT1 | 319985 base downstream | q31.33 | AG | 0.7517 | 0.634 | 0.0006815 |
| 4 | rs1358554 | 92512505 | TMSL3 | 533213 base downstream | q22.1 | CT | 0.2993 | 0.603 | 0.0003555 |
| 4 | rs6858268 | 8386637 | HTRA3 | 26907 base downstream | p16.1 | CT | 0.649 | 0.676 | 0.0007683 |
| 2 | rs9808407 | 38403917 | ARL6IP2 | intron 11 | p22.1 | AC | 0.4011 | 0.644 | 0.0003225 |
| 17 | rs12936268 | 9717002 | GLP2R | intron 10 | p13.1 | AT | 0.8464 | 0.601 | 0.0009002 |
| 3 | rs13082004 | 60197075 | FHIT | intron 5 | p14.2 | CT | 0.1879 | 0.523 | 0.0003843 |
| 2 | rs7593981 | 38403041 | ARL6IP2 | intron 11 | p22.1 | AT | 0.4011 | 0.644 | 0.000325 |
| 4 | rs10517571 | 154534381 | MND1 | intron 4 | q31.3 | AC | 0.4354 | 1.527 | 0.0004464 |
| 12 | rs1565723 | 68683295 | RAB3IP | 180046 base downstream | q15 | CT | 0.2609 | 0.589 | 0.0004326 |
| 1 | rs891373 | 205480867 | CD55 | 80572 base upstream | q32.2 | CT | 0.4276 | 1.487 | 0.0008291 |
| 2 | rs7425554 | 83407484 | SUCLG1 | 1096680 base upstream | p12 | CT | 0.5982 | 0.666 | 0.0005219 |
| 12 | rs7134411 | 68673713 | RAB3IP | 170464 base downstream | q15 | CT | 0.7404 | 1.681 | 0.0004565 |
| 4 | rs3796632 | 140897320 | MAML3 | intron 3 | q31.1 | CT | 0.0258 | 2.752 | 0.0009648 |
| 12 | rs980891 | 60689368 | FAM19A2 | intron 4 | q14.1 | CT | 0.7268 | 0.654 | 0.0007546 |
| 12 | rs348696 | 60704889 | FAM19A2 | intron 4 | q14.1 | CT | 0.7257 | 0.656 | 0.0007658 |
| 1 | rs6604542 | 215512121 | GPATCH2 | 158335 base upstream | q41 | AG | 0.5314 | 0.687 | 0.0009715 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 13 | rs9513497 | 98303633 | DOCK9 | intron 21 | q32.3 | CT | 0.4673 | 1.493 | 0.0007326 |
| 7 | rs4730806 | 78868858 | MAGI2 | intron 21 | q21.11 | AC | 0.7134 | 0.668 | 0.000749 |
| 1 | rs12058997 | 48880413 | AGBL4 | intron 3 | p33 | CT | 0.0812 | 1.849 | 0.0008688 |
| 7 | rs7805990 | 147249143 | CNTNAP2 | intron 14 | q35 | GT | 0.6633 | 1.618 | 0.0007391 |
| 4 | rs1377287 | 72355439 | SLC4A4 | intron 3 | q13.3 | AG | 0.8981 | 0.536 | 0.0002989 |
| 4 | rs7683541 | 92459340 | TMSL3 | 480048 base downstream | q22.1 | CT | 0.7078 | 1.718 | 0.0003267 |
| 12 | rs1565725 | 68683857 | RAB3IP | 180608 base downstream | q15 | CT | 0.7389 | 1.701 | 0.0004336 |
| 17 | rs902580 | 24510385 | MYO18A | intron 40 | q11.2 | AC | 0.5468 | 1.547 | 0.0002975 |
| 10 | rs1270449 | 30256668 | KIAA1462 | 86721 base upstream | p11.23 | CT | 0.7605 | 1.696 | 0.0007304 |
| 1 | rs4846404 | 215518894 | GPATCH2 | 151562 base upstream | q41 | AG | 0.5318 | 0.687 | 0.0009202 |
| 7 | rs7805223 | 147248660 | CNTNAP2 | intron 14 | q35 | CT | 0.663 | 1.619 | 0.0007348 |
| 11 | rs17142739 | 81039330 | MGC33846 | 1081368 base upstream | q14.1 | AC | 0.2373 | 1.55 | 0.0008271 |
| 1 | rs10863316 | 215512946 | GPATCH2 | 157510 base upstream | q41 | CT | 0.4686 | 1.455 | 0.0009711 |
| 1 | rs11117833 | 215514615 | GPATCH2 | 155841 base upstream | q41 | CT | 0.4651 | 1.462 | 0.0008857 |
| 1 | rs10863317 | 215513296 | GPATCH2 | 157160 base upstream | q41 | AC | 0.5314 | 0.687 | 0.000971 |
| 4 | rs6825003 | 8386558 | HTRA3 | 26828 base downstream | p16.1 | CT | 0.351 | 1.479 | 0.0007728 |
| 17 | rs6505114 | 24523266 | MYO18A | intron 41 | q11.2 | AG | 0.5531 | 1.543 | 0.0003138 |
| 4 | rs7698375 | 10669107 | HS3ST1 | 339979 base upstream | p16.1 | AG | 0.7854 | 0.64 | 0.0006671 |
| 1 | rs12741053 | 115209396 | SYCP1 | intron 8 | p13.2 | CT | 0.1243 | 1.689 | 0.000768 |
| 12 | rs1565724 | 68683835 | RAB3IP | 180586 base downstream | q15 | AC | 0.261 | 0.589 | 0.0004331 |
| 1 | rs6666935 | 215517984 | GPATCH2 | 152472 base upstream | q41 | CT | 0.5318 | 0.687 | 0.0009195 |
| 8 | rs12674947 | 4064166 | CSMD1 | intron 67 | p23.2 | AG | 0.96 | 0.441 | 0.0007123 |
| 11 | rs17142744 | 81039404 | MGC33846 | 1081294 base upstream | q14.1 | GT | 0.2373 | 1.549 | 0.0008288 |
| 7 | rs7805492 | 147248774 | CNTNAP2 | intron 14 | q35 | CT | 0.6631 | 1.619 | 0.0007348 |
| 7 | rs12718319 | 49039292 | ABCA13 | 381655 base downstream | p12.3 | CT | 0.7605 | 0.64 | 0.0007381 |
| 2 | rs875654 | 38366214 | ARL6IP2 | 10413 base upstream | p22.2 | CT | 0.1758 | 0.517 | 0.0004947 |
| 3 | rs10510834 | 60196556 | FHIT | intron 5 | p14.2 | AG | 0.8129 | 1.91 | 0.0004274 |
| 7 | rs7805515 | 147248819 | CNTNAP2 | intron 14 | q35 | CT | 0.6632 | 1.618 | 0.0007378 |
| 1 | rs4436446 | 215509686 | GPATCH2 | 160770 base upstream | q41 | CT | 0.5314 | 0.687 | 0.0009723 |
| 10 | rs604663 | 6544132 | PRKCQ | intron 4 | p15.1 | CT | 0.4502 | 0.651 | 0.0003581 |
| 11 | rs17142733 | 81037775 | MGC33846 | 1082923 base upstream | q14.1 | AG | 0.7627 | 0.645 | 0.0008247 |
| 7 | rs2538957 | 147247057 | CNTNAP2 | intron 14 | q35 | CT | 0.6628 | 1.619 | 0.0007319 |
| 1 | rs7525530 | 205549789 | CD55 | 11650 base upstream | q32.2 | AG | 0.5604 | 0.68 | 0.0009045 |
| 4 | rs3852108 | 154559969 | MND1 | 4276 base downstream | q31.3 | AC | 0.5647 | 0.656 | 0.0004676 |
| 8 | rs6989132 | 127608781 | FAM84B | 25087 base upstream | q24.21 | CT | 0.1511 | 1.688 | 0.0004784 |
| 4 | rs6816883 | 92460094 | TMSL3 | 480802 base downstream | q22.1 | AG | 0.3154 | 0.608 | 0.0003334 |
| 1 | rs10863318 | 215513377 | GPATCH2 | 157079 base upstream | q41 | AG | 0.5314 | 0.687 | 0.0009708 |

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|----|------------|-----------|-----------|-------------------------|--------|----|--------|-------|-----------|
| 1 | rs7532623 | 215516984 | GPATCH2 | 153472 base upstream | q41 | CT | 0.4684 | 1.456 | 0.0009449 |
| 5 | rs346405 | 62549494 | LOC389293 | 440568 base downstream | q12.1 | AC | 0.8742 | 2.176 | 0.0006101 |
| 3 | rs17024316 | 29757722 | RBMS3 | intron 5 | p24.1 | CG | 0.509 | 0.664 | 0.0005989 |
| 4 | rs4530647 | 127238127 | FAT4 | 604590 base downstream | q28.1 | CT | 0.1393 | 1.677 | 0.0005453 |
| 22 | rs713876 | 23839747 | CRYBB3 | 86077 base upstream | q11.23 | AG | 0.291 | 1.503 | 0.0008064 |
| 13 | rs9582269 | 98301752 | DOCK9 | intron 21 | q32.3 | AG | 0.1651 | 1.633 | 0.0005926 |
| 13 | rs2148775 | 89117527 | GPC5 | 1731360 base upstream | q31.3 | CT | 0.0597 | 1.912 | 0.0009976 |
| 1 | rs12074981 | 215514042 | GPATCH2 | 156414 base upstream | q41 | CT | 0.5314 | 0.687 | 0.0009704 |
| 18 | rs12454307 | 57445327 | CDH20 | 71982 base downstream | q21.33 | CT | 0.2097 | 0.568 | 0.0005978 |
| 8 | rs7007303 | 126994033 | TRIB1 | 474209 base downstream | q24.13 | AG | 0.6092 | 0.675 | 0.0009095 |
| 3 | rs1735538 | 129574792 | EEFSEC | intron 6 | q21.3 | AG | 0.7386 | 1.622 | 0.0009659 |
| 4 | rs2904382 | 92539047 | TMSL3 | 559755 base downstream | q22.1 | AG | 0.6997 | 1.642 | 0.000442 |
| 4 | rs955500 | 92464469 | TMSL3 | 485177 base downstream | q22.1 | CT | 0.3163 | 0.611 | 0.0003346 |
| 10 | rs12571128 | 36637209 | FZD8 | 666841 base downstream | p11.21 | AG | 0.9132 | 0.539 | 0.0005042 |
| 1 | rs12059973 | 215514427 | GPATCH2 | 156029 base upstream | q41 | CT | 0.4686 | 1.455 | 0.0009705 |
| 14 | rs1544623 | 78030008 | NRXN3 | intron 1 | q24.3 | AG | 0.6079 | 0.678 | 0.0008413 |
| 13 | rs4772150 | 98305323 | DOCK9 | intron 22 | q32.3 | CT | 0.429 | 1.485 | 0.0008734 |
| 9 | rs12554461 | 4855256 | RCL1 | 4192 base downstream | p24.1 | AG | 0.3145 | 0.644 | 0.0009996 |
| 18 | rs1377169 | 57433136 | CDH20 | 59791 base downstream | q21.33 | AG | 0.786 | 1.753 | 0.000692 |
| 6 | rs4712556 | 20964682 | CDKAL1 | intron 9 | p22.3 | AG | 0.3347 | 1.488 | 0.0009469 |
| 1 | rs6688376 | 152592990 | ATP8B2 | 2587 base downstream | q21.3 | CT | 0.7064 | 0.639 | 0.0007393 |
| 4 | rs12651062 | 116498891 | NDST4 | 244410 base downstream | q26 | AG | 0.3168 | 1.524 | 0.0004199 |
| 5 | rs346420 | 62564968 | LOC389293 | 456042 base downstream | q12.1 | GT | 0.1268 | 0.457 | 0.0006815 |
| 12 | rs2951468 | 60731556 | FAM19A2 | intron 4 | q14.1 | AC | 0.2615 | 1.539 | 0.0007555 |
| 16 | rs17205999 | 53285438 | IRX5 | 237173 base upstream | q12.2 | AG | 0.3573 | 1.496 | 0.0006675 |
| 2 | rs10932782 | 219061439 | USP37 | intron 12 | q35 | CT | 0.3702 | 0.641 | 0.0006242 |
| 7 | rs2538959 | 147244691 | CNTNAP2 | intron 14 | q35 | GT | 0.6597 | 1.613 | 0.0008126 |
| 2 | rs7571743 | 219060816 | USP37 | intron 11 | q35 | CT | 0.3702 | 0.641 | 0.0006238 |
| 5 | rs346421 | 62565739 | LOC389293 | 456813 base downstream | q12.1 | GT | 0.8731 | 2.191 | 0.0006858 |
| 13 | rs9536735 | 53936097 | OLFM4 | 1411910 base downstream | q21.1 | AG | 0.8756 | 2.239 | 0.0007985 |
| 1 | rs12567534 | 88273491 | PKN2 | 649018 base upstream | p22.2 | AG | 0.6075 | 1.533 | 0.0006716 |
| 8 | rs2385503 | 126997191 | TRIB1 | 477367 base downstream | q24.13 | AT | 0.39 | 1.483 | 0.0008874 |
| 5 | rs164105 | 62564201 | LOC389293 | 455275 base downstream | q12.1 | AG | 0.1263 | 0.46 | 0.0006618 |
| 10 | rs678304 | 6544142 | PRKCQ | intron 4 | p15.1 | CG | 0.5879 | 1.604 | 0.0004308 |
| 4 | rs6532290 | 92459948 | TMSL3 | 480656 base downstream | q22.1 | GT | 0.6856 | 1.653 | 0.0003449 |
| 1 | rs11117836 | 215514934 | GPATCH2 | 155522 base upstream | q41 | GT | 0.4686 | 1.455 | 0.00097 |
| 13 | rs7986477 | 98297352 | DOCK9 | intron 19 | q32.3 | AG | 0.8335 | 0.619 | 0.0007907 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 3 | rs6779932 | 29736947 | RBMS3 | intron 4 | p24.1 | GT | 0.6583 | 0.676 | 0.0008862 |
| 2 | rs6710383 | 219067929 | USP37 | intron 12 | q35 | GT | 0.6298 | 1.56 | 0.0006242 |
| 1 | rs6686201 | 205534725 | CD55 | 26714 base upstream | q32.2 | AG | 0.5604 | 0.681 | 0.0009313 |
| 2 | rs4668508 | 6853536 | LOC129607 | 52367 base upstream | p25.2 | AG | 0.2572 | 0.594 | 0.0007224 |
| 14 | rs1184875 | 37930129 | CLEC14A | 134804 base downstream | q21.1 | AC | 0.428 | 0.664 | 0.0007775 |
| 1 | rs12133500 | 88272291 | PKN2 | 650218 base upstream | p22.2 | CG | 0.3925 | 0.653 | 0.0006866 |
| 2 | rs10202238 | 38396294 | ARL6IP2 | intron 9 | p22.2 | CT | 0.3365 | 0.636 | 0.0006368 |
| 4 | rs11726082 | 127224194 | FAT4 | 590657 base downstream | q28.1 | CT | 0.862 | 0.601 | 0.0008 |
| 3 | rs1486796 | 151371682 | PFN2 | 200251 base downstream | q25.1 | CT | 0.197 | 0.558 | 0.0005957 |
| 10 | rs4934805 | 36634477 | FZD8 | 664109 base downstream | p11.21 | AG | 0.0868 | 1.858 | 0.0004729 |
| 8 | rs16902754 | 129318285 | MYC | 495432 base downstream | q24.21 | AC | 0.0552 | 2.176 | 0.0005214 |
| 1 | rs2217406 | 205524041 | CD55 | 37398 base upstream | q32.2 | AT | 0.5606 | 0.683 | 0.0009972 |
| 4 | rs6828907 | 116485614 | NDST4 | 231133 base downstream | q26 | CG | 0.6831 | 0.657 | 0.0004391 |
| 3 | rs7628950 | 60195347 | FHIT | intron 5 | p14.2 | AT | 0.1866 | 0.525 | 0.0004696 |
| 2 | rs10200467 | 6855044 | LOC129607 | 50859 base upstream | p25.2 | CT | 0.7431 | 1.664 | 0.0006955 |
| 13 | rs9582266 | 98294942 | DOCK9 | intron 18 | q32.3 | AG | 0.8333 | 0.621 | 0.0008397 |
| 8 | rs11990954 | 127612296 | FAM84B | 21572 base upstream | q24.21 | AC | 0.1488 | 1.691 | 0.0005056 |
| 1 | rs6675347 | 215516242 | GPATCH2 | 154214 base upstream | q41 | CT | 0.4686 | 1.455 | 0.0009703 |
| 1 | rs7540354 | 215516892 | GPATCH2 | 153564 base upstream | q41 | AG | 0.4686 | 1.454 | 0.0009705 |
| 2 | rs634590 | 219081012 | USP37 | intron 15 | q35 | AC | 0.6079 | 1.561 | 0.0006107 |
| 2 | rs2174865 | 17267063 | RAD51AP2 | 288403 base upstream | p24.2 | CG | 0.3301 | 0.629 | 0.0005174 |
| 2 | rs1507986 | 17266477 | RAD51AP2 | 288989 base upstream | p24.2 | CT | 0.3301 | 0.629 | 0.0005174 |
| 3 | rs1866773 | 29753247 | RBMS3 | intron 4 | p24.1 | CT | 0.4638 | 1.484 | 0.0005915 |
| 13 | rs9517467 | 98311123 | DOCK9 | intron 24 | q32.3 | AC | 0.5642 | 0.673 | 0.0007973 |
| 14 | rs1168555 | 37935967 | CLEC14A | 140642 base downstream | q21.1 | AG | 0.5694 | 1.504 | 0.0009281 |
| 2 | rs11677772 | 17265222 | RAD51AP2 | 290244 base upstream | p24.2 | GT | 0.3301 | 0.629 | 0.0005174 |
| 2 | rs2030357 | 17263874 | RAD51AP2 | 291592 base upstream | p24.2 | AG | 0.3301 | 0.629 | 0.0005171 |
| 2 | rs2030358 | 17263810 | RAD51AP2 | 291656 base upstream | p24.2 | CT | 0.6699 | 1.591 | 0.0005171 |
| 2 | rs7419572 | 17263221 | RAD51AP2 | 292245 base upstream | p24.2 | AG | 0.6699 | 1.591 | 0.0005171 |
| 2 | rs1519968 | 17262967 | RAD51AP2 | 292499 base upstream | p24.2 | AC | 0.3301 | 0.629 | 0.0005169 |
| 2 | rs16983357 | 17263402 | RAD51AP2 | 292064 base upstream | p24.2 | CG | 0.6699 | 1.591 | 0.0005172 |
| 2 | rs11673738 | 17264870 | RAD51AP2 | 290596 base upstream | p24.2 | AT | 0.6699 | 1.591 | 0.0005174 |
| 2 | rs11693140 | 17263551 | RAD51AP2 | 291915 base upstream | p24.2 | AT | 0.3301 | 0.629 | 0.0005172 |
| 6 | rs9368246 | 20974836 | CDKAL1 | intron 9 | p22.3 | CT | 0.3346 | 1.488 | 0.0009582 |
| 4 | rs6857556 | 114747468 | CAMK2D | intron 14 | q26 | AG | 0.0602 | 1.986 | 0.0008237 |
| 2 | rs1519969 | 17262933 | RAD51AP2 | 292533 base upstream | p24.2 | AT | 0.6699 | 1.591 | 0.0005167 |
| 1 | rs4265406 | 88270563 | PKN2 | 651946 base upstream | p22.2 | AG | 0.6075 | 1.531 | 0.0007016 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 3 | rs16862540 | 151370478 | PFN2 | 199047 base downstream | q25.1 | CG | 0.8031 | 1.792 | 0.0005962 |
| 4 | rs12648320 | 92541356 | TMSL3 | 562064 base downstream | q22.1 | AC | 0.6828 | 1.631 | 0.0005082 |
| 22 | rs5752064 | 23850095 | CRYBB3 | 75729 base upstream | q11.23 | CT | 0.7091 | 0.665 | 0.0007835 |
| 15 | rs11637847 | 31694343 | RYR3 | intron 19 | q14 | AG | 0.4124 | 0.662 | 0.0008922 |
| 11 | rs10160390 | 15157736 | INSC | intron 5 | p15.2 | CT | 0.6242 | 1.554 | 0.0005706 |
| 20 | rs1569604 | 8456036 | PLCB1 | intron 3 | p12.3 | AG | 0.4472 | 0.652 | 0.0004929 |
| 8 | rs2169623 | 140499179 | KCNK9 | 194806 base upstream | q24.3 | AG | 0.5346 | 0.677 | 0.0009219 |
| 2 | rs13020402 | 17267310 | RAD51AP2 | 288156 base upstream | p24.2 | CT | 0.3301 | 0.629 | 0.0005174 |
| 7 | rs6943725 | 48310276 | ABCA13 | intron 21 | p12.3 | AG | 0.465 | 1.509 | 0.0005585 |
| 14 | rs1168554 | 37935713 | CLEC14A | 140388 base downstream | q21.1 | AG | 0.5693 | 1.503 | 0.0009404 |
| 20 | rs4812022 | 56635234 | STX16 | 24499 base upstream | q13.32 | CT | 0.8361 | 1.959 | 0.0007733 |
| 4 | rs11731526 | 127224550 | FAT4 | 591013 base downstream | q28.1 | CG | 0.862 | 0.601 | 0.0007996 |
| 4 | rs7655124 | 116472360 | NDST4 | 217879 base downstream | q26 | CT | 0.317 | 1.519 | 0.0004573 |
| 2 | rs7601872 | 219028129 | USP37 | intron 1 | q35 | CG | 0.6225 | 1.536 | 0.0007453 |
| 21 | rs2252991 | 36478878 | DOPEY2 | intron 2 | q22.12 | AG | 0.2964 | 0.625 | 0.0009227 |
| 9 | rs11789876 | 2705349 | KCNV2 | 2176 base upstream | p24.2 | CT | 0.6765 | 1.602 | 0.0003909 |
| 2 | rs13031560 | 17251771 | RAD51AP2 | 303695 base upstream | p24.2 | CT | 0.67 | 1.59 | 0.000522 |
| 4 | rs12650886 | 116481279 | NDST4 | 226798 base downstream | q26 | CT | 0.3617 | 1.502 | 0.0005009 |
| 4 | rs987157 | 28926641 | PCDH7 | 1404493 base upstream | p15.1 | AG | 0.111 | 1.813 | 0.000576 |
| 3 | rs1386291 | 151376909 | PFN2 | 205478 base downstream | q25.1 | CT | 0.8025 | 1.793 | 0.0005918 |
| 2 | rs12467252 | 17248139 | RAD51AP2 | 307327 base upstream | p24.2 | CT | 0.3299 | 0.63 | 0.0005451 |
| 8 | rs9693045 | 129316558 | MYC | 493705 base downstream | q24.21 | CT | 0.0552 | 2.175 | 0.0005227 |
| 2 | rs3755042 | 219025492 | USP37 | EXON 1 | q35 | CT | 0.3776 | 0.651 | 0.0007437 |
| 2 | rs3731867 | 219180978 | PLCD4 | EXON 1 | q35 | AG | 0.376 | 0.645 | 0.000612 |
| 14 | rs1186370 | 37936185 | CLEC14A | 140860 base downstream | q21.1 | AG | 0.5696 | 1.505 | 0.0009154 |
| 2 | rs2710246 | 219242138 | RNF25 | intron 9 | q35 | CT | 0.376 | 0.64 | 0.0005051 |
| 2 | rs4674314 | 219131764 | USP37 | intron 23 | q35 | CT | 0.3778 | 0.65 | 0.0007202 |
| 2 | rs10495660 | 17260029 | RAD51AP2 | 295437 base upstream | p24.2 | GT | 0.6699 | 1.591 | 0.0005167 |
| 2 | rs664514 | 219038063 | USP37 | intron 5 | q35 | AG | 0.3716 | 0.646 | 0.0007343 |
| 2 | rs4674308 | 219018727 | VIL1 | intron 18 | q35 | AC | 0.3776 | 0.651 | 0.0007397 |
| 2 | rs3845835 | 219050528 | USP37 | intron 8 | q35 | CT | 0.3775 | 0.651 | 0.0007509 |
| 17 | rs12452739 | 24496369 | MYO18A | intron 40 | q11.2 | AG | 0.3202 | 0.607 | 0.0006282 |
| 18 | rs11876431 | 57438389 | CDH20 | 65044 base downstream | q21.33 | AG | 0.7921 | 1.735 | 0.0008113 |
| 14 | rs11844960 | 78084707 | NRXN3 | intron 1 | q24.3 | AC | 0.4131 | 1.478 | 0.0009047 |
| 2 | rs11898524 | 17250287 | RAD51AP2 | 305179 base upstream | p24.2 | CT | 0.6701 | 1.589 | 0.0005325 |
| 11 | rs4597100 | 117191666 | FXD2 | 4333 base upstream | q23.3 | AC | 0.4016 | 0.646 | 0.000703 |
| 2 | rs11893015 | 17250643 | RAD51AP2 | 304823 base upstream | p24.2 | CT | 0.3299 | 0.629 | 0.0005238 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs1983375 | 17289256 | RAD51AP2 | 266210 base upstream | p24.2 | CT | 0.1612 | 0.537 | 0.0009996 |
| 8 | rs10505507 | 129311983 | MYC | 489130 base downstream | q24.21 | CT | 0.0552 | 2.17 | 0.0005449 |
| 2 | rs13018947 | 17267368 | RAD51AP2 | 288098 base upstream | p24.2 | CG | 0.6699 | 1.591 | 0.0005174 |
| 10 | rs4303189 | 125987432 | OAT | 88429 base upstream | q26.13 | AG | 0.0395 | 2.357 | 0.0009687 |
| 2 | rs17572485 | 219004789 | VIL1 | intron 9 | q35 | AG | 0.3774 | 0.651 | 0.0007547 |
| 1 | rs7535028 | 215523070 | GPATCH2 | 147386 base upstream | q41 | GT | 0.4991 | 1.459 | 0.0009272 |
| 2 | rs747193 | 13999212 | FAM84A | 691094 base upstream | p24.3 | AG | 0.8955 | 0.533 | 0.0005929 |
| 2 | rs10200507 | 219044188 | USP37 | intron 6 | q35 | AC | 0.3775 | 0.651 | 0.0007486 |
| 8 | rs7840538 | 129311457 | MYC | 488604 base downstream | q24.21 | CG | 0.0552 | 2.169 | 0.0005469 |
| 1 | rs1536127 | 199353517 | CACNA1S | 5200 base downstream | q32.1 | AC | 0.2446 | 1.569 | 0.0008931 |
| 2 | rs11674840 | 17261376 | RAD51AP2 | 294090 base upstream | p24.2 | AG | 0.2123 | 0.547 | 0.0004859 |
| 2 | rs1589272 | 17253381 | RAD51AP2 | 302085 base upstream | p24.2 | AG | 0.7877 | 1.83 | 0.0004874 |
| 8 | rs10104031 | 140497072 | KCNK9 | 196913 base upstream | q24.3 | CT | 0.2339 | 1.531 | 0.0009582 |
| 16 | rs10500520 | 64006260 | LOC283867 | intron 7 | q21 | AG | 0.9304 | 0.538 | 0.0009109 |
| 16 | rs17439546 | 64006980 | LOC283867 | intron 7 | q21 | CT | 0.9304 | 0.539 | 0.0009237 |
| 8 | rs7812998 | 129307851 | MYC | 484998 base downstream | q24.21 | AG | 0.0552 | 2.168 | 0.0005525 |
| 2 | rs7574429 | 219207003 | PLCD4 | intron 11 | q35 | GT | 0.6241 | 1.551 | 0.0006067 |
| 22 | rs875352 | 23875909 | CRYBB3 | 49915 base upstream | q11.23 | CG | 0.2845 | 0.624 | 0.0007203 |
| 14 | rs1015964 | 78086868 | NRXN3 | intron 1 | q24.3 | AG | 0.5871 | 0.676 | 0.0009 |
| 8 | rs2447553 | 140501955 | KCNK9 | 192030 base upstream | q24.3 | CT | 0.5345 | 0.676 | 0.0008886 |
| 22 | rs9624730 | 23876617 | CRYBB3 | 49207 base upstream | q11.23 | CT | 0.7156 | 1.601 | 0.0007227 |
| 7 | rs10246267 | 103388421 | RELN | intron 64 | q22.1 | CT | 0.0526 | 2.059 | 0.0008913 |
| 2 | rs3770214 | 219217232 | ZNF142 | EXON 3 | q35 | CT | 0.624 | 1.55 | 0.0006133 |
| 22 | rs9624734 | 23878986 | CRYBB3 | 46838 base upstream | q11.23 | CT | 0.7157 | 1.601 | 0.0007289 |
| 4 | rs6532296 | 92469018 | TMSL3 | 489726 base downstream | q22.1 | AG | 0.6863 | 1.613 | 0.0004939 |
| 2 | rs585185 | 219165985 | RQCD1 | intron 7 | q35 | AG | 0.638 | 1.572 | 0.0006116 |
| 4 | rs6853566 | 116438169 | NDST4 | 183688 base downstream | q26 | CT | 0.6825 | 0.662 | 0.0005222 |
| 11 | rs12278218 | 113509338 | ZBTB16 | intron 2 | q23.2 | CT | 0.8998 | 0.554 | 0.0008695 |
| 2 | rs832798 | 219173054 | RQCD1 | 5812 base downstream | q35 | AG | 0.6235 | 1.543 | 0.0006774 |
| 22 | rs9624735 | 23879405 | CRYBB3 | 46419 base upstream | q11.23 | AG | 0.2842 | 0.625 | 0.0007358 |
| 11 | rs12419599 | 123073614 | ZNF202 | 26592 base upstream | q24.1 | GT | 0.9502 | 0.474 | 0.0006869 |
| 4 | rs17686110 | 116456988 | NDST4 | 202507 base downstream | q26 | AC | 0.3173 | 1.514 | 0.00049 |
| 11 | rs4406833 | 123073674 | ZNF202 | 26532 base upstream | q24.1 | AT | 0.9504 | 0.472 | 0.000647 |
| 1 | rs10158471 | 215522526 | GPATCH2 | 147930 base upstream | q41 | AG | 0.5008 | 0.685 | 0.0009194 |
| 8 | rs2468726 | 140503436 | KCNK9 | 190549 base upstream | q24.3 | CG | 0.4654 | 1.481 | 0.0009348 |
| 4 | rs10434023 | 116441466 | NDST4 | 186985 base downstream | q26 | CT | 0.3175 | 1.51 | 0.0005198 |
| 4 | rs6535917 | 154568191 | MND1 | 12498 base downstream | q31.3 | AG | 0.4155 | 1.505 | 0.0009343 |

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|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 8 | rs16901493 | 127614227 | FAM84B | 19641 base upstream | q24.21 | GT | 0.1488 | 1.693 | 0.0005138 |
| 16 | rs17530421 | 64011536 | LOC283867 | intron 7 | q21 | CT | 0.9304 | 0.54 | 0.0009701 |
| 2 | rs7603816 | 219104499 | USP37 | intron 17 | q35 | CT | 0.6286 | 1.548 | 0.0007443 |
| 22 | rs6004454 | 23885789 | CRYBB3 | 40035 base upstream | q11.23 | AG | 0.2837 | 0.626 | 0.0007556 |
| 1 | rs6604663 | 215504627 | GPATCH2 | 165829 base upstream | q41 | AG | 0.5009 | 0.687 | 0.0009876 |
| 4 | rs1528579 | 92528251 | TMSL3 | 548959 base downstream | q22.1 | AT | 0.2938 | 0.608 | 0.0004957 |
| 8 | rs16902742 | 129304629 | MYC | 481776 base downstream | q24.21 | AG | 0.0552 | 2.165 | 0.0005669 |
| 11 | rs10488696 | 113508557 | ZBTB16 | intron 2 | q23.2 | AG | 0.1 | 1.809 | 0.0008457 |
| 11 | rs1275055 | 123076941 | ZNF202 | 23265 base upstream | q24.1 | AT | 0.9498 | 0.473 | 0.0007025 |
| 12 | rs348692 | 60709833 | FAM19A2 | intron 4 | q14.1 | AG | 0.2701 | 1.516 | 0.0009855 |
| 22 | rs875353 | 23875612 | CRYBB3 | 50212 base upstream | q11.23 | AG | 0.2847 | 0.624 | 0.0007118 |
| 2 | rs636723 | 219081441 | USP37 | intron 15 | q35 | AG | 0.3774 | 0.651 | 0.0007551 |
| 5 | rs4921230 | 158812974 | IL12B | 122915 base downstream | q33.3 | CT | 0.7721 | 1.715 | 0.0005594 |
| 2 | rs620596 | 219170663 | RQCD1 | 3421 base downstream | q35 | AG | 0.6233 | 1.54 | 0.0007112 |
| 14 | rs10483907 | 78085918 | NRXN3 | intron 1 | q24.3 | AG | 0.413 | 1.479 | 0.000903 |
| 18 | rs12454424 | 57455491 | CDH20 | 82146 base downstream | q21.33 | AG | 0.2047 | 0.574 | 0.0009429 |
| 2 | rs662250 | 219082361 | USP37 | intron 15 | q35 | AT | 0.6226 | 1.536 | 0.0007555 |
| 2 | rs6717433 | 219083955 | USP37 | intron 16 | q35 | CG | 0.3774 | 0.651 | 0.0007564 |
| 4 | rs1881454 | 92484643 | TMSL3 | 505351 base downstream | q22.1 | CG | 0.6856 | 1.612 | 0.0004883 |
| 2 | rs526897 | 219141841 | RQCD1 | 80 base upstream | q35 | AG | 0.6228 | 1.533 | 0.0007833 |
| 4 | rs10856885 | 92528566 | TMSL3 | 549274 base downstream | q22.1 | CT | 0.2939 | 0.61 | 0.0005191 |
| 4 | rs1507942 | 116462047 | NDST4 | 207566 base downstream | q26 | AT | 0.317 | 1.515 | 0.0005612 |
| 22 | rs16979674 | 23885283 | CRYBB3 | 40541 base upstream | q11.23 | AG | 0.2632 | 0.618 | 0.0008486 |
| 2 | rs496674 | 219140813 | USP37 | intron 25 | q35 | AG | 0.6228 | 1.534 | 0.0007747 |
| 18 | rs12457154 | 57455551 | CDH20 | 82206 base downstream | q21.33 | AG | 0.7953 | 1.743 | 0.0009452 |
| 22 | rs6004449 | 23880247 | CRYBB3 | 45577 base upstream | q11.23 | AG | 0.716 | 1.599 | 0.0007432 |
| 2 | rs7583449 | 219111266 | USP37 | intron 18 | q35 | AC | 0.6227 | 1.535 | 0.0007643 |
| 2 | rs523305 | 219110935 | USP37 | intron 18 | q35 | CT | 0.6227 | 1.535 | 0.000764 |
| 2 | rs599973 | 219095517 | USP37 | intron 16 | q35 | CG | 0.3774 | 0.651 | 0.0007599 |
| 22 | rs16979684 | 23890601 | CRYBB3 | 35223 base upstream | q11.23 | AC | 0.7161 | 1.599 | 0.0007317 |
| 4 | rs6820807 | 92530648 | TMSL3 | 551356 base downstream | q22.1 | AT | 0.294 | 0.61 | 0.0005299 |
| 2 | rs3770213 | 219216616 | ZNF142 | EXON 3 | q35 | AT | 0.6191 | 1.546 | 0.0007043 |
| 4 | rs6841781 | 92489733 | TMSL3 | 510441 base downstream | q22.1 | CT | 0.6855 | 1.61 | 0.000493 |
| 2 | rs490483 | 219137296 | USP37 | intron 25 | q35 | AT | 0.3773 | 0.652 | 0.0007708 |
| 14 | rs10431730 | 78012231 | NRXN3 | intron 1 | q24.3 | AG | 0.6097 | 0.665 | 0.0006592 |
| 2 | rs687747 | 219107871 | USP37 | intron 18 | q35 | CT | 0.6226 | 1.535 | 0.0007624 |
| 4 | rs7654013 | 92510260 | TMSL3 | 530968 base downstream | q22.1 | GT | 0.7126 | 1.666 | 0.0005414 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs523937 | 219145840 | RQCD1 | intron 1 | q35 | CG | 0.6228 | 1.533 | 0.0007834 |
| 2 | rs3770216 | 219151961 | RQCD1 | intron 1 | q35 | AG | 0.6228 | 1.533 | 0.0007834 |
| 22 | rs7285325 | 23895420 | CRYBB3 | 30404 base upstream | q11.23 | AG | 0.2634 | 0.617 | 0.0008413 |
| 2 | rs576901 | 219132608 | USP37 | intron 23 | q35 | AG | 0.3773 | 0.652 | 0.0007677 |
| 2 | rs630858 | 219117933 | USP37 | intron 18 | q35 | AC | 0.6227 | 1.535 | 0.0007652 |
| 2 | rs12619347 | 219128179 | USP37 | intron 22 | q35 | CT | 0.3773 | 0.651 | 0.000766 |
| 4 | rs13147974 | 13322444 | FAM44A | 84018 base downstream | p15.33 | CG | 0.5855 | 1.533 | 0.00066 |
| 18 | rs2587634 | 37373309 | PIK3C3 | 415887 base upstream | q12.3 | CT | 0.3206 | 1.494 | 0.0007925 |
| 18 | rs2587632 | 37374178 | PIK3C3 | 415018 base upstream | q12.3 | CT | 0.321 | 1.496 | 0.0007881 |
| 21 | rs363569 | 29954574 | GRIK1 | intron 12 | q21.3 | CT | 0.9627 | 0.441 | 0.0006906 |
| 21 | rs7280245 | 33678481 | IFNGR2 | 18590 base upstream | q22.11 | AG | 0.8434 | 0.594 | 0.0005271 |
| 2 | rs6760584 | 83410251 | SUCLG1 | 1093913 base upstream | p12 | GT | 0.3991 | 1.478 | 0.0008855 |
| 10 | rs7913128 | 9906737 | CUGBP2 | 1180527 base upstream | p14 | AG | 0.8735 | 0.58 | 0.0009141 |
| 18 | rs2612339 | 37368108 | PIK3C3 | 421088 base upstream | q12.3 | AG | 0.3203 | 1.492 | 0.0007942 |
| 22 | rs16979683 | 23890579 | CRYBB3 | 35245 base upstream | q11.23 | AC | 0.7161 | 1.599 | 0.0007301 |
| 21 | rs12329794 | 33674908 | IFNAR1 | 20912 base downstream | q22.11 | AG | 0.1565 | 1.683 | 0.0005168 |
| 7 | rs826802 | 146666000 | CNTNAP2 | intron 9 | q35 | GT | 0.6825 | 1.58 | 0.0007718 |
| 4 | rs6532299 | 92470862 | TMSL3 | 491570 base downstream | q22.1 | CT | 0.3137 | 0.62 | 0.0004982 |
| 2 | rs11894455 | 38371019 | ARL6IP2 | 5608 base upstream | p22.2 | CT | 0.6104 | 1.505 | 0.0008666 |
| 13 | rs9519490 | 104284662 | DAOA | 631702 base upstream | q33.2 | CT | 0.2049 | 1.59 | 0.0007517 |
| 7 | rs849766 | 12646159 | SCIN | intron 10 | p21.3 | GT | 0.1185 | 1.798 | 0.000792 |
| 18 | rs2848770 | 37368855 | PIK3C3 | 420341 base upstream | q12.3 | AG | 0.3204 | 1.493 | 0.0007932 |
| 14 | rs727208 | 78050487 | NRXN3 | intron 1 | q24.3 | AC | 0.4128 | 1.475 | 0.0009097 |
| 14 | rs11622407 | 78058257 | NRXN3 | intron 1 | q24.3 | GT | 0.413 | 1.475 | 0.0009133 |
| 2 | rs2098446 | 51334759 | NRXN1 | 221581 base downstream | p16.3 | AG | 0.3593 | 1.494 | 0.0007645 |
| 2 | rs562510 | 219151245 | RQCD1 | intron 1 | q35 | AC | 0.3772 | 0.652 | 0.0007833 |
| 22 | rs6004456 | 23885948 | CRYBB3 | 39876 base upstream | q11.23 | AG | 0.2963 | 0.625 | 0.000829 |
| 2 | rs3755041 | 219150743 | RQCD1 | intron 1 | q35 | AT | 0.6228 | 1.533 | 0.0007835 |
| 7 | rs4370447 | 145214888 | CNTNAP2 | 229497 base upstream | q35 | AG | 0.9241 | 0.531 | 0.0008532 |
| 17 | rs1388175 | 24488142 | MYO18A | intron 40 | q11.2 | AC | 0.4539 | 0.66 | 0.0005601 |
| 2 | rs2098441 | 51330460 | NRXN1 | 217282 base downstream | p16.3 | AG | 0.6406 | 0.67 | 0.0007685 |
| 4 | rs4593093 | 92480699 | TMSL3 | 501407 base downstream | q22.1 | GT | 0.3143 | 0.62 | 0.0004862 |
| 21 | rs2832424 | 29945121 | GRIK1 | intron 10 | q21.3 | AC | 0.9627 | 0.442 | 0.0007279 |
| 3 | rs1371846 | 29736653 | RBMS3 | intron 4 | p24.1 | AC | 0.693 | 0.664 | 0.0006261 |
| 14 | rs11159368 | 78048416 | NRXN3 | intron 1 | q24.3 | AC | 0.5873 | 0.679 | 0.000966 |
| 2 | rs6712339 | 17296529 | RAD51AP2 | 258937 base upstream | p24.2 | CT | 0.8355 | 1.877 | 0.0009064 |
| 3 | rs6780134 | 29737133 | RBMS3 | intron 4 | p24.1 | AG | 0.3071 | 1.505 | 0.0006306 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 11 | rs1938928 | 86022325 | ME3 | intron 13 | q14.2 | CT | 0.0836 | 1.818 | 0.0009759 |
| 14 | rs11159367 | 78048326 | NRXN3 | intron 1 | q24.3 | AG | 0.5873 | 0.68 | 0.0009798 |
| 3 | rs1371844 | 29736510 | RBMS3 | intron 4 | p24.1 | CT | 0.6931 | 0.664 | 0.0006233 |
| 14 | rs11625200 | 77999119 | NRXN3 | intron 1 | q24.3 | AC | 0.386 | 1.491 | 0.0007936 |
| 14 | rs10782463 | 78048235 | NRXN3 | intron 1 | q24.3 | CT | 0.4127 | 1.471 | 0.0009919 |
| 9 | rs2376398 | 76896764 | OSTF1 | intron 1 | q21.13 | CT | 0.3991 | 0.643 | 0.0009438 |
| 2 | rs647990 | 219149672 | RQCD1 | intron 1 | q35 | CT | 0.6234 | 1.53 | 0.0008396 |
| 14 | rs11626916 | 78048581 | NRXN3 | intron 1 | q24.3 | AG | 0.5873 | 0.679 | 0.0009606 |
| 9 | rs1454629 | 2690620 | KCNV2 | 16905 base upstream | p24.2 | CT | 0.6754 | 1.577 | 0.0008215 |
| 2 | rs3755025 | 38374562 | ARL6IP2 | 2065 base upstream | p22.2 | CT | 0.3918 | 0.665 | 0.000888 |
| 11 | rs12289252 | 86016483 | ME3 | intron 13 | q14.2 | GT | 0.9164 | 0.55 | 0.0009758 |
| 2 | rs578450 | 219109481 | USP37 | intron 18 | q35 | CT | 0.3868 | 0.652 | 0.0008504 |
| 17 | rs7219630 | 24474555 | MYO18A | intron 40 | q11.2 | AG | 0.4537 | 0.663 | 0.0006304 |
| 21 | rs363586 | 29943925 | GRIK1 | intron 10 | q21.3 | GT | 0.0375 | 2.221 | 0.00098 |
| 17 | rs882729 | 24474102 | MYO18A | intron 40 | q11.2 | CT | 0.5463 | 1.508 | 0.0006341 |
| 3 | rs6783723 | 29738242 | RBMS3 | intron 4 | p24.1 | AG | 0.3076 | 1.505 | 0.0006423 |
| 16 | rs2220233 | 75607795 | MON1B | 174541 base upstream | q23.1 | CT | 0.2545 | 0.617 | 0.0008844 |
| 7 | rs849764 | 12644156 | SCIN | intron 10 | p21.3 | CG | 0.8813 | 0.555 | 0.0007983 |
| 2 | rs13417898 | 38369932 | ARL6IP2 | 6695 base upstream | p22.2 | CT | 0.3727 | 0.651 | 0.0007007 |
| 11 | rs1540176 | 81032483 | MGC33846 | 1088215 base upstream | q14.1 | CT | 0.3962 | 0.636 | 0.0007679 |
| 18 | rs2848760 | 37360470 | PIK3C3 | 428726 base upstream | q12.3 | AG | 0.6802 | 0.672 | 0.0008328 |
| 8 | rs1514708 | 19199623 | SH2D4A | 15863 base upstream | p21.3 | CG | 0.0408 | 2.173 | 0.0009791 |
| 18 | rs2848768 | 37367434 | PIK3C3 | 421762 base upstream | q12.3 | CT | 0.6801 | 0.672 | 0.0008281 |
| 2 | rs4670861 | 38374360 | ARL6IP2 | 2267 base upstream | p22.2 | CT | 0.3918 | 0.665 | 0.0008913 |
| 11 | rs2155035 | 86021251 | ME3 | intron 13 | q14.2 | AG | 0.0836 | 1.818 | 0.0009722 |
| 18 | rs2612343 | 37365054 | PIK3C3 | 424142 base upstream | q12.3 | CT | 0.6801 | 0.671 | 0.0008279 |
| 18 | rs2703183 | 37362872 | PIK3C3 | 426324 base upstream | q12.3 | AT | 0.6801 | 0.671 | 0.0008276 |
| 18 | rs2703176 | 37363038 | PIK3C3 | 426158 base upstream | q12.3 | CT | 0.3199 | 1.489 | 0.0008276 |
| 4 | rs6533856 | 116495156 | NDST4 | 240675 base downstream | q26 | GT | 0.3201 | 1.496 | 0.0007238 |
| 2 | rs287293 | 17251821 | RAD51AP2 | 303645 base upstream | p24.2 | CT | 0.8386 | 1.862 | 0.0009714 |
| 18 | rs2612344 | 37365020 | PIK3C3 | 424176 base upstream | q12.3 | CT | 0.3199 | 1.489 | 0.0008279 |
| 2 | rs13420545 | 51341929 | NRXN1 | 228751 base downstream | p16.3 | CT | 0.6436 | 0.668 | 0.0009116 |
| 18 | rs2587615 | 37364633 | PIK3C3 | 424563 base upstream | q12.3 | CT | 0.3199 | 1.489 | 0.0008277 |
| 2 | rs6720403 | 219002502 | VIL1 | intron 6 | q35 | AC | 0.6219 | 1.541 | 0.000689 |
| 2 | rs3821031 | 219003493 | VIL1 | intron 8 | q35 | CT | 0.622 | 1.541 | 0.0006956 |
| 18 | rs2848767 | 37366646 | PIK3C3 | 422550 base upstream | q12.3 | CT | 0.3199 | 1.489 | 0.0008279 |
| 18 | rs2848766 | 37366392 | PIK3C3 | 422804 base upstream | q12.3 | AG | 0.3199 | 1.489 | 0.0008279 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs287300 | 17263732 | RAD51AP2 | 291734 base upstream | p24.2 | AG | 0.8385 | 1.863 | 0.0009633 |
| 11 | rs10898515 | 86018768 | ME3 | intron 13 | q14.2 | CT | 0.9164 | 0.549 | 0.0009619 |
| 21 | rs363550 | 29968170 | GRIK1 | intron 13 | q21.3 | CG | 0.9625 | 0.441 | 0.0007736 |
| 9 | rs11793747 | 2705284 | KCNV2 | 2241 base upstream | p24.2 | CG | 0.3249 | 0.635 | 0.0005772 |
| 2 | rs484687 | 17222881 | RAD51AP2 | 332585 base upstream | p24.2 | CT | 0.8461 | 1.959 | 0.0008353 |
| 5 | rs1455845 | 114715541 | CCDC112 | 55184 base downstream | q22.3 | AG | 0.1007 | 1.78 | 0.0009561 |
| 3 | rs4679648 | 60194354 | FHIT | intron 5 | p14.2 | CT | 0.1838 | 0.548 | 0.0009246 |
| 7 | rs12703745 | 145228893 | CNTNAP2 | 215492 base upstream | q35 | AG | 0.0754 | 1.868 | 0.000997 |
| 2 | rs10497382 | 172973708 | ITGA6 | 26851 base upstream | q31.1 | CT | 0.8181 | 0.599 | 0.0007119 |
| 17 | rs9890077 | 45486459 | ITGA3 | 2270 base upstream | q21.33 | AG | 0.8864 | 0.579 | 0.0008887 |
| 5 | rs7701924 | 114734342 | CCDC112 | 73985 base downstream | q22.3 | AG | 0.1002 | 1.755 | 0.0009822 |
| 10 | rs11593067 | 122962348 | FGFR2 | 265497 base upstream | q26.12 | CT | 0.5312 | 0.675 | 0.0008253 |
| 4 | rs2091765 | 92557826 | TMSL3 | 578534 base downstream | q22.1 | AG | 0.3115 | 0.618 | 0.0006753 |
| 17 | rs4965417 | 24442232 | MYO18A | intron 8 | q11.2 | CT | 0.4585 | 0.667 | 0.000742 |
| 4 | rs7672281 | 92549378 | TMSL3 | 570086 base downstream | q22.1 | AC | 0.3113 | 0.619 | 0.0007032 |
| 17 | rs4795495 | 24438034 | MYO18A | intron 4 | q11.2 | CG | 0.4586 | 0.667 | 0.0007379 |
| 3 | rs11924206 | 14908226 | FGD5 | intron 4 | p24.3 | GT | 0.7559 | 0.666 | 0.0009021 |
| 17 | rs4794094 | 45487642 | ITGA3 | 1087 base upstream | q21.33 | CT | 0.1137 | 1.726 | 0.0008834 |
| 2 | rs972337 | 60184903 | BCL11A | 346902 base upstream | p16.1 | CT | 0.5692 | 0.656 | 0.0008451 |
| 4 | rs4301075 | 92549226 | TMSL3 | 569934 base downstream | q22.1 | AT | 0.3112 | 0.619 | 0.0007168 |
| 5 | rs10060558 | 114739103 | CCDC112 | 78746 base downstream | q22.3 | CT | 0.1001 | 1.753 | 0.0009659 |
| 16 | rs1485793 | 75659337 | MON1B | 122999 base upstream | q23.1 | AG | 0.7423 | 1.613 | 0.0009969 |
| 5 | rs17137669 | 114736927 | CCDC112 | 76570 base downstream | q22.3 | AG | 0.1002 | 1.749 | 0.0009901 |
| 11 | rs4430519 | 123073531 | ZNF202 | 26675 base upstream | q24.1 | GT | 0.9492 | 0.486 | 0.0009889 |
| 20 | rs6067766 | 49473493 | NFATC2 | intron 2 | q13.2 | AG | 0.1195 | 0.439 | 0.0009623 |
| 4 | rs4521314 | 72303517 | SLC4A4 | intron 1 | q13.3 | AC | 0.1123 | 2.101 | 4.19E-06 |
| 19 | rs12462673 | 56890466 | HAS1 | 17710 base upstream | q13.33 | AG | 0.9729 | 0.314 | 8.85E-06 |
| 4 | rs4311283 | 74585279 | AFM | intron 12 | q13.3 | CT | 0.9732 | 0.322 | 0.0001108 |
| 13 | rs1327342 | 89121163 | GPC5 | 1727724 base upstream | q31.3 | CG | 0.9741 | 0.35 | 0.0001396 |
| 6 | rs9474262 | 52599645 | TMEM14A | 44197 base upstream | p12.2 | CT | 0.0383 | 2.616 | 0.0001447 |
| 11 | rs11605616 | 131483057 | HNT | intron 2 | q25 | CG | 0.9901 | 0.178 | 0.0001737 |
| 20 | rs2143205 | 8459004 | PLCB1 | intron 3 | p12.3 | CT | 0.4991 | 1.604 | 0.0001827 |
| 20 | rs2423364 | 8464695 | PLCB1 | intron 3 | p12.3 | CT | 0.3113 | 0.593 | 0.0001909 |
| 5 | rs32973 | 115859204 | SEMA6A | intron 14 | q23.1 | AG | 0.6409 | 0.646 | 0.0002224 |
| 10 | rs17135903 | 3888018 | KLF6 | 70563 base downstream | p15.1 | CT | 0.9923 | 0.149 | 0.0002328 |
| 20 | rs2423366 | 8465451 | PLCB1 | intron 3 | p12.3 | AG | 0.3099 | 0.6 | 0.0002333 |
| 6 | rs1884456 | 52612989 | TMEM14A | 30853 base upstream | p12.1 | AG | 0.0344 | 2.532 | 0.0002409 |

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|----|------------|-----------|---------|------------------------|--------|----|--------|-------|-----------|
| 10 | rs6482659 | 129848954 | MKI67 | 34309 base downstream | q26.2 | AC | 0.3008 | 1.605 | 0.0002476 |
| 15 | rs8027032 | 58790190 | RORA | intron 10 | q22.2 | CT | 0.2106 | 0.512 | 0.0002557 |
| 14 | rs10133971 | 94392551 | GSC | 86299 base downstream | q32.13 | CT | 0.9358 | 0.467 | 0.0002586 |
| 4 | rs17710298 | 55661374 | KDR | intron 15 | q12 | CT | 0.9784 | 0.338 | 0.0002655 |
| 6 | rs9474264 | 52600553 | TMEM14A | 43289 base upstream | p12.1 | AT | 0.0344 | 2.528 | 0.0002673 |
| 6 | rs9463804 | 52591585 | TRAM2 | 41764 base downstream | p12.2 | AT | 0.9656 | 0.396 | 0.0002797 |
| 6 | rs9474257 | 52589637 | TRAM2 | 39816 base downstream | p12.2 | GT | 0.0344 | 2.526 | 0.0002823 |
| 2 | rs13032715 | 40178533 | SLC8A1 | 14256 base upstream | p22.1 | CT | 0.4345 | 1.585 | 0.0002837 |
| 2 | rs12614752 | 40169977 | SLC8A1 | 22812 base upstream | p22.1 | GT | 0.4378 | 1.573 | 0.0002938 |
| 17 | rs714422 | 12103857 | MAP2K4 | 116082 base downstream | p12 | AG | 0.0827 | 0.296 | 0.0002978 |
| 2 | rs10496069 | 57630160 | VRK2 | 497063 base upstream | p16.1 | AT | 0.9796 | 0.315 | 0.000305 |
| 2 | rs9309301 | 57629406 | VRK2 | 497817 base upstream | p16.1 | AG | 0.0204 | 3.176 | 0.0003075 |
| 2 | rs10166539 | 57629283 | VRK2 | 497940 base upstream | p16.1 | AG | 0.0204 | 3.175 | 0.0003083 |
| 17 | rs12150546 | 12108360 | MAP2K4 | 120585 base downstream | p12 | AG | 0.9171 | 3.381 | 0.000309 |
| 2 | rs9309299 | 57629006 | VRK2 | 498217 base upstream | p16.1 | CG | 0.0204 | 3.171 | 0.000313 |
| 17 | rs16945798 | 12110529 | MAP2K4 | 122754 base downstream | p12 | AG | 0.9169 | 3.381 | 0.0003243 |
| 3 | rs9857839 | 172439746 | TNIK | intron 31 | q26.2 | CT | 0.0078 | 6.213 | 0.0003401 |
| 14 | rs1777075 | 42261991 | LRFN5 | 818493 base downstream | q21.2 | AG | 0.0708 | 2.102 | 0.000342 |
| 2 | rs9309298 | 57626427 | VRK2 | 500796 base upstream | p16.1 | AG | 0.9794 | 0.319 | 0.0003496 |
| 2 | rs13412537 | 57636788 | VRK2 | 490435 base upstream | p16.1 | CG | 0.9797 | 0.316 | 0.0003499 |
| 2 | rs9309297 | 57625311 | VRK2 | 501912 base upstream | p16.1 | CG | 0.0206 | 3.132 | 0.0003556 |
| 8 | rs6981782 | 17542512 | PDGFRL | intron 5 | p22 | CT | 0.0137 | 3.771 | 0.0003564 |
| 2 | rs13410921 | 57624516 | VRK2 | 502707 base upstream | p16.1 | AC | 0.9794 | 0.319 | 0.0003577 |
| 6 | rs9474254 | 52586483 | TRAM2 | 36662 base downstream | p12.2 | AG | 0.9651 | 0.402 | 0.0003652 |
| 2 | rs13389335 | 57618472 | VRK2 | 508751 base upstream | p16.1 | AT | 0.9797 | 0.315 | 0.0003667 |
| 18 | rs8095590 | 10664815 | FAM38B | intron 2 | p11.22 | CT | 0.4977 | 1.561 | 0.0003671 |
| 14 | rs11160216 | 94394040 | GSC | 87788 base downstream | q32.13 | AG | 0.0638 | 2.026 | 0.0003714 |
| 2 | rs6746753 | 57617362 | VRK2 | 509861 base upstream | p16.1 | CG | 0.0199 | 3.241 | 0.0003729 |
| 14 | rs10149887 | 42262582 | LRFN5 | 819084 base downstream | q21.2 | AT | 0.0701 | 2.123 | 0.0003736 |
| 2 | rs13392012 | 57616717 | VRK2 | 510506 base upstream | p16.1 | CT | 0.0199 | 3.245 | 0.0003737 |
| 6 | rs9400871 | 116133539 | FRK | 235847 base upstream | q22.1 | AT | 0.8162 | 0.619 | 0.0003788 |
| 6 | rs9372449 | 116136091 | FRK | 233295 base upstream | q22.1 | CG | 0.813 | 0.615 | 0.0003843 |
| 6 | rs9374567 | 116136871 | FRK | 232515 base upstream | q22.1 | CT | 0.8162 | 0.619 | 0.0003873 |
| 2 | rs10153799 | 57633546 | VRK2 | 493677 base upstream | p16.1 | GT | 0.021 | 3.11 | 0.000391 |
| 6 | rs9320546 | 116137208 | FRK | 232178 base upstream | q22.1 | CT | 0.8163 | 0.619 | 0.0003952 |
| 3 | rs17066182 | 62091268 | PTPRG | intron 5 | p14.2 | CT | 0.9896 | 0.206 | 0.0003978 |
| 2 | rs917977 | 40174693 | SLC8A1 | 18096 base upstream | p22.1 | CT | 0.4434 | 1.559 | 0.0004039 |

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|----|------------|-----------|----------|------------------------|--------|----|--------|-------|-----------|
| 2 | rs12151560 | 40172384 | SLC8A1 | 20405 base upstream | p22.1 | CT | 0.4435 | 1.558 | 0.0004062 |
| 13 | rs6492439 | 89120930 | GPC5 | 1727957 base upstream | q31.3 | CT | 0.9253 | 0.498 | 0.0004101 |
| 6 | rs9463810 | 52615564 | TMEM14A | 28278 base upstream | p12.1 | GT | 0.9621 | 0.411 | 0.0004171 |
| 5 | rs11953897 | 26174463 | CDH9 | 742002 base upstream | p14.1 | AG | 0.0854 | 1.941 | 0.0004296 |
| 9 | rs748787 | 2684201 | KCNV2 | 23324 base upstream | p24.2 | AG | 0.0721 | 2.075 | 0.0004516 |
| 20 | rs6056488 | 924269 | RSPO4 | intron 4 | p13 | AG | 0.954 | 0.445 | 0.0004531 |
| 9 | rs4741038 | 10573907 | PTPRD | intron 44 | p23 | AT | 0.1044 | 1.85 | 0.0004966 |
| 6 | rs6904410 | 83342419 | TPBG | 209086 base downstream | q14.1 | CT | 0.0322 | 2.5 | 0.000497 |
| 6 | rs9361943 | 83341774 | TPBG | 208441 base downstream | q14.1 | AG | 0.9678 | 0.4 | 0.0004973 |
| 6 | rs16885899 | 83339411 | TPBG | 206078 base downstream | q14.1 | AG | 0.0322 | 2.51 | 0.0005037 |
| 6 | rs9443987 | 83346508 | TPBG | 213175 base downstream | q14.1 | CT | 0.0322 | 2.496 | 0.0005088 |
| 6 | rs1999411 | 83348901 | TPBG | 215568 base downstream | q14.1 | CT | 0.9678 | 0.401 | 0.0005242 |
| 6 | rs1999412 | 83348993 | TPBG | 215660 base downstream | q14.1 | AC | 0.9678 | 0.401 | 0.0005275 |
| 6 | rs6939695 | 83349658 | TPBG | 216325 base downstream | q14.1 | AC | 0.9678 | 0.402 | 0.0005513 |
| 11 | rs12292038 | 23636292 | SVIP | 828334 base downstream | p14.3 | AG | 0.0117 | 4.509 | 0.0005712 |
| 11 | rs11037068 | 5350363 | OR51M1 | 16841 base upstream | p15.4 | GT | 0.0603 | 2.004 | 0.0005809 |
| 2 | rs6544307 | 40152968 | SLC8A1 | 39821 base upstream | p22.1 | CT | 0.7233 | 0.627 | 0.0005834 |
| 2 | rs9288698 | 150391583 | C2orf25 | 239066 base downstream | q23.3 | GT | 0.6381 | 0.636 | 0.0005838 |
| 5 | rs4701526 | 26178629 | CDH9 | 737836 base upstream | p14.1 | CG | 0.085 | 1.889 | 0.0005867 |
| 18 | rs600419 | 10667979 | FAM38B | intron 4 | p11.22 | CT | 0.5009 | 0.651 | 0.0005947 |
| 18 | rs510529 | 10666564 | FAM38B | intron 3 | p11.22 | CT | 0.4989 | 1.534 | 0.000597 |
| 5 | rs11959230 | 85551089 | COX7C | 398450 base upstream | q14.3 | CT | 0.9884 | 0.231 | 0.0006025 |
| 11 | rs12279140 | 23653839 | LUZP2 | 821292 base upstream | p14.3 | AC | 0.0133 | 3.769 | 0.0006091 |
| 11 | rs12269913 | 23656340 | LUZP2 | 818791 base upstream | p14.3 | AC | 0.9866 | 0.266 | 0.0006094 |
| 11 | rs11027431 | 23662377 | LUZP2 | 812754 base upstream | p14.3 | AT | 0.0135 | 3.721 | 0.000614 |
| 11 | rs11027434 | 23665756 | LUZP2 | 809375 base upstream | p14.3 | CT | 0.0136 | 3.685 | 0.000623 |
| 11 | rs12293501 | 23666708 | LUZP2 | 808423 base upstream | p14.3 | AG | 0.0137 | 3.683 | 0.0006239 |
| 11 | rs12294691 | 23649890 | LUZP2 | 825241 base upstream | p14.3 | AG | 0.987 | 0.263 | 0.000627 |
| 11 | rs11027436 | 23667238 | LUZP2 | 807893 base upstream | p14.3 | CT | 0.9863 | 0.272 | 0.0006278 |
| 11 | rs11027438 | 23669184 | LUZP2 | 805947 base upstream | p14.3 | AT | 0.0137 | 3.659 | 0.0006336 |
| 12 | rs5028648 | 118973019 | CCDC64 | intron 2 | q24.23 | AG | 0.7962 | 0.623 | 0.0006341 |
| 11 | rs11027440 | 23669845 | LUZP2 | 805286 base upstream | p14.3 | AT | 0.9863 | 0.274 | 0.0006353 |
| 11 | rs12274900 | 23671438 | LUZP2 | 803693 base upstream | p14.3 | CT | 0.9862 | 0.274 | 0.0006386 |
| 11 | rs12283754 | 23672278 | LUZP2 | 802853 base upstream | p14.3 | AT | 0.0138 | 3.635 | 0.0006562 |
| 12 | rs3852585 | 118998008 | CCDC64 | intron 6 | q24.23 | CT | 0.7976 | 0.629 | 0.0006721 |
| 18 | rs7236228 | 8866666 | KIAA0802 | 43891 base downstream | p11.22 | CT | 0.5721 | 1.542 | 0.0006864 |
| 11 | rs10789607 | 106690064 | CWF19L2 | 12228 base upstream | q22.3 | CT | 0.9811 | 0.31 | 0.0006882 |

| | | | | | | | | | |
|----|------------|-----------|-----------|------------------------|--------|----|--------|-------|-----------|
| 11 | rs12280993 | 23675755 | LUZP2 | 799376 base upstream | p14.3 | CT | 0.0139 | 3.617 | 0.0006938 |
| 12 | rs3852587 | 119024673 | RAB35 | intron 3 | q24.23 | AC | 0.2001 | 1.572 | 0.0007225 |
| 12 | rs3936255 | 119031310 | RAB35 | intron 5 | q24.23 | GT | 0.8003 | 0.637 | 0.0007339 |
| 5 | rs346423 | 62568648 | LOC389293 | 459722 base downstream | q12.1 | AG | 0.8717 | 2.223 | 0.0007521 |
| 20 | rs16985881 | 39586586 | CHD6 | intron 34 | q12 | AG | 0.9827 | 0.331 | 0.0007527 |
| 20 | rs6102451 | 39591123 | CHD6 | intron 34 | q12 | AG | 0.0173 | 3.017 | 0.0007527 |
| 20 | rs16985879 | 39585961 | CHD6 | intron 34 | q12 | CT | 0.0173 | 3.017 | 0.0007529 |
| 20 | rs6124365 | 39687101 | CHD6 | 6554 base downstream | q12 | AC | 0.9829 | 0.327 | 0.000755 |
| 11 | rs7114872 | 23645887 | LUZP2 | 829244 base upstream | p14.3 | CT | 0.0133 | 3.675 | 0.0007567 |
| 20 | rs6129876 | 39646291 | CHD6 | intron 36 | q12 | AG | 0.0173 | 3.023 | 0.0007587 |
| 20 | rs6093497 | 39634949 | CHD6 | intron 36 | q12 | AG | 0.9827 | 0.331 | 0.0007596 |
| 15 | rs17539990 | 91523799 | RGMA | 90362 base downstream | q26.1 | CG | 0.7569 | 0.645 | 0.0007808 |
| 7 | rs10085746 | 82779344 | SEMA3E | 51813 base upstream | q21.11 | CT | 0.9822 | 0.332 | 0.0007929 |
| 20 | rs224159 | 24128615 | GGTLA4 | 211199 base downstream | p11.21 | CT | 0.9774 | 0.349 | 0.0008067 |
| 11 | rs1879035 | 23644526 | LUZP2 | 830605 base upstream | p14.3 | CT | 0.9869 | 0.274 | 0.000828 |
| 6 | rs3734662 | 90707807 | BACH2 | intron 2 | q15 | CT | 0.4704 | 0.664 | 0.0008315 |
| 20 | rs2208014 | 24094378 | GGTLA4 | 176962 base downstream | p11.21 | CT | 0.9785 | 0.355 | 0.0008381 |
| 11 | rs11027422 | 23641651 | LUZP2 | 833480 base upstream | p14.3 | CG | 0.0131 | 3.637 | 0.0008562 |
| 11 | rs12295501 | 23637818 | SVIP | 829860 base downstream | p14.3 | CG | 0.0131 | 3.643 | 0.0008568 |
| 11 | rs7122399 | 23639466 | SVIP | 831508 base downstream | p14.3 | CG | 0.9869 | 0.275 | 0.0008583 |
| 11 | rs1879036 | 23644504 | LUZP2 | 830627 base upstream | p14.3 | AG | 0.013 | 3.635 | 0.0008589 |
| 7 | rs1557787 | 82671810 | PCLO | 41677 base downstream | q21.11 | CT | 0.982 | 0.331 | 0.0008611 |
| 12 | rs7961195 | 78710196 | PPP1R12A | intron 6 | q21.31 | CT | 0.0183 | 3.062 | 0.0008671 |
| 11 | rs12277987 | 23678195 | LUZP2 | 796936 base upstream | p14.3 | CT | 0.9871 | 0.257 | 0.0008818 |
| 12 | rs12833727 | 78691492 | PPP1R12A | 824 base upstream | q21.2 | CG | 0.9816 | 0.328 | 0.0008977 |
| 12 | rs17005986 | 78733055 | PPP1R12A | intron 16 | q21.31 | CT | 0.018 | 3.031 | 0.000904 |
| 1 | rs11207145 | 58233385 | DAB1 | intron 16 | p32.2 | AG | 0.0086 | 4.61 | 0.0009134 |
| 20 | rs2179441 | 8465895 | PLCB1 | intron 3 | p12.3 | AC | 0.4075 | 0.644 | 0.0009177 |
| 4 | rs12512046 | 182929319 | ODZ3 | 552811 base upstream | q35.1 | GT | 0.4678 | 1.509 | 0.0009219 |
| 4 | rs12508055 | 182929362 | ODZ3 | 552768 base upstream | q35.1 | AG | 0.4678 | 1.508 | 0.0009246 |
| 3 | rs16855954 | 172404356 | TNIK | intron 29 | q26.2 | AC | 0.9939 | 0.155 | 0.000925 |
| 10 | rs11185747 | 91289457 | SLC16A12 | 4164 base downstream | q23.31 | AT | 0.0506 | 2.084 | 0.0009606 |

| CHR | BP | SNP | A1 | A2 | N | P | P(R) | OR | OR(R) | Q | I ² |
|-----|----------|------------|----|----|---|----------|----------|--------|--------|--------|----------------|
| 10 | 97112231 | rs4918918 | C | T | 4 | 3.28E-06 | 3.28E-06 | 0.8456 | 0.8456 | 0.8086 | 0 |
| 10 | 97113875 | rs955760 | A | G | 4 | 4.87E-06 | 4.87E-06 | 0.8513 | 0.8513 | 0.5216 | 0 |
| 10 | 97109039 | rs7900095 | C | T | 4 | 5.58E-06 | 5.58E-06 | 0.8501 | 0.8501 | 0.8056 | 0 |
| 21 | 39943622 | rs10854398 | C | T | 4 | 6.06E-06 | 6.06E-06 | 1.178 | 1.178 | 0.6215 | 0 |
| 10 | 97109583 | rs7079293 | C | T | 4 | 6.19E-06 | 6.19E-06 | 0.8507 | 0.8507 | 0.7916 | 0 |
| 21 | 39947754 | rs8132770 | A | T | 4 | 7.15E-06 | 7.15E-06 | 0.8559 | 0.8559 | 0.6162 | 0 |
| 10 | 30530710 | rs2462021 | C | T | 4 | 8.30E-06 | 8.30E-06 | 1.1755 | 1.1755 | 0.4293 | 0 |
| 10 | 97106209 | rs7076888 | C | T | 4 | 8.62E-06 | 8.62E-06 | 1.1696 | 1.1696 | 0.3939 | 0 |
| 10 | 30527766 | rs1360550 | A | G | 4 | 8.95E-06 | 8.95E-06 | 0.8511 | 0.8511 | 0.43 | 0 |
| 2 | 46174598 | rs12373805 | A | G | 4 | 9.20E-06 | 9.20E-06 | 1.2169 | 1.2169 | 0.912 | 0 |
| 10 | 30531413 | rs2488010 | A | G | 4 | 1.00E-05 | 1.00E-05 | 1.1738 | 1.1738 | 0.4698 | 0 |
| 10 | 30536131 | rs503598 | A | G | 4 | 1.04E-05 | 1.04E-05 | 0.8531 | 0.8531 | 0.5019 | 0 |
| 14 | 33759807 | rs6571636 | A | G | 4 | 1.41E-05 | 1.41E-05 | 1.1704 | 1.1704 | 0.74 | 0 |
| 10 | 30507811 | rs2488003 | A | G | 4 | 1.56E-05 | 1.56E-05 | 0.8559 | 0.8559 | 0.4251 | 0 |
| 2 | 46174837 | rs10202504 | C | G | 4 | 1.60E-05 | 1.60E-05 | 0.8261 | 0.8261 | 0.903 | 0 |
| 2 | 46174384 | rs2345955 | C | T | 4 | 1.69E-05 | 1.69E-05 | 0.8275 | 0.8275 | 0.8881 | 0 |
| 20 | 5197302 | rs2038410 | C | T | 4 | 1.12E-06 | 1.89E-05 | 1.1933 | 1.1936 | 0.3164 | 15.1 |
| 8 | 1779092 | rs11136435 | A | G | 4 | 2.11E-05 | 2.11E-05 | 1.1614 | 1.1614 | 0.508 | 0 |
| 1 | 4548433 | rs504274 | C | T | 4 | 2.18E-05 | 2.18E-05 | 0.738 | 0.738 | 0.9341 | 0 |
| 10 | 30540273 | rs2795863 | A | G | 4 | 2.54E-05 | 2.54E-05 | 0.8591 | 0.8591 | 0.4916 | 0 |
| 6 | 92134035 | rs2180130 | A | G | 4 | 3.00E-05 | 3.00E-05 | 0.8635 | 0.8635 | 0.596 | 0 |
| 10 | 30497139 | rs2488035 | A | C | 4 | 3.26E-05 | 3.26E-05 | 1.1646 | 1.1646 | 0.4269 | 0 |
| 10 | 30500212 | rs2482828 | A | G | 4 | 3.29E-05 | 3.29E-05 | 1.1632 | 1.1632 | 0.4159 | 0 |
| 10 | 30512209 | rs2795858 | A | G | 4 | 3.41E-05 | 3.41E-05 | 0.8614 | 0.8614 | 0.4415 | 0 |
| 10 | 30512398 | rs1977583 | A | G | 4 | 3.42E-05 | 3.42E-05 | 1.1609 | 1.1609 | 0.4408 | 0 |
| 10 | 30510906 | rs2505110 | A | G | 4 | 3.46E-05 | 3.46E-05 | 1.1609 | 1.1609 | 0.4817 | 0 |
| 2 | 46174610 | rs10167555 | G | T | 4 | 3.47E-05 | 3.47E-05 | 1.2066 | 1.2066 | 0.8436 | 0 |
| 10 | 30517781 | rs2482824 | C | T | 4 | 3.51E-05 | 3.51E-05 | 0.8616 | 0.8616 | 0.4199 | 0 |
| 10 | 30512779 | rs2798907 | A | G | 4 | 3.54E-05 | 3.54E-05 | 0.8616 | 0.8616 | 0.4209 | 0 |
| 10 | 30508511 | rs2505109 | C | T | 4 | 3.56E-05 | 3.56E-05 | 0.8616 | 0.8616 | 0.4739 | 0 |
| 10 | 30494239 | rs2488034 | A | G | 4 | 3.74E-05 | 3.74E-05 | 1.1633 | 1.1633 | 0.4305 | 0 |
| 2 | 46176270 | rs4953309 | C | G | 4 | 3.81E-05 | 3.81E-05 | 0.8365 | 0.8365 | 0.8024 | 0 |
| 10 | 30509940 | rs1571957 | C | T | 4 | 4.14E-05 | 4.14E-05 | 1.1592 | 1.1592 | 0.4786 | 0 |
| 10 | 30514592 | rs2798906 | A | G | 4 | 4.27E-05 | 4.27E-05 | 1.1588 | 1.1588 | 0.4561 | 0 |
| 10 | 30514493 | rs2795859 | C | T | 4 | 4.28E-05 | 4.28E-05 | 0.863 | 0.863 | 0.4641 | 0 |
| 6 | 92125869 | rs6910080 | A | G | 4 | 4.32E-05 | 4.32E-05 | 0.8661 | 0.8661 | 0.5847 | 0 |

| | | | | | | | | | | | |
|----|----------|------------|---|---|---|-----------|-----------|--------|--------|--------|------|
| 10 | 30512070 | rs2795857 | C | G | 4 | 4.85E-05 | 4.85E-05 | 1.1579 | 1.1579 | 0.468 | 0 |
| 10 | 30515649 | rs2798920 | A | G | 4 | 4.86E-05 | 4.86E-05 | 1.1575 | 1.1575 | 0.452 | 0 |
| 10 | 30543585 | rs2779068 | G | T | 4 | 4.93E-05 | 4.93E-05 | 1.1603 | 1.1603 | 0.5857 | 0 |
| 10 | 30543961 | rs2689216 | A | G | 4 | 5.21E-05 | 5.21E-05 | 0.8623 | 0.8623 | 0.5881 | 0 |
| 10 | 30517210 | rs2505112 | C | T | 4 | 5.43E-05 | 5.43E-05 | 1.1566 | 1.1566 | 0.4019 | 0 |
| 10 | 97076365 | rs4542335 | C | G | 4 | 5.59E-05 | 5.59E-05 | 1.1653 | 1.1653 | 0.5374 | 0 |
| 6 | 92124822 | rs7762541 | C | T | 4 | 6.13E-05 | 6.13E-05 | 1.1513 | 1.1513 | 0.5642 | 0 |
| 6 | 92118422 | rs9353824 | A | G | 4 | 6.21E-05 | 6.21E-05 | 0.8687 | 0.8687 | 0.5936 | 0 |
| 8 | 1780249 | rs10099567 | A | G | 4 | 6.81E-05 | 6.91E-05 | 0.8682 | 0.8682 | 0.3912 | 0.09 |
| 5 | 2547273 | rs895658 | C | T | 4 | 7.52E-05 | 7.52E-05 | 1.1568 | 1.1568 | 0.4932 | 0 |
| 15 | 86366855 | rs1381112 | A | G | 4 | 6.90E-05 | 7.81E-05 | 0.8122 | 0.8124 | 0.388 | 0.77 |
| 5 | 64018562 | rs275828 | A | G | 4 | 8.40E-05 | 8.40E-05 | 0.8682 | 0.8682 | 0.4424 | 0 |
| 8 | 1778840 | rs11136431 | C | T | 4 | 4.90E-05 | 8.57E-05 | 1.1563 | 1.1558 | 0.3748 | 3.56 |
| 5 | 2550120 | rs1562414 | A | G | 4 | 9.32E-05 | 9.32E-05 | 0.8661 | 0.8661 | 0.473 | 0 |
| 2 | 46197239 | rs12619351 | G | T | 4 | 9.83E-05 | 9.83E-05 | 0.8478 | 0.8478 | 0.4807 | 0 |
| 5 | 64017230 | rs275829 | A | T | 4 | 0.0001103 | 0.0001103 | 0.8687 | 0.8687 | 0.4725 | 0 |
| 5 | 64047836 | rs183917 | C | T | 4 | 0.0001144 | 0.0001184 | 0.8741 | 0.8742 | 0.3907 | 0.2 |
| 5 | 2511057 | rs315892 | C | T | 4 | 0.0001187 | 0.0001187 | 0.8609 | 0.8609 | 0.5747 | 0 |
| 5 | 64055597 | rs10075967 | C | T | 4 | 0.000119 | 0.000119 | 1.1436 | 1.1436 | 0.3927 | 0 |
| 10 | 97100869 | rs6583995 | C | T | 4 | 0.0001217 | 0.0001217 | 1.1586 | 1.1586 | 0.4032 | 0 |
| 2 | 46181464 | rs12477409 | C | G | 4 | 0.0001237 | 0.0001237 | 1.1759 | 1.1759 | 0.6654 | 0 |
| 5 | 64029942 | rs275832 | A | G | 4 | 0.0001073 | 0.0001297 | 1.1448 | 1.1443 | 0.3866 | 1.08 |
| 2 | 46183371 | rs1116246 | A | G | 4 | 0.0001311 | 0.0001311 | 1.1752 | 1.1752 | 0.6593 | 0 |
| 2 | 45964078 | rs13431763 | A | G | 4 | 0.0001343 | 0.0001343 | 0.8511 | 0.8511 | 0.6322 | 0 |
| 2 | 46181374 | rs12477342 | C | T | 4 | 0.0001348 | 0.0001348 | 0.8512 | 0.8512 | 0.6679 | 0 |
| 2 | 46185673 | rs12712969 | C | T | 4 | 0.0001422 | 0.0001422 | 0.8516 | 0.8516 | 0.6506 | 0 |
| 6 | 48336297 | rs2503674 | C | T | 4 | 0.0001474 | 0.0001474 | 0.8014 | 0.8014 | 0.5655 | 0 |
| 2 | 46187198 | rs12712970 | A | G | 4 | 0.0001616 | 0.0001616 | 1.1715 | 1.1715 | 0.6838 | 0 |
| 2 | 45962449 | rs11125041 | C | T | 4 | 0.0001633 | 0.0001633 | 1.1714 | 1.1714 | 0.5871 | 0 |
| 2 | 46196507 | rs3768752 | A | C | 4 | 0.0001668 | 0.0001668 | 1.171 | 1.171 | 0.6605 | 0 |
| 20 | 5203899 | rs996389 | G | T | 4 | 0.0001521 | 0.000174 | 1.1441 | 1.1441 | 0.3872 | 0.96 |
| 2 | 46193882 | rs1375055 | A | G | 4 | 0.0001812 | 0.0001812 | 1.17 | 1.17 | 0.671 | 0 |
| 2 | 46192218 | rs1597156 | C | T | 4 | 0.0001837 | 0.0001837 | 0.8549 | 0.8549 | 0.6725 | 0 |
| 5 | 2532789 | rs10475154 | G | T | 4 | 0.0001859 | 0.0001859 | 0.8674 | 0.8674 | 0.535 | 0 |
| 9 | 19646396 | rs16937690 | A | G | 4 | 0.0001906 | 0.0001906 | 1.1471 | 1.1471 | 0.5006 | 0 |
| 5 | 64066108 | rs2610243 | G | T | 4 | 0.0001917 | 0.0001917 | 0.8769 | 0.8769 | 0.4191 | 0 |
| 5 | 64077497 | rs188027 | C | T | 4 | 0.000194 | 0.000194 | 1.1387 | 1.1387 | 0.4247 | 0 |

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|----|-----------|------------|---|---|---|-----------|-----------|--------|--------|--------|-------|
| 17 | 11467738 | rs16945089 | C | G | 3 | 0.0001941 | 0.0001941 | 1.273 | 1.273 | 0.8332 | 0 |
| 5 | 64088118 | rs275823 | C | T | 4 | 0.0001949 | 0.0001949 | 1.1401 | 1.1401 | 0.4159 | 0 |
| 2 | 46182056 | rs7568264 | A | G | 4 | 0.0001951 | 0.0001951 | 0.8519 | 0.8519 | 0.5786 | 0 |
| 5 | 64063348 | rs4700651 | A | T | 4 | 0.0001956 | 0.0001956 | 0.8782 | 0.8782 | 0.4106 | 0 |
| 5 | 64076579 | rs275820 | G | T | 4 | 0.0002059 | 0.0002059 | 0.8787 | 0.8787 | 0.4185 | 0 |
| 20 | 5210119 | rs6107609 | C | T | 4 | 0.0002601 | 0.0002601 | 0.8771 | 0.8771 | 0.4523 | 0 |
| 3 | 141211649 | rs16849682 | C | T | 3 | 0.0002724 | 0.0002724 | 0.6972 | 0.6972 | 0.4624 | 0 |
| 20 | 5203159 | rs6038111 | A | C | 4 | 0.0001452 | 0.0002729 | 0.8737 | 0.8735 | 0.3694 | 4.69 |
| 6 | 127762249 | rs6938872 | G | T | 4 | 0.0002506 | 0.0002768 | 0.7316 | 0.732 | 0.3888 | 0.6 |
| 5 | 64084924 | rs7715910 | C | T | 4 | 0.0002928 | 0.0002928 | 0.8804 | 0.8804 | 0.4124 | 0 |
| 5 | 64072297 | rs6449751 | C | G | 4 | 0.0002949 | 0.0002949 | 1.1344 | 1.1344 | 0.4074 | 0 |
| 2 | 45955645 | rs12467641 | A | T | 4 | 0.0003114 | 0.0003114 | 1.1661 | 1.1661 | 0.4727 | 0 |
| 20 | 5211444 | rs2326618 | A | G | 4 | 0.0003227 | 0.0003227 | 1.1378 | 1.1378 | 0.4241 | 0 |
| 5 | 64028945 | rs182149 | C | T | 4 | 0.0001225 | 0.0003783 | 1.1435 | 1.1407 | 0.3588 | 6.87 |
| 2 | 123052210 | rs1439838 | A | T | 4 | 7.70E-05 | 0.0003953 | 0.8644 | 0.8667 | 0.3396 | 10.67 |
| 5 | 2516858 | rs6877519 | A | G | 4 | 7.24E-05 | 0.0004129 | 1.1609 | 1.1598 | 0.3288 | 12.76 |
| 20 | 5201641 | rs6038108 | C | T | 4 | 0.0001351 | 0.0004218 | 0.8732 | 0.8727 | 0.3488 | 8.85 |
| 5 | 5754291 | rs11134123 | C | G | 3 | 0.0004313 | 0.0004313 | 0.583 | 0.583 | 0.7763 | 0 |
| 8 | 127250276 | rs2385523 | A | C | 4 | 0.0004694 | 0.0004694 | 0.863 | 0.863 | 0.5383 | 0 |
| 20 | 5202928 | rs6038110 | A | G | 4 | 0.00016 | 0.0004973 | 0.8745 | 0.874 | 0.3482 | 8.98 |
| 1 | 167156181 | rs17514245 | A | G | 4 | 0.0005025 | 0.0005025 | 1.2194 | 1.2194 | 0.4024 | 0 |
| 6 | 127666637 | rs9401948 | C | T | 4 | 0.0003183 | 0.000525 | 0.7356 | 0.7377 | 0.3767 | 3.18 |
| 20 | 5202768 | rs6038109 | C | T | 4 | 0.000159 | 0.000525 | 0.8745 | 0.8739 | 0.3455 | 9.51 |
| 6 | 127692809 | rs9401949 | C | T | 4 | 0.0003082 | 0.0005271 | 1.3605 | 1.3562 | 0.3756 | 3.4 |
| 6 | 127691077 | rs9372865 | C | T | 4 | 0.0003224 | 0.0005335 | 0.7358 | 0.738 | 0.3766 | 3.2 |
| 6 | 127720097 | rs2073298 | C | T | 4 | 0.0003256 | 0.0005345 | 0.7353 | 0.7375 | 0.3768 | 3.15 |
| 6 | 127717884 | rs6569485 | C | T | 4 | 0.0003266 | 0.0005422 | 0.736 | 0.7382 | 0.3764 | 3.23 |
| 6 | 127643410 | rs9388559 | A | G | 4 | 0.0003675 | 0.0005565 | 1.3552 | 1.3518 | 0.3791 | 2.67 |
| 6 | 127697120 | rs9372866 | C | T | 4 | 0.000316 | 0.0005716 | 1.3597 | 1.3549 | 0.3738 | 3.78 |
| 20 | 5204774 | rs6515995 | G | T | 4 | 0.0001561 | 0.0005776 | 0.8743 | 0.8737 | 0.3408 | 10.45 |
| 2 | 55891570 | rs6723695 | C | T | 4 | 0.0001111 | 0.0005852 | 1.3261 | 1.3186 | 0.335 | 11.56 |
| 5 | 159180592 | rs17057166 | C | T | 3 | 0.0005856 | 0.0005856 | 1.3649 | 1.3649 | 0.6077 | 0 |
| 6 | 127698485 | rs9375502 | G | T | 4 | 0.0003164 | 0.0005868 | 0.7355 | 0.7382 | 0.373 | 3.95 |
| 20 | 5204385 | rs6053245 | C | T | 4 | 0.0001468 | 0.0005904 | 0.8738 | 0.8731 | 0.3373 | 11.13 |
| 9 | 20232344 | rs10811336 | A | C | 4 | 0.0005982 | 0.0005982 | 1.1907 | 1.1907 | 0.5134 | 0 |
| 2 | 55889730 | rs10196888 | A | G | 4 | 0.000106 | 0.0006126 | 0.7514 | 0.756 | 0.3323 | 12.08 |
| 6 | 127637134 | rs9375498 | A | G | 4 | 0.0004025 | 0.0006208 | 1.3524 | 1.3489 | 0.3784 | 2.82 |

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|----|-----------|------------|---|---|---|-----------|-----------|--------|--------|--------|-------|
| 6 | 127643754 | rs9401947 | C | T | 4 | 0.0003993 | 0.0006522 | 0.7405 | 0.7427 | 0.3765 | 3.22 |
| 6 | 127655994 | rs6936084 | A | G | 4 | 0.000364 | 0.0006543 | 1.3554 | 1.3507 | 0.3737 | 3.81 |
| 6 | 127647360 | rs7764180 | A | C | 4 | 0.000376 | 0.0006547 | 0.7383 | 0.7408 | 0.3746 | 3.61 |
| 6 | 127659891 | rs9372863 | A | G | 4 | 0.000376 | 0.0006547 | 0.7383 | 0.7408 | 0.3746 | 3.61 |
| 6 | 127662563 | rs761842 | A | T | 4 | 0.000376 | 0.0006547 | 0.7383 | 0.7408 | 0.3746 | 3.61 |
| 6 | 127642939 | rs9372862 | C | T | 4 | 0.0003687 | 0.0006659 | 1.3551 | 1.3502 | 0.3735 | 3.85 |
| 6 | 127690339 | rs4141423 | C | T | 4 | 0.0003808 | 0.0006666 | 0.7385 | 0.741 | 0.3744 | 3.65 |
| 6 | 127642888 | rs9372861 | C | T | 4 | 0.0003726 | 0.0006688 | 0.7382 | 0.7408 | 0.3737 | 3.81 |
| 6 | 127744028 | rs9385420 | A | G | 4 | 0.0003964 | 0.000684 | 0.738 | 0.7404 | 0.3749 | 3.56 |
| 6 | 127739111 | rs9375505 | C | T | 4 | 0.0003812 | 0.0006869 | 1.3552 | 1.3503 | 0.3735 | 3.84 |
| 6 | 127688899 | rs9375500 | C | T | 4 | 0.0003783 | 0.0006902 | 1.3543 | 1.3494 | 0.3731 | 3.93 |
| 2 | 55903459 | rs13394642 | A | G | 4 | 0.0001485 | 0.0007057 | 0.7551 | 0.7594 | 0.3372 | 11.14 |
| 6 | 127638279 | rs9388558 | A | T | 4 | 0.0003789 | 0.0007076 | 0.7384 | 0.7412 | 0.3723 | 4.09 |
| 6 | 127767426 | rs6941233 | A | G | 4 | 0.0002304 | 0.0007488 | 0.7262 | 0.7315 | 0.355 | 7.61 |
| 20 | 5221382 | rs2234397 | A | G | 3 | 0.0007701 | 0.0007701 | 0.8843 | 0.8843 | 0.3912 | 0 |
| 5 | 143534973 | rs6887917 | A | G | 4 | 0.0003554 | 0.0008447 | 1.1391 | 1.1401 | 0.3495 | 8.72 |
| 6 | 127648042 | rs9321072 | C | T | 4 | 0.0004497 | 0.0008528 | 0.7413 | 0.7442 | 0.3713 | 4.29 |
| 1 | 167157044 | rs7530207 | C | G | 4 | 0.0006682 | 0.0008992 | 0.8229 | 0.8236 | 0.381 | 2.27 |
| 5 | 55358652 | rs17348299 | A | C | 4 | 0.0009495 | 0.0009495 | 1.1739 | 1.1739 | 0.4061 | 0 |
| 2 | 123043417 | rs6759289 | A | C | 4 | 0.0001149 | 0.001018 | 0.8676 | 0.871 | 0.3146 | 15.44 |
| 6 | 127754044 | rs9401954 | A | C | 4 | 0.0005464 | 0.001046 | 0.746 | 0.7491 | 0.3706 | 4.45 |
| 5 | 2517882 | rs13175490 | A | G | 4 | 4.85E-05 | 0.001087 | 1.1701 | 1.1657 | 0.274 | 22.81 |
| 2 | 55892233 | rs7577580 | G | T | 4 | 0.0001796 | 0.001164 | 1.3184 | 1.3091 | 0.3219 | 14.07 |
| 4 | 9846004 | rs877619 | A | G | 3 | 0.001188 | 0.001188 | 0.5091 | 0.5091 | 0.5525 | 0 |
| 10 | 97117254 | rs6583997 | C | T | 4 | 0.000504 | 0.001254 | 0.8741 | 0.874 | 0.3485 | 8.93 |
| 1 | 167156031 | rs17514217 | A | T | 4 | 0.0006895 | 0.00134 | 0.8233 | 0.825 | 0.3671 | 5.18 |
| 2 | 55901698 | rs6759150 | A | T | 4 | 0.000216 | 0.001369 | 0.7603 | 0.7659 | 0.3214 | 14.17 |
| 5 | 2532446 | rs10075636 | C | T | 4 | 0.0004468 | 0.001373 | 1.1501 | 1.1487 | 0.3446 | 9.7 |
| 10 | 115736409 | rs17653713 | C | T | 4 | 2.07E-05 | 0.001377 | 0.7393 | 0.7347 | 0.1912 | 36.81 |
| 5 | 2527518 | rs9312996 | C | G | 4 | 0.0004652 | 0.001398 | 1.1516 | 1.1497 | 0.3468 | 9.26 |
| 2 | 123035921 | rs7573865 | C | G | 4 | 0.0001453 | 0.001423 | 1.1502 | 1.1454 | 0.3072 | 16.83 |
| 4 | 175712054 | rs2877818 | C | T | 4 | 0.001461 | 0.001461 | 1.2219 | 1.2219 | 0.4167 | 0 |
| 5 | 2530430 | rs10055939 | G | T | 4 | 0.000325 | 0.001462 | 1.154 | 1.1528 | 0.3265 | 13.2 |
| 2 | 123036498 | rs9308638 | G | T | 4 | 0.0001463 | 0.001499 | 1.1501 | 1.1452 | 0.305 | 17.22 |
| 2 | 123038464 | rs7581875 | C | T | 4 | 0.0001401 | 0.001514 | 0.8691 | 0.873 | 0.3031 | 17.58 |
| 2 | 123041003 | rs6541834 | G | T | 4 | 0.0001401 | 0.001514 | 0.8691 | 0.873 | 0.3031 | 17.58 |
| 2 | 123058863 | rs10864879 | C | G | 4 | 8.77E-05 | 0.001593 | 1.1566 | 1.1496 | 0.2875 | 20.41 |

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|----|-----------|------------|---|---|---|-----------|----------|--------|--------|--------|-------|
| 1 | 110900289 | rs903050 | C | T | 4 | 8.56E-05 | 0.001613 | 1.2584 | 1.2566 | 0.2585 | 25.52 |
| 2 | 123038857 | rs1527255 | A | C | 4 | 0.0001468 | 0.001667 | 1.1501 | 1.1449 | 0.3001 | 18.13 |
| 14 | 55248246 | rs12431962 | A | G | 4 | 0.0001539 | 0.001823 | 1.2436 | 1.2414 | 0.2784 | 22.03 |
| 2 | 123050723 | rs2272315 | A | G | 4 | 9.55E-05 | 0.001871 | 0.8653 | 0.8707 | 0.2824 | 21.33 |
| 2 | 123035471 | rs1561552 | G | T | 4 | 0.0001682 | 0.001902 | 1.1487 | 1.1434 | 0.2982 | 18.46 |
| 3 | 22438352 | rs11129059 | A | G | 4 | 0.001936 | 0.001936 | 1.161 | 1.161 | 0.4193 | 0 |
| 14 | 55246612 | rs2880396 | A | C | 4 | 0.0001508 | 0.001973 | 1.2444 | 1.2428 | 0.2709 | 23.35 |
| 2 | 123042613 | rs11122916 | C | T | 4 | 0.0001622 | 0.002015 | 0.8703 | 0.8745 | 0.2942 | 19.2 |
| 4 | 175713571 | rs10019035 | C | T | 4 | 0.001964 | 0.002048 | 1.2164 | 1.2164 | 0.3895 | 0.46 |
| 5 | 2517988 | rs13156277 | C | T | 4 | 5.86E-05 | 0.002066 | 1.1656 | 1.1614 | 0.2442 | 27.97 |
| 13 | 89560729 | rs7325881 | C | T | 4 | 0.0003498 | 0.002171 | 0.8504 | 0.8532 | 0.3143 | 15.51 |
| 14 | 55248459 | rs12432019 | C | G | 4 | 0.000166 | 0.002175 | 1.2423 | 1.24 | 0.2708 | 23.37 |
| 14 | 55246211 | rs8015301 | C | T | 4 | 0.0001528 | 0.00221 | 0.8027 | 0.8033 | 0.2625 | 24.81 |
| 2 | 123069387 | rs2418570 | A | G | 4 | 9.12E-05 | 0.002255 | 0.8648 | 0.8703 | 0.2689 | 23.71 |
| 20 | 5207966 | rs6085062 | C | G | 4 | 0.0001736 | 0.002256 | 1.1432 | 1.1458 | 0.2713 | 23.28 |
| 20 | 5207931 | rs6085061 | C | T | 4 | 0.0001694 | 0.00226 | 0.8746 | 0.8725 | 0.2701 | 23.48 |
| 14 | 55245765 | rs7152314 | C | T | 4 | 0.0001466 | 0.002285 | 0.8022 | 0.8029 | 0.2588 | 25.46 |
| 2 | 123045361 | rs13425998 | C | T | 4 | 0.0001326 | 0.002309 | 1.1505 | 1.1426 | 0.2861 | 20.65 |
| 10 | 115728492 | rs17653278 | C | G | 4 | 1.03E-05 | 0.002348 | 0.7291 | 0.721 | 0.126 | 47.56 |
| 2 | 123024644 | rs1080548 | C | T | 4 | 0.0002039 | 0.002492 | 0.8722 | 0.8765 | 0.2913 | 19.73 |
| 3 | 22537241 | rs4392438 | C | T | 4 | 0.0002175 | 0.002532 | 0.8559 | 0.8616 | 0.2955 | 18.97 |
| 2 | 123048824 | rs999492 | A | C | 4 | 0.0001128 | 0.002575 | 0.8687 | 0.8753 | 0.2756 | 22.52 |
| 2 | 123061530 | rs1304771 | A | G | 4 | 0.0001235 | 0.002838 | 1.153 | 1.1451 | 0.2697 | 23.56 |
| 2 | 123031238 | rs11695611 | C | T | 4 | 0.0002279 | 0.002902 | 0.8743 | 0.8796 | 0.2921 | 19.57 |
| 2 | 123068787 | rs10171928 | C | T | 4 | 0.0001133 | 0.002941 | 0.8657 | 0.8717 | 0.2627 | 24.78 |
| 4 | 82339936 | rs984924 | A | G | 3 | 0.0007466 | 0.002963 | 0.7676 | 0.7681 | 0.305 | 15.78 |
| 20 | 5219710 | rs910970 | C | T | 4 | 4.39E-05 | 0.002983 | 1.154 | 1.1626 | 0.1687 | 40.51 |
| 2 | 123031511 | rs9308637 | C | T | 4 | 0.0002267 | 0.002988 | 0.8731 | 0.8776 | 0.2855 | 20.76 |
| 2 | 123091471 | rs1918273 | G | T | 4 | 6.88E-05 | 0.002992 | 0.8618 | 0.869 | 0.2469 | 27.51 |
| 4 | 175714448 | rs9998916 | C | G | 4 | 0.002024 | 0.003001 | 0.8216 | 0.8214 | 0.3707 | 4.43 |
| 2 | 123098289 | rs1371489 | C | T | 4 | 6.06E-05 | 0.003041 | 0.8608 | 0.8683 | 0.242 | 28.35 |
| 13 | 89566249 | rs9588875 | A | T | 4 | 0.0004212 | 0.003104 | 0.8522 | 0.8551 | 0.3017 | 17.84 |
| 2 | 123022799 | rs10201094 | C | G | 4 | 0.000226 | 0.003226 | 0.873 | 0.8777 | 0.2816 | 21.46 |
| 2 | 123023527 | rs2091427 | C | G | 4 | 0.0002592 | 0.003238 | 0.8741 | 0.8786 | 0.2865 | 20.58 |
| 10 | 115729399 | rs17574901 | C | T | 4 | 1.41E-05 | 0.003294 | 0.7335 | 0.7245 | 0.1136 | 49.66 |
| 14 | 55251053 | rs11621130 | C | T | 4 | 0.0002052 | 0.003592 | 0.8078 | 0.8093 | 0.246 | 27.66 |
| 2 | 123046194 | rs10195812 | C | T | 4 | 0.0001584 | 0.003604 | 0.8706 | 0.8776 | 0.2697 | 23.56 |

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|----|-----------|------------|---|---|---|-----------|----------|--------|--------|--------|-------|
| 13 | 89566889 | rs9805500 | C | T | 4 | 0.0004579 | 0.003655 | 1.1722 | 1.168 | 0.2955 | 18.96 |
| 2 | 123048317 | rs1527253 | C | T | 4 | 0.0001534 | 0.003742 | 1.149 | 1.1396 | 0.2668 | 24.07 |
| 2 | 123037185 | rs766757 | C | T | 4 | 0.0002268 | 0.00376 | 0.873 | 0.878 | 0.2727 | 23.03 |
| 10 | 30537356 | rs560559 | A | G | 4 | 0.0001623 | 0.003938 | 1.1609 | 1.1492 | 0.2741 | 22.79 |
| 12 | 94632343 | rs4077227 | C | T | 4 | 0.001106 | 0.004118 | 0.874 | 0.8748 | 0.3215 | 14.15 |
| 2 | 123070752 | rs1405604 | A | G | 4 | 0.0001272 | 0.00414 | 0.8697 | 0.8772 | 0.2539 | 26.3 |
| 20 | 5221314 | rs6038126 | C | T | 4 | 3.89E-05 | 0.004287 | 1.1551 | 1.167 | 0.131 | 46.72 |
| 11 | 23675755 | rs12280993 | C | T | 2 | 0.0009513 | 0.004434 | 2.9248 | 2.8415 | 0.2769 | 15.42 |
| 11 | 23672278 | rs12283754 | A | T | 2 | 0.0009139 | 0.004719 | 2.9355 | 2.8458 | 0.2739 | 16.46 |
| 5 | 2532515 | rs16869822 | A | G | 4 | 0.0006631 | 0.00484 | 1.1452 | 1.1427 | 0.2904 | 19.88 |
| 11 | 23669845 | rs11027440 | A | T | 2 | 0.0008847 | 0.004957 | 0.3397 | 0.351 | 0.2715 | 17.29 |
| 11 | 23671438 | rs12274900 | C | T | 2 | 0.0008847 | 0.004957 | 0.3397 | 0.351 | 0.2715 | 17.29 |
| 14 | 55252880 | rs12587803 | A | G | 4 | 0.0002761 | 0.004985 | 1.2329 | 1.2288 | 0.2407 | 28.56 |
| 20 | 5222381 | rs6053263 | C | G | 4 | 5.85E-05 | 0.005004 | 1.1526 | 1.1652 | 0.1289 | 47.07 |
| 13 | 45339540 | rs4941534 | A | T | 4 | 6.44E-06 | 0.005027 | 0.6782 | 0.649 | 0.0771 | 56.16 |
| 2 | 123087692 | rs1595755 | C | T | 4 | 0.0001122 | 0.005058 | 1.1511 | 1.1396 | 0.241 | 28.51 |
| 2 | 123075396 | rs6753885 | A | T | 4 | 0.0001168 | 0.005092 | 1.1507 | 1.1393 | 0.2418 | 28.38 |
| 7 | 115977929 | rs3815412 | C | T | 4 | 0.0007957 | 0.005137 | 1.1416 | 1.1368 | 0.3045 | 17.32 |
| 11 | 23669184 | rs11027438 | A | T | 2 | 0.0008949 | 0.005154 | 2.9473 | 2.8502 | 0.2703 | 17.7 |
| 2 | 123083369 | rs2043940 | C | T | 4 | 0.0001179 | 0.005371 | 1.1506 | 1.139 | 0.2392 | 28.82 |
| 11 | 23667238 | rs11027436 | C | T | 2 | 0.0008611 | 0.005448 | 0.3381 | 0.3503 | 0.2675 | 18.65 |
| 11 | 23666708 | rs12293501 | A | G | 2 | 0.0008767 | 0.005605 | 2.9589 | 2.8547 | 0.2668 | 18.89 |
| 11 | 23665756 | rs11027434 | C | T | 2 | 0.0008729 | 0.005639 | 2.9601 | 2.8551 | 0.2665 | 19 |
| 2 | 123052783 | rs10445851 | G | T | 4 | 0.0001869 | 0.005686 | 1.1458 | 1.1357 | 0.2494 | 27.07 |
| 20 | 5208540 | rs2145083 | A | G | 4 | 0.0001467 | 0.005699 | 1.145 | 1.1522 | 0.1888 | 37.2 |
| 20 | 5203078 | rs6116721 | G | T | 4 | 0.0003928 | 0.005756 | 0.8774 | 0.877 | 0.244 | 28 |
| 20 | 5209399 | rs6116726 | C | T | 4 | 0.0003825 | 0.005848 | 1.1406 | 1.1406 | 0.2463 | 27.61 |
| 3 | 59331465 | rs6446043 | A | T | 4 | 0.0007246 | 0.005929 | 0.8845 | 0.8908 | 0.3057 | 17.09 |
| 7 | 52133795 | rs9690478 | C | G | 4 | 0.000516 | 0.006058 | 0.8607 | 0.8588 | 0.2423 | 28.29 |
| 2 | 106695948 | rs1006472 | A | C | 4 | 0.0004637 | 0.006076 | 1.1452 | 1.1373 | 0.2766 | 22.34 |
| 12 | 94615189 | rs12423171 | A | G | 4 | 0.00101 | 0.006333 | 0.8719 | 0.8729 | 0.2866 | 20.57 |
| 11 | 23662377 | rs11027431 | A | T | 2 | 0.000889 | 0.006417 | 2.9736 | 2.8599 | 0.2619 | 20.56 |
| 22 | 17963106 | rs5746794 | C | G | 4 | 0.002061 | 0.006653 | 0.8954 | 0.8957 | 0.3198 | 14.46 |
| 20 | 5209029 | rs6038114 | A | G | 4 | 0.0001388 | 0.006748 | 0.8729 | 0.8663 | 0.1702 | 40.26 |
| 14 | 82831246 | rs162637 | C | T | 4 | 0.001448 | 0.006871 | 0.8689 | 0.8732 | 0.3136 | 15.64 |
| 5 | 149554727 | rs17652448 | C | T | 3 | 0.002578 | 0.006885 | 0.6545 | 0.6637 | 0.3467 | 5.61 |
| 12 | 94627360 | rs12824729 | A | G | 4 | 0.001214 | 0.007147 | 1.143 | 1.1413 | 0.2893 | 20.08 |

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|----|-----------|------------|---|---|---|-----------|----------|--------|--------|--------|-------|
| 11 | 23656340 | rs12269913 | A | C | 2 | 0.0008733 | 0.007229 | 0.3344 | 0.3488 | 0.2567 | 22.27 |
| 20 | 5209132 | rs6038115 | A | G | 4 | 0.0001298 | 0.007255 | 0.8724 | 0.8651 | 0.1597 | 41.98 |
| 12 | 94615484 | rs17286390 | A | T | 4 | 0.001075 | 0.007639 | 0.8728 | 0.874 | 0.2757 | 22.5 |
| 12 | 94635249 | rs17287370 | A | G | 4 | 0.00138 | 0.007743 | 0.8763 | 0.8774 | 0.2884 | 20.24 |
| 20 | 5209440 | rs4384857 | C | G | 4 | 0.0001305 | 0.00793 | 0.8724 | 0.8646 | 0.1518 | 43.27 |
| 3 | 22446750 | rs9852024 | A | T | 4 | 0.001907 | 0.00795 | 1.1691 | 1.1632 | 0.3185 | 14.71 |
| 20 | 5209206 | rs4553880 | C | T | 4 | 0.0001414 | 0.007966 | 0.873 | 0.8654 | 0.1547 | 42.81 |
| 17 | 51900513 | rs12945850 | C | T | 4 | 0.0004312 | 0.008013 | 1.1515 | 1.1416 | 0.2596 | 25.33 |
| 2 | 106705890 | rs898457 | A | G | 4 | 0.0005072 | 0.008017 | 1.1441 | 1.1352 | 0.2633 | 24.68 |
| 12 | 94629965 | rs10507059 | C | T | 4 | 0.001332 | 0.00806 | 0.8759 | 0.8771 | 0.2836 | 21.09 |
| 5 | 2522415 | rs6880842 | A | G | 4 | 3.20E-05 | 0.008085 | 1.163 | 1.1548 | 0.1452 | 44.37 |
| 1 | 110896325 | rs1281173 | C | T | 4 | 0.001393 | 0.008151 | 0.817 | 0.8181 | 0.2801 | 21.72 |
| 2 | 106707725 | rs13393451 | A | G | 4 | 0.0004936 | 0.008176 | 0.8738 | 0.8809 | 0.2615 | 25 |
| 11 | 23649890 | rs12294691 | A | G | 2 | 0.0009355 | 0.008329 | 0.3331 | 0.3483 | 0.252 | 23.79 |
| 2 | 106706061 | rs898456 | A | G | 4 | 0.0005105 | 0.008486 | 0.8741 | 0.8812 | 0.2602 | 25.22 |
| 8 | 11156393 | rs10503418 | C | T | 4 | 0.0002777 | 0.008532 | 1.1621 | 1.1762 | 0.175 | 39.48 |
| 5 | 2515225 | rs11133949 | A | G | 4 | 0.0002875 | 0.008729 | 1.139 | 1.1325 | 0.2215 | 31.8 |
| 10 | 111992160 | rs12412423 | C | G | 4 | 0.0009875 | 0.008788 | 1.2501 | 1.2591 | 0.2469 | 27.51 |
| 2 | 123098501 | rs11684281 | G | T | 4 | 0.0001209 | 0.008821 | 0.8693 | 0.88 | 0.2113 | 33.49 |
| 10 | 112303893 | rs7901527 | A | G | 4 | 0.001107 | 0.008844 | 0.8833 | 0.886 | 0.2747 | 22.68 |
| 2 | 106716044 | rs11124131 | A | C | 4 | 0.0004416 | 0.008981 | 1.1445 | 1.1343 | 0.2537 | 26.35 |
| 17 | 51894034 | rs1548809 | C | T | 4 | 0.0004768 | 0.009176 | 1.1503 | 1.1402 | 0.2542 | 26.26 |
| 17 | 51893701 | rs9913702 | C | T | 4 | 0.0004743 | 0.009282 | 0.8693 | 0.877 | 0.2533 | 26.42 |
| 10 | 30516612 | rs576505 | C | T | 4 | 0.000284 | 0.009352 | 1.1502 | 1.136 | 0.2472 | 27.46 |
| 7 | 82779344 | rs10085746 | T | C | 3 | 0.0004455 | 0.009371 | 1.6925 | 1.7804 | 0.1435 | 48.5 |
| 5 | 2526843 | rs3104229 | C | G | 4 | 2.96E-05 | 0.009532 | 1.1637 | 1.1537 | 0.1367 | 45.77 |
| 12 | 94624381 | rs11108202 | A | G | 4 | 0.001293 | 0.009632 | 1.1422 | 1.14 | 0.2701 | 23.49 |
| 4 | 82313069 | rs1546651 | C | T | 3 | 0.0006026 | 0.009658 | 0.7764 | 0.7795 | 0.2291 | 32.14 |
| 5 | 2506377 | rs1908159 | A | G | 4 | 0.0003433 | 0.009802 | 1.136 | 1.1294 | 0.2226 | 31.61 |
| 6 | 29829284 | rs2523407 | C | G | 4 | 0.0003847 | 0.01046 | 0.8447 | 0.8574 | 0.2518 | 26.68 |
| 2 | 106709532 | rs13391600 | C | T | 4 | 0.0005841 | 0.01082 | 0.8754 | 0.883 | 0.2495 | 27.07 |
| 4 | 82333327 | rs3733552 | C | G | 3 | 0.0005421 | 0.01115 | 0.7529 | 0.7563 | 0.2089 | 36.15 |
| 11 | 23678195 | rs12277987 | C | T | 2 | 0.001344 | 0.01127 | 0.3329 | 0.3485 | 0.2454 | 25.88 |
| 10 | 112308514 | rs6584994 | C | G | 4 | 0.001141 | 0.01128 | 0.881 | 0.8834 | 0.2523 | 26.58 |
| 3 | 22448847 | rs11716879 | A | T | 4 | 0.002298 | 0.01131 | 1.158 | 1.1509 | 0.3077 | 16.72 |
| 4 | 182937652 | rs12504073 | A | C | 4 | 0.0004632 | 0.01141 | 0.8803 | 0.8654 | 0.1135 | 49.68 |
| 17 | 51908311 | rs8070836 | C | T | 4 | 0.0008407 | 0.01176 | 0.8748 | 0.8816 | 0.2587 | 25.48 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 17 | 51907580 | rs1442831 | A | T | 4 | 0.000816 | 0.01214 | 1.1435 | 1.1344 | 0.2553 | 26.06 |
| 10 | 112017646 | rs3793889 | A | G | 4 | 0.001232 | 0.01234 | 1.2507 | 1.2535 | 0.2388 | 28.89 |
| 20 | 5209578 | rs4597612 | G | T | 4 | 0.0001171 | 0.01236 | 0.8715 | 0.859 | 0.0986 | 52.25 |
| 17 | 51911802 | rs11653462 | G | T | 4 | 0.0008719 | 0.01269 | 0.8751 | 0.8822 | 0.255 | 26.12 |
| 6 | 155209126 | rs9384246 | C | T | 3 | 0.0003802 | 0.01289 | 0.6207 | 0.6514 | 0.2847 | 20.4 |
| 8 | 3339206 | rs10103966 | C | G | 4 | 0.000532 | 0.01326 | 1.1636 | 1.1626 | 0.1863 | 37.63 |
| 13 | 45339590 | rs4942456 | A | G | 4 | 2.24E-05 | 0.01369 | 0.6923 | 0.6557 | 0.0409 | 63.68 |
| 10 | 111979315 | rs17127166 | A | G | 4 | 0.001271 | 0.01393 | 0.7996 | 0.793 | 0.2192 | 32.18 |
| 17 | 51884770 | rs7218500 | C | T | 4 | 0.0005648 | 0.0141 | 0.871 | 0.8798 | 0.2312 | 30.17 |
| 4 | 82337376 | rs4149 | C | T | 3 | 0.0006824 | 0.01411 | 0.756 | 0.7593 | 0.2002 | 37.84 |
| 19 | 56890466 | rs12462673 | A | G | 3 | 9.34E-06 | 0.01422 | 0.5674 | 0.5028 | 0.024 | 73.19 |
| 3 | 59332476 | rs2366434 | A | G | 4 | 0.000909 | 0.01438 | 1.1272 | 1.1153 | 0.2642 | 24.52 |
| 7 | 52130574 | rs4473990 | A | G | 4 | 0.001023 | 0.01466 | 0.8679 | 0.8651 | 0.1975 | 35.78 |
| 2 | 123106179 | rs11897702 | C | T | 4 | 4.73E-05 | 0.01473 | 1.1615 | 1.1403 | 0.1555 | 42.68 |
| 7 | 52130379 | rs4498494 | A | G | 4 | 0.001107 | 0.01489 | 1.15 | 1.1547 | 0.1975 | 35.79 |
| 10 | 30520525 | rs6481661 | C | T | 4 | 0.0001449 | 0.01581 | 0.8635 | 0.8792 | 0.1954 | 36.12 |
| 4 | 82313093 | rs1972127 | A | G | 3 | 0.0007979 | 0.0166 | 1.2831 | 1.2761 | 0.2031 | 37.26 |
| 13 | 45341521 | rs17067329 | A | T | 4 | 3.07E-05 | 0.01687 | 0.6982 | 0.6642 | 0.038 | 64.4 |
| 13 | 45341888 | rs7998666 | G | T | 4 | 3.21E-05 | 0.01706 | 1.4327 | 1.5166 | 0.0349 | 65.18 |
| 4 | 82314024 | rs3943629 | A | T | 3 | 0.0008114 | 0.01724 | 0.7796 | 0.7839 | 0.2009 | 37.7 |
| 10 | 30526790 | rs11007929 | C | T | 4 | 0.0001673 | 0.01781 | 0.8639 | 0.8802 | 0.1928 | 36.55 |
| 16 | 26204460 | rs12443717 | A | T | 4 | 0.002338 | 0.01787 | 0.877 | 0.8838 | 0.2797 | 21.8 |
| 17 | 47289896 | rs8076116 | G | T | 4 | 0.001502 | 0.01802 | 1.3178 | 1.3011 | 0.2389 | 28.86 |
| 5 | 2532184 | rs10058639 | A | G | 3 | 0.0007471 | 0.0181 | 0.8701 | 0.8743 | 0.1906 | 39.66 |
| 3 | 22448096 | rs9861611 | C | T | 4 | 0.002784 | 0.01836 | 1.1539 | 1.1456 | 0.2805 | 21.66 |
| 7 | 69791004 | rs6946693 | G | T | 4 | 0.0008838 | 0.0186 | 1.1321 | 1.1666 | 0.0624 | 59 |
| 22 | 37038552 | rs867198 | C | T | 4 | 0.004549 | 0.01892 | 0.798 | 0.8057 | 0.3151 | 15.35 |
| 13 | 45343013 | rs7982931 | C | T | 4 | 3.87E-05 | 0.01924 | 1.4238 | 1.5083 | 0.032 | 65.93 |
| 11 | 19040692 | rs12222200 | C | T | 4 | 0.00223 | 0.01941 | 0.8954 | 0.8621 | 0.0622 | 59.06 |
| 2 | 200960600 | rs3769450 | A | G | 4 | 0.001514 | 0.01951 | 1.1275 | 1.126 | 0.21 | 33.72 |
| 11 | 23644504 | rs1879036 | A | G | 2 | 0.001499 | 0.01998 | 2.8436 | 2.6724 | 0.2276 | 31.3 |
| 11 | 23641651 | rs11027422 | C | G | 2 | 0.001492 | 0.02005 | 2.8447 | 2.6729 | 0.2274 | 31.38 |
| 5 | 2546280 | rs2453814 | A | C | 4 | 0.0001917 | 0.02011 | 1.1406 | 1.1374 | 0.1171 | 49.06 |
| 17 | 51825310 | rs4794639 | A | G | 4 | 0.0003365 | 0.02014 | 0.8628 | 0.8755 | 0.1909 | 36.87 |
| 11 | 23639466 | rs7122399 | C | G | 2 | 0.001497 | 0.02019 | 0.3516 | 0.3743 | 0.2271 | 31.46 |
| 11 | 23644526 | rs1879035 | C | T | 2 | 0.001454 | 0.02048 | 0.3506 | 0.3737 | 0.2255 | 31.92 |
| 11 | 23637818 | rs12295501 | C | G | 2 | 0.001522 | 0.02052 | 2.845 | 2.6721 | 0.2265 | 31.64 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 5 | 2525928 | rs6555113 | A | T | 4 | 4.29E-05 | 0.02065 | 1.1674 | 1.1554 | 0.0916 | 53.51 |
| 4 | 175716769 | rs10520281 | A | G | 3 | 0.002138 | 0.02083 | 1.2286 | 1.2312 | 0.2162 | 34.71 |
| 8 | 3342219 | rs1499682 | A | T | 4 | 0.0007761 | 0.02117 | 0.8647 | 0.864 | 0.1551 | 42.73 |
| 11 | 23645887 | rs7114872 | C | T | 2 | 0.001337 | 0.02126 | 2.8689 | 2.6838 | 0.2216 | 33.06 |
| 6 | 17953140 | rs9396812 | A | G | 4 | 0.001399 | 0.02146 | 0.8938 | 0.8572 | 0.0353 | 65.08 |
| 4 | 175716127 | rs7671048 | C | T | 3 | 0.002364 | 0.02203 | 1.2261 | 1.2288 | 0.2163 | 34.69 |
| 10 | 30510832 | rs473195 | C | T | 4 | 0.0001006 | 0.0223 | 0.8606 | 0.8797 | 0.164 | 41.28 |
| 4 | 82315844 | rs10516650 | A | C | 3 | 0.001007 | 0.02248 | 1.2784 | 1.2717 | 0.1868 | 40.39 |
| 5 | 2534088 | rs3112426 | A | C | 4 | 7.26E-05 | 0.02255 | 1.1565 | 1.1471 | 0.0948 | 52.92 |
| 10 | 30535057 | rs10826770 | A | G | 4 | 0.0001361 | 0.02291 | 0.8623 | 0.8812 | 0.1716 | 40.04 |
| 5 | 2521375 | rs924134 | A | C | 4 | 4.79E-05 | 0.02348 | 0.8617 | 0.8699 | 0.0835 | 54.96 |
| 10 | 30532611 | rs2151114 | A | G | 4 | 0.000155 | 0.02354 | 1.1584 | 1.1338 | 0.1751 | 39.47 |
| 2 | 123108773 | rs987707 | C | T | 4 | 2.16E-05 | 0.02358 | 1.1718 | 1.143 | 0.1086 | 50.51 |
| 17 | 51771638 | rs8082579 | G | T | 4 | 7.72E-05 | 0.02393 | 0.8501 | 0.865 | 0.1197 | 48.62 |
| 4 | 82316475 | rs10516651 | C | T | 3 | 0.001163 | 0.02411 | 0.7838 | 0.7873 | 0.1854 | 40.67 |
| 8 | 59543277 | rs6471719 | C | T | 4 | 0.004522 | 0.02438 | 0.8927 | 0.8959 | 0.2703 | 23.46 |
| 4 | 82316801 | rs10003341 | A | C | 3 | 0.001254 | 0.02469 | 0.7842 | 0.7873 | 0.185 | 40.74 |
| 4 | 82316860 | rs10005912 | G | T | 3 | 0.001382 | 0.02489 | 1.2739 | 1.2698 | 0.187 | 40.37 |
| 17 | 51856204 | rs2215759 | A | G | 4 | 0.0002815 | 0.02582 | 1.1622 | 1.1411 | 0.1714 | 40.07 |
| 20 | 46386093 | rs6066696 | A | T | 4 | 0.0007842 | 0.02587 | 0.8783 | 0.8796 | 0.1491 | 43.72 |
| 2 | 123110041 | rs17039782 | C | T | 4 | 1.96E-05 | 0.02595 | 0.8526 | 0.8752 | 0.1013 | 51.78 |
| 6 | 29820738 | rs2844845 | A | T | 4 | 0.0006465 | 0.02612 | 1.1719 | 1.1507 | 0.2082 | 34.01 |
| 2 | 123110875 | rs4848185 | A | G | 4 | 1.78E-05 | 0.02647 | 1.1738 | 1.1431 | 0.0982 | 52.33 |
| 10 | 111996476 | rs716595 | A | G | 4 | 0.00202 | 0.02705 | 0.8087 | 0.8032 | 0.1799 | 38.67 |
| 1 | 38656605 | rs6600426 | A | G | 4 | 0.0007462 | 0.02799 | 1.1672 | 1.2126 | 0.0333 | 65.6 |
| 13 | 45344451 | rs17067344 | C | T | 4 | 6.70E-05 | 0.02815 | 0.7091 | 0.6655 | 0.0213 | 69.06 |
| 11 | 23636292 | rs12292038 | A | G | 2 | 0.001071 | 0.02833 | 3.2369 | 2.9944 | 0.1832 | 43.55 |
| 17 | 51850895 | rs9899359 | C | G | 4 | 0.000379 | 0.02868 | 1.1584 | 1.138 | 0.1729 | 39.82 |
| 8 | 59547229 | rs6471720 | A | G | 4 | 0.004912 | 0.02883 | 0.8937 | 0.8968 | 0.2561 | 25.92 |
| 4 | 82319684 | rs11099460 | A | C | 3 | 0.001632 | 0.02956 | 1.2705 | 1.2672 | 0.1773 | 42.19 |
| 7 | 148246576 | rs7804456 | C | T | 4 | 0.001229 | 0.02972 | 1.1453 | 1.1702 | 0.0666 | 58.18 |
| 3 | 22206935 | rs1994727 | A | T | 4 | 0.003928 | 0.02996 | 0.8772 | 0.883 | 0.2494 | 27.09 |
| 5 | 168156259 | rs4867939 | C | T | 4 | 0.0009817 | 0.03038 | 1.1242 | 1.1328 | 0.0982 | 52.32 |
| 3 | 32247502 | rs9813563 | C | G | 4 | 0.004039 | 0.03079 | 1.1417 | 1.132 | 0.2622 | 24.87 |
| 12 | 13267994 | rs7962943 | A | G | 4 | 0.002104 | 0.03106 | 1.2496 | 1.3154 | 0.0845 | 54.78 |
| 13 | 45343085 | rs7983269 | A | G | 4 | 9.72E-05 | 0.03149 | 0.7165 | 0.6686 | 0.0182 | 70.14 |
| 1 | 150047352 | rs11588258 | A | T | 4 | 0.00166 | 0.03156 | 1.1921 | 1.2039 | 0.1359 | 45.91 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 12 | 13268178 | rs7966096 | C | T | 4 | 0.002168 | 0.0326 | 0.7998 | 0.7602 | 0.0819 | 55.26 |
| 1 | 150047310 | rs11588634 | A | T | 4 | 0.001483 | 0.0327 | 0.8371 | 0.8303 | 0.1309 | 46.74 |
| 5 | 149554979 | rs17708892 | A | G | 3 | 0.003344 | 0.03314 | 1.5077 | 1.4434 | 0.3016 | 16.56 |
| 4 | 9887927 | rs16895848 | A | T | 3 | 0.000614 | 0.0346 | 2.6334 | 2.3028 | 0.1941 | 39 |
| 5 | 2541341 | rs1992827 | C | T | 4 | 0.0001258 | 0.0353 | 0.8689 | 0.8759 | 0.0744 | 56.66 |
| 21 | 40065876 | rs2837202 | A | T | 4 | 0.0002497 | 0.03634 | 0.877 | 0.8891 | 0.1164 | 49.18 |
| 4 | 9892151 | rs16895934 | G | T | 3 | 0.0005487 | 0.03678 | 2.6418 | 2.2957 | 0.1879 | 40.19 |
| 11 | 11073168 | rs745231 | C | T | 3 | 0.0007694 | 0.03711 | 1.164 | 1.1374 | 0.2485 | 28.18 |
| 7 | 52134879 | rs6965611 | G | T | 3 | 0.0009679 | 0.03721 | 0.8611 | 0.859 | 0.1167 | 53.46 |
| 8 | 3343653 | rs2100119 | A | G | 4 | 0.001063 | 0.03777 | 1.151 | 1.1526 | 0.1098 | 50.32 |
| 3 | 124840968 | rs1254403 | A | C | 4 | 0.0007755 | 0.03786 | 0.7742 | 0.7857 | 0.116 | 49.24 |
| 14 | 77087999 | rs11159275 | C | T | 4 | 0.005001 | 0.03828 | 1.111 | 1.1734 | 0.0187 | 69.94 |
| 5 | 2563027 | rs3099592 | A | G | 4 | 0.001516 | 0.03859 | 1.1209 | 1.1165 | 0.1512 | 43.38 |
| 4 | 82314170 | rs1545287 | A | G | 3 | 0.001461 | 0.03901 | 1.2683 | 1.2612 | 0.1531 | 46.71 |
| 5 | 164229034 | rs7723455 | A | C | 4 | 0.002599 | 0.04053 | 0.8852 | 0.8796 | 0.1254 | 47.66 |
| 10 | 91289457 | rs11185747 | A | T | 2 | 0.00199 | 0.04229 | 1.8414 | 1.74 | 0.2225 | 32.82 |
| 17 | 51779870 | rs1547966 | C | T | 4 | 0.0001114 | 0.04293 | 1.1722 | 1.1479 | 0.09 | 53.78 |
| 9 | 19654081 | rs4258076 | G | T | 4 | 0.001569 | 0.04305 | 1.1242 | 1.1091 | 0.1893 | 37.12 |
| 17 | 51873068 | rs7220133 | C | T | 4 | 0.0003202 | 0.04385 | 1.1595 | 1.135 | 0.1348 | 46.09 |
| 1 | 89361971 | rs10922574 | C | T | 4 | 0.009713 | 0.04539 | 0.8849 | 0.8319 | 0.0379 | 64.41 |
| 8 | 120020186 | rs3102725 | A | G | 4 | 0.001911 | 0.04564 | 1.2543 | 1.2653 | 0.1003 | 51.96 |
| 5 | 164230439 | rs2962852 | A | G | 4 | 0.004158 | 0.04596 | 0.8906 | 0.889 | 0.1581 | 42.24 |
| 9 | 77922888 | rs1467773 | A | G | 3 | 0.0008821 | 0.04755 | 1.2074 | 1.2194 | 0.0799 | 60.42 |
| 5 | 164230392 | rs2962851 | A | G | 4 | 0.004329 | 0.04823 | 0.8911 | 0.8894 | 0.1544 | 42.85 |
| 5 | 141067873 | rs17097481 | C | T | 4 | 0.004361 | 0.04827 | 1.1682 | 1.1537 | 0.2141 | 33.03 |
| 1 | 219585205 | rs4465211 | A | G | 4 | 0.008567 | 0.04852 | 1.0989 | 1.1492 | 0.0287 | 66.85 |
| 17 | 51862430 | rs7213627 | G | T | 4 | 0.0003816 | 0.04891 | 0.8632 | 0.8835 | 0.1363 | 45.84 |
| 12 | 115293528 | rs6490059 | C | T | 4 | 0.005832 | 0.04903 | 1.2171 | 1.2074 | 0.214 | 33.04 |
| 7 | 52086483 | rs10256394 | C | T | 4 | 0.0004993 | 0.04904 | 0.8638 | 0.8596 | 0.0499 | 61.62 |
| 1 | 219584095 | rs6671621 | C | G | 4 | 0.008858 | 0.04908 | 1.0985 | 1.1489 | 0.0285 | 66.88 |
| 22 | 17962066 | rs5992433 | C | T | 4 | 0.004432 | 0.04932 | 1.1046 | 1.1027 | 0.175 | 39.48 |
| 1 | 219588044 | rs10863604 | C | G | 4 | 0.0088 | 0.04934 | 1.0986 | 1.1492 | 0.0278 | 67.1 |
| 1 | 89403309 | rs2893089 | G | T | 4 | 0.01211 | 0.04942 | 1.1262 | 1.2021 | 0.0341 | 65.38 |
| 6 | 41399102 | rs9462696 | A | T | 4 | 0.0003237 | 0.04967 | 0.8791 | 0.8923 | 0.0989 | 52.21 |
| 17 | 51868565 | rs4793818 | G | T | 4 | 0.0002563 | 0.04985 | 1.1621 | 1.1346 | 0.1204 | 48.5 |
| 6 | 41398747 | rs9471555 | C | T | 4 | 0.0003387 | 0.05 | 0.8794 | 0.8929 | 0.1011 | 51.81 |
| 3 | 63493882 | rs1505600 | C | G | 4 | 0.0001053 | 0.05043 | 0.8444 | 0.8697 | 0.094 | 53.06 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 15 | 36725969 | rs1122891 | C | G | 4 | 0.00456 | 0.05062 | 0.9054 | 0.9117 | 0.2094 | 33.82 |
| 4 | 132492216 | rs1316758 | C | T | 4 | 0.001775 | 0.05078 | 1.365 | 1.4102 | 0.0616 | 59.17 |
| 10 | 124144159 | rs17103488 | C | T | 4 | 0.002964 | 0.05086 | 0.8509 | 0.8642 | 0.1995 | 35.45 |
| 9 | 19652307 | rs10811225 | A | G | 4 | 0.002302 | 0.05095 | 0.8966 | 0.9094 | 0.2018 | 35.07 |
| 11 | 15201694 | rs1714336 | C | T | 4 | 0.008437 | 0.05096 | 0.9108 | 0.8799 | 0.0443 | 62.89 |
| 1 | 89277631 | rs2149186 | G | T | 4 | 0.008458 | 0.05101 | 0.8787 | 0.8232 | 0.0281 | 67.01 |
| 6 | 29819726 | rs2523386 | A | G | 4 | 0.001164 | 0.05272 | 1.163 | 1.1385 | 0.1715 | 40.04 |
| 7 | 82671810 | rs1557787 | C | T | 3 | 0.003708 | 0.05283 | 0.6457 | 0.5732 | 0.0413 | 68.62 |
| 11 | 15203462 | rs1714337 | A | G | 4 | 0.009253 | 0.05293 | 0.9118 | 0.8806 | 0.0436 | 63.04 |
| 14 | 82451964 | rs7160795 | C | T | 4 | 0.001913 | 0.05308 | 0.8792 | 0.8893 | 0.1554 | 42.7 |
| 22 | 17961830 | rs5993714 | A | G | 4 | 0.004672 | 0.05357 | 1.1039 | 1.1023 | 0.1663 | 40.9 |
| 2 | 126453217 | rs10496652 | A | G | 4 | 0.007216 | 0.05502 | 0.8995 | 0.8679 | 0.0455 | 62.61 |
| 5 | 2561221 | rs3112414 | C | G | 4 | 0.0009342 | 0.05516 | 1.126 | 1.1238 | 0.0778 | 56.02 |
| 4 | 132488079 | rs11931096 | C | T | 4 | 0.002023 | 0.0552 | 0.7347 | 0.7104 | 0.0578 | 59.95 |
| 1 | 219578338 | rs4313406 | C | T | 4 | 0.01152 | 0.05562 | 0.9133 | 0.8721 | 0.0255 | 67.75 |
| 1 | 219579859 | rs6690986 | C | T | 4 | 0.01152 | 0.05562 | 0.9133 | 0.8721 | 0.0255 | 67.75 |
| 8 | 53656739 | rs17329730 | A | T | 4 | 0.002968 | 0.05581 | 1.1115 | 1.1298 | 0.0569 | 60.13 |
| 4 | 182929362 | rs12508055 | A | G | 3 | 0.001541 | 0.05587 | 1.1619 | 1.1989 | 0.0686 | 62.68 |
| 4 | 132486892 | rs17051178 | G | T | 4 | 0.002095 | 0.056 | 1.3608 | 1.4072 | 0.0577 | 59.97 |
| 4 | 132501459 | rs4585325 | C | T | 4 | 0.00224 | 0.05617 | 0.7371 | 0.7129 | 0.0597 | 59.56 |
| 7 | 52115801 | rs11979834 | A | G | 4 | 0.0005475 | 0.05665 | 0.8647 | 0.86 | 0.0406 | 63.75 |
| 4 | 132508352 | rs8180150 | A | C | 4 | 0.002366 | 0.05674 | 1.3533 | 1.3985 | 0.0611 | 59.27 |
| 11 | 15201097 | rs1792556 | G | T | 4 | 0.011 | 0.05691 | 1.0944 | 1.1339 | 0.0422 | 63.37 |
| 13 | 31563969 | rs17591593 | C | G | 4 | 0.01613 | 0.05728 | 1.096 | 1.1467 | 0.0377 | 64.46 |
| 8 | 120025500 | rs3134061 | A | T | 4 | 0.002502 | 0.0575 | 1.2471 | 1.2591 | 0.0861 | 54.49 |
| 1 | 219590026 | rs10863605 | A | G | 4 | 0.01126 | 0.05757 | 1.0993 | 1.1499 | 0.0274 | 67.21 |
| 4 | 132509434 | rs17051181 | C | T | 4 | 0.002469 | 0.05786 | 1.3516 | 1.397 | 0.0606 | 59.37 |
| 1 | 219574484 | rs6704485 | C | G | 4 | 0.01212 | 0.05804 | 1.0941 | 1.1466 | 0.0231 | 68.5 |
| 8 | 120025033 | rs3134059 | C | T | 4 | 0.002509 | 0.05848 | 1.2479 | 1.2589 | 0.0859 | 54.52 |
| 4 | 182929319 | rs12512046 | G | T | 3 | 0.001757 | 0.05899 | 1.1598 | 1.198 | 0.0658 | 63.25 |
| 22 | 17961946 | rs5993715 | G | T | 4 | 0.005061 | 0.05914 | 1.103 | 1.1013 | 0.1582 | 42.24 |
| 8 | 120024531 | rs3102726 | A | T | 4 | 0.002572 | 0.05915 | 0.8018 | 0.7946 | 0.0854 | 54.62 |
| 4 | 132486687 | rs17051177 | A | G | 4 | 0.002374 | 0.05919 | 1.3547 | 1.4021 | 0.0562 | 60.27 |
| 8 | 120028459 | rs3134062 | A | G | 4 | 0.002583 | 0.0594 | 0.8019 | 0.7948 | 0.0853 | 54.64 |
| 8 | 120025686 | rs3102729 | A | G | 4 | 0.002552 | 0.05941 | 1.2474 | 1.2585 | 0.0848 | 54.73 |
| 8 | 120028570 | rs3102731 | A | G | 4 | 0.002552 | 0.05941 | 1.2474 | 1.2585 | 0.0848 | 54.73 |
| 8 | 120029532 | rs3134066 | A | T | 4 | 0.002507 | 0.05942 | 0.8014 | 0.7944 | 0.0839 | 54.89 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 8 | 120030619 | rs3134067 | C | T | 4 | 0.002507 | 0.05942 | 0.8014 | 0.7944 | 0.0839 | 54.89 |
| 8 | 120031301 | rs3102733 | C | T | 4 | 0.002523 | 0.05957 | 1.2476 | 1.2586 | 0.084 | 54.88 |
| 8 | 120031840 | rs3134068 | C | T | 4 | 0.002488 | 0.05962 | 1.248 | 1.2589 | 0.0834 | 54.99 |
| 8 | 120033197 | rs3102734 | A | G | 4 | 0.002488 | 0.05962 | 1.248 | 1.2589 | 0.0834 | 54.99 |
| 4 | 82301012 | rs6828114 | C | T | 4 | 0.001851 | 0.05976 | 1.2469 | 1.2134 | 0.1741 | 39.62 |
| 4 | 132509387 | rs8180189 | C | T | 4 | 0.002664 | 0.05982 | 0.7416 | 0.7172 | 0.0599 | 59.52 |
| 1 | 219574269 | rs6704281 | C | T | 4 | 0.01289 | 0.05989 | 1.0933 | 1.1462 | 0.0221 | 68.8 |
| 4 | 132503523 | rs1343670 | C | T | 4 | 0.002758 | 0.06018 | 1.346 | 1.3924 | 0.0602 | 59.46 |
| 17 | 51788210 | rs9915451 | A | G | 4 | 0.000125 | 0.06023 | 1.1709 | 1.1377 | 0.0885 | 54.05 |
| 12 | 82371672 | rs17010837 | A | G | 3 | 0.001342 | 0.06069 | 1.3773 | 1.3982 | 0.0617 | 64.1 |
| 13 | 98303633 | rs9513497 | C | T | 4 | 0.0256 | 0.06108 | 1.0819 | 1.152 | 0.0131 | 72.13 |
| 7 | 84546498 | rs13222785 | A | G | 4 | 0.005003 | 0.06119 | 1.1528 | 1.2417 | 0.0056 | 76.19 |
| 8 | 73172373 | rs2587579 | C | T | 4 | 0.01208 | 0.06157 | 1.1117 | 1.16 | 0.035 | 65.14 |
| 8 | 73173101 | rs2587580 | C | G | 4 | 0.01199 | 0.0618 | 0.9 | 0.8625 | 0.0345 | 65.27 |
| 4 | 132476044 | rs11940669 | C | T | 4 | 0.002532 | 0.06185 | 0.7391 | 0.7138 | 0.0541 | 60.72 |
| 4 | 132508470 | rs4146422 | C | T | 4 | 0.002994 | 0.06298 | 0.7437 | 0.719 | 0.0589 | 59.72 |
| 8 | 120025224 | rs3134060 | A | G | 4 | 0.002808 | 0.06314 | 0.8039 | 0.7957 | 0.0797 | 55.67 |
| 4 | 132536774 | rs11099102 | C | T | 4 | 0.00315 | 0.06321 | 1.3458 | 1.3858 | 0.0662 | 58.26 |
| 8 | 73175604 | rs2701439 | C | G | 4 | 0.01319 | 0.06368 | 0.9001 | 0.862 | 0.0338 | 65.45 |
| 8 | 120034205 | rs3134070 | C | T | 4 | 0.002679 | 0.06397 | 0.8026 | 0.7958 | 0.0793 | 55.74 |
| 4 | 132537559 | rs11936773 | G | T | 4 | 0.003289 | 0.06421 | 0.7435 | 0.7221 | 0.0663 | 58.24 |
| 6 | 29810185 | rs2844833 | C | G | 3 | 0.0009201 | 0.0645 | 0.804 | 0.8369 | 0.231 | 31.75 |
| 8 | 120034169 | rs3134069 | A | C | 4 | 0.002725 | 0.06494 | 0.8029 | 0.796 | 0.0782 | 55.94 |
| 8 | 120035902 | rs3134073 | A | G | 4 | 0.002723 | 0.06496 | 0.8029 | 0.7964 | 0.0789 | 55.82 |
| 9 | 7904008 | rs10815714 | C | T | 4 | 0.002873 | 0.06501 | 1.1809 | 1.2027 | 0.0508 | 61.43 |
| 8 | 120037209 | rs12386956 | A | G | 4 | 0.002709 | 0.06522 | 1.2456 | 1.2557 | 0.0784 | 55.91 |
| 1 | 176952870 | rs2811280 | A | G | 4 | 0.0008286 | 0.06528 | 1.1299 | 1.1067 | 0.1414 | 45.01 |
| 8 | 120034718 | rs3134072 | C | T | 4 | 0.002748 | 0.06548 | 0.803 | 0.7962 | 0.078 | 55.98 |
| 4 | 136728154 | rs13146643 | A | G | 4 | 0.007011 | 0.06576 | 0.8913 | 0.8938 | 0.1662 | 40.92 |
| 17 | 51864068 | rs980080 | C | T | 4 | 0.0004076 | 0.06615 | 0.8638 | 0.8863 | 0.1126 | 49.83 |
| 4 | 136728035 | rs13122550 | C | T | 4 | 0.006909 | 0.06636 | 1.1222 | 1.119 | 0.1642 | 41.25 |
| 8 | 73174272 | rs2701441 | A | G | 4 | 0.01551 | 0.06679 | 0.9024 | 0.8638 | 0.0345 | 65.26 |
| 8 | 120038338 | rs4876872 | A | G | 4 | 0.002723 | 0.0668 | 0.803 | 0.7966 | 0.0761 | 56.34 |
| 4 | 82302241 | rs11722020 | C | T | 4 | 0.00208 | 0.06681 | 1.2451 | 1.2103 | 0.169 | 40.46 |
| 4 | 132412751 | rs17051170 | A | C | 4 | 0.001843 | 0.06687 | 1.3799 | 1.4529 | 0.0283 | 66.96 |
| 4 | 132421378 | rs10006868 | C | G | 4 | 0.001819 | 0.06698 | 0.7244 | 0.6878 | 0.0277 | 67.12 |
| 4 | 132412892 | rs17051172 | C | T | 4 | 0.001865 | 0.06703 | 1.3794 | 1.4525 | 0.0283 | 66.96 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 8 | 120039201 | rs4876873 | A | C | 4 | 0.002753 | 0.06704 | 1.245 | 1.2549 | 0.0763 | 56.31 |
| 4 | 132550197 | rs11945624 | A | G | 4 | 0.003563 | 0.06722 | 1.3406 | 1.3816 | 0.064 | 58.69 |
| 17 | 51864305 | rs10852984 | A | G | 4 | 0.0004122 | 0.06726 | 1.1575 | 1.1281 | 0.1113 | 50.05 |
| 8 | 120041852 | rs12335174 | G | T | 4 | 0.002746 | 0.06736 | 0.8031 | 0.7969 | 0.0759 | 56.39 |
| 7 | 84545533 | rs7809347 | A | G | 4 | 0.006094 | 0.06739 | 0.8703 | 0.8077 | 0.005 | 76.66 |
| 4 | 132409675 | rs12641606 | C | T | 4 | 0.001956 | 0.06743 | 1.3789 | 1.451 | 0.0292 | 66.68 |
| 8 | 120042745 | rs17758011 | G | T | 4 | 0.00281 | 0.06744 | 1.2445 | 1.2542 | 0.0767 | 56.23 |
| 4 | 132410530 | rs11947432 | A | G | 4 | 0.001997 | 0.06777 | 1.378 | 1.4503 | 0.0293 | 66.68 |
| 1 | 89290783 | rs2296883 | A | G | 4 | 0.02007 | 0.06782 | 1.1111 | 1.1699 | 0.0457 | 62.56 |
| 4 | 132422269 | rs11941498 | C | T | 4 | 0.001647 | 0.06787 | 1.3842 | 1.458 | 0.025 | 67.92 |
| 4 | 132424433 | rs17051173 | C | T | 4 | 0.001648 | 0.06824 | 1.3841 | 1.4583 | 0.0246 | 68.04 |
| 4 | 82312214 | rs1517547 | C | T | 2 | 0.001023 | 0.06825 | 0.7774 | 0.7807 | 0.0769 | 68.04 |
| 4 | 132426397 | rs2861393 | A | G | 4 | 0.001679 | 0.06859 | 1.3834 | 1.4576 | 0.0246 | 68.04 |
| 4 | 132565936 | rs12648650 | A | C | 4 | 0.003585 | 0.06894 | 0.7449 | 0.7231 | 0.0619 | 59.11 |
| 21 | 42619764 | rs225424 | A | G | 4 | 0.008243 | 0.06898 | 1.1019 | 1.1037 | 0.1483 | 43.86 |
| 4 | 136726126 | rs7662409 | C | G | 4 | 0.007048 | 0.06916 | 0.8914 | 0.8943 | 0.1616 | 41.67 |
| 8 | 73169428 | rs1530402 | A | G | 4 | 0.01686 | 0.06916 | 1.1081 | 1.157 | 0.0357 | 64.97 |
| 4 | 132404922 | rs9992638 | A | T | 4 | 0.002232 | 0.0692 | 0.7281 | 0.6915 | 0.0301 | 66.44 |
| 7 | 84537323 | rs6966472 | C | T | 4 | 0.00565 | 0.06939 | 1.1502 | 1.2352 | 0.005 | 76.66 |
| 8 | 73170538 | rs2701449 | C | T | 4 | 0.0176 | 0.06945 | 0.903 | 0.865 | 0.037 | 64.64 |
| 4 | 136725872 | rs13131704 | A | T | 4 | 0.007104 | 0.06955 | 0.8915 | 0.8945 | 0.1617 | 41.66 |
| 7 | 84540088 | rs6957484 | G | T | 4 | 0.005776 | 0.06964 | 0.8696 | 0.8092 | 0.0049 | 76.75 |
| 4 | 74413190 | rs4694161 | A | G | 4 | 0.01015 | 0.06971 | 1.3005 | 1.4144 | 0.0326 | 65.77 |
| 6 | 29816396 | rs2517941 | C | G | 4 | 0.001363 | 0.06979 | 0.8615 | 0.8823 | 0.1546 | 42.82 |
| 4 | 136725857 | rs12643192 | C | G | 4 | 0.007161 | 0.06996 | 0.8916 | 0.8946 | 0.1618 | 41.65 |
| 7 | 84534250 | rs16887821 | C | G | 4 | 0.005698 | 0.07002 | 1.1492 | 1.2334 | 0.005 | 76.62 |
| 4 | 74411672 | rs6821554 | A | G | 4 | 0.01221 | 0.07013 | 1.2969 | 1.421 | 0.0336 | 65.5 |
| 4 | 136728247 | rs13122996 | A | T | 4 | 0.007434 | 0.07034 | 1.1211 | 1.118 | 0.1602 | 41.9 |
| 13 | 74984164 | rs17064600 | C | T | 3 | 0.001028 | 0.07042 | 0.8689 | 0.8858 | 0.1269 | 51.55 |
| 1 | 89290761 | rs2296882 | A | T | 4 | 0.02202 | 0.07049 | 1.11 | 1.1693 | 0.0451 | 62.7 |
| 12 | 2779406 | rs3021522 | C | G | 4 | 0.002187 | 0.07075 | 0.7589 | 0.7907 | 0.1804 | 38.59 |
| 4 | 132410710 | rs10518587 | G | T | 4 | 0.002325 | 0.07076 | 1.3705 | 1.4437 | 0.0292 | 66.69 |
| 4 | 132429544 | rs2861394 | A | G | 4 | 0.00187 | 0.07087 | 1.3757 | 1.4509 | 0.0243 | 68.13 |
| 7 | 84542645 | rs2286192 | C | T | 4 | 0.006318 | 0.07091 | 1.1486 | 1.2364 | 0.0048 | 76.81 |
| 3 | 124831466 | rs820446 | C | T | 4 | 0.00164 | 0.07116 | 1.2687 | 1.2581 | 0.0681 | 57.88 |
| 8 | 73171160 | rs1443942 | A | C | 4 | 0.01884 | 0.07121 | 0.904 | 0.8658 | 0.0369 | 64.67 |
| 20 | 8465895 | rs2179441 | A | C | 3 | 0.005354 | 0.07126 | 0.8716 | 0.8259 | 0.0491 | 66.82 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 4 | 74412327 | rs6446920 | C | T | 4 | 0.01077 | 0.07136 | 1.3013 | 1.4163 | 0.0323 | 65.84 |
| 4 | 74419872 | rs4336191 | C | T | 4 | 0.01024 | 0.07136 | 1.3027 | 1.4184 | 0.0308 | 66.25 |
| 18 | 48362228 | rs4940191 | A | G | 4 | 0.00441 | 0.07142 | 0.8662 | 0.8655 | 0.1166 | 49.14 |
| 4 | 132434465 | rs4624669 | A | G | 4 | 0.001321 | 0.0715 | 0.718 | 0.68 | 0.018 | 70.21 |
| 7 | 84529379 | rs16887818 | C | G | 4 | 0.005795 | 0.0715 | 0.8737 | 0.8252 | 0.0095 | 73.81 |
| 17 | 47371272 | rs1501259 | A | T | 4 | 0.007544 | 0.0715 | 0.7383 | 0.7501 | 0.1688 | 40.5 |
| 4 | 74415477 | rs6446922 | A | G | 4 | 0.01092 | 0.07158 | 0.7694 | 0.7062 | 0.0318 | 65.97 |
| 11 | 10833019 | rs2232918 | A | G | 4 | 0.001726 | 0.07176 | 0.8106 | 0.8234 | 0.1051 | 51.13 |
| 8 | 73171725 | rs1838285 | C | T | 4 | 0.01928 | 0.07181 | 0.9044 | 0.866 | 0.0368 | 64.69 |
| 4 | 1664607 | rs8051 | C | T | 3 | 0.0001863 | 0.07188 | 1.1556 | 1.1267 | 0.0856 | 59.31 |
| 8 | 73168913 | rs2701450 | A | T | 4 | 0.0188 | 0.07195 | 0.904 | 0.8654 | 0.0353 | 65.06 |
| 7 | 84530877 | rs2240394 | C | T | 4 | 0.005749 | 0.07218 | 1.1455 | 1.2123 | 0.0096 | 73.77 |
| 2 | 40152968 | rs6544307 | T | C | 3 | 0.006001 | 0.07221 | 1.1532 | 1.2797 | 0.0082 | 79.17 |
| 11 | 10831170 | rs2232928 | A | G | 4 | 0.001745 | 0.07225 | 1.2334 | 1.2141 | 0.1049 | 51.16 |
| 4 | 74418309 | rs4274815 | A | T | 4 | 0.01099 | 0.07286 | 1.2994 | 1.4147 | 0.0314 | 66.1 |
| 4 | 132437567 | rs10008591 | C | T | 4 | 0.001341 | 0.07301 | 0.7183 | 0.6809 | 0.0177 | 70.33 |
| 21 | 33332334 | rs2834072 | A | G | 4 | 0.003881 | 0.07307 | 0.9042 | 0.8783 | 0.0175 | 70.39 |
| 8 | 73175388 | rs2701440 | C | T | 4 | 0.02013 | 0.07319 | 1.1037 | 1.1539 | 0.0344 | 65.29 |
| 1 | 89290506 | rs12408132 | C | T | 4 | 0.02455 | 0.07357 | 0.9014 | 0.8529 | 0.0397 | 63.97 |
| 21 | 33329836 | rs743331 | C | T | 4 | 0.003938 | 0.07362 | 1.1058 | 1.1363 | 0.0197 | 69.6 |
| 6 | 29817265 | rs2743950 | C | T | 4 | 0.001379 | 0.07387 | 0.8617 | 0.883 | 0.1491 | 43.72 |
| 1 | 89290653 | rs1048848 | C | G | 4 | 0.02445 | 0.07391 | 0.9025 | 0.8564 | 0.0442 | 62.91 |
| 8 | 26559908 | rs4076071 | C | T | 4 | 0.01204 | 0.07415 | 1.1555 | 1.2269 | 0.0297 | 66.54 |
| 8 | 10719627 | rs7005531 | A | G | 4 | 0.01378 | 0.07454 | 0.9048 | 0.8729 | 0.0476 | 62.15 |
| 8 | 10717307 | rs2409651 | C | T | 4 | 0.01387 | 0.07465 | 1.1051 | 1.1457 | 0.0476 | 62.15 |
| 4 | 74419733 | rs4408930 | A | G | 4 | 0.01183 | 0.07522 | 1.2953 | 1.4113 | 0.0307 | 66.29 |
| 13 | 98305163 | rs4772149 | C | T | 4 | 0.0273 | 0.07569 | 1.0817 | 1.1369 | 0.0214 | 69.05 |
| 1 | 89290398 | rs6675866 | C | T | 4 | 0.02562 | 0.07571 | 1.1071 | 1.1672 | 0.043 | 63.2 |
| 13 | 98311123 | rs9517467 | A | C | 4 | 0.03697 | 0.07578 | 0.928 | 0.8741 | 0.0142 | 71.67 |
| 10 | 80752296 | rs11002926 | A | C | 4 | 0.01604 | 0.07584 | 1.1041 | 1.1663 | 0.0174 | 70.4 |
| 4 | 136727429 | rs13145036 | A | G | 4 | 0.007593 | 0.07617 | 0.8923 | 0.8952 | 0.152 | 43.26 |
| 7 | 84530345 | rs4461846 | C | T | 4 | 0.006508 | 0.07618 | 0.8747 | 0.8261 | 0.009 | 74.1 |
| 15 | 46652089 | rs12915677 | C | T | 4 | 0.004047 | 0.07621 | 0.8838 | 0.8826 | 0.0937 | 53.13 |
| 13 | 98300600 | rs2296991 | C | T | 4 | 0.0185 | 0.07633 | 0.8903 | 0.8047 | 0.0013 | 80.93 |
| 4 | 74420504 | rs4345145 | C | T | 4 | 0.01191 | 0.07662 | 0.7722 | 0.7077 | 0.0287 | 66.84 |
| 4 | 132578708 | rs12649130 | C | G | 4 | 0.004418 | 0.07678 | 0.7499 | 0.727 | 0.058 | 59.91 |
| 4 | 82292319 | rs3733550 | C | T | 4 | 0.002288 | 0.07694 | 0.8057 | 0.8298 | 0.1571 | 42.41 |

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|----|-----------|------------|---|---|---|----------|---------|--------|--------|--------|-------|
| 8 | 10721186 | rs2271356 | A | T | 4 | 0.01484 | 0.07784 | 0.9052 | 0.8719 | 0.043 | 63.2 |
| 13 | 98288560 | rs7333687 | A | G | 4 | 0.03144 | 0.07791 | 0.9277 | 0.8776 | 0.014 | 71.73 |
| 3 | 124839727 | rs820463 | A | G | 4 | 0.002085 | 0.07795 | 0.8006 | 0.798 | 0.0526 | 61.04 |
| 13 | 98293824 | rs913560 | A | G | 4 | 0.03117 | 0.07839 | 0.9275 | 0.8768 | 0.0131 | 72.11 |
| 6 | 28316514 | rs1150711 | C | T | 4 | 0.02655 | 0.07868 | 0.9164 | 0.8658 | 0.0206 | 69.29 |
| 15 | 58798563 | rs2414680 | A | G | 4 | 0.01592 | 0.07874 | 1.1063 | 1.2309 | 0.0004 | 83.69 |
| 13 | 98302606 | rs7321357 | C | T | 4 | 0.02705 | 0.07881 | 0.8967 | 0.8068 | 0.0015 | 80.56 |
| 13 | 98305323 | rs4772150 | C | T | 4 | 0.03646 | 0.07893 | 1.0779 | 1.1334 | 0.0257 | 67.71 |
| 8 | 10720735 | rs7824384 | A | C | 4 | 0.0154 | 0.07931 | 1.1041 | 1.1451 | 0.0453 | 62.67 |
| 4 | 136735906 | rs7692855 | C | T | 4 | 0.007584 | 0.07941 | 0.8909 | 0.8886 | 0.1273 | 47.34 |
| 15 | 58797094 | rs17303111 | C | T | 4 | 0.01594 | 0.07992 | 0.906 | 0.815 | 0.0003 | 84 |
| 13 | 98286664 | rs9300518 | C | T | 4 | 0.03333 | 0.08006 | 1.0783 | 1.1414 | 0.0128 | 72.25 |
| 10 | 3888018 | rs17135903 | C | T | 3 | 0.002374 | 0.08009 | 0.5193 | 0.4382 | 0.029 | 71.75 |
| 6 | 29818607 | rs730858 | A | G | 4 | 0.001514 | 0.08055 | 1.159 | 1.1305 | 0.144 | 44.57 |
| 2 | 26381302 | rs11902679 | C | T | 4 | 0.006007 | 0.08078 | 0.7273 | 0.6854 | 0.0372 | 64.58 |
| 4 | 82313570 | rs11933194 | C | T | 3 | 0.002506 | 0.08092 | 0.8009 | 0.8041 | 0.0975 | 57.05 |
| 4 | 132482173 | rs1911882 | C | T | 4 | 0.004552 | 0.08112 | 1.3414 | 1.3868 | 0.0509 | 61.42 |
| 8 | 73179080 | rs2701437 | A | G | 4 | 0.01276 | 0.0812 | 0.8982 | 0.8602 | 0.0207 | 69.27 |
| 4 | 136726319 | rs7667350 | A | G | 4 | 0.00802 | 0.0813 | 0.893 | 0.8958 | 0.1458 | 44.27 |
| 4 | 74453060 | rs6844516 | A | T | 4 | 0.009836 | 0.08142 | 1.3024 | 1.4174 | 0.0223 | 68.75 |
| 4 | 74496772 | rs16849331 | G | T | 4 | 0.008304 | 0.08178 | 0.7671 | 0.7084 | 0.0213 | 69.08 |
| 8 | 10722996 | rs10109550 | G | T | 4 | 0.01706 | 0.0819 | 1.1024 | 1.1456 | 0.0416 | 63.52 |
| 2 | 6432676 | rs11899039 | A | T | 4 | 0.01287 | 0.08194 | 1.1713 | 1.2286 | 0.0384 | 64.29 |
| 6 | 29817819 | rs2517938 | C | T | 4 | 0.001556 | 0.08217 | 1.1586 | 1.13 | 0.143 | 44.73 |
| 8 | 73175792 | rs2701438 | G | T | 4 | 0.01254 | 0.08229 | 1.1137 | 1.1622 | 0.0205 | 69.33 |
| 15 | 36725309 | rs10438404 | G | T | 4 | 0.006016 | 0.08263 | 0.9077 | 0.9164 | 0.1729 | 39.81 |
| 21 | 33331127 | rs12233311 | A | G | 4 | 0.005049 | 0.08265 | 1.1028 | 1.1322 | 0.0194 | 69.7 |
| 20 | 8465451 | rs2423366 | A | G | 3 | 0.004998 | 0.0831 | 0.8679 | 0.7983 | 0.0151 | 76.15 |
| 2 | 26379923 | rs6753473 | G | T | 4 | 0.004746 | 0.08347 | 1.3859 | 1.456 | 0.0349 | 65.17 |
| 8 | 10723495 | rs6989846 | C | T | 4 | 0.01793 | 0.08375 | 1.1016 | 1.1453 | 0.0402 | 63.85 |
| 13 | 98301752 | rs9582269 | A | G | 4 | 0.03253 | 0.084 | 1.107 | 1.2121 | 0.0031 | 78.38 |
| 20 | 8464695 | rs2423364 | C | T | 3 | 0.003887 | 0.08431 | 0.8643 | 0.7982 | 0.0149 | 76.24 |
| 2 | 40172384 | rs12151560 | C | T | 3 | 0.003658 | 0.08456 | 1.148 | 1.3297 | 0.0004 | 87.4 |
| 19 | 38737515 | rs1864132 | A | G | 4 | 0.005565 | 0.0848 | 0.86 | 0.8658 | 0.1345 | 46.15 |
| 4 | 136739233 | rs2089184 | C | G | 4 | 0.009507 | 0.08508 | 0.8953 | 0.8982 | 0.1519 | 43.27 |
| 4 | 74455492 | rs7675336 | A | G | 4 | 0.01136 | 0.08563 | 0.7718 | 0.7085 | 0.022 | 68.83 |
| 4 | 74460813 | rs16849293 | A | G | 4 | 0.01143 | 0.08591 | 0.77 | 0.7068 | 0.0221 | 68.8 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 16 | 16026525 | rs246240 | A | G | 4 | 0.01266 | 0.08592 | 1.1287 | 1.2036 | 0.0115 | 72.85 |
| 8 | 73172159 | rs2587578 | A | G | 4 | 0.01515 | 0.08627 | 1.1103 | 1.1591 | 0.0212 | 69.12 |
| 11 | 32223969 | rs11031664 | C | T | 4 | 0.002053 | 0.08681 | 1.1302 | 1.1101 | 0.1267 | 47.45 |
| 4 | 136730370 | rs2035291 | C | G | 4 | 0.008943 | 0.08797 | 1.1181 | 1.1152 | 0.1383 | 45.51 |
| 6 | 14489463 | rs7748589 | A | G | 4 | 0.006548 | 0.08824 | 0.9089 | 0.9034 | 0.0821 | 55.22 |
| 3 | 71412562 | rs4613421 | C | G | 4 | 0.009749 | 0.08876 | 0.9072 | 0.915 | 0.1959 | 36.05 |
| 12 | 13259589 | rs2069086 | G | T | 4 | 0.008183 | 0.08924 | 0.8279 | 0.7763 | 0.0249 | 67.95 |
| 21 | 40082808 | rs2837220 | C | T | 4 | 0.000517 | 0.0894 | 1.1313 | 1.131 | 0.021 | 69.16 |
| 6 | 121574075 | rs9490138 | C | T | 4 | 0.001623 | 0.08973 | 1.1568 | 1.1224 | 0.1571 | 42.41 |
| 4 | 74514655 | rs16849372 | A | T | 4 | 0.01063 | 0.08975 | 1.2925 | 1.4002 | 0.0209 | 69.19 |
| 16 | 47659380 | rs2967303 | C | G | 4 | 0.006425 | 0.09005 | 0.9067 | 0.9009 | 0.0737 | 56.79 |
| 13 | 28458146 | rs1570309 | A | G | 4 | 0.006237 | 0.09031 | 0.8572 | 0.8491 | 0.0645 | 58.6 |
| 10 | 24662335 | rs10741051 | A | G | 4 | 0.02911 | 0.09067 | 1.1015 | 1.1848 | 0.0057 | 76.09 |
| 11 | 10824525 | rs771377 | C | G | 4 | 0.00226 | 0.09131 | 1.228 | 1.2082 | 0.0882 | 54.12 |
| 4 | 132440597 | rs10018289 | A | G | 4 | 0.003037 | 0.0914 | 1.3528 | 1.4353 | 0.0164 | 70.79 |
| 2 | 40169977 | rs12614752 | G | T | 3 | 0.004786 | 0.09164 | 1.1472 | 1.3207 | 0.0004 | 87.2 |
| 8 | 73172073 | rs2701444 | C | T | 4 | 0.01848 | 0.09172 | 0.9035 | 0.8648 | 0.021 | 69.18 |
| 10 | 124167869 | rs17103522 | C | T | 4 | 0.004929 | 0.0918 | 0.8562 | 0.8729 | 0.1606 | 41.83 |
| 4 | 136723916 | rs1842259 | A | G | 4 | 0.01073 | 0.09209 | 0.8974 | 0.8998 | 0.147 | 44.07 |
| 8 | 10715391 | rs1544980 | C | T | 4 | 0.01954 | 0.0922 | 0.902 | 0.8558 | 0.0196 | 69.65 |
| 4 | 136736073 | rs13142176 | C | T | 4 | 0.009838 | 0.09221 | 1.1165 | 1.1143 | 0.1349 | 46.08 |
| 11 | 10826485 | rs2687489 | A | G | 4 | 0.002342 | 0.09249 | 1.2271 | 1.2075 | 0.088 | 54.15 |
| 7 | 122420709 | rs1525489 | A | G | 4 | 0.01741 | 0.09253 | 0.8281 | 0.7825 | 0.0362 | 64.84 |
| 13 | 98301534 | rs2026026 | C | T | 4 | 0.04111 | 0.09265 | 1.1014 | 1.2093 | 0.0024 | 79.2 |
| 8 | 10713033 | rs2052963 | G | T | 4 | 0.01741 | 0.0929 | 1.102 | 1.1421 | 0.0379 | 64.41 |
| 13 | 21757616 | rs2038712 | C | T | 4 | 0.006017 | 0.09362 | 0.9052 | 0.9006 | 0.0722 | 57.08 |
| 4 | 136737904 | rs6816076 | A | G | 4 | 0.009808 | 0.09368 | 0.8956 | 0.8976 | 0.133 | 46.39 |
| 8 | 10720537 | rs7840785 | C | T | 4 | 0.01934 | 0.09404 | 1.0968 | 1.1408 | 0.03 | 66.48 |
| 11 | 10832929 | rs2232919 | C | T | 4 | 0.002316 | 0.09426 | 0.8154 | 0.8265 | 0.0793 | 55.74 |
| 1 | 74129798 | rs2789708 | A | T | 4 | 0.02184 | 0.09436 | 1.0842 | 1.1605 | 0.0018 | 80.05 |
| 4 | 136724400 | rs1479789 | A | G | 4 | 0.009228 | 0.09447 | 1.1175 | 1.1137 | 0.1339 | 46.25 |
| 8 | 73171999 | rs2701445 | G | T | 4 | 0.02041 | 0.09472 | 1.1051 | 1.1549 | 0.0209 | 69.21 |
| 1 | 74129950 | rs2792075 | C | T | 4 | 0.02226 | 0.09492 | 0.9226 | 0.8618 | 0.0018 | 80.09 |
| 4 | 135192004 | rs12642075 | A | G | 4 | 0.02713 | 0.09506 | 0.9128 | 0.8722 | 0.0328 | 65.72 |
| 4 | 136734593 | rs11944567 | C | T | 4 | 0.01017 | 0.09521 | 1.116 | 1.1134 | 0.1342 | 46.19 |
| 2 | 133199169 | rs4953986 | C | T | 4 | 0.0009475 | 0.09534 | 1.1326 | 1.1163 | 0.0639 | 58.7 |
| 8 | 73197756 | rs4614034 | C | T | 4 | 0.0254 | 0.09544 | 0.9075 | 0.8686 | 0.0265 | 67.46 |

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|----|-----------|------------|---|---|---|-----------|---------|--------|--------|--------|-------|
| 8 | 26555006 | rs4733048 | C | T | 4 | 0.01816 | 0.09558 | 0.8731 | 0.8261 | 0.0286 | 66.87 |
| 14 | 31527742 | rs10132087 | C | T | 4 | 0.007038 | 0.09568 | 1.1298 | 1.1274 | 0.105 | 51.14 |
| 3 | 41535096 | rs1495693 | C | T | 4 | 0.01223 | 0.09574 | 1.1978 | 1.2445 | 0.0393 | 64.06 |
| 2 | 209868043 | rs6752290 | C | T | 4 | 0.007986 | 0.09581 | 1.1198 | 1.1098 | 0.1559 | 42.61 |
| 16 | 26198350 | rs12925611 | C | T | 4 | 0.0006838 | 0.09587 | 0.866 | 0.8918 | 0.1001 | 51.99 |
| 3 | 124836431 | rs1254401 | C | G | 4 | 0.002463 | 0.09604 | 1.2492 | 1.2494 | 0.0421 | 63.41 |
| 21 | 32322781 | rs9977744 | C | T | 4 | 0.005581 | 0.09627 | 0.8709 | 0.8813 | 0.1287 | 47.11 |
| 11 | 10829758 | rs7925687 | C | T | 4 | 0.002486 | 0.0963 | 0.8165 | 0.8292 | 0.0844 | 54.8 |
| 4 | 136728703 | rs13101421 | C | T | 4 | 0.009722 | 0.0968 | 0.8955 | 0.8978 | 0.1292 | 47.02 |
| 8 | 10708670 | rs6995541 | A | G | 4 | 0.0151 | 0.09686 | 1.1037 | 1.1394 | 0.0352 | 65.1 |
| 3 | 41535386 | rs1795312 | A | T | 4 | 0.01298 | 0.09698 | 1.1959 | 1.2428 | 0.04 | 63.89 |
| 3 | 41542696 | rs1565960 | A | G | 4 | 0.01319 | 0.09713 | 1.1947 | 1.2425 | 0.0395 | 64.02 |
| 8 | 73193049 | rs4467976 | A | G | 4 | 0.02786 | 0.09717 | 1.0995 | 1.1494 | 0.0271 | 67.28 |
| 8 | 73191306 | rs4738207 | A | G | 4 | 0.02398 | 0.09719 | 0.9078 | 0.8692 | 0.0243 | 68.12 |
| 8 | 73185849 | rs16938030 | C | T | 4 | 0.02226 | 0.09726 | 1.1029 | 1.1514 | 0.0229 | 68.55 |
| 8 | 12770433 | rs13272401 | G | T | 3 | 0.0002785 | 0.09754 | 1.8427 | 1.647 | 0.1014 | 56.32 |
| 16 | 16022393 | rs246214 | C | T | 4 | 0.01675 | 0.09768 | 1.1238 | 1.1982 | 0.0106 | 73.25 |
| 4 | 136734221 | rs11099350 | A | G | 4 | 0.01044 | 0.09803 | 1.1155 | 1.113 | 0.1313 | 46.67 |
| 4 | 135194503 | rs1565911 | G | T | 4 | 0.02904 | 0.09821 | 1.0943 | 1.1465 | 0.0304 | 66.37 |
| 4 | 136730572 | rs2035292 | A | G | 4 | 0.0102 | 0.0985 | 1.1159 | 1.1133 | 0.129 | 47.05 |
| 9 | 76896764 | rs2376398 | C | T | 4 | 0.0734 | 0.09864 | 0.9359 | 0.8792 | 0.0163 | 70.84 |
| 3 | 41534618 | rs1631168 | A | C | 4 | 0.01368 | 0.09889 | 1.1943 | 1.2415 | 0.0398 | 63.96 |
| 12 | 123620722 | rs6488934 | A | T | 3 | 0.002045 | 0.09897 | 1.2701 | 1.2732 | 0.056 | 65.31 |
| 3 | 124833978 | rs1254397 | C | T | 4 | 0.002622 | 0.09925 | 0.8016 | 0.8011 | 0.0405 | 63.78 |
| 4 | 135184692 | rs10021844 | A | G | 4 | 0.03178 | 0.09927 | 0.9152 | 0.8757 | 0.0373 | 64.56 |
| 10 | 124149040 | rs4565845 | A | C | 3 | 0.003347 | 0.0993 | 1.1826 | 1.1658 | 0.1109 | 54.53 |
| 2 | 133207895 | rs4953987 | A | G | 4 | 0.001022 | 0.09946 | 0.8844 | 0.897 | 0.0617 | 59.16 |
| 8 | 73191692 | rs4738208 | C | T | 4 | 0.02802 | 0.09982 | 1.0994 | 1.1487 | 0.0262 | 67.55 |
| 8 | 73191724 | rs4738209 | A | C | 4 | 0.02824 | 0.09983 | 1.0993 | 1.1483 | 0.0268 | 67.37 |
| 4 | 136740519 | rs11737477 | G | T | 4 | 0.01097 | 0.1001 | 0.8972 | 0.9001 | 0.1364 | 45.83 |
| 18 | 48343516 | rs1550567 | A | G | 4 | 0.006729 | 0.1002 | 0.8722 | 0.8708 | 0.091 | 53.61 |
| 4 | 132454388 | rs9995748 | C | T | 4 | 0.003742 | 0.1003 | 1.3415 | 1.4043 | 0.0216 | 68.97 |
| 2 | 133209220 | rs984521 | A | G | 4 | 0.0007894 | 0.1004 | 0.8811 | 0.8943 | 0.0519 | 61.2 |
| 16 | 24389161 | rs3096190 | A | C | 4 | 0.03478 | 0.1005 | 1.0792 | 1.1247 | 0.0234 | 68.41 |
| 1 | 74232437 | rs4650237 | G | T | 4 | 0.02328 | 0.1006 | 0.9197 | 0.864 | 0.0033 | 78.11 |
| 13 | 98297352 | rs7986477 | A | G | 4 | 0.05163 | 0.1007 | 0.9116 | 0.8333 | 0.0032 | 78.25 |
| 2 | 40174693 | rs917977 | C | T | 3 | 0.007471 | 0.1009 | 1.1357 | 1.3261 | 0.0002 | 88.3 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 4 | 136732580 | rs2016168 | C | T | 4 | 0.01073 | 0.1009 | 1.1151 | 1.1126 | 0.1285 | 47.15 |
| 4 | 136733600 | rs11723306 | C | T | 4 | 0.01073 | 0.1009 | 1.1151 | 1.1126 | 0.1285 | 47.15 |
| 6 | 99026958 | rs1494770 | C | T | 4 | 0.0006625 | 0.101 | 0.7169 | 0.7566 | 0.0641 | 58.66 |
| 4 | 136724155 | rs1479787 | C | T | 4 | 0.00996 | 0.1012 | 0.8958 | 0.899 | 0.1289 | 47.08 |
| 4 | 136732373 | rs1038152 | A | T | 4 | 0.01056 | 0.1012 | 0.8966 | 0.8987 | 0.1269 | 47.41 |
| 1 | 212361177 | rs1660375 | A | G | 4 | 0.002202 | 0.1013 | 1.3781 | 1.2943 | 0.1606 | 41.84 |
| 7 | 84576431 | rs1029563 | G | T | 4 | 0.04518 | 0.1014 | 1.0842 | 1.1448 | 0.0206 | 69.31 |
| 10 | 114466456 | rs11196072 | C | T | 4 | 0.004632 | 0.1016 | 1.2093 | 1.1915 | 0.1139 | 49.62 |
| 4 | 136723951 | rs2127459 | G | T | 4 | 0.01004 | 0.1018 | 0.8959 | 0.8992 | 0.1289 | 47.07 |
| 1 | 91987216 | rs284170 | C | T | 4 | 0.008224 | 0.1019 | 1.1458 | 1.1648 | 0.0564 | 60.25 |
| 2 | 133195447 | rs6736839 | C | T | 4 | 0.002053 | 0.102 | 1.1148 | 1.1181 | 0.0327 | 65.74 |
| 4 | 136731046 | rs7694930 | A | C | 4 | 0.01065 | 0.102 | 0.8967 | 0.8989 | 0.1267 | 47.45 |
| 1 | 58233385 | rs11207145 | A | G | 3 | 0.002621 | 0.1022 | 2.0312 | 2.0041 | 0.0655 | 63.3 |
| 4 | 136723423 | rs2054506 | C | G | 4 | 0.01011 | 0.1023 | 0.896 | 0.8993 | 0.129 | 47.06 |
| 3 | 41611668 | rs17059208 | C | G | 4 | 0.007932 | 0.1024 | 0.796 | 0.7563 | 0.0216 | 68.97 |
| 4 | 74412384 | rs6446921 | A | G | 4 | 0.02847 | 0.1025 | 1.2351 | 1.3612 | 0.0255 | 67.75 |
| 11 | 34519515 | rs836123 | C | T | 4 | 0.002853 | 0.1027 | 0.8164 | 0.829 | 0.0837 | 54.94 |
| 11 | 32223435 | rs1033627 | A | G | 4 | 0.001123 | 0.1035 | 0.8852 | 0.9017 | 0.0767 | 56.22 |
| 4 | 136724188 | rs1479788 | A | T | 4 | 0.01015 | 0.1036 | 0.8961 | 0.8992 | 0.126 | 47.56 |
| 2 | 98792270 | rs1356424 | C | T | 4 | 0.004806 | 0.1037 | 0.8983 | 0.8988 | 0.0693 | 57.64 |
| 4 | 136733042 | rs11935087 | A | G | 4 | 0.01084 | 0.1041 | 0.8969 | 0.899 | 0.1241 | 47.88 |
| 13 | 98294942 | rs9582266 | A | G | 4 | 0.05857 | 0.1041 | 0.9144 | 0.8382 | 0.0041 | 77.38 |
| 4 | 136731472 | rs7654065 | A | C | 4 | 0.01076 | 0.1042 | 1.115 | 1.1125 | 0.1234 | 47.99 |
| 4 | 136722856 | rs11935664 | C | T | 4 | 0.01029 | 0.1043 | 0.8963 | 0.8995 | 0.1264 | 47.49 |
| 4 | 136723371 | rs2054505 | C | T | 4 | 0.01029 | 0.1043 | 0.8963 | 0.8995 | 0.1264 | 47.49 |
| 11 | 32207041 | rs2418582 | A | G | 4 | 0.001605 | 0.1043 | 1.1255 | 1.1045 | 0.0952 | 52.85 |
| 1 | 97696087 | rs7531138 | A | T | 4 | 0.07793 | 0.1044 | 0.9379 | 0.8645 | 0.0027 | 78.77 |
| 21 | 32336948 | rs9982468 | C | T | 4 | 0.005404 | 0.1044 | 1.1488 | 1.1358 | 0.1114 | 50.04 |
| 4 | 135194459 | rs1565912 | A | G | 4 | 0.03522 | 0.1046 | 0.9168 | 0.8748 | 0.0311 | 66.17 |
| 1 | 74227364 | rs11210390 | C | T | 4 | 0.02417 | 0.1047 | 1.0867 | 1.156 | 0.0031 | 78.33 |
| 4 | 135195163 | rs2421069 | C | T | 4 | 0.03192 | 0.1047 | 1.0928 | 1.144 | 0.0298 | 66.53 |
| 4 | 136722879 | rs11940405 | G | T | 4 | 0.01026 | 0.1047 | 1.1158 | 1.1118 | 0.1258 | 47.59 |
| 5 | 153749486 | rs13154706 | C | T | 4 | 0.04849 | 0.105 | 0.921 | 0.8618 | 0.0102 | 73.45 |
| 6 | 40752262 | rs11962303 | A | C | 4 | 0.006777 | 0.1051 | 1.1217 | 1.1438 | 0.031 | 66.2 |
| 7 | 20862587 | rs17143423 | A | G | 4 | 0.007407 | 0.1059 | 0.8807 | 0.8822 | 0.0939 | 53.09 |
| 4 | 132446415 | rs12641562 | A | C | 4 | 0.003393 | 0.1066 | 0.7427 | 0.7093 | 0.0166 | 70.7 |
| 7 | 84598360 | rs2159575 | C | T | 4 | 0.05053 | 0.1066 | 0.9225 | 0.8729 | 0.0195 | 69.67 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 4 | 136722837 | rs11935719 | A | G | 4 | 0.01049 | 0.1071 | 1.1154 | 1.1115 | 0.1232 | 48.03 |
| 10 | 24661175 | rs7897007 | A | G | 4 | 0.0368 | 0.1073 | 0.9109 | 0.8493 | 0.0064 | 75.66 |
| 10 | 80764708 | rs16937080 | A | T | 4 | 0.05602 | 0.1073 | 0.9278 | 0.8737 | 0.0155 | 71.14 |
| 18 | 69425930 | rs2051413 | A | G | 4 | 0.0471 | 0.1075 | 1.0738 | 1.1268 | 0.021 | 69.17 |
| 11 | 32209862 | rs1998003 | A | C | 4 | 0.00158 | 0.1076 | 1.1254 | 1.1039 | 0.0915 | 53.52 |
| 7 | 84575619 | rs10486848 | A | G | 4 | 0.0363 | 0.1081 | 1.0962 | 1.1676 | 0.0097 | 73.69 |
| 4 | 132453787 | rs12641624 | C | T | 4 | 0.004482 | 0.1082 | 0.7492 | 0.7151 | 0.0201 | 69.48 |
| 4 | 132449623 | rs12650292 | A | G | 4 | 0.003724 | 0.1084 | 1.3426 | 1.4066 | 0.0169 | 70.62 |
| 4 | 135194549 | rs1565910 | A | G | 4 | 0.03746 | 0.1085 | 1.0892 | 1.1409 | 0.0308 | 66.24 |
| 18 | 69430600 | rs1943869 | C | G | 4 | 0.04907 | 0.1087 | 1.0731 | 1.1252 | 0.0225 | 68.68 |
| 11 | 32207093 | rs2418583 | C | T | 4 | 0.001682 | 0.1088 | 1.1247 | 1.1034 | 0.0919 | 53.44 |
| 9 | 104678314 | rs1826415 | C | T | 4 | 0.0427 | 0.109 | 0.9149 | 0.8763 | 0.0362 | 64.84 |
| 7 | 146312527 | rs10808041 | A | T | 4 | 0.001297 | 0.1094 | 0.8227 | 0.8588 | 0.1197 | 48.63 |
| 7 | 84577029 | rs17561679 | C | T | 4 | 0.04814 | 0.1096 | 1.083 | 1.1386 | 0.0238 | 68.27 |
| 10 | 6552587 | rs11597105 | A | G | 4 | 0.07448 | 0.1096 | 0.9127 | 0.7937 | 0.0005 | 83.07 |
| 7 | 107414230 | rs2021886 | A | G | 3 | 0.007393 | 0.1097 | 1.1057 | 1.1003 | 0.1212 | 52.61 |
| 18 | 69429890 | rs4892117 | C | T | 4 | 0.05067 | 0.1098 | 0.9323 | 0.8892 | 0.0229 | 68.55 |
| 4 | 132449990 | rs12641430 | C | T | 4 | 0.004393 | 0.1099 | 1.3357 | 1.3995 | 0.0188 | 69.92 |
| 1 | 212356390 | rs1660381 | C | T | 3 | 0.001183 | 0.1101 | 1.4069 | 1.3283 | 0.1063 | 55.39 |
| 11 | 32207354 | rs926968 | C | T | 4 | 0.001526 | 0.1102 | 1.1259 | 1.104 | 0.0873 | 54.26 |
| 1 | 74227289 | rs11210389 | A | C | 4 | 0.02949 | 0.1103 | 1.083 | 1.1527 | 0.0031 | 78.39 |
| 11 | 32207798 | rs926967 | A | G | 4 | 0.001586 | 0.1116 | 0.8886 | 0.9061 | 0.0875 | 54.23 |
| 21 | 40067833 | rs16998436 | C | T | 4 | 0.005305 | 0.1118 | 1.1901 | 1.2181 | 0.0252 | 67.86 |
| 7 | 84577791 | rs1029564 | G | T | 4 | 0.05032 | 0.112 | 1.0822 | 1.1382 | 0.0231 | 68.48 |
| 2 | 128358837 | rs10183605 | C | G | 4 | 0.002387 | 0.1121 | 0.8935 | 0.8977 | 0.0469 | 62.3 |
| 2 | 209855352 | rs4673461 | A | G | 4 | 0.00911 | 0.1121 | 0.8953 | 0.9029 | 0.1372 | 45.7 |
| 11 | 32208659 | rs2418584 | C | T | 4 | 0.001664 | 0.1122 | 1.1248 | 1.1023 | 0.0924 | 53.36 |
| 4 | 132453477 | rs12647579 | A | T | 4 | 0.00489 | 0.1124 | 0.7513 | 0.7167 | 0.0191 | 69.8 |
| 4 | 149309538 | rs6535584 | C | T | 4 | 0.01224 | 0.1124 | 1.0916 | 1.1176 | 0.0258 | 67.67 |
| 7 | 84532070 | rs7800255 | A | T | 4 | 0.0103 | 0.1129 | 1.1469 | 1.193 | 0.0168 | 70.66 |
| 18 | 69451956 | rs11662228 | C | T | 4 | 0.05017 | 0.1129 | 1.0706 | 1.1257 | 0.0146 | 71.49 |
| 3 | 41530567 | rs2017454 | A | G | 4 | 0.02321 | 0.113 | 1.1763 | 1.2279 | 0.0419 | 63.46 |
| 6 | 41385833 | rs9357353 | C | T | 4 | 0.00136 | 0.1132 | 1.1213 | 1.0982 | 0.0925 | 53.33 |
| 11 | 10781116 | rs10743150 | A | G | 4 | 0.001917 | 0.1133 | 1.231 | 1.2066 | 0.0625 | 58.98 |
| 1 | 97673140 | rs12129397 | A | T | 4 | 0.08645 | 0.1134 | 1.0621 | 1.1512 | 0.002 | 79.78 |
| 4 | 132450305 | rs11946051 | G | T | 4 | 0.005034 | 0.1138 | 0.752 | 0.7173 | 0.0189 | 69.88 |
| 6 | 14489412 | rs926924 | C | T | 4 | 0.0094 | 0.1143 | 1.0945 | 1.1091 | 0.0416 | 63.53 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 3 | 41526055 | rs1256396 | A | T | 4 | 0.02244 | 0.1146 | 1.1767 | 1.2267 | 0.0412 | 63.61 |
| 11 | 32211971 | rs7124928 | C | T | 4 | 0.001529 | 0.1146 | 0.8882 | 0.9059 | 0.0822 | 55.2 |
| 10 | 30438125 | rs12220246 | C | T | 4 | 0.0007857 | 0.1147 | 1.1358 | 1.1 | 0.1192 | 48.71 |
| 1 | 97675378 | rs11165873 | A | T | 4 | 0.08883 | 0.1149 | 1.0616 | 1.1507 | 0.0019 | 79.81 |
| 3 | 41524937 | rs9831248 | C | G | 4 | 0.02247 | 0.115 | 1.1766 | 1.2267 | 0.0409 | 63.7 |
| 21 | 40068571 | rs16998444 | A | G | 4 | 0.006016 | 0.1151 | 1.187 | 1.2153 | 0.0257 | 67.68 |
| 2 | 133201434 | rs11692408 | A | G | 4 | 0.001263 | 0.1153 | 0.8863 | 0.8991 | 0.0531 | 60.94 |
| 6 | 25256945 | rs12663706 | C | G | 4 | 0.003686 | 0.1153 | 1.1414 | 1.1235 | 0.0984 | 52.29 |
| 14 | 31529811 | rs10132140 | A | G | 4 | 0.008069 | 0.1158 | 0.8868 | 0.8905 | 0.0939 | 53.08 |
| 12 | 2777987 | rs1981655 | A | T | 4 | 0.004163 | 0.116 | 0.7731 | 0.8081 | 0.1537 | 42.97 |
| 3 | 41519427 | rs4258937 | A | G | 4 | 0.02343 | 0.1162 | 0.8504 | 0.8156 | 0.0414 | 63.57 |
| 1 | 97668350 | rs11165870 | C | T | 4 | 0.1006 | 0.1163 | 0.9439 | 0.867 | 0.0014 | 80.63 |
| 4 | 135193417 | rs1390026 | G | T | 4 | 0.04777 | 0.1165 | 0.9216 | 0.8789 | 0.0318 | 65.98 |
| 11 | 32212187 | rs10742273 | C | G | 4 | 0.001594 | 0.1165 | 1.1254 | 1.1036 | 0.082 | 55.24 |
| 1 | 97699427 | rs7550959 | A | G | 4 | 0.0935 | 0.1167 | 0.9422 | 0.8698 | 0.0023 | 79.37 |
| 10 | 114461555 | rs11196070 | C | G | 4 | 0.005055 | 0.1169 | 0.8285 | 0.8418 | 0.1007 | 51.89 |
| 3 | 60196556 | rs10510834 | A | G | 4 | 0.1213 | 0.117 | 1.076 | 1.1872 | 0.0074 | 75.02 |
| 11 | 32212217 | rs10742274 | C | T | 4 | 0.001623 | 0.1171 | 0.8887 | 0.9063 | 0.0822 | 55.21 |
| 3 | 60197075 | rs13082004 | C | T | 4 | 0.1256 | 0.1176 | 0.9306 | 0.8421 | 0.0067 | 75.44 |
| 1 | 97693544 | rs12354219 | C | T | 4 | 0.09758 | 0.1177 | 0.9434 | 0.8687 | 0.0017 | 80.19 |
| 21 | 32329234 | rs9974134 | A | C | 4 | 0.006386 | 0.1177 | 0.8728 | 0.883 | 0.1038 | 51.35 |
| 4 | 28926641 | rs987157 | A | G | 4 | 0.06876 | 0.1182 | 1.1064 | 1.1937 | 0.0167 | 70.67 |
| 11 | 10779614 | rs7103202 | A | G | 4 | 0.002068 | 0.1184 | 0.8142 | 0.8299 | 0.0588 | 59.75 |
| 1 | 97690894 | rs3897854 | C | T | 4 | 0.0949 | 0.1187 | 1.0605 | 1.1497 | 0.0019 | 79.92 |
| 6 | 40749271 | rs4714357 | A | G | 4 | 0.01025 | 0.1188 | 0.8961 | 0.8785 | 0.032 | 65.93 |
| 2 | 6855044 | rs10200467 | C | T | 4 | 0.2119 | 0.1189 | 1.0513 | 1.1747 | 0.002 | 79.75 |
| 2 | 229840402 | rs10185903 | C | T | 4 | 0.003574 | 0.1191 | 1.1556 | 1.1214 | 0.1558 | 42.62 |
| 1 | 74116329 | rs967881 | A | G | 4 | 0.05199 | 0.1192 | 0.9305 | 0.8871 | 0.0172 | 70.5 |
| 11 | 32212512 | rs12795402 | C | T | 4 | 0.001559 | 0.1192 | 1.1257 | 1.1035 | 0.0792 | 55.76 |
| 7 | 91252060 | rs1208998 | C | T | 4 | 0.001419 | 0.1193 | 0.7862 | 0.8187 | 0.07 | 57.52 |
| 1 | 74233585 | rs6663201 | C | T | 4 | 0.03839 | 0.1199 | 1.0801 | 1.1656 | 0.0008 | 81.97 |
| 7 | 84580693 | rs17561700 | G | T | 4 | 0.03885 | 0.1199 | 1.0954 | 1.1594 | 0.0115 | 72.82 |
| 1 | 74138234 | rs1340434 | C | T | 4 | 0.02395 | 0.1202 | 1.085 | 1.1607 | 0.0008 | 82.15 |
| 8 | 27723712 | rs1052873 | C | T | 4 | 0.004011 | 0.1204 | 1.1359 | 1.1128 | 0.1211 | 48.38 |
| 1 | 74233724 | rs6660710 | A | G | 4 | 0.03898 | 0.1206 | 0.926 | 0.8579 | 0.0008 | 82.05 |
| 1 | 97677368 | rs4949953 | C | T | 4 | 0.1012 | 0.1206 | 0.9441 | 0.8699 | 0.0017 | 80.17 |
| 3 | 60195347 | rs7628950 | A | T | 4 | 0.1314 | 0.1207 | 0.9311 | 0.8439 | 0.0075 | 74.95 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 74149450 | rs7544252 | C | G | 4 | 0.024 | 0.1209 | 1.0849 | 1.1609 | 0.0007 | 82.26 |
| 1 | 74150383 | rs12062996 | C | T | 4 | 0.024 | 0.1209 | 1.0849 | 1.1609 | 0.0007 | 82.26 |
| 20 | 8455713 | rs6055881 | C | T | 4 | 0.05949 | 0.1209 | 1.0709 | 1.141 | 0.0052 | 76.51 |
| 6 | 40749486 | rs16893894 | C | T | 4 | 0.01069 | 0.1211 | 1.1153 | 1.1375 | 0.0318 | 65.98 |
| 1 | 74111118 | rs6672527 | C | T | 4 | 0.05454 | 0.1212 | 0.9306 | 0.8862 | 0.0165 | 70.76 |
| 1 | 74112532 | rs11210361 | C | T | 4 | 0.05461 | 0.1214 | 1.0738 | 1.1265 | 0.0173 | 70.46 |
| 6 | 25265596 | rs1900554 | C | T | 4 | 0.004718 | 0.1214 | 0.882 | 0.9002 | 0.1366 | 45.8 |
| 1 | 74117298 | rs17579506 | C | T | 4 | 0.05538 | 0.1216 | 1.0731 | 1.1262 | 0.0166 | 70.71 |
| 1 | 74117107 | rs17520168 | C | T | 4 | 0.05559 | 0.1217 | 1.073 | 1.126 | 0.0169 | 70.61 |
| 1 | 74151900 | rs7550937 | A | G | 4 | 0.02455 | 0.1217 | 1.0846 | 1.1608 | 0.0007 | 82.32 |
| 1 | 74152537 | rs1768649 | A | G | 4 | 0.02455 | 0.1217 | 1.0846 | 1.1608 | 0.0007 | 82.32 |
| 1 | 74153059 | rs11210368 | A | G | 4 | 0.02455 | 0.1217 | 1.0846 | 1.1608 | 0.0007 | 82.32 |
| 4 | 136740556 | rs11737486 | A | G | 4 | 0.006824 | 0.1217 | 1.1621 | 1.1504 | 0.0779 | 56.01 |
| 6 | 40749374 | rs4714358 | A | C | 4 | 0.01096 | 0.1221 | 1.1149 | 1.1372 | 0.0317 | 66 |
| 21 | 40081547 | rs11088495 | C | T | 4 | 0.001244 | 0.1222 | 0.8917 | 0.8918 | 0.0166 | 70.7 |
| 1 | 74159865 | rs2733260 | C | T | 4 | 0.02496 | 0.1223 | 0.9222 | 0.8616 | 0.0007 | 82.33 |
| 12 | 82308633 | rs7136505 | A | G | 3 | 0.004254 | 0.1223 | 0.7624 | 0.736 | 0.0232 | 73.44 |
| 14 | 37935967 | rs1168555 | A | G | 4 | 0.0676 | 0.1225 | 1.0663 | 1.1114 | 0.034 | 65.4 |
| 1 | 74165700 | rs7533599 | A | G | 4 | 0.02501 | 0.1226 | 1.0843 | 1.1609 | 0.0007 | 82.42 |
| 1 | 74168149 | rs12081389 | A | T | 4 | 0.02501 | 0.1226 | 1.0843 | 1.1609 | 0.0007 | 82.42 |
| 6 | 28377642 | rs1997660 | A | G | 4 | 0.04545 | 0.1226 | 1.0814 | 1.1319 | 0.023 | 68.53 |
| 18 | 69453896 | rs11876675 | A | G | 4 | 0.06164 | 0.1231 | 0.9359 | 0.89 | 0.0148 | 71.4 |
| 3 | 60194354 | rs4679648 | C | T | 4 | 0.1314 | 0.1232 | 0.9316 | 0.8535 | 0.0135 | 71.93 |
| 15 | 81227450 | rs12592976 | C | T | 4 | 0.01657 | 0.1232 | 0.8749 | 0.8392 | 0.0283 | 66.95 |
| 11 | 32214418 | rs1155855 | A | G | 4 | 0.001358 | 0.1233 | 0.887 | 0.9057 | 0.072 | 57.12 |
| 11 | 32214070 | rs1155856 | A | G | 4 | 0.001382 | 0.1234 | 1.1272 | 1.1039 | 0.0725 | 57.03 |
| 18 | 13790956 | rs9949908 | G | T | 4 | 0.01088 | 0.1234 | 0.8633 | 0.8019 | 0.0017 | 80.18 |
| 18 | 13793024 | rs948271 | C | T | 4 | 0.01094 | 0.1234 | 1.1584 | 1.2473 | 0.0017 | 80.16 |
| 2 | 6853536 | rs4668508 | A | G | 4 | 0.2157 | 0.1241 | 0.9501 | 0.8498 | 0.002 | 79.72 |
| 14 | 37935713 | rs1168554 | A | G | 4 | 0.06959 | 0.1241 | 1.0658 | 1.1109 | 0.0341 | 65.37 |
| 6 | 83339411 | rs16885899 | A | G | 2 | 0.00222 | 0.1244 | 1.9161 | 1.7841 | 0.0879 | 65.66 |
| 8 | 10739369 | rs7010709 | C | T | 4 | 0.04741 | 0.1244 | 0.9172 | 0.8607 | 0.0103 | 73.42 |
| 11 | 80994506 | rs7949287 | A | G | 4 | 0.1198 | 0.1244 | 0.9476 | 0.8775 | 0.0028 | 78.68 |
| 2 | 40178533 | rs13032715 | C | T | 3 | 0.01709 | 0.1245 | 1.1252 | 1.3042 | 0.0002 | 88.04 |
| 1 | 74122434 | rs11210363 | A | G | 4 | 0.05916 | 0.1248 | 1.0725 | 1.1263 | 0.0163 | 70.84 |
| 8 | 10739944 | rs6990589 | A | G | 4 | 0.0467 | 0.1248 | 0.9165 | 0.8603 | 0.0104 | 73.35 |
| 8 | 10741808 | rs11990167 | C | T | 4 | 0.04801 | 0.1249 | 1.09 | 1.163 | 0.0095 | 73.83 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 10 | 30429219 | rs3847404 | C | T | 4 | 0.000328 | 0.1252 | 0.8749 | 0.9079 | 0.0903 | 53.73 |
| 1 | 74235010 | rs2343196 | C | T | 4 | 0.04221 | 0.1256 | 1.0787 | 1.1629 | 0.0009 | 81.85 |
| 1 | 212358932 | rs1795036 | A | G | 4 | 0.001961 | 0.1257 | 1.3805 | 1.2852 | 0.1351 | 46.03 |
| 4 | 72355439 | rs1377287 | A | G | 4 | 0.0827 | 0.1257 | 0.9062 | 0.8181 | 0.0038 | 77.69 |
| 6 | 28403018 | rs853683 | A | G | 4 | 0.04964 | 0.1257 | 1.0798 | 1.1293 | 0.0252 | 67.86 |
| 3 | 63500043 | rs4616634 | A | G | 4 | 8.62E-05 | 0.126 | 1.1855 | 1.1345 | 0.0365 | 64.77 |
| 3 | 41517346 | rs1691983 | A | G | 4 | 0.0303 | 0.1261 | 0.8569 | 0.8207 | 0.0422 | 63.37 |
| 1 | 212356865 | rs1660378 | C | T | 4 | 0.001624 | 0.1264 | 1.3647 | 1.2709 | 0.1313 | 46.68 |
| 6 | 28399219 | rs707907 | A | G | 4 | 0.0506 | 0.1267 | 1.0795 | 1.1291 | 0.0249 | 67.93 |
| 11 | 107990612 | rs7125479 | A | C | 4 | 0.05127 | 0.1267 | 0.9341 | 0.9032 | 0.037 | 64.63 |
| 3 | 41516991 | rs2643977 | C | T | 4 | 0.0297 | 0.1271 | 1.1677 | 1.2193 | 0.0404 | 63.8 |
| 11 | 107987483 | rs2852205 | A | G | 4 | 0.05356 | 0.1277 | 1.0699 | 1.107 | 0.0371 | 64.62 |
| 20 | 57284330 | rs6100397 | G | T | 4 | 0.0006886 | 0.1277 | 1.3981 | 1.3821 | 0.0109 | 73.09 |
| 2 | 229839689 | rs6754229 | C | T | 4 | 0.004091 | 0.1279 | 1.1532 | 1.1189 | 0.1535 | 42.99 |
| 4 | 136739022 | rs2102279 | C | T | 4 | 0.007456 | 0.1279 | 1.1596 | 1.1474 | 0.0765 | 56.26 |
| 11 | 32214720 | rs12287573 | C | T | 4 | 0.00145 | 0.1284 | 1.1266 | 1.1032 | 0.0697 | 57.56 |
| 3 | 41516845 | rs2643976 | A | G | 4 | 0.031 | 0.1286 | 1.1669 | 1.2183 | 0.0412 | 63.61 |
| 6 | 25260653 | rs6941417 | A | G | 4 | 0.007927 | 0.1288 | 0.8831 | 0.8942 | 0.1195 | 48.66 |
| 6 | 40745631 | rs6901833 | A | G | 4 | 0.002475 | 0.1288 | 1.1416 | 1.1476 | 0.0194 | 69.69 |
| 11 | 10721194 | rs924111 | A | G | 4 | 0.005926 | 0.1288 | 1.1027 | 1.0839 | 0.1441 | 44.55 |
| 11 | 32215762 | rs10767925 | A | G | 4 | 0.001362 | 0.1288 | 1.1274 | 1.1035 | 0.068 | 57.9 |
| 8 | 10744211 | rs1469557 | C | T | 4 | 0.05384 | 0.1289 | 1.0877 | 1.1662 | 0.007 | 75.25 |
| 14 | 37936185 | rs1186370 | A | G | 4 | 0.07616 | 0.1291 | 1.0643 | 1.1105 | 0.0317 | 66.01 |
| 11 | 32220627 | rs6484557 | A | C | 4 | 0.001211 | 0.1292 | 0.8859 | 0.9052 | 0.0633 | 58.84 |
| 1 | 74224911 | rs9662322 | G | T | 4 | 0.03892 | 0.1294 | 0.9256 | 0.8581 | 0.0006 | 82.71 |
| 3 | 41561312 | rs1629284 | C | G | 4 | 0.01903 | 0.1297 | 1.1847 | 1.2316 | 0.0295 | 66.6 |
| 2 | 236090677 | rs2316435 | A | T | 4 | 0.03637 | 0.1301 | 0.9087 | 0.8494 | 0.0033 | 78.12 |
| 2 | 209659240 | rs1439736 | G | T | 4 | 0.001546 | 0.1302 | 0.8536 | 0.8798 | 0.0786 | 55.87 |
| 1 | 74185240 | rs10493528 | A | T | 4 | 0.02383 | 0.1306 | 1.0857 | 1.1591 | 0.0006 | 82.67 |
| 2 | 236075691 | rs7599284 | A | G | 4 | 0.03428 | 0.1307 | 0.9067 | 0.8459 | 0.0026 | 78.94 |
| 11 | 80986103 | rs1945649 | C | T | 4 | 0.1325 | 0.1307 | 1.0534 | 1.1366 | 0.0028 | 78.65 |
| 1 | 212357674 | rs1440619 | A | G | 4 | 0.001927 | 0.1308 | 1.3692 | 1.2776 | 0.1257 | 47.61 |
| 5 | 153738544 | rs7728507 | C | T | 4 | 0.08266 | 0.131 | 1.0721 | 1.1583 | 0.0036 | 77.89 |
| 17 | 45486194 | rs9895410 | C | T | 4 | 0.07892 | 0.131 | 1.0981 | 1.1924 | 0.0079 | 74.68 |
| 2 | 236094249 | rs4663604 | A | G | 4 | 0.03713 | 0.1312 | 1.1001 | 1.1765 | 0.0034 | 78.06 |
| 3 | 41516460 | rs11919885 | C | T | 4 | 0.03353 | 0.1314 | 0.8589 | 0.8232 | 0.0436 | 63.04 |
| 11 | 107991327 | rs7934388 | A | T | 4 | 0.05591 | 0.1314 | 1.0692 | 1.1062 | 0.0361 | 64.86 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 3 | 15005549 | rs9839660 | A | T | 4 | 0.04199 | 0.1315 | 1.1752 | 1.2852 | 0.0117 | 72.73 |
| 2 | 236094532 | rs10460276 | C | T | 4 | 0.03775 | 0.1316 | 0.9093 | 0.8502 | 0.0034 | 78.04 |
| 2 | 236095585 | rs6731720 | G | T | 4 | 0.03213 | 0.1317 | 1.1046 | 1.1763 | 0.0039 | 77.53 |
| 3 | 63499920 | rs1505598 | C | G | 4 | 0.0001213 | 0.1319 | 1.1812 | 1.1316 | 0.0379 | 64.41 |
| 18 | 37303085 | rs2703175 | A | G | 4 | 0.03422 | 0.1319 | 0.8802 | 0.7928 | 0.0023 | 79.28 |
| 6 | 25262375 | rs11752102 | A | G | 4 | 0.007811 | 0.132 | 1.1326 | 1.1176 | 0.1182 | 48.88 |
| 11 | 81001119 | rs2097171 | C | T | 4 | 0.1228 | 0.1321 | 1.0547 | 1.1313 | 0.0042 | 77.26 |
| 5 | 153737245 | rs1422665 | C | T | 4 | 0.08645 | 0.1323 | 1.0711 | 1.1568 | 0.0038 | 77.69 |
| 2 | 236087152 | rs938675 | C | T | 4 | 0.0368 | 0.1326 | 0.9089 | 0.8494 | 0.003 | 78.49 |
| 1 | 74161472 | rs12076161 | A | C | 4 | 0.02844 | 0.1329 | 0.924 | 0.8658 | 0.0008 | 82.21 |
| 8 | 10720187 | rs17152571 | A | G | 4 | 0.08882 | 0.133 | 0.9118 | 0.8198 | 0.0046 | 76.94 |
| 2 | 236091352 | rs4663602 | A | G | 4 | 0.03838 | 0.1332 | 1.0994 | 1.1767 | 0.0031 | 78.33 |
| 3 | 124837883 | rs820460 | C | T | 4 | 0.004051 | 0.1333 | 1.2352 | 1.2378 | 0.0263 | 67.52 |
| 1 | 74191995 | rs7544238 | A | C | 4 | 0.02584 | 0.1337 | 1.084 | 1.1586 | 0.0005 | 82.95 |
| 3 | 63490926 | rs6777474 | A | G | 4 | 7.28E-05 | 0.1337 | 1.1904 | 1.1371 | 0.0298 | 66.51 |
| 1 | 74161523 | rs12077198 | A | G | 4 | 0.02919 | 0.1338 | 0.9243 | 0.866 | 0.0007 | 82.23 |
| 18 | 48360097 | rs12961437 | G | T | 4 | 0.006429 | 0.1338 | 0.8731 | 0.8672 | 0.0393 | 64.07 |
| 2 | 159755255 | rs12617786 | A | G | 4 | 0.01303 | 0.1339 | 1.4395 | 1.4253 | 0.0828 | 55.1 |
| 4 | 154534381 | rs10517571 | A | C | 4 | 0.1615 | 0.134 | 1.0506 | 1.1372 | 0.003 | 78.43 |
| 4 | 154559969 | rs3852108 | A | C | 4 | 0.1585 | 0.134 | 0.9511 | 0.879 | 0.0031 | 78.32 |
| 11 | 10804775 | rs4243917 | C | T | 4 | 0.001385 | 0.134 | 0.8097 | 0.8299 | 0.0399 | 63.93 |
| 11 | 32220968 | rs2418587 | C | T | 4 | 0.001313 | 0.134 | 0.8867 | 0.906 | 0.0618 | 59.14 |
| 4 | 29199244 | rs1441670 | A | G | 4 | 0.1868 | 0.1341 | 1.0475 | 1.1509 | 0.0008 | 82.2 |
| 1 | 74191025 | rs1417259 | G | T | 4 | 0.02596 | 0.1343 | 1.0839 | 1.1584 | 0.0005 | 82.96 |
| 3 | 15059018 | rs9825022 | C | T | 4 | 0.04796 | 0.1343 | 0.8557 | 0.7854 | 0.0148 | 71.4 |
| 11 | 32216421 | rs1884382 | A | G | 4 | 0.001193 | 0.1343 | 1.1289 | 1.1038 | 0.0606 | 59.38 |
| 1 | 212357165 | rs1795037 | A | G | 4 | 0.001828 | 0.1344 | 1.3611 | 1.2663 | 0.1295 | 46.98 |
| 1 | 74195971 | rs11210377 | G | T | 4 | 0.03005 | 0.1345 | 0.9251 | 0.8643 | 0.0006 | 82.88 |
| 3 | 41515056 | rs12639280 | C | T | 4 | 0.03586 | 0.1345 | 1.1621 | 1.2128 | 0.0437 | 63.03 |
| 8 | 10769957 | rs10903331 | C | G | 4 | 0.04483 | 0.1346 | 0.9073 | 0.8279 | 0.0015 | 80.55 |
| 8 | 120078754 | rs4876434 | C | T | 4 | 0.00804 | 0.1346 | 1.2269 | 1.2324 | 0.0515 | 61.29 |
| 1 | 74196206 | rs12116914 | G | T | 4 | 0.03027 | 0.1348 | 1.0809 | 1.157 | 0.0005 | 82.89 |
| 3 | 15058788 | rs9820676 | C | G | 4 | 0.04883 | 0.1348 | 0.8562 | 0.7861 | 0.0152 | 71.25 |
| 13 | 26340889 | rs9553915 | A | G | 4 | 0.003893 | 0.1349 | 0.8563 | 0.8821 | 0.1251 | 47.71 |
| 21 | 40093555 | rs16998556 | G | T | 4 | 0.01043 | 0.1349 | 0.8522 | 0.8278 | 0.0216 | 68.98 |
| 1 | 205534725 | rs6686201 | A | G | 4 | 0.1497 | 0.1356 | 0.9506 | 0.8824 | 0.0038 | 77.67 |
| 5 | 153740522 | rs17116042 | C | T | 4 | 0.08897 | 0.1357 | 0.9341 | 0.8648 | 0.0034 | 78.03 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 1 | 212355741 | rs1660382 | A | G | 4 | 0.001589 | 0.1358 | 1.3808 | 1.2757 | 0.1257 | 47.61 |
| 12 | 13256321 | rs2291060 | A | G | 4 | 0.01666 | 0.1361 | 1.1868 | 1.2748 | 0.0106 | 73.24 |
| 4 | 72354592 | rs7436806 | A | G | 4 | 0.08416 | 0.1362 | 1.1118 | 1.2387 | 0.0029 | 78.56 |
| 8 | 10723261 | rs17152584 | A | G | 4 | 0.09952 | 0.1362 | 0.9145 | 0.8207 | 0.0045 | 77.07 |
| 3 | 102220701 | rs13091963 | A | G | 4 | 0.06209 | 0.1363 | 1.0749 | 1.1452 | 0.0039 | 77.53 |
| 8 | 10741204 | rs11250082 | C | T | 4 | 0.05754 | 0.1364 | 1.0863 | 1.1582 | 0.0093 | 73.93 |
| 3 | 63490780 | rs6766087 | C | T | 4 | 7.74E-05 | 0.1365 | 0.8405 | 0.8798 | 0.0291 | 66.72 |
| 1 | 74170715 | rs12082647 | A | C | 4 | 0.02849 | 0.1366 | 0.924 | 0.8644 | 0.0005 | 83.01 |
| 1 | 74202690 | rs12064998 | A | G | 4 | 0.03184 | 0.1366 | 0.9259 | 0.8647 | 0.0005 | 82.95 |
| 11 | 32216841 | rs7109202 | C | T | 4 | 0.001243 | 0.1366 | 1.1284 | 1.1034 | 0.0599 | 59.51 |
| 1 | 74202532 | rs12064944 | A | G | 4 | 0.03269 | 0.1375 | 0.9262 | 0.8649 | 0.0005 | 82.97 |
| 3 | 124845546 | rs820470 | C | T | 4 | 0.003046 | 0.1376 | 1.2538 | 1.2344 | 0.0343 | 65.33 |
| 2 | 57624516 | rs13410921 | A | C | 3 | 7.59E-05 | 0.1377 | 0.5133 | 0.5791 | 0.035 | 70.17 |
| 6 | 28390627 | rs853693 | A | G | 4 | 0.06293 | 0.1378 | 0.9302 | 0.8888 | 0.0241 | 68.18 |
| 3 | 102221017 | rs2713775 | A | T | 4 | 0.06458 | 0.138 | 0.931 | 0.8737 | 0.0039 | 77.53 |
| 9 | 70346115 | rs10120859 | C | T | 4 | 0.01145 | 0.138 | 0.8799 | 0.8889 | 0.1191 | 48.72 |
| 2 | 57625311 | rs9309297 | C | G | 3 | 7.81E-05 | 0.1382 | 1.9459 | 1.7253 | 0.0351 | 70.15 |
| 1 | 74215111 | rs12138557 | A | C | 4 | 0.03273 | 0.1383 | 1.0796 | 1.1552 | 0.0006 | 82.82 |
| 5 | 153745624 | rs6870010 | C | T | 4 | 0.1001 | 0.1383 | 0.9367 | 0.8699 | 0.005 | 76.63 |
| 1 | 91987439 | rs284172 | A | T | 4 | 0.01276 | 0.1385 | 0.8802 | 0.8647 | 0.0381 | 64.35 |
| 2 | 57618472 | rs13389335 | A | T | 3 | 7.60E-05 | 0.1385 | 0.509 | 0.5759 | 0.0344 | 70.31 |
| 1 | 74158268 | rs10493526 | C | T | 4 | 0.03372 | 0.1387 | 1.0797 | 1.1527 | 0.0007 | 82.24 |
| 4 | 136728656 | rs13129036 | C | T | 3 | 0.008213 | 0.1388 | 1.1243 | 1.1186 | 0.0826 | 59.9 |
| 8 | 27642120 | rs13282289 | A | G | 4 | 0.004474 | 0.139 | 1.1289 | 1.1022 | 0.1254 | 47.66 |
| 3 | 106415848 | rs10933810 | C | T | 4 | 0.004956 | 0.1394 | 1.1315 | 1.1117 | 0.0968 | 52.58 |
| 7 | 12650865 | rs2691810 | C | T | 4 | 0.08902 | 0.1396 | 1.0945 | 1.1851 | 0.0092 | 73.94 |
| 3 | 63503954 | rs11130944 | C | T | 4 | 0.0001525 | 0.1397 | 0.8449 | 0.8824 | 0.0349 | 65.18 |
| 3 | 124847003 | rs820472 | C | T | 4 | 0.003244 | 0.1397 | 1.2505 | 1.2344 | 0.0318 | 65.99 |
| 2 | 57616717 | rs13392012 | C | T | 3 | 7.63E-05 | 0.1399 | 1.9928 | 1.7528 | 0.0334 | 70.57 |
| 7 | 24845137 | rs1541363 | C | T | 4 | 0.01262 | 0.14 | 1.1554 | 1.2318 | 0.0046 | 76.95 |
| 2 | 57626427 | rs9309298 | A | G | 3 | 8.29E-05 | 0.1401 | 0.5151 | 0.5806 | 0.0347 | 70.24 |
| 12 | 89968187 | rs7959834 | C | T | 4 | 0.01573 | 0.1401 | 0.8393 | 0.7931 | 0.0138 | 71.8 |
| 12 | 89968856 | rs7973791 | A | C | 4 | 0.01576 | 0.1402 | 1.1914 | 1.2608 | 0.0139 | 71.8 |
| 1 | 74194799 | rs1361463 | A | T | 4 | 0.03534 | 0.1403 | 1.0785 | 1.1554 | 0.0005 | 83.05 |
| 1 | 205524041 | rs2217406 | A | T | 4 | 0.1625 | 0.1405 | 0.952 | 0.8838 | 0.0038 | 77.65 |
| 2 | 64133110 | rs10171434 | C | T | 4 | 0.00459 | 0.1405 | 0.8263 | 0.8562 | 0.1264 | 47.5 |
| 1 | 205549789 | rs7525530 | A | G | 4 | 0.1624 | 0.1407 | 0.952 | 0.8825 | 0.0033 | 78.18 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 3 | 63487802 | rs11928896 | A | G | 4 | 7.46E-05 | 0.1407 | 1.1918 | 1.1431 | 0.0195 | 69.68 |
| 13 | 43927733 | rs11619041 | A | G | 4 | 0.01936 | 0.1408 | 1.0876 | 1.117 | 0.0171 | 70.54 |
| 13 | 44106744 | rs9567450 | C | T | 4 | 0.03785 | 0.1408 | 1.0784 | 1.1201 | 0.0156 | 71.09 |
| 4 | 95487295 | rs1991316 | G | T | 4 | 0.006318 | 0.1409 | 1.1036 | 1.1149 | 0.019 | 69.84 |
| 2 | 236080078 | rs1865951 | A | G | 4 | 0.04341 | 0.141 | 0.9112 | 0.8475 | 0.002 | 79.75 |
| 1 | 61296851 | rs12402756 | C | T | 4 | 0.01464 | 0.1415 | 1.157 | 1.1796 | 0.037 | 64.64 |
| 6 | 116166045 | rs9384957 | C | T | 4 | 0.002786 | 0.1415 | 1.1558 | 1.1566 | 0.0159 | 70.99 |
| 18 | 48306360 | rs12964400 | A | G | 4 | 0.006962 | 0.1415 | 1.1438 | 1.1494 | 0.0406 | 63.76 |
| 1 | 205480867 | rs891373 | C | T | 4 | 0.1646 | 0.1416 | 1.0511 | 1.135 | 0.0034 | 78.02 |
| 3 | 63504654 | rs1027764 | G | T | 4 | 0.0001639 | 0.1417 | 0.8438 | 0.8813 | 0.0338 | 65.45 |
| 21 | 40067939 | rs2837204 | C | T | 4 | 0.007639 | 0.1417 | 1.1741 | 1.2014 | 0.0176 | 70.36 |
| 11 | 32217307 | rs2207820 | A | C | 4 | 0.001305 | 0.1418 | 1.1278 | 1.1027 | 0.0575 | 60.01 |
| 4 | 29184029 | rs1348188 | C | T | 4 | 0.2112 | 0.1419 | 0.9566 | 0.8694 | 0.0007 | 82.51 |
| 12 | 89954104 | rs12228056 | C | T | 4 | 0.01779 | 0.142 | 1.187 | 1.2674 | 0.0105 | 73.3 |
| 2 | 98798495 | rs1568213 | A | T | 4 | 0.006052 | 0.1424 | 1.1092 | 1.1081 | 0.0433 | 63.13 |
| 1 | 88270563 | rs4265406 | A | G | 4 | 0.2904 | 0.1426 | 1.0389 | 1.1505 | 0.001 | 81.6 |
| 1 | 74175413 | rs10890093 | G | T | 4 | 0.03608 | 0.1428 | 0.9271 | 0.8665 | 0.0005 | 82.89 |
| 1 | 74175476 | rs10890094 | A | G | 4 | 0.03628 | 0.143 | 0.9272 | 0.8665 | 0.0005 | 82.91 |
| 6 | 99016428 | rs9491625 | A | G | 4 | 0.0008617 | 0.143 | 0.7262 | 0.7818 | 0.055 | 60.54 |
| 13 | 21757893 | rs9510084 | A | C | 4 | 0.01053 | 0.143 | 1.0963 | 1.0973 | 0.0626 | 58.97 |
| 6 | 30228616 | rs9468693 | C | T | 3 | 0.007737 | 0.1432 | 1.2242 | 1.2337 | 0.048 | 67.07 |
| 2 | 57617362 | rs6746753 | C | G | 3 | 8.13E-05 | 0.1434 | 1.9701 | 1.7412 | 0.0328 | 70.75 |
| 11 | 32216036 | rs1884379 | G | T | 4 | 0.001575 | 0.1436 | 0.8885 | 0.9081 | 0.0608 | 59.33 |
| 4 | 95484845 | rs7438414 | C | T | 4 | 0.00685 | 0.1438 | 0.907 | 0.8976 | 0.0188 | 69.91 |
| 3 | 63499833 | rs1505599 | A | C | 4 | 0.0002113 | 0.1439 | 1.1753 | 1.1272 | 0.0396 | 63.99 |
| 4 | 34724145 | rs968774 | A | G | 4 | 0.0123 | 0.1439 | 1.4149 | 1.3419 | 0.1589 | 42.12 |
| 11 | 10783496 | rs7932171 | C | T | 4 | 0.002801 | 0.144 | 1.2225 | 1.1978 | 0.0489 | 61.85 |
| 11 | 32218732 | rs10835876 | A | T | 4 | 0.001383 | 0.1443 | 0.8873 | 0.9074 | 0.0573 | 60.06 |
| 11 | 117191666 | rs4597100 | A | C | 4 | 0.1059 | 0.1445 | 0.9427 | 0.8954 | 0.0203 | 69.41 |
| 1 | 88272291 | rs12133500 | C | G | 4 | 0.3002 | 0.1446 | 0.9633 | 0.8695 | 0.001 | 81.67 |
| 4 | 95481688 | rs11727030 | A | G | 4 | 0.007153 | 0.1448 | 1.1019 | 1.1138 | 0.019 | 69.86 |
| 1 | 74208096 | rs11210383 | A | C | 4 | 0.03813 | 0.1449 | 1.0778 | 1.1541 | 0.0005 | 82.99 |
| 1 | 212356402 | rs1660380 | A | G | 4 | 0.00202 | 0.1451 | 0.7374 | 0.7932 | 0.1238 | 47.93 |
| 5 | 158812974 | rs4921230 | C | T | 4 | 0.155 | 0.1451 | 1.0605 | 1.1429 | 0.0115 | 72.85 |
| 3 | 15120491 | rs13318013 | A | G | 4 | 0.04363 | 0.1456 | 1.1743 | 1.279 | 0.0098 | 73.67 |
| 3 | 63485004 | rs6775133 | A | G | 4 | 9.44E-05 | 0.1456 | 1.1889 | 1.1424 | 0.0184 | 70.05 |
| 6 | 99007342 | rs9482736 | C | T | 4 | 0.001074 | 0.1456 | 1.373 | 1.2706 | 0.0665 | 58.2 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 18 | 41955585 | rs12607480 | A | G | 4 | 0.01575 | 0.1457 | 0.8813 | 0.8512 | 0.0182 | 70.11 |
| 3 | 63485884 | rs17068905 | C | T | 4 | 8.89E-05 | 0.1459 | 1.1897 | 1.1418 | 0.0189 | 69.89 |
| 18 | 41948674 | rs8083916 | A | C | 4 | 0.0161 | 0.1459 | 0.8817 | 0.8534 | 0.0208 | 69.25 |
| 3 | 15097982 | rs13326820 | A | G | 4 | 0.04939 | 0.146 | 0.857 | 0.7804 | 0.0081 | 74.6 |
| 21 | 40087119 | rs16998519 | G | T | 4 | 0.01203 | 0.146 | 1.1705 | 1.206 | 0.0187 | 69.97 |
| 1 | 88273491 | rs12567534 | A | G | 4 | 0.3086 | 0.1462 | 1.0375 | 1.1499 | 0.0009 | 81.8 |
| 3 | 15125801 | rs9867224 | A | G | 4 | 0.04392 | 0.1462 | 0.8517 | 0.7835 | 0.0105 | 73.3 |
| 3 | 63488445 | rs6770081 | A | G | 4 | 8.90E-05 | 0.1462 | 1.1896 | 1.1413 | 0.0194 | 69.7 |
| 3 | 63488625 | rs11921529 | A | G | 4 | 8.61E-05 | 0.1462 | 0.8403 | 0.8761 | 0.0192 | 69.78 |
| 3 | 63489025 | rs9848074 | C | G | 4 | 8.67E-05 | 0.1463 | 1.19 | 1.1414 | 0.0193 | 69.76 |
| 3 | 63489216 | rs7641936 | C | T | 4 | 8.67E-05 | 0.1463 | 1.19 | 1.1414 | 0.0193 | 69.76 |
| 10 | 22887793 | rs7097972 | C | T | 4 | 0.002212 | 0.1466 | 0.8948 | 0.9209 | 0.1194 | 48.67 |
| 11 | 32219434 | rs1115704 | C | T | 4 | 0.001415 | 0.1466 | 1.1268 | 1.1017 | 0.0562 | 60.28 |
| 15 | 36725830 | rs3923022 | A | G | 3 | 0.006271 | 0.1468 | 1.1051 | 1.0948 | 0.086 | 59.23 |
| 6 | 99015010 | rs12213284 | G | T | 4 | 0.0009078 | 0.1469 | 0.725 | 0.7829 | 0.0563 | 60.26 |
| 3 | 63495515 | rs985367 | G | T | 4 | 0.0002403 | 0.147 | 1.1736 | 1.126 | 0.04 | 63.9 |
| 2 | 38224980 | rs10188379 | C | G | 4 | 0.003951 | 0.1471 | 1.1302 | 1.1093 | 0.0826 | 55.13 |
| 4 | 95479708 | rs724260 | A | G | 4 | 0.007604 | 0.1473 | 1.1011 | 1.1131 | 0.0188 | 69.91 |
| 3 | 124823568 | rs820455 | A | G | 4 | 0.003726 | 0.1479 | 0.8028 | 0.8106 | 0.027 | 67.31 |
| 3 | 63487061 | rs7617487 | G | T | 4 | 8.67E-05 | 0.1481 | 0.8404 | 0.8762 | 0.0185 | 70.01 |
| 6 | 116106532 | rs9320545 | C | T | 4 | 0.01101 | 0.1482 | 0.8973 | 0.8831 | 0.0204 | 69.36 |
| 10 | 22886741 | rs4748813 | C | T | 4 | 0.002462 | 0.1482 | 1.1139 | 1.0839 | 0.1202 | 48.54 |
| 4 | 34724210 | rs968773 | A | C | 4 | 0.01311 | 0.1483 | 1.3997 | 1.3365 | 0.1498 | 43.62 |
| 11 | 123073614 | rs12419599 | G | T | 4 | 0.06993 | 0.1484 | 0.8659 | 0.8055 | 0.0305 | 66.33 |
| 3 | 63494767 | rs1394901 | C | T | 4 | 0.0002577 | 0.1491 | 0.8527 | 0.8887 | 0.04 | 63.89 |
| 3 | 63495077 | rs4392412 | G | T | 4 | 0.0002577 | 0.1491 | 0.8527 | 0.8887 | 0.04 | 63.89 |
| 1 | 205553098 | rs11120691 | G | T | 4 | 0.1839 | 0.1492 | 1.0479 | 1.1316 | 0.0028 | 78.64 |
| 3 | 63494733 | rs1394902 | C | T | 4 | 0.0002616 | 0.1492 | 1.1725 | 1.1251 | 0.0402 | 63.85 |
| 3 | 63495157 | rs985370 | A | G | 4 | 0.0002616 | 0.1492 | 1.1725 | 1.1251 | 0.0402 | 63.85 |
| 3 | 63495430 | rs985368 | C | T | 4 | 0.0002616 | 0.1492 | 1.1725 | 1.1251 | 0.0402 | 63.85 |
| 1 | 74143228 | rs4650235 | A | G | 4 | 0.03612 | 0.1493 | 1.0799 | 1.1253 | 0.0077 | 74.78 |
| 9 | 70346769 | rs10746875 | A | T | 4 | 0.01036 | 0.1498 | 0.8779 | 0.8902 | 0.111 | 50.1 |
| 1 | 4560412 | rs589176 | A | G | 4 | 0.01065 | 0.15 | 0.9106 | 0.9125 | 0.0667 | 58.15 |
| 6 | 102373779 | rs9498719 | C | T | 4 | 0.08047 | 0.15 | 0.8909 | 0.7992 | 0.0029 | 78.57 |
| 2 | 57629006 | rs9309299 | C | G | 3 | 0.0001039 | 0.1501 | 1.9234 | 1.7106 | 0.032 | 70.95 |
| 4 | 136712040 | rs11946618 | C | G | 4 | 0.01629 | 0.1503 | 1.1063 | 1.1007 | 0.106 | 50.97 |
| 1 | 212358567 | rs12568811 | A | G | 4 | 0.00245 | 0.1504 | 0.7297 | 0.7873 | 0.1236 | 47.97 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 7 | 12646159 | rs849766 | G | T | 4 | 0.1212 | 0.1504 | 1.0882 | 1.1755 | 0.0155 | 71.12 |
| 6 | 102368610 | rs12333317 | A | G | 4 | 0.07549 | 0.1505 | 1.1259 | 1.2558 | 0.0025 | 79.09 |
| 1 | 199828298 | rs625436 | A | G | 4 | 0.1111 | 0.1509 | 0.8913 | 0.7599 | 0.0005 | 83.14 |
| 2 | 236072455 | rs2316431 | C | T | 4 | 0.04664 | 0.151 | 0.9096 | 0.8492 | 0.0026 | 78.9 |
| 1 | 61295468 | rs12565220 | C | T | 4 | 0.01475 | 0.1516 | 0.8649 | 0.8497 | 0.0333 | 65.6 |
| 1 | 225256592 | rs12409428 | C | T | 4 | 0.03663 | 0.1516 | 1.0744 | 1.116 | 0.0093 | 73.92 |
| 13 | 21757961 | rs9510085 | G | T | 4 | 0.01159 | 0.1517 | 0.9132 | 0.9135 | 0.0651 | 58.46 |
| 1 | 225249982 | rs10495273 | G | T | 4 | 0.0374 | 0.1518 | 1.0741 | 1.116 | 0.0092 | 73.96 |
| 6 | 99020505 | rs9401880 | C | G | 4 | 0.0009572 | 0.1518 | 1.3744 | 1.2755 | 0.0525 | 61.06 |
| 6 | 99021401 | rs9491633 | A | C | 4 | 0.00101 | 0.1519 | 0.7279 | 0.7837 | 0.0528 | 61 |
| 6 | 99021767 | rs1908399 | A | G | 4 | 0.0009912 | 0.1523 | 1.3745 | 1.2762 | 0.0522 | 61.14 |
| 1 | 225244354 | rs1186 | A | T | 4 | 0.03739 | 0.1528 | 0.931 | 0.8958 | 0.0087 | 74.23 |
| 1 | 225254994 | rs7541033 | A | C | 4 | 0.03771 | 0.1529 | 1.074 | 1.116 | 0.009 | 74.09 |
| 6 | 99021290 | rs9491632 | A | T | 4 | 0.001067 | 0.1529 | 0.7291 | 0.7846 | 0.0533 | 60.9 |
| 16 | 47661065 | rs7205094 | G | T | 4 | 0.008578 | 0.1529 | 0.9074 | 0.9081 | 0.0726 | 57 |
| 3 | 101331030 | rs17315194 | G | T | 4 | 0.09536 | 0.1531 | 1.092 | 1.1744 | 0.0117 | 72.73 |
| 1 | 225256856 | rs6684821 | A | G | 4 | 0.03764 | 0.1534 | 1.074 | 1.1157 | 0.009 | 74.05 |
| 2 | 57629283 | rs10166539 | A | G | 3 | 0.0001145 | 0.1534 | 1.9158 | 1.7055 | 0.0315 | 71.09 |
| 1 | 225268494 | rs17600669 | A | G | 4 | 0.03325 | 0.1535 | 0.9294 | 0.9007 | 0.0147 | 71.44 |
| 21 | 40092123 | rs16998550 | C | T | 4 | 0.01519 | 0.1535 | 1.1644 | 1.2009 | 0.0194 | 69.71 |
| 3 | 63483291 | rs13067087 | A | T | 4 | 9.86E-05 | 0.1537 | 1.19 | 1.143 | 0.016 | 70.93 |
| 6 | 99020082 | rs9388491 | A | C | 4 | 0.0009789 | 0.1538 | 1.3735 | 1.2744 | 0.0519 | 61.19 |
| 6 | 99021203 | rs9482746 | C | T | 4 | 0.0009758 | 0.154 | 0.728 | 0.7847 | 0.0518 | 61.22 |
| 6 | 99021192 | rs9491631 | C | T | 4 | 0.0009707 | 0.1541 | 1.3739 | 1.2745 | 0.0516 | 61.26 |
| 2 | 57629406 | rs9309301 | A | G | 3 | 0.0001174 | 0.1542 | 1.9138 | 1.7042 | 0.0313 | 71.13 |
| 1 | 225249748 | rs1343743 | C | T | 4 | 0.03879 | 0.1548 | 0.9315 | 0.8964 | 0.0088 | 74.19 |
| 1 | 225250697 | rs10916075 | A | G | 4 | 0.03895 | 0.1549 | 1.0735 | 1.1155 | 0.0089 | 74.15 |
| 1 | 212358976 | rs1795035 | C | T | 4 | 0.002614 | 0.1553 | 0.7297 | 0.7874 | 0.1234 | 48 |
| 7 | 12644156 | rs849764 | C | G | 4 | 0.1326 | 0.1553 | 0.921 | 0.8513 | 0.0145 | 71.54 |
| 1 | 225245585 | rs1045287 | C | T | 4 | 0.03948 | 0.1554 | 1.0733 | 1.1155 | 0.0087 | 74.22 |
| 3 | 63505317 | rs1505595 | C | T | 4 | 0.0002693 | 0.1554 | 1.1787 | 1.1304 | 0.034 | 65.4 |
| 5 | 85551089 | rs11959230 | C | T | 3 | 0.004479 | 0.1554 | 0.5665 | 0.5526 | 0.0344 | 70.33 |
| 16 | 24384824 | rs2560922 | G | T | 4 | 0.05849 | 0.1554 | 0.9304 | 0.8973 | 0.0223 | 68.74 |
| 3 | 63482702 | rs2202492 | C | T | 4 | 0.0001117 | 0.1556 | 0.8405 | 0.8747 | 0.0161 | 70.92 |
| 1 | 212359212 | rs1795034 | C | T | 4 | 0.002693 | 0.1557 | 1.3691 | 1.2693 | 0.1242 | 47.86 |
| 1 | 225245677 | rs1045285 | A | G | 3 | 0.03581 | 0.1558 | 1.0775 | 1.1413 | 0.0033 | 82.46 |
| 3 | 63482584 | rs2221476 | A | G | 4 | 0.0001077 | 0.1558 | 1.1904 | 1.144 | 0.0156 | 71.09 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 14 | 37930129 | rs1184875 | A | C | 4 | 0.09031 | 0.156 | 0.9419 | 0.9056 | 0.0295 | 66.6 |
| 20 | 8459004 | rs2143205 | C | T | 3 | 0.02025 | 0.1561 | 1.1168 | 1.202 | 0.008 | 79.31 |
| 1 | 225254519 | rs11587443 | C | T | 4 | 0.03983 | 0.1562 | 1.0732 | 1.1151 | 0.0089 | 74.16 |
| 2 | 57630160 | rs10496069 | A | T | 3 | 0.0001274 | 0.1565 | 0.5243 | 0.5883 | 0.0311 | 71.18 |
| 11 | 123073674 | rs4406833 | A | T | 4 | 0.07714 | 0.1566 | 0.8686 | 0.8054 | 0.0261 | 67.58 |
| 1 | 74134374 | rs10890086 | A | C | 4 | 0.0459 | 0.1567 | 0.931 | 0.8934 | 0.0083 | 74.44 |
| 1 | 225244750 | rs3768425 | A | G | 3 | 0.0358 | 0.1567 | 0.9281 | 0.8759 | 0.0031 | 82.65 |
| 3 | 124820628 | rs820459 | A | G | 4 | 0.004215 | 0.1569 | 0.8056 | 0.8121 | 0.0238 | 68.29 |
| 1 | 225245323 | rs1045290 | A | G | 3 | 0.03616 | 0.1571 | 0.9282 | 0.8763 | 0.0033 | 82.53 |
| 1 | 225245336 | rs1045289 | C | T | 3 | 0.03616 | 0.1571 | 0.9282 | 0.8763 | 0.0033 | 82.53 |
| 4 | 136730007 | rs2086327 | A | C | 4 | 0.003334 | 0.1574 | 0.9026 | 0.9181 | 0.0712 | 57.28 |
| 8 | 10767033 | rs2409667 | A | G | 4 | 0.09322 | 0.158 | 1.0821 | 1.1673 | 0.0069 | 75.3 |
| 4 | 95498237 | rs6839224 | G | T | 4 | 0.01489 | 0.1582 | 0.916 | 0.9 | 0.0168 | 70.63 |
| 18 | 41961878 | rs4243278 | A | G | 4 | 0.01953 | 0.1584 | 1.1307 | 1.1717 | 0.0167 | 70.68 |
| 1 | 225270854 | rs17600725 | A | G | 4 | 0.03634 | 0.1586 | 0.9306 | 0.901 | 0.0135 | 71.95 |
| 1 | 225248546 | rs3795451 | C | T | 3 | 0.0372 | 0.1589 | 0.9286 | 0.8766 | 0.0032 | 82.62 |
| 1 | 225262834 | rs11588904 | C | T | 4 | 0.0403 | 0.1592 | 1.073 | 1.1147 | 0.0085 | 74.35 |
| 21 | 40087288 | rs16998521 | A | G | 4 | 0.01577 | 0.1594 | 1.1627 | 1.2001 | 0.0171 | 70.53 |
| 1 | 225248461 | rs3795449 | G | T | 3 | 0.03789 | 0.1595 | 1.0766 | 1.1407 | 0.0031 | 82.65 |
| 3 | 15118432 | rs9839836 | G | T | 4 | 0.05938 | 0.1595 | 1.1615 | 1.2706 | 0.0088 | 74.16 |
| 3 | 124819672 | rs848145 | A | G | 4 | 0.00426 | 0.1597 | 1.2417 | 1.2304 | 0.0236 | 68.35 |
| 3 | 63493103 | rs11130939 | G | T | 4 | 0.0001427 | 0.1598 | 1.1889 | 1.1367 | 0.0231 | 68.48 |
| 4 | 95497524 | rs1593554 | C | T | 4 | 0.01481 | 0.1598 | 1.0917 | 1.111 | 0.0165 | 70.76 |
| 16 | 6606821 | rs7199694 | A | G | 4 | 0.004618 | 0.1598 | 0.9047 | 0.9048 | 0.0242 | 68.16 |
| 18 | 26046673 | rs2960028 | A | T | 4 | 0.07612 | 0.16 | 1.0641 | 1.1013 | 0.031 | 66.19 |
| 1 | 225248177 | rs1062908 | C | G | 3 | 0.03858 | 0.1601 | 0.9291 | 0.8769 | 0.0032 | 82.6 |
| 6 | 99010182 | rs12208539 | G | T | 4 | 0.001274 | 0.1601 | 1.3657 | 1.2642 | 0.0605 | 59.39 |
| 3 | 15090482 | rs9830744 | C | T | 4 | 0.06212 | 0.1602 | 0.8629 | 0.7919 | 0.0114 | 72.9 |
| 6 | 116121301 | rs9374564 | C | T | 4 | 0.01964 | 0.1602 | 0.9044 | 0.8899 | 0.0285 | 66.9 |
| 7 | 22565267 | rs9655226 | C | T | 4 | 0.06 | 0.1603 | 0.9339 | 0.9062 | 0.0345 | 65.28 |
| 4 | 95489901 | rs2865353 | C | T | 4 | 0.007475 | 0.1605 | 0.9074 | 0.8992 | 0.0159 | 71 |
| 3 | 15003482 | rs17040623 | A | G | 4 | 0.07313 | 0.1606 | 0.8671 | 0.7895 | 0.0105 | 73.29 |
| 1 | 225248178 | rs1045252 | A | G | 3 | 0.03826 | 0.1607 | 0.929 | 0.8768 | 0.0031 | 82.71 |
| 1 | 225259202 | rs2297418 | A | C | 3 | 0.03826 | 0.1607 | 0.929 | 0.8768 | 0.0031 | 82.71 |
| 10 | 30254709 | rs1246758 | A | C | 4 | 0.2028 | 0.1608 | 0.9484 | 0.8738 | 0.0072 | 75.14 |
| 3 | 63482284 | rs7614676 | A | G | 4 | 0.0001355 | 0.1609 | 1.1912 | 1.1454 | 0.0147 | 71.47 |
| 11 | 123073531 | rs4430519 | G | T | 4 | 0.09518 | 0.1609 | 0.8769 | 0.813 | 0.0319 | 65.96 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 18 | 48306727 | rs1349930 | C | G | 4 | 0.01083 | 0.161 | 1.1351 | 1.1378 | 0.048 | 62.06 |
| 1 | 199813623 | rs633696 | C | T | 4 | 0.1654 | 0.1616 | 1.1085 | 1.2911 | 0.0017 | 80.17 |
| 1 | 199829227 | rs685982 | A | T | 4 | 0.38 | 0.1616 | 1.0354 | 1.1811 | 0.0001 | 86.26 |
| 4 | 154168497 | rs1111986 | A | G | 4 | 0.009855 | 0.1618 | 1.0999 | 1.1085 | 0.0261 | 67.57 |
| 6 | 99009252 | rs12200527 | A | T | 4 | 0.001437 | 0.1621 | 1.3612 | 1.261 | 0.0629 | 58.91 |
| 13 | 21758087 | rs9550833 | A | C | 4 | 0.01333 | 0.1621 | 0.9148 | 0.9148 | 0.0616 | 59.17 |
| 1 | 212356924 | rs1660377 | A | T | 4 | 0.002373 | 0.1622 | 1.3577 | 1.2544 | 0.1229 | 48.08 |
| 9 | 70347279 | rs7860486 | A | C | 4 | 0.01175 | 0.1623 | 0.8799 | 0.8925 | 0.1072 | 50.76 |
| 3 | 15104541 | rs17040729 | G | T | 4 | 0.06618 | 0.1627 | 1.1557 | 1.2733 | 0.007 | 75.23 |
| 1 | 225262499 | rs6426559 | C | T | 4 | 0.04251 | 0.163 | 1.0722 | 1.1142 | 0.0081 | 74.6 |
| 13 | 21759295 | rs9506821 | A | G | 4 | 0.009367 | 0.163 | 0.9095 | 0.9093 | 0.0419 | 63.46 |
| 6 | 25253691 | rs9379723 | C | T | 4 | 0.01495 | 0.1632 | 1.1189 | 1.1036 | 0.1336 | 46.3 |
| 1 | 225238913 | rs12593 | C | T | 4 | 0.03722 | 0.1633 | 0.9309 | 0.8956 | 0.0066 | 75.5 |
| 11 | 10776960 | rs4909953 | A | C | 4 | 0.003709 | 0.1635 | 0.8245 | 0.8385 | 0.0393 | 64.08 |
| 2 | 57636788 | rs13412537 | C | G | 3 | 0.0001735 | 0.1638 | 0.5305 | 0.5931 | 0.0314 | 71.11 |
| 3 | 15088046 | rs3773478 | C | T | 4 | 0.07169 | 0.164 | 0.8672 | 0.7888 | 0.0087 | 74.23 |
| 3 | 15034334 | rs11128731 | C | T | 4 | 0.08026 | 0.1641 | 1.1486 | 1.2552 | 0.0137 | 71.84 |
| 17 | 45487642 | rs4794094 | C | T | 4 | 0.1587 | 0.1641 | 1.0781 | 1.1723 | 0.01 | 73.55 |
| 11 | 123076941 | rs1275055 | A | T | 4 | 0.0804 | 0.1642 | 0.8691 | 0.8085 | 0.0284 | 66.92 |
| 12 | 2805760 | rs2334868 | A | G | 4 | 0.005535 | 0.1642 | 0.7805 | 0.8222 | 0.1322 | 46.52 |
| 1 | 74169484 | rs2733262 | C | T | 4 | 0.05395 | 0.1645 | 0.9333 | 0.8957 | 0.0088 | 74.17 |
| 1 | 199826786 | rs608356 | A | G | 4 | 0.3863 | 0.1646 | 0.9663 | 0.8484 | 0.0001 | 86.16 |
| 4 | 136730586 | rs2035293 | A | G | 4 | 0.003358 | 0.1648 | 0.9027 | 0.9185 | 0.0652 | 58.45 |
| 11 | 120728846 | rs17125182 | A | G | 4 | 0.01866 | 0.1648 | 0.7755 | 0.7539 | 0.0347 | 65.21 |
| 1 | 116595268 | rs11583110 | A | C | 4 | 0.01155 | 0.1649 | 1.0991 | 1.0907 | 0.0845 | 54.78 |
| 18 | 48292120 | rs1031062 | G | T | 4 | 0.01114 | 0.1655 | 0.882 | 0.8771 | 0.0389 | 64.16 |
| 6 | 99023189 | rs9482747 | C | T | 4 | 0.001242 | 0.1657 | 1.3662 | 1.27 | 0.048 | 62.04 |
| 1 | 74212970 | rs6424568 | A | G | 4 | 0.05823 | 0.1658 | 0.9333 | 0.8883 | 0.0044 | 77.12 |
| 6 | 99028026 | rs9482751 | C | T | 4 | 0.001135 | 0.1659 | 1.3697 | 1.2718 | 0.0462 | 62.45 |
| 3 | 15094808 | rs2306855 | C | T | 4 | 0.07291 | 0.1661 | 1.1525 | 1.2684 | 0.0081 | 74.61 |
| 7 | 146317484 | rs1524344 | C | G | 4 | 0.003631 | 0.1664 | 1.1946 | 1.1439 | 0.1119 | 49.95 |
| 18 | 10667979 | rs600419 | C | T | 3 | 0.08501 | 0.1664 | 0.9225 | 0.7997 | 0.0005 | 86.93 |
| 6 | 99023244 | rs9885878 | A | C | 4 | 0.001216 | 0.1666 | 0.7314 | 0.7873 | 0.0474 | 62.18 |
| 6 | 99024090 | rs9491637 | A | G | 4 | 0.001208 | 0.1667 | 1.3674 | 1.2704 | 0.0472 | 62.23 |
| 6 | 99025985 | rs9491640 | A | C | 4 | 0.001178 | 0.1668 | 0.7308 | 0.7868 | 0.0466 | 62.37 |
| 4 | 95492168 | rs4282187 | C | T | 4 | 0.008066 | 0.1669 | 0.9082 | 0.9002 | 0.0151 | 71.29 |
| 9 | 120842902 | rs11794075 | A | G | 4 | 0.0859 | 0.167 | 0.9024 | 0.8217 | 0.0028 | 78.68 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 4 | 95497016 | rs10020236 | A | G | 4 | 0.01894 | 0.1673 | 1.0905 | 1.1111 | 0.0168 | 70.66 |
| 11 | 79787547 | rs10792479 | C | T | 4 | 0.1748 | 0.1676 | 1.057 | 1.14 | 0.0049 | 76.69 |
| 13 | 21758866 | rs4770264 | A | G | 4 | 0.01387 | 0.1677 | 1.0932 | 1.0943 | 0.0535 | 60.85 |
| 11 | 80981521 | rs7933268 | G | T | 4 | 0.2326 | 0.168 | 0.9592 | 0.8828 | 0.0012 | 81.19 |
| 1 | 225267653 | rs6704144 | C | G | 4 | 0.04201 | 0.1681 | 1.0724 | 1.1133 | 0.0077 | 74.81 |
| 3 | 15109324 | rs17040733 | C | G | 4 | 0.06734 | 0.1681 | 0.8645 | 0.7831 | 0.0057 | 76.08 |
| 1 | 88292306 | rs12568661 | A | G | 4 | 0.4292 | 0.1682 | 0.971 | 0.8707 | 0.0008 | 82.22 |
| 4 | 95494865 | rs6840479 | A | G | 4 | 0.009087 | 0.1682 | 1.0995 | 1.1099 | 0.0161 | 70.92 |
| 18 | 10666564 | rs510529 | T | C | 3 | 0.08945 | 0.1683 | 0.9235 | 0.8003 | 0.0005 | 86.92 |
| 1 | 199818411 | rs677390 | A | G | 4 | 0.4011 | 0.1685 | 0.9674 | 0.8493 | 0.0001 | 86.33 |
| 1 | 88297128 | rs4656008 | G | T | 4 | 0.4576 | 0.1687 | 1.028 | 1.1524 | 0.0005 | 83.09 |
| 1 | 88301956 | rs10754315 | C | T | 4 | 0.4511 | 0.1687 | 0.9718 | 0.8621 | 0.0003 | 84.08 |
| 2 | 106764565 | rs728241 | A | G | 4 | 0.0009952 | 0.1689 | 0.8768 | 0.905 | 0.049 | 61.82 |
| 6 | 99028948 | rs9482752 | A | C | 4 | 0.001165 | 0.1689 | 0.7306 | 0.787 | 0.0453 | 62.67 |
| 11 | 80981836 | rs7950006 | A | G | 4 | 0.2342 | 0.1689 | 0.9594 | 0.8832 | 0.0012 | 81.15 |
| 9 | 70346371 | rs10869020 | A | G | 4 | 0.01193 | 0.169 | 1.1362 | 1.1195 | 0.1025 | 51.57 |
| 10 | 30256403 | rs2776630 | C | T | 4 | 0.1984 | 0.1691 | 0.9483 | 0.8803 | 0.0101 | 73.53 |
| 2 | 209684516 | rs1439724 | A | G | 4 | 0.002308 | 0.1695 | 1.1631 | 1.1299 | 0.0569 | 60.14 |
| 3 | 15093737 | rs746665 | A | T | 4 | 0.07712 | 0.1695 | 0.8695 | 0.7896 | 0.0079 | 74.7 |
| 2 | 106764687 | rs728239 | C | T | 4 | 0.001247 | 0.1699 | 0.8782 | 0.9054 | 0.0513 | 61.32 |
| 2 | 106764888 | rs728240 | G | T | 4 | 0.001148 | 0.1701 | 1.1398 | 1.1052 | 0.0496 | 61.69 |
| 3 | 14995353 | rs10510434 | A | G | 4 | 0.08555 | 0.1703 | 0.8731 | 0.7942 | 0.01 | 73.57 |
| 1 | 74186512 | rs2789706 | C | T | 4 | 0.05726 | 0.1704 | 0.9342 | 0.8938 | 0.006 | 75.88 |
| 2 | 30855634 | rs6754923 | C | G | 4 | 0.002351 | 0.1705 | 1.113 | 1.084 | 0.0852 | 54.66 |
| 1 | 110908053 | rs6537671 | C | T | 4 | 0.01288 | 0.1707 | 1.1027 | 1.1137 | 0.0238 | 68.28 |
| 3 | 15094724 | rs2306854 | A | C | 4 | 0.07931 | 0.171 | 0.8707 | 0.7903 | 0.0078 | 74.78 |
| 4 | 154491352 | rs6821156 | A | T | 4 | 0.2967 | 0.171 | 0.9631 | 0.876 | 0.0007 | 82.45 |
| 17 | 24561368 | rs7213514 | C | T | 4 | 0.2558 | 0.1712 | 0.9606 | 0.885 | 0.0019 | 79.83 |
| 1 | 225267729 | rs6665290 | C | T | 4 | 0.03359 | 0.1713 | 0.9279 | 0.8967 | 0.0076 | 74.87 |
| 2 | 128352457 | rs7566163 | A | G | 4 | 0.003727 | 0.1717 | 1.1068 | 1.0971 | 0.0324 | 65.83 |
| 2 | 128353695 | rs2405635 | A | G | 4 | 0.003673 | 0.1719 | 0.9034 | 0.9114 | 0.032 | 65.93 |
| 1 | 199817630 | rs585041 | A | T | 4 | 0.4373 | 0.1723 | 1.031 | 1.1757 | 0.0001 | 86.45 |
| 3 | 18376571 | rs11927883 | A | G | 4 | 0.002684 | 0.1727 | 0.7612 | 0.7425 | 0.0042 | 77.29 |
| 3 | 63498351 | rs11926493 | C | T | 4 | 0.0002859 | 0.1727 | 1.1792 | 1.1296 | 0.0271 | 67.28 |
| 1 | 212355520 | rs1660383 | A | G | 4 | 0.002049 | 0.1729 | 1.3719 | 1.2655 | 0.0959 | 52.73 |
| 10 | 30256668 | rs1270449 | C | T | 4 | 0.2194 | 0.1733 | 1.052 | 1.1351 | 0.0097 | 73.73 |
| 1 | 225271954 | rs3795453 | C | T | 4 | 0.04682 | 0.1736 | 1.0707 | 1.1048 | 0.0148 | 71.4 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 12 | 13260841 | rs3191064 | A | G | 3 | 0.01324 | 0.1736 | 1.1977 | 1.2401 | 0.0235 | 73.33 |
| 7 | 84683482 | rs2159579 | G | T | 4 | 0.1668 | 0.1744 | 0.9467 | 0.8818 | 0.0049 | 76.73 |
| 1 | 225266341 | rs1929862 | A | G | 4 | 0.04528 | 0.1752 | 1.0712 | 1.1119 | 0.0073 | 75.04 |
| 18 | 37290341 | rs2703167 | A | C | 4 | 0.04223 | 0.1753 | 0.8789 | 0.7862 | 0.0005 | 83.1 |
| 4 | 136716070 | rs11935796 | A | G | 4 | 0.01629 | 0.1755 | 0.9046 | 0.9112 | 0.0891 | 53.95 |
| 11 | 79783565 | rs7482266 | C | T | 4 | 0.1886 | 0.1759 | 0.9469 | 0.8816 | 0.0072 | 75.1 |
| 6 | 99006740 | rs9491610 | A | G | 4 | 0.001839 | 0.1763 | 1.3575 | 1.257 | 0.0597 | 59.56 |
| 1 | 225264498 | rs6659424 | A | G | 4 | 0.04559 | 0.1764 | 0.9336 | 0.8994 | 0.0071 | 75.17 |
| 11 | 41020808 | rs355220 | C | T | 4 | 0.0152 | 0.1765 | 1.2759 | 1.2589 | 0.0714 | 57.23 |
| 17 | 45486459 | rs9890077 | A | G | 4 | 0.1672 | 0.1765 | 0.929 | 0.861 | 0.0137 | 71.85 |
| 11 | 79783016 | rs2448273 | A | C | 4 | 0.1831 | 0.177 | 1.0563 | 1.1362 | 0.0055 | 76.26 |
| 3 | 106404720 | rs6794974 | A | G | 4 | 0.003319 | 0.1772 | 0.8746 | 0.9026 | 0.087 | 54.34 |
| 4 | 95496334 | rs6532481 | G | T | 4 | 0.01535 | 0.1772 | 0.9164 | 0.9022 | 0.0138 | 71.84 |
| 4 | 154496631 | rs7340984 | C | G | 4 | 0.3073 | 0.1772 | 0.9649 | 0.8826 | 0.0009 | 81.8 |
| 6 | 30041240 | rs6457109 | C | T | 3 | 0.0005814 | 0.1772 | 1.3878 | 1.2709 | 0.0936 | 57.77 |
| 21 | 32310264 | rs17666683 | G | T | 4 | 0.02275 | 0.1772 | 1.1189 | 1.1107 | 0.1111 | 50.08 |
| 1 | 19518260 | rs4912069 | A | G | 4 | 0.05823 | 0.1776 | 1.0768 | 1.1147 | 0.019 | 69.84 |
| 4 | 95496437 | rs6532482 | A | G | 4 | 0.01563 | 0.1777 | 1.0909 | 1.1081 | 0.0139 | 71.78 |
| 4 | 136738151 | rs2174394 | A | G | 4 | 0.0114 | 0.1791 | 1.1503 | 1.1345 | 0.0677 | 57.95 |
| 3 | 18377595 | rs3922895 | A | T | 4 | 0.003064 | 0.1793 | 1.3087 | 1.3413 | 0.0041 | 77.42 |
| 1 | 74174906 | rs10890092 | C | T | 4 | 0.05952 | 0.1798 | 1.0698 | 1.1149 | 0.0068 | 75.35 |
| 1 | 225263572 | rs12409755 | A | T | 4 | 0.0479 | 0.1798 | 0.9343 | 0.9005 | 0.0074 | 74.98 |
| 2 | 106757512 | rs1448103 | A | G | 4 | 0.0009263 | 0.18 | 0.8796 | 0.9096 | 0.0493 | 61.76 |
| 11 | 79784289 | rs2448274 | C | G | 4 | 0.1944 | 0.18 | 0.9476 | 0.8829 | 0.0076 | 74.89 |
| 4 | 95497050 | rs9997915 | C | T | 4 | 0.0167 | 0.1801 | 1.09 | 1.1078 | 0.0136 | 71.92 |
| 14 | 31526109 | rs8017647 | C | T | 4 | 0.01395 | 0.1801 | 1.1127 | 1.1081 | 0.0593 | 59.63 |
| 1 | 88285953 | rs10923014 | C | T | 4 | 0.3806 | 0.1803 | 1.0322 | 1.1369 | 0.001 | 81.47 |
| 13 | 21758269 | rs9506819 | G | T | 4 | 0.01567 | 0.1806 | 0.9167 | 0.9164 | 0.0527 | 61.03 |
| 18 | 10664815 | rs8095590 | T | C | 3 | 0.1169 | 0.1807 | 0.9299 | 0.7996 | 0.0003 | 87.61 |
| 1 | 88284959 | rs12117077 | C | T | 4 | 0.3854 | 0.1811 | 0.9691 | 0.8797 | 0.001 | 81.51 |
| 4 | 72358121 | rs980363 | A | G | 4 | 0.1898 | 0.1813 | 0.9492 | 0.866 | 0.0005 | 83.06 |
| 1 | 74234416 | rs4556311 | A | G | 4 | 0.2661 | 0.1815 | 0.9597 | 0.8889 | 0.0039 | 77.59 |
| 11 | 81054378 | rs17142764 | C | G | 4 | 0.2055 | 0.1816 | 0.9483 | 0.879 | 0.0051 | 76.58 |
| 20 | 8456036 | rs1569604 | A | G | 4 | 0.1547 | 0.1817 | 0.9502 | 0.9033 | 0.0142 | 71.67 |
| 18 | 48349538 | rs11665228 | C | T | 4 | 0.01181 | 0.1819 | 0.8822 | 0.8733 | 0.0234 | 68.41 |
| 2 | 106759973 | rs17033251 | C | T | 4 | 0.001057 | 0.182 | 0.88 | 0.9093 | 0.0488 | 61.87 |
| 1 | 74140143 | rs11210366 | C | T | 4 | 0.1583 | 0.1821 | 0.9488 | 0.8837 | 0.0021 | 79.56 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 2 | 219061439 | rs10932782 | C | T | 3 | 0.121 | 0.1823 | 0.9435 | 0.885 | 0.008 | 79.29 |
| 10 | 30437845 | rs12220219 | C | T | 4 | 0.001128 | 0.1824 | 1.131 | 1.0882 | 0.0846 | 54.77 |
| 6 | 99005624 | rs9491608 | A | G | 4 | 0.002217 | 0.1825 | 0.7379 | 0.7954 | 0.0579 | 59.94 |
| 1 | 88276958 | rs12143926 | C | T | 4 | 0.3866 | 0.1827 | 0.9692 | 0.8808 | 0.0011 | 81.26 |
| 3 | 106423032 | rs12639365 | A | T | 4 | 0.007369 | 0.1827 | 1.1404 | 1.1118 | 0.0975 | 52.45 |
| 13 | 89501299 | rs9583775 | A | G | 4 | 0.009174 | 0.1828 | 0.8912 | 0.9105 | 0.1081 | 50.61 |
| 2 | 106761667 | rs1448105 | A | T | 4 | 0.0009782 | 0.183 | 0.8792 | 0.9091 | 0.0472 | 62.24 |
| 3 | 106400088 | rs1568420 | C | T | 4 | 0.003441 | 0.1831 | 0.8751 | 0.9034 | 0.0846 | 54.76 |
| 8 | 127597922 | rs11986722 | C | G | 4 | 0.05688 | 0.1836 | 0.9009 | 0.8529 | 0.0107 | 73.21 |
| 10 | 30338528 | rs10826749 | C | T | 4 | 0.01995 | 0.1836 | 1.0845 | 1.077 | 0.1062 | 50.94 |
| 4 | 154494114 | rs6841435 | C | T | 4 | 0.3195 | 0.1838 | 0.9649 | 0.882 | 0.0009 | 81.75 |
| 1 | 88286774 | rs4655998 | A | C | 4 | 0.4045 | 0.1839 | 1.0306 | 1.1372 | 0.0009 | 81.87 |
| 3 | 15090876 | rs9868848 | A | G | 4 | 0.09794 | 0.1841 | 0.8779 | 0.7952 | 0.0072 | 75.1 |
| 3 | 172404356 | rs16855954 | A | C | 2 | 0.004868 | 0.1841 | 0.2805 | 0.331 | 0.0763 | 68.16 |
| 2 | 57633546 | rs10153799 | G | T | 3 | 0.0003334 | 0.1842 | 1.8133 | 1.6418 | 0.0305 | 71.34 |
| 2 | 106756383 | rs6747891 | A | G | 4 | 0.0009687 | 0.1842 | 0.8801 | 0.9102 | 0.0484 | 61.97 |
| 1 | 74160464 | rs1340424 | C | G | 4 | 0.06678 | 0.1846 | 1.0679 | 1.111 | 0.0087 | 74.22 |
| 1 | 88287316 | rs4656002 | C | T | 4 | 0.4003 | 0.1846 | 1.0309 | 1.1368 | 0.0009 | 81.84 |
| 1 | 88286988 | rs4656000 | A | G | 4 | 0.4013 | 0.1847 | 0.9701 | 0.88 | 0.0009 | 81.74 |
| 21 | 40053815 | rs2837175 | C | T | 4 | 0.01752 | 0.1851 | 1.0927 | 1.0834 | 0.0971 | 52.52 |
| 1 | 225263125 | rs12403236 | C | G | 4 | 0.05092 | 0.1854 | 0.9351 | 0.9012 | 0.007 | 75.25 |
| 1 | 88287567 | rs10923015 | A | T | 4 | 0.4009 | 0.1855 | 0.9701 | 0.88 | 0.0009 | 81.79 |
| 1 | 88288082 | rs4656003 | C | T | 4 | 0.4019 | 0.1856 | 1.0308 | 1.1364 | 0.0009 | 81.82 |
| 1 | 94942350 | rs841329 | A | G | 4 | 0.08782 | 0.1856 | 1.0632 | 1.0982 | 0.0279 | 67.07 |
| 1 | 88287018 | rs4656001 | A | G | 4 | 0.407 | 0.1859 | 1.0305 | 1.1364 | 0.0009 | 81.85 |
| 6 | 99031598 | rs11154359 | A | G | 4 | 0.001465 | 0.186 | 0.7318 | 0.7906 | 0.0427 | 63.27 |
| 1 | 19517442 | rs2064378 | A | G | 4 | 0.06575 | 0.1861 | 1.0752 | 1.1143 | 0.0175 | 70.38 |
| 12 | 78733055 | rs17005986 | C | T | 3 | 0.03628 | 0.1863 | 1.4006 | 1.5639 | 0.0298 | 71.55 |
| 4 | 74585279 | rs4311283 | C | T | 3 | 0.02105 | 0.1869 | 0.7312 | 0.6339 | 0.0065 | 80.16 |
| 12 | 78691492 | rs12833727 | C | G | 3 | 0.03661 | 0.1869 | 0.7126 | 0.6385 | 0.0298 | 71.52 |
| 6 | 99032521 | rs9491644 | A | G | 4 | 0.00155 | 0.1872 | 1.3656 | 1.2649 | 0.0423 | 63.36 |
| 11 | 9123690 | rs2291840 | A | C | 4 | 0.008373 | 0.1874 | 1.1266 | 1.1102 | 0.0654 | 58.41 |
| 12 | 78710196 | rs7961195 | C | T | 3 | 0.03614 | 0.1874 | 1.4045 | 1.5685 | 0.0289 | 71.77 |
| 2 | 106755485 | rs11888992 | C | G | 4 | 0.0009812 | 0.1877 | 1.1361 | 1.0983 | 0.0469 | 62.31 |
| 3 | 18374868 | rs7621961 | A | G | 4 | 0.002462 | 0.1877 | 1.3243 | 1.3446 | 0.0039 | 77.55 |
| 6 | 41405361 | rs9471573 | A | G | 4 | 0.0006457 | 0.188 | 0.8856 | 0.9008 | 0.0086 | 74.28 |
| 4 | 166318168 | rs4132377 | C | G | 3 | 0.01012 | 0.1882 | 0.8221 | 0.8152 | 0.0302 | 71.43 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 2 | 128340581 | rs2118204 | C | T | 4 | 0.009668 | 0.1889 | 1.0967 | 1.09 | 0.0482 | 62 |
| 1 | 110906436 | rs1105101 | C | G | 4 | 0.01409 | 0.1891 | 0.9074 | 0.9002 | 0.0213 | 69.06 |
| 1 | 74176368 | rs1340447 | A | C | 4 | 0.07158 | 0.1894 | 0.938 | 0.8988 | 0.0062 | 75.75 |
| 2 | 30856523 | rs17041560 | A | G | 4 | 0.002911 | 0.1901 | 0.9005 | 0.925 | 0.0795 | 55.71 |
| 4 | 136732205 | rs1038151 | G | T | 4 | 0.004313 | 0.1905 | 1.1048 | 1.0856 | 0.0556 | 60.42 |
| 10 | 30337993 | rs1418276 | C | T | 4 | 0.02014 | 0.1905 | 1.0849 | 1.0764 | 0.1048 | 51.17 |
| 1 | 199814155 | rs617053 | A | G | 4 | 0.5144 | 0.1906 | 1.0261 | 1.1648 | 0.0001 | 85.77 |
| 2 | 30846223 | rs17010236 | G | T | 4 | 0.0002358 | 0.1906 | 1.145 | 1.0973 | 0.0335 | 65.53 |
| 21 | 40078450 | rs4337554 | A | G | 4 | 0.006698 | 0.1906 | 0.9024 | 0.914 | 0.0508 | 61.44 |
| 7 | 145214888 | rs4370447 | A | G | 4 | 0.1212 | 0.1908 | 0.9101 | 0.8553 | 0.0289 | 66.79 |
| 2 | 106755321 | rs11887836 | C | G | 4 | 0.001019 | 0.1909 | 1.1356 | 1.0978 | 0.0461 | 62.48 |
| 20 | 24094378 | rs2208014 | C | T | 3 | 0.0526 | 0.1909 | 0.7576 | 0.6479 | 0.0168 | 75.54 |
| 1 | 110905211 | rs6656346 | A | G | 4 | 0.01494 | 0.191 | 1.1002 | 1.1091 | 0.0217 | 68.95 |
| 17 | 51764470 | rs759107 | A | G | 4 | 0.0002643 | 0.191 | 1.1513 | 1.1088 | 0.0217 | 68.95 |
| 1 | 88293965 | rs12118601 | C | T | 4 | 0.4641 | 0.1921 | 1.0283 | 1.1482 | 0.0005 | 83.23 |
| 3 | 124839752 | rs820464 | C | G | 4 | 0.01391 | 0.1923 | 1.1862 | 1.2217 | 0.0086 | 74.32 |
| 2 | 106754304 | rs2377685 | G | T | 4 | 0.0009336 | 0.1924 | 0.8797 | 0.9105 | 0.0435 | 63.07 |
| 1 | 199813717 | rs1267131 | A | C | 4 | 0.4937 | 0.1926 | 0.9731 | 0.8578 | 0.0001 | 85.96 |
| 1 | 74177642 | rs2733267 | A | G | 4 | 0.07306 | 0.193 | 0.9378 | 0.8986 | 0.0059 | 75.98 |
| 1 | 160514028 | rs7511679 | C | T | 4 | 0.08094 | 0.193 | 1.1138 | 1.1951 | 0.0124 | 72.42 |
| 6 | 99032544 | rs9491645 | C | T | 4 | 0.001548 | 0.193 | 1.3671 | 1.266 | 0.0428 | 63.25 |
| 11 | 81005553 | rs1945662 | C | T | 4 | 0.2981 | 0.1932 | 0.9644 | 0.8971 | 0.0037 | 77.79 |
| 1 | 110912891 | rs7526907 | A | G | 4 | 0.0164 | 0.1933 | 0.91 | 0.9049 | 0.0286 | 66.86 |
| 4 | 154177648 | rs17029520 | C | T | 4 | 0.01195 | 0.1935 | 0.9114 | 0.9034 | 0.0154 | 71.19 |
| 4 | 154165619 | rs4696159 | C | T | 4 | 0.01617 | 0.1936 | 0.9132 | 0.9033 | 0.0178 | 70.29 |
| 1 | 160514702 | rs11800645 | G | T | 4 | 0.08226 | 0.1937 | 0.8982 | 0.8367 | 0.0121 | 72.56 |
| 7 | 84686625 | rs2732738 | A | G | 4 | 0.102 | 0.1938 | 0.9347 | 0.8923 | 0.0139 | 71.77 |
| 1 | 199815919 | rs511201 | A | G | 4 | 0.5215 | 0.1939 | 0.9752 | 0.8589 | 0.0001 | 86.18 |
| 4 | 72354319 | rs2602098 | G | T | 4 | 0.1441 | 0.194 | 1.0657 | 1.1897 | 0 | 87.04 |
| 2 | 115905074 | rs7581748 | A | T | 4 | 0.1999 | 0.1944 | 0.9261 | 0.8163 | 0.0006 | 82.75 |
| 6 | 41404359 | rs9471568 | C | T | 4 | 0.0004048 | 0.1947 | 1.1319 | 1.1119 | 0.0052 | 76.49 |
| 7 | 84686884 | rs2732737 | A | G | 4 | 0.1037 | 0.1947 | 0.935 | 0.8923 | 0.0136 | 71.93 |
| 17 | 24510385 | rs902580 | A | C | 4 | 0.2375 | 0.1947 | 1.0426 | 1.1114 | 0.006 | 75.87 |
| 17 | 51775701 | rs2110200 | G | T | 4 | 0.0002615 | 0.1948 | 1.1527 | 1.1091 | 0.0204 | 69.36 |
| 2 | 106754935 | rs11894298 | C | T | 4 | 0.001031 | 0.1954 | 0.8807 | 0.9113 | 0.0443 | 62.89 |
| 2 | 106755254 | rs11894451 | C | T | 4 | 0.001031 | 0.1954 | 0.8807 | 0.9113 | 0.0443 | 62.89 |
| 9 | 77923214 | rs2185227 | A | G | 4 | 0.00375 | 0.1954 | 1.1687 | 1.1409 | 0.039 | 64.15 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 2 | 40410780 | rs2160236 | C | G | 4 | 0.00207 | 0.1957 | 1.1206 | 1.0838 | 0.0851 | 54.68 |
| 1 | 225264308 | rs6693535 | A | G | 4 | 0.07268 | 0.196 | 1.0648 | 1.1074 | 0.0079 | 74.71 |
| 18 | 37293712 | rs4318293 | A | C | 4 | 0.1203 | 0.1962 | 1.0595 | 1.1147 | 0.0072 | 75.12 |
| 7 | 84685921 | rs2732741 | A | T | 4 | 0.101 | 0.1963 | 1.0705 | 1.1246 | 0.0101 | 73.51 |
| 6 | 41403590 | rs2395773 | C | T | 4 | 0.0004061 | 0.1966 | 1.1318 | 1.1118 | 0.005 | 76.66 |
| 6 | 41403603 | rs2395774 | A | G | 4 | 0.0004061 | 0.1966 | 1.1318 | 1.1118 | 0.005 | 76.66 |
| 4 | 154177907 | rs10012544 | A | T | 4 | 0.01164 | 0.1968 | 1.0982 | 1.1065 | 0.0156 | 71.11 |
| 16 | 6609627 | rs8062885 | C | G | 4 | 0.006605 | 0.1968 | 1.1008 | 1.107 | 0.0093 | 73.93 |
| 4 | 154191355 | rs17029545 | C | T | 4 | 0.007308 | 0.1969 | 1.1045 | 1.0997 | 0.0286 | 66.86 |
| 6 | 41403756 | rs4605877 | G | T | 4 | 0.0004128 | 0.197 | 0.8837 | 0.8996 | 0.005 | 76.64 |
| 12 | 88790264 | rs12424558 | C | G | 4 | 0.008189 | 0.1971 | 0.8459 | 0.8771 | 0.1016 | 51.72 |
| 13 | 43897258 | rs2325129 | C | T | 4 | 0.03638 | 0.1974 | 0.9277 | 0.9003 | 0.0078 | 74.77 |
| 16 | 53798452 | rs12935507 | A | T | 4 | 0.009751 | 0.1974 | 0.8762 | 0.8687 | 0.0144 | 71.57 |
| 1 | 74175716 | rs2733265 | C | G | 4 | 0.081 | 0.1976 | 0.9399 | 0.9 | 0.0058 | 76.07 |
| 4 | 154568191 | rs6535917 | A | G | 4 | 0.2577 | 0.1978 | 1.0422 | 1.1108 | 0.0087 | 74.25 |
| 4 | 92465367 | rs3762827 | A | G | 3 | 0.1813 | 0.198 | 1.0559 | 1.1573 | 0.0019 | 83.98 |
| 18 | 37374178 | rs2587632 | C | T | 4 | 0.1287 | 0.1982 | 1.0584 | 1.1 | 0.0257 | 67.7 |
| 18 | 37373309 | rs2587634 | C | T | 4 | 0.1296 | 0.1985 | 1.0582 | 1.0996 | 0.0265 | 67.47 |
| 6 | 41404430 | rs13208294 | A | G | 4 | 0.0004265 | 0.1987 | 1.1313 | 1.1113 | 0.005 | 76.66 |
| 6 | 41404488 | rs13208406 | A | C | 4 | 0.0004265 | 0.1987 | 1.1313 | 1.1113 | 0.005 | 76.66 |
| 6 | 41405993 | rs2395775 | C | G | 4 | 0.0004835 | 0.1988 | 1.1312 | 1.112 | 0.005 | 76.64 |
| 17 | 24523266 | rs6505114 | A | G | 4 | 0.2518 | 0.1989 | 1.0413 | 1.1112 | 0.0056 | 76.15 |
| 6 | 41406187 | rs10755717 | A | G | 4 | 0.0005452 | 0.199 | 1.1311 | 1.1128 | 0.005 | 76.63 |
| 18 | 37368108 | rs2612339 | A | G | 4 | 0.1285 | 0.199 | 1.0579 | 1.0994 | 0.025 | 67.89 |
| 6 | 41400115 | rs10807260 | C | T | 4 | 0.0004575 | 0.1991 | 0.8845 | 0.8993 | 0.0046 | 76.99 |
| 6 | 41400213 | rs10807261 | A | C | 4 | 0.0004575 | 0.1991 | 0.8845 | 0.8993 | 0.0046 | 76.99 |
| 7 | 84686087 | rs2534851 | G | T | 4 | 0.1054 | 0.1993 | 0.9353 | 0.8937 | 0.0143 | 71.63 |
| 11 | 81004683 | rs10897849 | A | G | 4 | 0.3174 | 0.1993 | 0.9657 | 0.8983 | 0.0036 | 77.84 |
| 21 | 40101946 | rs2410182 | A | G | 4 | 0.005898 | 0.1996 | 0.9074 | 0.923 | 0.0621 | 59.07 |
| 6 | 41402893 | rs13219519 | A | T | 4 | 0.0004458 | 0.1998 | 0.8843 | 0.8993 | 0.0045 | 77.04 |
| 6 | 41401304 | rs12198812 | C | T | 4 | 0.000461 | 0.2004 | 0.8846 | 0.8994 | 0.0045 | 77.05 |
| 6 | 41402924 | rs13203392 | C | T | 4 | 0.000442 | 0.2007 | 1.131 | 1.1119 | 0.0044 | 77.12 |
| 4 | 154181234 | rs4583737 | A | C | 3 | 0.006525 | 0.2008 | 1.1095 | 1.1227 | 0.0093 | 78.62 |
| 6 | 41402041 | rs9462699 | A | G | 4 | 0.0004556 | 0.2008 | 1.1306 | 1.1118 | 0.0044 | 77.11 |
| 18 | 37343203 | rs2587642 | C | T | 4 | 0.1273 | 0.2008 | 1.0568 | 1.114 | 0.0053 | 76.43 |
| 6 | 41399757 | rs9471557 | C | T | 4 | 0.0004697 | 0.2009 | 1.1303 | 1.1118 | 0.0044 | 77.1 |
| 6 | 41406742 | rs7771870 | A | T | 4 | 0.000532 | 0.2009 | 1.1314 | 1.1127 | 0.0048 | 76.81 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 6 | 41399986 | rs9471560 | A | G | 4 | 0.0004499 | 0.201 | 0.8844 | 0.8992 | 0.0043 | 77.21 |
| 11 | 81005829 | rs7946763 | A | C | 4 | 0.328 | 0.201 | 1.0347 | 1.1134 | 0.0034 | 78.07 |
| 6 | 41404657 | rs12525710 | C | T | 4 | 0.0004374 | 0.2013 | 1.131 | 1.1106 | 0.005 | 76.67 |
| 7 | 145228893 | rs12703745 | A | G | 4 | 0.1398 | 0.2014 | 1.0935 | 1.163 | 0.0308 | 66.26 |
| 6 | 41405925 | rs1905568 | C | T | 4 | 0.0005201 | 0.2018 | 1.1303 | 1.1113 | 0.0049 | 76.74 |
| 15 | 58790190 | rs8027032 | C | T | 3 | 0.22 | 0.2019 | 0.9287 | 0.7528 | 0.0004 | 87.17 |
| 2 | 115906362 | rs1712005 | A | G | 4 | 0.2063 | 0.2021 | 1.0789 | 1.2298 | 0.0003 | 83.88 |
| 12 | 60704889 | rs348696 | C | T | 4 | 0.1411 | 0.2021 | 0.9419 | 0.8987 | 0.0172 | 70.5 |
| 6 | 99034084 | rs9491646 | A | G | 4 | 0.00185 | 0.2027 | 0.737 | 0.7949 | 0.0382 | 64.35 |
| 2 | 115906019 | rs1717054 | C | T | 4 | 0.2144 | 0.203 | 0.9281 | 0.8146 | 0.0004 | 83.67 |
| 3 | 27906342 | rs993668 | C | G | 4 | 0.02469 | 0.2032 | 1.1471 | 1.1327 | 0.0976 | 52.44 |
| 2 | 44191376 | rs6732415 | A | G | 4 | 0.002166 | 0.2033 | 1.4306 | 1.4036 | 0.0147 | 71.44 |
| 18 | 37368855 | rs2848770 | A | G | 4 | 0.1335 | 0.2033 | 1.0576 | 1.0994 | 0.0241 | 68.17 |
| 5 | 28807655 | rs1423298 | C | T | 4 | 0.03204 | 0.2034 | 1.0966 | 1.1292 | 0.0081 | 74.56 |
| 12 | 94738331 | rs7134181 | C | T | 4 | 0.01541 | 0.2036 | 0.9097 | 0.9241 | 0.1087 | 50.5 |
| 2 | 30846381 | rs17324843 | A | G | 4 | 0.0002913 | 0.204 | 0.8751 | 0.9132 | 0.0316 | 66.03 |
| 7 | 84684755 | rs2732742 | A | G | 4 | 0.1075 | 0.204 | 0.9365 | 0.8948 | 0.0128 | 72.26 |
| 20 | 924269 | rs6056488 | A | G | 3 | 0.04088 | 0.2041 | 0.7977 | 0.7043 | 0.0135 | 76.77 |
| 3 | 63499138 | rs12054371 | C | T | 4 | 0.0005025 | 0.2042 | 1.1765 | 1.1245 | 0.028 | 67.03 |
| 16 | 6607296 | rs17664315 | G | T | 4 | 0.006629 | 0.2054 | 1.1015 | 1.1004 | 0.0149 | 71.37 |
| 11 | 81037775 | rs17142733 | A | G | 4 | 0.2665 | 0.2056 | 0.9553 | 0.8884 | 0.0061 | 75.84 |
| 7 | 84680820 | rs2732744 | C | T | 4 | 0.1061 | 0.206 | 1.0681 | 1.1161 | 0.0139 | 71.79 |
| 2 | 115891622 | rs843390 | C | G | 4 | 0.2273 | 0.2061 | 1.0752 | 1.2262 | 0.0004 | 83.7 |
| 10 | 19333212 | rs10763789 | C | G | 4 | 0.00452 | 0.2061 | 1.1444 | 1.11 | 0.064 | 58.68 |
| 2 | 115904553 | rs843394 | G | T | 4 | 0.2265 | 0.2065 | 1.0754 | 1.2259 | 0.0004 | 83.68 |
| 10 | 85961327 | rs4933978 | A | G | 4 | 0.02362 | 0.2067 | 0.9146 | 0.9122 | 0.0495 | 61.73 |
| 11 | 106690064 | rs10789607 | C | T | 3 | 0.08739 | 0.2073 | 0.7769 | 0.6077 | 0.0037 | 82.16 |
| 18 | 37292163 | rs11874148 | C | T | 4 | 0.1256 | 0.2074 | 0.9438 | 0.8984 | 0.0073 | 75.06 |
| 17 | 24442232 | rs4965417 | C | T | 4 | 0.2694 | 0.2076 | 0.9618 | 0.9079 | 0.0115 | 72.85 |
| 10 | 6933270 | rs1013250 | A | G | 4 | 0.04051 | 0.2079 | 1.2518 | 1.3041 | 0.0303 | 66.38 |
| 4 | 154185069 | rs2406144 | C | T | 4 | 0.008398 | 0.208 | 1.1023 | 1.1005 | 0.0207 | 69.28 |
| 6 | 25277765 | rs16890179 | C | T | 4 | 0.008509 | 0.2082 | 0.888 | 0.9131 | 0.1094 | 50.37 |
| 2 | 219216616 | rs3770213 | A | T | 3 | 0.1727 | 0.2083 | 1.052 | 1.1215 | 0.0078 | 79.42 |
| 5 | 25900515 | rs11949113 | G | T | 4 | 0.456 | 0.2083 | 1.0282 | 1.1319 | 0.0009 | 81.7 |
| 10 | 131545202 | rs4751138 | C | T | 4 | 0.01459 | 0.2084 | 1.1017 | 1.0838 | 0.1002 | 51.98 |
| 12 | 94722758 | rs12582105 | A | G | 4 | 0.01655 | 0.2086 | 1.0981 | 1.0817 | 0.1057 | 51.03 |
| 2 | 115974128 | rs6712054 | C | T | 4 | 0.2669 | 0.2087 | 0.9362 | 0.8332 | 0.0017 | 80.12 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 10 | 30338084 | rs1418278 | A | G | 4 | 0.0228 | 0.2087 | 0.9237 | 0.9303 | 0.091 | 53.61 |
| 16 | 53802538 | rs17291845 | A | G | 4 | 0.009472 | 0.2091 | 1.1417 | 1.1486 | 0.0126 | 72.34 |
| 17 | 24570756 | rs727999 | A | G | 4 | 0.3626 | 0.2091 | 0.9665 | 0.8937 | 0.004 | 77.49 |
| 10 | 30336364 | rs4749520 | A | G | 4 | 0.0216 | 0.2093 | 1.0839 | 1.0747 | 0.0947 | 52.95 |
| 17 | 24438034 | rs4795495 | C | G | 4 | 0.2685 | 0.2093 | 0.9617 | 0.9085 | 0.0118 | 72.68 |
| 20 | 24128615 | rs224159 | C | T | 3 | 0.06828 | 0.2093 | 0.7688 | 0.6499 | 0.0135 | 76.78 |
| 6 | 90708506 | rs210052 | C | T | 4 | 0.1053 | 0.2104 | 0.9416 | 0.9008 | 0.0091 | 74.01 |
| 16 | 70636408 | rs1424241 | A | G | 4 | 0.01418 | 0.2107 | 0.8935 | 0.9023 | 0.0605 | 59.4 |
| 17 | 24488142 | rs1388175 | A | C | 4 | 0.2685 | 0.2107 | 0.9617 | 0.9067 | 0.0093 | 73.92 |
| 2 | 37367267 | rs10181140 | G | T | 4 | 0.2576 | 0.2108 | 1.0488 | 1.1256 | 0.0085 | 74.36 |
| 5 | 25905847 | rs1366465 | C | T | 4 | 0.4694 | 0.2109 | 1.0271 | 1.1299 | 0.001 | 81.63 |
| 9 | 133647911 | rs7851410 | C | T | 4 | 0.2697 | 0.2109 | 1.042 | 1.1225 | 0.0026 | 78.89 |
| 2 | 128337564 | rs1045832 | A | G | 4 | 0.008999 | 0.2111 | 0.9111 | 0.9182 | 0.0361 | 64.86 |
| 5 | 26041000 | rs6880807 | G | T | 4 | 0.565 | 0.2113 | 1.0217 | 1.1386 | 0.0003 | 83.91 |
| 18 | 37367434 | rs2848768 | C | T | 4 | 0.1503 | 0.2113 | 0.9481 | 0.9119 | 0.0251 | 67.89 |
| 20 | 55505059 | rs2182970 | G | T | 3 | 0.01217 | 0.2114 | 0.9122 | 0.9189 | 0.0593 | 64.6 |
| 5 | 25900953 | rs11949195 | A | T | 4 | 0.4832 | 0.2115 | 0.9744 | 0.8844 | 0.0009 | 81.84 |
| 2 | 229868406 | rs1419948 | A | C | 4 | 0.01439 | 0.2121 | 0.848 | 0.8577 | 0.0523 | 61.1 |
| 5 | 25906087 | rs12658597 | C | T | 4 | 0.4755 | 0.2121 | 0.9739 | 0.8855 | 0.001 | 81.56 |
| 9 | 133647188 | rs10793897 | C | T | 4 | 0.2644 | 0.2121 | 0.9588 | 0.8916 | 0.0031 | 78.39 |
| 1 | 74229988 | rs2343194 | A | G | 4 | 0.359 | 0.2122 | 0.9667 | 0.8961 | 0.004 | 77.47 |
| 12 | 130855942 | rs12319878 | C | T | 4 | 0.02159 | 0.2123 | 0.9216 | 0.9321 | 0.1117 | 49.99 |
| 12 | 94738697 | rs12366571 | A | C | 4 | 0.009252 | 0.2127 | 0.9048 | 0.9228 | 0.0831 | 55.04 |
| 6 | 116094037 | rs9387353 | C | T | 4 | 0.02385 | 0.2129 | 0.9059 | 0.8923 | 0.0141 | 71.69 |
| 2 | 128338961 | rs13411546 | A | G | 4 | 0.01212 | 0.2131 | 1.0936 | 1.0856 | 0.0469 | 62.3 |
| 1 | 215512121 | rs6604542 | A | G | 4 | 0.08472 | 0.2133 | 0.9419 | 0.9196 | 0.0304 | 66.36 |
| 5 | 13536969 | rs3915771 | A | G | 4 | 0.01919 | 0.2133 | 0.9207 | 0.9304 | 0.0946 | 52.97 |
| 17 | 24474102 | rs882729 | C | T | 4 | 0.2808 | 0.2135 | 1.0391 | 1.1024 | 0.0096 | 73.75 |
| 1 | 225275244 | rs2104861 | C | T | 4 | 0.01766 | 0.2136 | 0.9186 | 0.8981 | 0.0038 | 77.66 |
| 17 | 24548368 | rs4965978 | C | T | 4 | 0.2843 | 0.2136 | 1.0386 | 1.1072 | 0.0058 | 76.05 |
| 3 | 124852418 | rs1254389 | A | T | 4 | 0.007698 | 0.2137 | 1.2223 | 1.2156 | 0.0125 | 72.37 |
| 7 | 84683866 | rs2732743 | C | T | 4 | 0.1117 | 0.214 | 1.0673 | 1.1157 | 0.0125 | 72.36 |
| 1 | 215512946 | rs10863316 | C | T | 4 | 0.08539 | 0.2141 | 1.0616 | 1.0872 | 0.0306 | 66.3 |
| 17 | 24474555 | rs7219630 | A | G | 4 | 0.2812 | 0.2144 | 0.9624 | 0.9074 | 0.0096 | 73.74 |
| 3 | 116985171 | rs2972491 | A | G | 4 | 0.002151 | 0.2145 | 0.8413 | 0.8887 | 0.0802 | 55.57 |
| 2 | 128341634 | rs7572242 | C | T | 4 | 0.01117 | 0.2148 | 0.9135 | 0.9188 | 0.0364 | 64.79 |
| 2 | 115890266 | rs843393 | A | G | 4 | 0.2558 | 0.2149 | 1.0706 | 1.2226 | 0.0003 | 83.86 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 1 | 215513296 | rs10863317 | A | C | 4 | 0.08667 | 0.2153 | 0.9422 | 0.9198 | 0.0302 | 66.42 |
| 11 | 113509338 | rs12278218 | C | T | 4 | 0.1063 | 0.2153 | 0.9078 | 0.8664 | 0.0281 | 67 |
| 2 | 30858988 | rs6548034 | A | G | 4 | 0.003309 | 0.2156 | 1.1099 | 1.0783 | 0.0726 | 57.01 |
| 6 | 87197144 | rs9362322 | A | T | 4 | 0.01358 | 0.2158 | 1.1201 | 1.1164 | 0.03 | 66.47 |
| 21 | 40052396 | rs4816652 | C | T | 4 | 0.02256 | 0.216 | 0.9171 | 0.9239 | 0.0778 | 56.03 |
| 6 | 40754017 | rs7759444 | A | G | 4 | 0.01052 | 0.217 | 1.1167 | 1.126 | 0.0094 | 73.86 |
| 1 | 215519038 | rs6604543 | A | G | 4 | 0.0844 | 0.2171 | 0.9418 | 0.9187 | 0.026 | 67.6 |
| 2 | 229880420 | rs1226954 | C | T | 4 | 0.02191 | 0.2174 | 0.8511 | 0.8491 | 0.0399 | 63.94 |
| 1 | 74218172 | rs10890101 | C | T | 4 | 0.3996 | 0.2177 | 0.9701 | 0.892 | 0.0013 | 80.86 |
| 17 | 24532830 | rs8080958 | A | T | 4 | 0.2937 | 0.2178 | 1.0378 | 1.1067 | 0.0053 | 76.38 |
| 2 | 113514036 | rs1900287 | A | G | 4 | 0.007337 | 0.218 | 0.9049 | 0.9196 | 0.0507 | 61.47 |
| 2 | 115885861 | rs1402446 | A | G | 4 | 0.2639 | 0.2181 | 0.9345 | 0.8181 | 0.0004 | 83.76 |
| 2 | 115885270 | rs1717040 | C | T | 4 | 0.265 | 0.2184 | 1.0699 | 1.2221 | 0.0004 | 83.76 |
| 6 | 116111190 | rs9374562 | C | T | 4 | 0.07844 | 0.2188 | 0.9333 | 0.9063 | 0.0202 | 69.42 |
| 8 | 54312587 | rs16918909 | A | G | 4 | 0.009957 | 0.2189 | 1.1683 | 1.1265 | 0.1008 | 51.86 |
| 2 | 30855725 | rs4952181 | A | T | 4 | 0.0001408 | 0.2191 | 0.8701 | 0.9132 | 0.0228 | 68.57 |
| 14 | 31527434 | rs1952969 | G | T | 4 | 0.01832 | 0.2195 | 0.9026 | 0.9065 | 0.0441 | 62.93 |
| 3 | 178788491 | rs539967 | A | C | 4 | 0.01636 | 0.2196 | 1.0927 | 1.0834 | 0.0618 | 59.14 |
| 2 | 30860228 | rs6548036 | C | G | 4 | 0.000129 | 0.2197 | 1.1571 | 1.101 | 0.0186 | 69.99 |
| 6 | 6097407 | rs3024457 | A | C | 4 | 0.01802 | 0.2197 | 1.1148 | 1.0935 | 0.1126 | 49.82 |
| 11 | 113508557 | rs10488696 | A | G | 4 | 0.1143 | 0.2199 | 1.1002 | 1.1536 | 0.0284 | 66.92 |
| 18 | 37366392 | rs2848766 | A | G | 4 | 0.1634 | 0.22 | 1.0529 | 1.0956 | 0.0233 | 68.44 |
| 18 | 37366646 | rs2848767 | C | T | 4 | 0.1634 | 0.22 | 1.0529 | 1.0956 | 0.0233 | 68.44 |
| 6 | 116092185 | rs12205135 | C | G | 4 | 0.0265 | 0.2202 | 1.1026 | 1.1196 | 0.0137 | 71.85 |
| 2 | 115959914 | rs10496495 | C | T | 4 | 0.2721 | 0.2207 | 1.0682 | 1.2128 | 0.0005 | 82.9 |
| 2 | 229871291 | rs1226973 | A | C | 4 | 0.01663 | 0.221 | 0.851 | 0.8601 | 0.0521 | 61.14 |
| 7 | 69842984 | rs7777347 | A | G | 4 | 0.1929 | 0.2211 | 0.9552 | 0.9094 | 0.0097 | 73.71 |
| 11 | 15157736 | rs10160390 | C | T | 4 | 0.1866 | 0.2212 | 1.0488 | 1.0982 | 0.0153 | 71.21 |
| 1 | 215513377 | rs10863318 | A | G | 4 | 0.09276 | 0.2213 | 0.9433 | 0.9206 | 0.0295 | 66.61 |
| 2 | 229875214 | rs17257436 | A | G | 4 | 0.01751 | 0.2219 | 0.8527 | 0.8617 | 0.0549 | 60.56 |
| 18 | 37363038 | rs2703176 | C | T | 4 | 0.1666 | 0.222 | 1.0525 | 1.0953 | 0.023 | 68.54 |
| 18 | 37364633 | rs2587615 | C | T | 4 | 0.1666 | 0.222 | 1.0525 | 1.0953 | 0.023 | 68.54 |
| 18 | 37365020 | rs2612344 | C | T | 4 | 0.1666 | 0.222 | 1.0525 | 1.0953 | 0.023 | 68.54 |
| 4 | 154187592 | rs908535 | A | G | 4 | 0.008781 | 0.2221 | 0.9076 | 0.9112 | 0.0206 | 69.3 |
| 1 | 215518894 | rs4846404 | A | G | 4 | 0.08814 | 0.2222 | 0.9425 | 0.9201 | 0.0272 | 67.26 |
| 18 | 37365054 | rs2612343 | C | T | 4 | 0.1674 | 0.2224 | 0.9502 | 0.9128 | 0.0224 | 68.7 |
| 20 | 925164 | rs6056491 | A | G | 4 | 0.05936 | 0.2224 | 0.8664 | 0.8119 | 0.0072 | 75.12 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 1 | 215514615 | rs11117833 | C | T | 4 | 0.09157 | 0.2227 | 1.0604 | 1.0872 | 0.0264 | 67.49 |
| 6 | 94799746 | rs679881 | A | G | 4 | 0.0001534 | 0.2232 | 1.1493 | 1.0914 | 0.0329 | 65.7 |
| 12 | 49895867 | rs6580809 | C | T | 4 | 0.01644 | 0.2239 | 0.9145 | 0.9189 | 0.0428 | 63.24 |
| 2 | 113506112 | rs6724667 | A | G | 4 | 0.009232 | 0.2241 | 0.9042 | 0.9158 | 0.0436 | 63.06 |
| 1 | 215514042 | rs12074981 | C | T | 4 | 0.09334 | 0.2242 | 0.9434 | 0.9209 | 0.029 | 66.76 |
| 1 | 215517984 | rs6666935 | C | T | 4 | 0.09016 | 0.2242 | 0.9429 | 0.9204 | 0.027 | 67.33 |
| 6 | 94778822 | rs4707818 | C | G | 4 | 0.00588 | 0.2242 | 0.9072 | 0.9319 | 0.0961 | 52.69 |
| 10 | 26606462 | rs11015025 | C | T | 3 | 0.002794 | 0.2242 | 1.2034 | 1.1526 | 0.0569 | 65.1 |
| 12 | 60689368 | rs980891 | C | T | 4 | 0.1557 | 0.2244 | 0.9435 | 0.903 | 0.0176 | 70.33 |
| 12 | 65684056 | rs11176528 | C | T | 4 | 0.1304 | 0.2244 | 1.0887 | 1.16 | 0.0101 | 73.5 |
| 1 | 180321600 | rs3856106 | C | T | 4 | 0.3141 | 0.2246 | 1.0386 | 1.1241 | 0.0017 | 80.16 |
| 8 | 135194786 | rs1457473 | A | G | 4 | 0.008655 | 0.2248 | 1.0959 | 1.0821 | 0.0433 | 63.13 |
| 1 | 23097909 | rs309543 | A | G | 4 | 0.01259 | 0.225 | 1.0945 | 1.0737 | 0.1012 | 51.8 |
| 1 | 215516984 | rs7532623 | C | T | 4 | 0.09391 | 0.225 | 1.0599 | 1.0858 | 0.0287 | 66.84 |
| 2 | 115970570 | rs17362720 | A | G | 4 | 0.2922 | 0.2252 | 1.0646 | 1.1874 | 0.0026 | 78.9 |
| 2 | 30859743 | rs11675229 | C | T | 4 | 0.00362 | 0.2253 | 1.1108 | 1.0791 | 0.066 | 58.29 |
| 12 | 65692893 | rs992738 | C | T | 4 | 0.1151 | 0.2255 | 0.9152 | 0.8612 | 0.0093 | 73.89 |
| 3 | 15090727 | rs9851219 | C | T | 3 | 0.09967 | 0.2258 | 1.1457 | 1.2943 | 0.0027 | 83.07 |
| 18 | 37362872 | rs2703183 | A | T | 4 | 0.1697 | 0.2258 | 0.9504 | 0.9133 | 0.0224 | 68.73 |
| 6 | 41404395 | rs13208606 | A | G | 4 | 0.01118 | 0.2259 | 0.9145 | 0.9147 | 0.0165 | 70.77 |
| 7 | 69839751 | rs10270627 | G | T | 4 | 0.1762 | 0.2259 | 1.0488 | 1.0977 | 0.0106 | 73.28 |
| 2 | 229868477 | rs1419947 | A | G | 4 | 0.01588 | 0.2263 | 0.85 | 0.8596 | 0.047 | 62.27 |
| 2 | 229877443 | rs1226959 | A | C | 4 | 0.01819 | 0.2263 | 0.8525 | 0.86 | 0.0499 | 61.64 |
| 12 | 65682486 | rs11176527 | A | G | 4 | 0.1336 | 0.2266 | 1.0875 | 1.1543 | 0.0132 | 72.1 |
| 2 | 115894049 | rs843385 | C | T | 4 | 0.296 | 0.2269 | 1.0648 | 1.2181 | 0.0003 | 84.11 |
| 2 | 17248139 | rs12467252 | C | T | 4 | 0.2446 | 0.2271 | 0.9576 | 0.907 | 0.0129 | 72.21 |
| 1 | 215514427 | rs12059973 | C | T | 4 | 0.09673 | 0.2272 | 1.0594 | 1.0853 | 0.0289 | 66.77 |
| 16 | 64006980 | rs17439546 | C | T | 4 | 0.224 | 0.2273 | 0.9222 | 0.844 | 0.0097 | 73.71 |
| 13 | 41468201 | rs11619622 | A | G | 4 | 0.04708 | 0.2274 | 0.9324 | 0.9154 | 0.0181 | 70.18 |
| 14 | 31528650 | rs10143992 | C | G | 4 | 0.01932 | 0.2277 | 1.107 | 1.1023 | 0.0415 | 63.53 |
| 1 | 215509686 | rs4436446 | C | T | 4 | 0.09216 | 0.228 | 0.9432 | 0.9212 | 0.0282 | 66.97 |
| 21 | 40052413 | rs4816653 | C | T | 4 | 0.02308 | 0.2281 | 0.9186 | 0.9264 | 0.0755 | 56.45 |
| 16 | 64006260 | rs10500520 | A | G | 4 | 0.2274 | 0.2283 | 0.923 | 0.8442 | 0.0093 | 73.9 |
| 6 | 15948412 | rs16877105 | A | G | 4 | 0.02207 | 0.2286 | 1.1244 | 1.111 | 0.0742 | 56.71 |
| 12 | 60709833 | rs348692 | A | G | 4 | 0.1459 | 0.2287 | 1.0605 | 1.1007 | 0.025 | 67.9 |
| 18 | 44768190 | rs2635509 | A | G | 4 | 0.3941 | 0.2289 | 1.031 | 1.1252 | 0.0005 | 83.21 |
| 2 | 229868175 | rs1922458 | A | G | 4 | 0.01623 | 0.2293 | 0.8505 | 0.8602 | 0.0463 | 62.43 |

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|----|-----------|-------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 22 | 23875909 | rs875352 | C | G | 4 | 0.2818 | 0.2296 | 0.9582 | 0.9017 | 0.0123 | 72.46 |
| 2 | 30860140 | rs17010271 | C | T | 4 | 0.003626 | 0.2298 | 1.1109 | 1.0788 | 0.0641 | 58.66 |
| 6 | 80193185 | rs3846739 | A | G | 4 | 0.02927 | 0.2299 | 1.1172 | 1.1411 | 0.0116 | 72.79 |
| 14 | 31530235 | rs10483393 | C | T | 4 | 0.01867 | 0.2304 | 0.9028 | 0.9071 | 0.0397 | 63.99 |
| 9 | 133646531 | rs11243525 | A | T | 4 | 0.2843 | 0.2305 | 0.9605 | 0.8954 | 0.0031 | 78.37 |
| 11 | 41016901 | rs996263 | A | T | 4 | 0.02861 | 0.2307 | 1.2414 | 1.2273 | 0.0654 | 58.42 |
| 17 | 24573932 | rs9900880 | A | G | 4 | 0.3976 | 0.2307 | 0.9689 | 0.8994 | 0.0045 | 77.01 |
| 22 | 23876617 | rs9624730 | C | T | 4 | 0.2851 | 0.2309 | 1.0433 | 1.1086 | 0.0125 | 72.4 |
| 12 | 17411380 | rs2936206 | A | G | 4 | 0.01174 | 0.231 | 1.0918 | 1.0721 | 0.0861 | 54.5 |
| 16 | 64011536 | rs17530421 | C | T | 4 | 0.2324 | 0.231 | 0.9238 | 0.8459 | 0.01 | 73.57 |
| 20 | 19740762 | rs6136840 | C | G | 4 | 0.06276 | 0.2314 | 0.8935 | 0.8553 | 0.0094 | 73.88 |
| 2 | 113507953 | rs2862772 | C | G | 4 | 0.007018 | 0.2317 | 0.9095 | 0.9281 | 0.06 | 59.51 |
| 4 | 154482001 | rs6535914 | C | T | 4 | 0.4875 | 0.2319 | 1.027 | 1.1294 | 0.0007 | 82.4 |
| 1 | 215514934 | rs11117836 | G | T | 4 | 0.1019 | 0.2321 | 1.0584 | 1.0846 | 0.0283 | 66.94 |
| 6 | 94785340 | rs582835 | C | T | 4 | 0.0001174 | 0.2324 | 0.868 | 0.9163 | 0.0277 | 67.1 |
| 22 | 23878986 | rs9624734 | C | T | 4 | 0.2898 | 0.2324 | 1.0428 | 1.1082 | 0.0124 | 72.43 |
| 11 | 81032483 | rs1540176 | C | T | 4 | 0.2533 | 0.2328 | 0.9581 | 0.9091 | 0.0157 | 71.06 |
| 2 | 17251771 | rs13031560 | C | T | 4 | 0.2626 | 0.2333 | 1.0426 | 1.1019 | 0.012 | 72.61 |
| 2 | 17250287 | rs11898524 | C | T | 4 | 0.2629 | 0.2335 | 1.0425 | 1.1017 | 0.0122 | 72.49 |
| 21 | 40057208 | rs2837183 | C | T | 4 | 0.0233 | 0.2335 | 1.0884 | 1.0791 | 0.0717 | 57.18 |
| 22 | 23879405 | rs9624735 | A | G | 4 | 0.2929 | 0.2336 | 0.9592 | 0.9026 | 0.0124 | 72.4 |
| 2 | 30858801 | rs4597574 | C | T | 4 | 0.003313 | 0.2341 | 0.9017 | 0.9294 | 0.0658 | 58.33 |
| 12 | 45757706 | rs2269828 | A | G | 3 | 0.0001301 | 0.2342 | 0.8505 | 0.8973 | 0.0215 | 73.97 |
| 2 | 17250643 | rs11893015 | C | T | 4 | 0.2668 | 0.2347 | 0.9595 | 0.9078 | 0.012 | 72.59 |
| 1 | 173288830 | rs12409660 | C | G | 4 | 0.1366 | 0.235 | 1.0613 | 1.1324 | 0.0009 | 81.76 |
| 2 | 113514395 | rs2862776 | A | G | 4 | 0.008244 | 0.235 | 0.9062 | 0.9211 | 0.0452 | 62.69 |
| 3 | 59333230 | rs111130703 | C | T | 4 | 0.0004337 | 0.2357 | 1.1421 | 1.0918 | 0.0292 | 66.7 |
| 2 | 17263221 | rs7419572 | A | G | 4 | 0.2683 | 0.2358 | 1.042 | 1.1018 | 0.0115 | 72.82 |
| 2 | 116082577 | rs17454262 | C | T | 4 | 0.2767 | 0.2358 | 1.0723 | 1.1977 | 0.0028 | 78.69 |
| 12 | 65718923 | rs7955793 | A | G | 4 | 0.1948 | 0.2358 | 1.0681 | 1.1462 | 0.0061 | 75.81 |
| 20 | 19742718 | rs6136842 | C | G | 4 | 0.06698 | 0.2359 | 0.8951 | 0.8572 | 0.0099 | 73.63 |
| 1 | 173301266 | rs10912878 | A | T | 4 | 0.144 | 0.236 | 0.943 | 0.8832 | 0.0009 | 81.78 |
| 22 | 23885789 | rs6004454 | A | G | 4 | 0.2991 | 0.236 | 0.9597 | 0.9033 | 0.0128 | 72.25 |
| 2 | 229875567 | rs16825971 | C | T | 4 | 0.01927 | 0.2366 | 0.8548 | 0.8637 | 0.0492 | 61.78 |
| 6 | 94792276 | rs1488324 | A | G | 4 | 0.0003618 | 0.2366 | 1.1413 | 1.0863 | 0.0423 | 63.35 |
| 6 | 94789896 | rs1586510 | C | T | 4 | 0.0001415 | 0.2368 | 1.1501 | 1.0901 | 0.0285 | 66.88 |
| 6 | 90708821 | rs210051 | A | G | 4 | 0.1354 | 0.2369 | 1.0574 | 1.1094 | 0.005 | 76.6 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 8 | 19199623 | rs1514708 | C | G | 4 | 0.2221 | 0.2369 | 1.1008 | 1.2074 | 0.0181 | 70.16 |
| 6 | 94800718 | rs1463678 | A | G | 4 | 0.0001952 | 0.2371 | 1.1468 | 1.089 | 0.0317 | 66 |
| 13 | 43934565 | rs9595128 | A | G | 4 | 0.1239 | 0.2371 | 1.0565 | 1.0945 | 0.0142 | 71.64 |
| 10 | 30437462 | rs17295031 | A | G | 4 | 0.0008664 | 0.2372 | 0.8832 | 0.9243 | 0.0605 | 59.4 |
| 22 | 23875612 | rs875353 | A | G | 4 | 0.3051 | 0.2373 | 0.9602 | 0.903 | 0.012 | 72.61 |
| 2 | 17262933 | rs1519969 | A | T | 4 | 0.2732 | 0.2375 | 1.0416 | 1.1014 | 0.0115 | 72.85 |
| 22 | 23890601 | rs16979684 | A | C | 4 | 0.3056 | 0.2376 | 1.0412 | 1.1062 | 0.0126 | 72.32 |
| 2 | 17262967 | rs1519968 | A | C | 4 | 0.2733 | 0.2377 | 0.9601 | 0.908 | 0.0116 | 72.8 |
| 2 | 17263402 | rs16983357 | C | G | 4 | 0.2735 | 0.2377 | 1.0416 | 1.1015 | 0.0113 | 72.9 |
| 2 | 17263810 | rs2030358 | C | T | 4 | 0.2735 | 0.2377 | 1.0416 | 1.1015 | 0.0113 | 72.9 |
| 2 | 17263874 | rs2030357 | A | G | 4 | 0.2733 | 0.2377 | 0.9601 | 0.908 | 0.0116 | 72.8 |
| 12 | 94729110 | rs10859956 | C | T | 4 | 0.01947 | 0.2377 | 1.0955 | 1.0784 | 0.0938 | 53.11 |
| 1 | 159363865 | rs12727614 | A | T | 4 | 0.08523 | 0.2383 | 1.0691 | 1.0982 | 0.0198 | 69.58 |
| 2 | 17265222 | rs11677772 | G | T | 4 | 0.2743 | 0.2387 | 0.9601 | 0.9082 | 0.0116 | 72.8 |
| 2 | 17266477 | rs1507986 | C | T | 4 | 0.2743 | 0.2387 | 0.9601 | 0.9082 | 0.0116 | 72.8 |
| 2 | 17267063 | rs2174865 | C | G | 4 | 0.2743 | 0.2387 | 0.9601 | 0.9082 | 0.0116 | 72.8 |
| 2 | 30855109 | rs17010264 | C | G | 4 | 0.0001856 | 0.2387 | 0.8722 | 0.9158 | 0.021 | 69.18 |
| 2 | 30861183 | rs6754455 | C | T | 4 | 0.004346 | 0.2387 | 1.1111 | 1.0801 | 0.0573 | 60.06 |
| 11 | 15188429 | rs16931216 | A | G | 4 | 0.1091 | 0.2387 | 0.856 | 0.7879 | 0.0123 | 72.48 |
| 2 | 30860893 | rs2090734 | A | T | 4 | 0.003954 | 0.2389 | 1.1115 | 1.0797 | 0.0573 | 60.05 |
| 22 | 23880247 | rs6004449 | A | G | 4 | 0.3105 | 0.2389 | 1.0407 | 1.1061 | 0.0124 | 72.42 |
| 5 | 28990579 | rs17583873 | C | T | 4 | 0.04911 | 0.239 | 1.0885 | 1.1221 | 0.0065 | 75.58 |
| 2 | 17263551 | rs11693140 | A | T | 4 | 0.2783 | 0.2394 | 0.9605 | 0.9083 | 0.0115 | 72.84 |
| 2 | 107772978 | rs7569095 | C | G | 3 | 0.009653 | 0.2394 | 1.1095 | 1.0868 | 0.0768 | 61.05 |
| 10 | 85956301 | rs7084853 | A | G | 4 | 0.03483 | 0.2398 | 1.0882 | 1.0946 | 0.0372 | 64.6 |
| 1 | 215516242 | rs6675347 | C | T | 4 | 0.1105 | 0.2399 | 1.057 | 1.0835 | 0.0274 | 67.2 |
| 1 | 215516892 | rs7540354 | A | G | 4 | 0.1109 | 0.2401 | 1.0569 | 1.0833 | 0.0278 | 67.08 |
| 2 | 17264870 | rs11673738 | A | T | 4 | 0.2794 | 0.2403 | 1.0411 | 1.1009 | 0.0113 | 72.93 |
| 20 | 55503911 | rs6025590 | A | G | 4 | 0.01783 | 0.2407 | 1.0881 | 1.0734 | 0.0809 | 55.45 |
| 13 | 43946832 | rs9595132 | A | G | 4 | 0.1318 | 0.2413 | 1.0553 | 1.094 | 0.0137 | 71.87 |
| 6 | 90702947 | rs292251 | A | G | 4 | 0.151 | 0.2417 | 1.0552 | 1.1056 | 0.0067 | 75.42 |
| 2 | 219247043 | rs7604319 | A | C | 4 | 0.1681 | 0.242 | 1.0506 | 1.0965 | 0.0112 | 72.99 |
| 2 | 17267310 | rs13020402 | C | T | 4 | 0.2843 | 0.2421 | 0.9609 | 0.9087 | 0.0114 | 72.87 |
| 13 | 43922370 | rs12583155 | C | T | 4 | 0.1311 | 0.2421 | 0.9475 | 0.9147 | 0.0144 | 71.59 |
| 6 | 87194834 | rs9351097 | G | T | 4 | 0.01937 | 0.2424 | 0.8959 | 0.9017 | 0.0379 | 64.4 |
| 10 | 6924140 | rs17400327 | C | T | 4 | 0.0459 | 0.2426 | 0.8088 | 0.7787 | 0.0203 | 69.41 |
| 10 | 9906737 | rs7913128 | A | G | 4 | 0.1708 | 0.2427 | 0.9301 | 0.8837 | 0.023 | 68.53 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 7 | 146666000 | rs826802 | G | T | 4 | 0.2019 | 0.243 | 1.0489 | 1.0951 | 0.0193 | 69.74 |
| 1 | 66628614 | rs12406429 | A | G | 4 | 0.01931 | 0.2433 | 0.8487 | 0.8766 | 0.102 | 51.66 |
| 11 | 23653839 | rs12279140 | A | C | 3 | 0.2059 | 0.2435 | 1.1805 | 1.7585 | 0.0046 | 81.4 |
| 6 | 90703875 | rs292250 | A | G | 4 | 0.153 | 0.2436 | 1.0549 | 1.1059 | 0.0061 | 75.84 |
| 12 | 114340512 | rs11067588 | C | G | 4 | 0.006991 | 0.2437 | 1.1184 | 1.0894 | 0.0572 | 60.07 |
| 19 | 37368199 | rs4334417 | A | G | 4 | 0.4456 | 0.2437 | 0.9721 | 0.9039 | 0.0045 | 77.01 |
| 21 | 40054047 | rs9983659 | C | T | 4 | 0.02547 | 0.2437 | 1.087 | 1.0777 | 0.0696 | 57.59 |
| 13 | 89489076 | rs9583770 | A | G | 4 | 0.02489 | 0.244 | 0.906 | 0.9216 | 0.1042 | 51.28 |
| 22 | 23890579 | rs16979683 | A | C | 4 | 0.3256 | 0.244 | 1.0395 | 1.105 | 0.0123 | 72.46 |
| 2 | 17260029 | rs10495660 | G | T | 4 | 0.2933 | 0.2442 | 1.0399 | 1.1002 | 0.0111 | 73 |
| 2 | 38458897 | rs3806552 | A | C | 3 | 0.2514 | 0.2443 | 1.0438 | 1.1243 | 0.0025 | 83.3 |
| 22 | 23885948 | rs6004456 | A | G | 4 | 0.2878 | 0.2443 | 0.9582 | 0.9051 | 0.0147 | 71.44 |
| 2 | 113516520 | rs4849144 | A | G | 4 | 0.009134 | 0.2454 | 1.102 | 1.0843 | 0.0432 | 63.15 |
| 11 | 81039404 | rs17142744 | G | T | 4 | 0.318 | 0.2454 | 1.0418 | 1.1111 | 0.0081 | 74.56 |
| 2 | 229865352 | rs11678426 | A | G | 4 | 0.01713 | 0.2455 | 1.1741 | 1.1575 | 0.0442 | 62.91 |
| 6 | 15947234 | rs4716002 | G | T | 4 | 0.0245 | 0.2457 | 0.8917 | 0.9011 | 0.0618 | 59.14 |
| 6 | 94825178 | rs1416058 | A | T | 4 | 0.0001861 | 0.2459 | 1.1483 | 1.0894 | 0.027 | 67.31 |
| 13 | 43928799 | rs4942331 | C | T | 4 | 0.1396 | 0.2461 | 1.0542 | 1.0925 | 0.0142 | 71.64 |
| 1 | 159370069 | rs10797093 | G | T | 4 | 0.08206 | 0.2462 | 1.0678 | 1.1024 | 0.0086 | 74.28 |
| 6 | 90704480 | rs182382 | C | G | 4 | 0.1541 | 0.2463 | 1.0543 | 1.1049 | 0.0059 | 75.94 |
| 2 | 38220587 | rs10469900 | C | T | 4 | 0.00564 | 0.2464 | 1.1246 | 1.0957 | 0.0447 | 62.81 |
| 6 | 99029526 | rs9482753 | A | G | 4 | 0.00128 | 0.2464 | 1.3661 | 1.2491 | 0.0205 | 69.33 |
| 5 | 149561777 | rs2240785 | C | T | 4 | 0.01561 | 0.2467 | 1.2696 | 1.2327 | 0.0471 | 62.27 |
| 7 | 69846869 | rs7806434 | A | G | 4 | 0.1915 | 0.2467 | 0.9551 | 0.9142 | 0.0098 | 73.64 |
| 16 | 75607795 | rs2220233 | C | T | 4 | 0.2832 | 0.2468 | 0.9581 | 0.9063 | 0.0165 | 70.75 |
| 4 | 116454363 | rs6533850 | A | T | 4 | 0.2479 | 0.2469 | 0.9596 | 0.9058 | 0.0034 | 78.02 |
| 6 | 15948658 | rs16877108 | A | G | 4 | 0.02598 | 0.247 | 0.8932 | 0.902 | 0.0631 | 58.87 |
| 1 | 215504627 | rs6604663 | A | G | 4 | 0.1345 | 0.2472 | 0.9497 | 0.9242 | 0.0269 | 67.35 |
| 5 | 28895838 | rs17616969 | A | G | 4 | 0.05466 | 0.2472 | 0.9211 | 0.8904 | 0.0043 | 77.2 |
| 11 | 5350363 | rs11037068 | G | T | 3 | 0.00973 | 0.2472 | 1.2655 | 1.3022 | 0.0258 | 72.65 |
| 2 | 113505787 | rs2305150 | C | T | 4 | 0.007356 | 0.2473 | 1.0983 | 1.0772 | 0.048 | 62.05 |
| 1 | 66607403 | rs2311985 | A | G | 4 | 0.01908 | 0.2474 | 1.1778 | 1.1397 | 0.0988 | 52.22 |
| 15 | 89947230 | rs4420510 | A | G | 4 | 0.09102 | 0.2474 | 0.9369 | 0.8937 | 0.0018 | 79.95 |
| 4 | 116448276 | rs6533848 | G | T | 4 | 0.2654 | 0.2476 | 0.9613 | 0.9058 | 0.0031 | 78.35 |
| 4 | 116450640 | rs7698264 | C | T | 4 | 0.2654 | 0.2476 | 0.9613 | 0.9058 | 0.0031 | 78.35 |
| 1 | 88279379 | rs12566596 | C | G | 4 | 0.4616 | 0.2477 | 0.9711 | 0.8919 | 0.0023 | 79.31 |
| 9 | 10655668 | rs4380991 | A | T | 4 | 0.2892 | 0.2477 | 1.0551 | 1.1647 | 0.0007 | 82.44 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 16 | 50235764 | rs7204626 | C | T | 4 | 0.09437 | 0.2478 | 1.0664 | 1.1117 | 0.0033 | 78.1 |
| 12 | 65691760 | rs11176534 | C | T | 4 | 0.1389 | 0.2479 | 0.9202 | 0.8655 | 0.0081 | 74.6 |
| 12 | 65704574 | rs905699 | C | T | 4 | 0.2212 | 0.2479 | 0.9393 | 0.8741 | 0.0057 | 76.12 |
| 11 | 81039330 | rs17142739 | A | C | 4 | 0.324 | 0.2483 | 1.0413 | 1.1107 | 0.0079 | 74.69 |
| 20 | 55508313 | rs2209885 | C | G | 4 | 0.02114 | 0.2485 | 1.0863 | 1.0725 | 0.0809 | 55.44 |
| 6 | 94818482 | rs667243 | A | G | 4 | 0.0002356 | 0.2487 | 1.1447 | 1.0872 | 0.0304 | 66.37 |
| 12 | 65708448 | rs11176540 | G | T | 4 | 0.2227 | 0.2487 | 1.0643 | 1.1441 | 0.0055 | 76.23 |
| 14 | 42258660 | rs1777077 | C | T | 4 | 0.07721 | 0.2489 | 1.0787 | 1.1093 | 0.0167 | 70.69 |
| 1 | 180318899 | rs8179259 | C | G | 4 | 0.3625 | 0.2497 | 1.0353 | 1.1189 | 0.0017 | 80.24 |
| 12 | 65706048 | rs6581729 | A | G | 4 | 0.2254 | 0.2497 | 1.0639 | 1.144 | 0.0054 | 76.3 |
| 2 | 219081012 | rs634590 | A | C | 4 | 0.1771 | 0.2499 | 1.0504 | 1.0926 | 0.0166 | 70.73 |
| 4 | 116442250 | rs1396064 | G | T | 4 | 0.2721 | 0.2501 | 1.0397 | 1.1035 | 0.0031 | 78.36 |
| 7 | 69844069 | rs4718991 | C | G | 4 | 0.1899 | 0.2505 | 0.9549 | 0.915 | 0.01 | 73.56 |
| 18 | 37360470 | rs2848760 | A | G | 4 | 0.1952 | 0.2506 | 0.9532 | 0.9172 | 0.0214 | 69.04 |
| 2 | 155411014 | rs2937600 | A | G | 4 | 0.01909 | 0.2507 | 1.0939 | 1.0794 | 0.07 | 57.5 |
| 2 | 107777551 | rs1583938 | A | C | 3 | 0.009777 | 0.2509 | 1.1093 | 1.0859 | 0.0711 | 62.17 |
| 4 | 92470862 | rs6532299 | C | T | 3 | 0.2985 | 0.2509 | 0.96 | 0.8887 | 0.0039 | 81.99 |
| 12 | 65706599 | rs11176539 | C | G | 4 | 0.2247 | 0.2509 | 1.064 | 1.1434 | 0.0056 | 76.22 |
| 6 | 94830671 | rs9354083 | C | T | 4 | 0.0002068 | 0.2511 | 0.8717 | 0.9186 | 0.0265 | 67.47 |
| 2 | 219270919 | rs1863704 | A | G | 4 | 0.1821 | 0.2512 | 0.9534 | 0.9117 | 0.0089 | 74.12 |
| 4 | 116455401 | rs1979975 | A | G | 4 | 0.2752 | 0.2514 | 0.9621 | 0.9062 | 0.003 | 78.49 |
| 4 | 116455651 | rs11098294 | C | G | 4 | 0.2752 | 0.2514 | 0.9621 | 0.9062 | 0.003 | 78.49 |
| 4 | 116459223 | rs6851203 | A | G | 4 | 0.2752 | 0.2514 | 0.9621 | 0.9062 | 0.003 | 78.49 |
| 4 | 175703538 | rs6811079 | A | G | 4 | 0.00901 | 0.2514 | 0.8523 | 0.8767 | 0.0418 | 63.48 |
| 2 | 106754740 | rs1349065 | C | G | 3 | 0.0007936 | 0.2517 | 1.1446 | 1.1043 | 0.0214 | 74 |
| 12 | 65709564 | rs11176545 | A | T | 4 | 0.2245 | 0.2518 | 1.0644 | 1.1437 | 0.0055 | 76.23 |
| 10 | 36687776 | rs11593579 | A | G | 4 | 0.06287 | 0.2523 | 1.1037 | 1.148 | 0.0063 | 75.67 |
| 5 | 28874857 | rs10520944 | A | C | 4 | 0.05947 | 0.2525 | 0.9226 | 0.891 | 0.0041 | 77.43 |
| 12 | 65705663 | rs17103210 | A | T | 4 | 0.2259 | 0.2526 | 1.0642 | 1.1436 | 0.0055 | 76.27 |
| 6 | 15948891 | rs16877113 | A | C | 4 | 0.02634 | 0.2529 | 1.1199 | 1.108 | 0.0619 | 59.12 |
| 6 | 99010723 | rs3104078 | A | T | 4 | 0.002078 | 0.253 | 0.7505 | 0.8262 | 0.0448 | 62.78 |
| 6 | 94807741 | rs2875662 | C | T | 4 | 0.0002667 | 0.2531 | 0.8747 | 0.9209 | 0.0314 | 66.1 |
| 7 | 17138564 | rs7341406 | C | G | 4 | 0.07155 | 0.2535 | 0.88 | 0.8495 | 0.0212 | 69.11 |
| 13 | 73018296 | rs17215110 | A | C | 4 | 0.02431 | 0.2535 | 0.8919 | 0.8826 | 0.0114 | 72.89 |
| 9 | 10643484 | rs4131202 | C | T | 4 | 0.1092 | 0.2537 | 0.9325 | 0.8833 | 0.0017 | 80.27 |
| 6 | 94816613 | rs6919516 | A | G | 4 | 0.0003089 | 0.2542 | 1.1418 | 1.0855 | 0.0322 | 65.86 |
| 6 | 51288724 | rs2465043 | A | G | 4 | 0.2232 | 0.2543 | 1.0466 | 1.0958 | 0.012 | 72.59 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 1 | 116602943 | rs2184484 | A | G | 4 | 0.01929 | 0.2555 | 0.9162 | 0.924 | 0.0429 | 63.22 |
| 2 | 30858680 | rs4597573 | C | T | 4 | 0.004059 | 0.2557 | 0.9038 | 0.9317 | 0.0613 | 59.23 |
| 1 | 110903737 | rs12407862 | C | T | 4 | 0.01983 | 0.256 | 0.9002 | 0.8969 | 0.0139 | 71.77 |
| 12 | 65700060 | rs7953084 | A | C | 4 | 0.2463 | 0.2561 | 1.0615 | 1.1426 | 0.0056 | 76.15 |
| 1 | 215523070 | rs7535028 | G | T | 4 | 0.132 | 0.2563 | 1.0537 | 1.0818 | 0.0244 | 68.1 |
| 3 | 116979664 | rs2972493 | A | C | 4 | 0.008041 | 0.2564 | 0.8677 | 0.9066 | 0.1052 | 51.1 |
| 6 | 99015679 | rs3125579 | A | G | 4 | 0.002532 | 0.2564 | 1.3074 | 1.2031 | 0.04 | 63.91 |
| 16 | 47660593 | rs2967260 | A | T | 4 | 0.01721 | 0.2566 | 1.091 | 1.0818 | 0.0579 | 59.92 |
| 4 | 8386637 | rs6858268 | C | T | 4 | 0.1028 | 0.2571 | 0.9427 | 0.9197 | 0.0201 | 69.48 |
| 4 | 116535799 | rs7434366 | A | T | 4 | 0.2992 | 0.2572 | 1.0385 | 1.1077 | 0.0021 | 79.55 |
| 6 | 94855791 | rs669021 | C | T | 4 | 0.0003001 | 0.2576 | 1.1446 | 1.0876 | 0.0284 | 66.92 |
| 2 | 30858633 | rs2030385 | C | T | 4 | 0.0002338 | 0.2581 | 1.144 | 1.0886 | 0.0199 | 69.55 |
| 9 | 10637333 | rs10809144 | C | T | 4 | 0.163 | 0.2581 | 1.0584 | 1.1186 | 0.0024 | 79.15 |
| 22 | 17946365 | rs5748309 | C | T | 4 | 0.02839 | 0.2581 | 0.9121 | 0.9243 | 0.0877 | 54.21 |
| 12 | 60731556 | rs2951468 | A | C | 4 | 0.1593 | 0.2583 | 1.0599 | 1.1 | 0.0187 | 69.94 |
| 12 | 65699454 | rs12369132 | A | G | 4 | 0.2469 | 0.2588 | 0.9419 | 0.8753 | 0.0055 | 76.23 |
| 6 | 94824189 | rs1538283 | A | G | 4 | 0.0001785 | 0.2589 | 0.8713 | 0.919 | 0.0235 | 68.38 |
| 6 | 94834038 | rs9351405 | A | G | 4 | 0.000216 | 0.2591 | 0.8729 | 0.9195 | 0.0244 | 68.1 |
| 1 | 173301060 | rs10798331 | A | G | 4 | 0.2816 | 0.2593 | 1.04 | 1.1119 | 0.0013 | 80.97 |
| 8 | 32647451 | rs12541855 | C | T | 4 | 0.1054 | 0.2596 | 1.0608 | 1.1031 | 0.0043 | 77.24 |
| 5 | 118636074 | rs13361153 | A | G | 4 | 0.3886 | 0.2598 | 1.0373 | 1.1192 | 0.0066 | 75.46 |
| 4 | 116484342 | rs6821637 | G | T | 4 | 0.2618 | 0.26 | 1.0409 | 1.1046 | 0.0023 | 79.32 |
| 6 | 94830956 | rs9445199 | A | G | 4 | 0.0002116 | 0.2606 | 0.8727 | 0.9197 | 0.0241 | 68.17 |
| 11 | 80658536 | rs7941624 | A | G | 4 | 0.2834 | 0.2606 | 1.0501 | 1.1214 | 0.0104 | 73.36 |
| 20 | 56635234 | rs4812022 | C | T | 4 | 0.5388 | 0.2606 | 1.0304 | 1.1363 | 0.0073 | 75.07 |
| 2 | 113520034 | rs7569284 | A | G | 4 | 0.01036 | 0.2607 | 0.9089 | 0.9234 | 0.0382 | 64.33 |
| 2 | 229863370 | rs1226936 | G | T | 4 | 0.01717 | 0.2607 | 0.8511 | 0.865 | 0.038 | 64.38 |
| 6 | 94849976 | rs658208 | A | G | 4 | 0.01158 | 0.2613 | 1.0932 | 1.0668 | 0.098 | 52.35 |
| 10 | 22883117 | rs12146350 | C | G | 4 | 0.003252 | 0.2615 | 0.9001 | 0.9331 | 0.0712 | 57.28 |
| 9 | 10638898 | rs1923439 | G | T | 4 | 0.1714 | 0.2617 | 1.0572 | 1.119 | 0.0021 | 79.65 |
| 3 | 14908226 | rs11924206 | G | T | 4 | 0.1771 | 0.2618 | 0.947 | 0.9144 | 0.0245 | 68.05 |
| 2 | 133485247 | rs1437896 | C | T | 4 | 0.7055 | 0.2619 | 0.9864 | 0.8928 | 0.0004 | 83.6 |
| 2 | 113514439 | rs7557928 | G | T | 4 | 0.01052 | 0.2622 | 0.9091 | 0.9238 | 0.0389 | 64.18 |
| 4 | 116486031 | rs6829587 | C | T | 4 | 0.2673 | 0.2622 | 1.0404 | 1.1041 | 0.0023 | 79.33 |
| 2 | 219245468 | rs2241527 | A | G | 4 | 0.1752 | 0.2624 | 0.9526 | 0.915 | 0.0107 | 73.21 |
| 2 | 229863870 | rs11676521 | G | T | 4 | 0.01934 | 0.2625 | 0.8536 | 0.8668 | 0.0411 | 63.65 |
| 6 | 94830432 | rs9354082 | C | T | 4 | 0.0002136 | 0.2626 | 0.8728 | 0.9199 | 0.0239 | 68.25 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 2 | 229856782 | rs1226946 | C | T | 4 | 0.01662 | 0.2628 | 1.1758 | 1.1557 | 0.0371 | 64.61 |
| 6 | 94814119 | rs678036 | C | G | 4 | 0.000303 | 0.2629 | 0.8757 | 0.9222 | 0.0305 | 66.34 |
| 6 | 30074705 | rs9261043 | C | T | 3 | 0.0002851 | 0.2631 | 0.7088 | 0.7984 | 0.0515 | 66.28 |
| 10 | 47991283 | rs3814160 | C | T | 4 | 0.008811 | 0.2636 | 0.8701 | 0.8977 | 0.0485 | 61.95 |
| 4 | 8386558 | rs6825003 | C | T | 4 | 0.1089 | 0.2637 | 1.0597 | 1.0863 | 0.0195 | 69.67 |
| 13 | 41467528 | rs2324845 | C | T | 4 | 0.1397 | 0.2641 | 1.0535 | 1.093 | 0.008 | 74.65 |
| 15 | 86294466 | rs4887337 | A | C | 4 | 0.003477 | 0.2641 | 1.1813 | 1.1414 | 0.0167 | 70.67 |
| 4 | 116463016 | rs11727958 | C | T | 4 | 0.3271 | 0.2643 | 1.0363 | 1.1037 | 0.0031 | 78.39 |
| 4 | 116460667 | rs10516610 | C | T | 4 | 0.2826 | 0.2646 | 0.9626 | 0.9065 | 0.0022 | 79.41 |
| 5 | 28851719 | rs16898178 | A | C | 4 | 0.06786 | 0.2651 | 0.9249 | 0.893 | 0.0037 | 77.73 |
| 4 | 116483034 | rs4834466 | C | G | 4 | 0.2821 | 0.2653 | 1.0389 | 1.1033 | 0.0021 | 79.53 |
| 6 | 94855506 | rs471348 | A | G | 4 | 0.01194 | 0.2656 | 0.9151 | 0.9376 | 0.0964 | 52.65 |
| 1 | 215522526 | rs10158471 | A | G | 4 | 0.1442 | 0.2657 | 0.9505 | 0.9254 | 0.0232 | 68.48 |
| 9 | 10639309 | rs1322303 | A | G | 4 | 0.1785 | 0.2659 | 0.9468 | 0.8942 | 0.002 | 79.77 |
| 11 | 106222728 | rs1954864 | G | T | 4 | 0.1156 | 0.2659 | 0.9377 | 0.9075 | 0.0145 | 71.54 |
| 2 | 219025492 | rs3755042 | C | T | 4 | 0.1733 | 0.2664 | 0.9525 | 0.9198 | 0.0174 | 70.42 |
| 2 | 13999212 | rs747193 | A | G | 4 | 0.3362 | 0.2665 | 0.9485 | 0.8754 | 0.0101 | 73.51 |
| 3 | 129574792 | rs1735538 | A | G | 4 | 0.3242 | 0.2667 | 1.0401 | 1.1011 | 0.0137 | 71.87 |
| 2 | 219028129 | rs7601872 | C | G | 4 | 0.1741 | 0.2668 | 1.0498 | 1.0871 | 0.0174 | 70.42 |
| 3 | 102284333 | rs13096071 | C | T | 4 | 0.06519 | 0.2668 | 1.1254 | 1.2146 | 0.0004 | 83.74 |
| 10 | 85962578 | rs10887255 | C | T | 4 | 0.03675 | 0.2668 | 0.9209 | 0.9175 | 0.0309 | 66.21 |
| 13 | 43987160 | rs9533885 | A | G | 3 | 0.002074 | 0.2668 | 1.6542 | 1.3877 | 0.1412 | 48.92 |
| 8 | 14884772 | rs10097898 | A | G | 4 | 0.02915 | 0.2674 | 1.0841 | 1.0766 | 0.0518 | 61.23 |
| 4 | 116491650 | rs12503088 | C | G | 4 | 0.2802 | 0.2675 | 0.9622 | 0.9063 | 0.0021 | 79.54 |
| 10 | 85956138 | rs960731 | G | T | 4 | 0.04484 | 0.2675 | 1.0842 | 1.0901 | 0.0343 | 65.32 |
| 2 | 60184903 | rs972337 | C | T | 4 | 0.3647 | 0.2676 | 0.9671 | 0.9164 | 0.0134 | 71.97 |
| 11 | 15191628 | rs16931218 | C | T | 4 | 0.1376 | 0.2681 | 1.1548 | 1.2508 | 0.0124 | 72.44 |
| 4 | 116461695 | rs6533852 | G | T | 4 | 0.2929 | 0.2684 | 0.9634 | 0.907 | 0.0021 | 79.54 |
| 7 | 17140404 | rs7341466 | G | T | 4 | 0.08469 | 0.2685 | 0.883 | 0.8468 | 0.0167 | 70.66 |
| 6 | 94830027 | rs1338341 | A | G | 4 | 0.0002109 | 0.2688 | 0.8727 | 0.9204 | 0.0225 | 68.67 |
| 13 | 43902494 | rs2875552 | C | T | 4 | 0.176 | 0.2688 | 1.0496 | 1.0908 | 0.0108 | 73.18 |
| 4 | 116474793 | rs13101335 | G | T | 4 | 0.2834 | 0.2691 | 1.0391 | 1.103 | 0.0021 | 79.54 |
| 8 | 127013476 | rs2087688 | A | G | 4 | 0.327 | 0.2692 | 1.0361 | 1.1019 | 0.0029 | 78.52 |
| 3 | 102279569 | rs16843216 | C | T | 4 | 0.2004 | 0.2693 | 0.9374 | 0.8357 | 0 | 88.08 |
| 6 | 15953087 | rs1927587 | C | T | 4 | 0.03004 | 0.2695 | 0.8954 | 0.9037 | 0.0533 | 60.9 |
| 6 | 94856518 | rs682644 | C | T | 4 | 0.01424 | 0.2696 | 1.0912 | 1.066 | 0.0996 | 52.08 |
| 6 | 94856881 | rs2787948 | C | T | 4 | 0.01424 | 0.2696 | 1.0912 | 1.066 | 0.0996 | 52.08 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 2 | 17267368 | rs13018947 | C | G | 4 | 0.3333 | 0.2698 | 1.0366 | 1.095 | 0.0107 | 73.2 |
| 8 | 127018859 | rs4568586 | A | T | 4 | 0.3254 | 0.27 | 0.9651 | 0.9076 | 0.0029 | 78.59 |
| 8 | 127007226 | rs1491476 | A | G | 4 | 0.326 | 0.2702 | 0.9651 | 0.9098 | 0.004 | 77.5 |
| 2 | 219050528 | rs3845835 | C | T | 4 | 0.1806 | 0.2704 | 0.9532 | 0.9204 | 0.0172 | 70.48 |
| 12 | 94741290 | rs10777742 | C | T | 4 | 0.02251 | 0.2704 | 0.9148 | 0.9303 | 0.0821 | 55.23 |
| 8 | 127015428 | rs7819223 | C | T | 4 | 0.3296 | 0.2706 | 0.9654 | 0.9076 | 0.0029 | 78.61 |
| 12 | 94730019 | rs7307769 | A | G | 4 | 0.0235 | 0.2709 | 1.0925 | 1.075 | 0.0808 | 55.46 |
| 4 | 116435600 | rs4464590 | C | T | 4 | 0.2898 | 0.271 | 1.0385 | 1.1025 | 0.0022 | 79.51 |
| 8 | 140501955 | rs2447553 | C | T | 4 | 0.52 | 0.2715 | 0.9781 | 0.9172 | 0.0073 | 75.03 |
| 5 | 149562853 | rs2240791 | A | G | 4 | 0.02084 | 0.2716 | 1.256 | 1.2262 | 0.0386 | 64.24 |
| 21 | 40054216 | rs2837176 | C | G | 4 | 0.03014 | 0.2716 | 1.0843 | 1.0752 | 0.059 | 59.71 |
| 6 | 92320349 | rs9342290 | C | T | 4 | 0.4975 | 0.2718 | 0.9719 | 0.8982 | 0.0067 | 75.4 |
| 6 | 99803170 | rs12194369 | A | G | 4 | 0.1191 | 0.2722 | 0.9361 | 0.9045 | 0.011 | 73.06 |
| 4 | 116464246 | rs1948983 | C | G | 4 | 0.3034 | 0.2723 | 0.9641 | 0.9074 | 0.002 | 79.67 |
| 1 | 66603687 | rs2275644 | A | G | 4 | 0.02299 | 0.2725 | 0.8516 | 0.8811 | 0.0933 | 53.2 |
| 16 | 75659337 | rs1485793 | A | G | 4 | 0.4454 | 0.2728 | 1.0315 | 1.1025 | 0.0131 | 72.1 |
| 2 | 219060816 | rs7571743 | C | T | 4 | 0.1743 | 0.2732 | 0.9521 | 0.9189 | 0.015 | 71.33 |
| 8 | 32664543 | rs12541309 | A | G | 4 | 0.4505 | 0.2734 | 0.964 | 0.8801 | 0.0056 | 76.2 |
| 4 | 116465817 | rs4349617 | C | T | 4 | 0.2979 | 0.2736 | 0.9635 | 0.9072 | 0.002 | 79.65 |
| 2 | 98863360 | rs17022036 | G | T | 4 | 0.03722 | 0.2737 | 0.8641 | 0.8608 | 0.0254 | 67.78 |
| 8 | 36281532 | rs12544826 | A | G | 4 | 0.01658 | 0.2737 | 0.8957 | 0.9221 | 0.1079 | 50.63 |
| 1 | 66603910 | rs7538869 | G | T | 4 | 0.02328 | 0.2742 | 0.852 | 0.8814 | 0.0925 | 53.34 |
| 2 | 219044188 | rs10200507 | A | C | 4 | 0.1881 | 0.2745 | 0.954 | 0.921 | 0.0171 | 70.54 |
| 4 | 116466112 | rs4519812 | A | G | 4 | 0.2987 | 0.2745 | 0.9636 | 0.9074 | 0.002 | 79.65 |
| 20 | 19738602 | rs16981148 | A | G | 4 | 0.118 | 0.2745 | 1.0984 | 1.1524 | 0.0096 | 73.76 |
| 1 | 81222832 | rs1863618 | A | G | 4 | 0.01302 | 0.2746 | 1.0943 | 1.0704 | 0.0742 | 56.7 |
| 6 | 15945269 | rs13211010 | C | T | 4 | 0.02466 | 0.2748 | 1.1214 | 1.1076 | 0.0469 | 62.29 |
| 4 | 116481902 | rs7439118 | C | T | 4 | 0.2985 | 0.2749 | 1.0378 | 1.1022 | 0.002 | 79.73 |
| 3 | 102284910 | rs16843229 | A | G | 4 | 0.2278 | 0.2762 | 1.064 | 1.1971 | 0 | 88.11 |
| 5 | 93821414 | rs9314112 | A | G | 4 | 0.5456 | 0.2762 | 1.0211 | 1.0924 | 0.0055 | 76.27 |
| 4 | 116473561 | rs6533855 | A | G | 4 | 0.3142 | 0.2766 | 1.0364 | 1.1016 | 0.0019 | 79.88 |
| 5 | 164985118 | rs17065434 | C | T | 4 | 0.005867 | 0.2768 | 0.8911 | 0.9099 | 0.0172 | 70.48 |
| 6 | 94821751 | rs2787944 | C | T | 4 | 0.0002667 | 0.277 | 1.1434 | 1.0849 | 0.0229 | 68.55 |
| 9 | 10625939 | rs10756072 | A | G | 4 | 0.1921 | 0.277 | 0.9491 | 0.9037 | 0.0046 | 76.94 |
| 4 | 127224550 | rs11731526 | C | G | 4 | 0.1281 | 0.2776 | 0.9268 | 0.8968 | 0.0217 | 68.95 |
| 1 | 154309539 | rs11264432 | A | G | 3 | 0.01294 | 0.278 | 0.9085 | 0.908 | 0.0123 | 77.28 |
| 2 | 219067929 | rs6710383 | G | T | 4 | 0.1832 | 0.278 | 1.0493 | 1.0874 | 0.0148 | 71.42 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 21 | 40054313 | rs2837178 | A | G | 4 | 0.03042 | 0.2781 | 1.0842 | 1.0749 | 0.0558 | 60.37 |
| 9 | 119035785 | rs1335406 | A | T | 4 | 0.006204 | 0.2787 | 0.8115 | 0.8585 | 0.0521 | 61.15 |
| 4 | 116469038 | rs7676815 | C | T | 4 | 0.3089 | 0.2788 | 1.037 | 1.1017 | 0.0019 | 79.86 |
| 5 | 93827557 | rs7728878 | C | T | 4 | 0.5815 | 0.279 | 0.9809 | 0.9139 | 0.0046 | 76.93 |
| 3 | 124820104 | rs860224 | C | G | 4 | 0.03754 | 0.2792 | 0.9109 | 0.897 | 0.0068 | 75.36 |
| 3 | 172439746 | rs9857839 | C | T | 2 | 0.001595 | 0.2792 | 4.2554 | 2.8514 | 0.0894 | 65.33 |
| 4 | 72339718 | rs4694387 | A | C | 4 | 0.09756 | 0.2794 | 1.0913 | 1.1699 | 0.0006 | 82.55 |
| 12 | 130815441 | rs6598153 | C | T | 4 | 0.02054 | 0.2794 | 0.921 | 0.9366 | 0.0766 | 56.25 |
| 1 | 65104374 | rs12093269 | C | T | 4 | 0.02181 | 0.2796 | 1.136 | 1.1302 | 0.0197 | 69.62 |
| 6 | 92328542 | rs9342293 | A | T | 4 | 0.5013 | 0.2797 | 1.0286 | 1.1121 | 0.0063 | 75.7 |
| 20 | 19738531 | rs16981142 | C | G | 4 | 0.07233 | 0.2798 | 1.1152 | 1.1545 | 0.0084 | 74.42 |
| 6 | 94852999 | rs606061 | A | G | 4 | 0.01342 | 0.2799 | 1.0912 | 1.0649 | 0.0935 | 53.15 |
| 6 | 94854912 | rs591551 | C | T | 4 | 0.01342 | 0.2799 | 1.0912 | 1.0649 | 0.0935 | 53.15 |
| 11 | 106336866 | rs12364403 | C | T | 4 | 0.0573 | 0.2803 | 0.9251 | 0.9032 | 0.0064 | 75.65 |
| 3 | 102273952 | rs13081830 | A | G | 4 | 0.2497 | 0.2808 | 1.0598 | 1.191 | 0 | 88.02 |
| 1 | 66627158 | rs12239708 | A | T | 4 | 0.02391 | 0.2811 | 0.8531 | 0.8825 | 0.0898 | 53.82 |
| 3 | 102283947 | rs16843225 | G | T | 4 | 0.2477 | 0.2813 | 1.0604 | 1.1919 | 0 | 88.05 |
| 6 | 87192966 | rs9362321 | C | T | 4 | 0.03221 | 0.2814 | 0.9048 | 0.9086 | 0.0355 | 65.02 |
| 1 | 66624485 | rs6701234 | G | T | 4 | 0.02462 | 0.2815 | 0.8538 | 0.8831 | 0.0915 | 53.52 |
| 8 | 127011528 | rs1491474 | A | C | 4 | 0.3664 | 0.2818 | 0.9679 | 0.9085 | 0.0024 | 79.15 |
| 8 | 140503436 | rs2468726 | C | G | 4 | 0.5394 | 0.282 | 1.0216 | 1.0884 | 0.0079 | 74.68 |
| 4 | 127239590 | rs6820042 | A | G | 4 | 0.1142 | 0.2823 | 1.0806 | 1.1173 | 0.0147 | 71.45 |
| 6 | 15943835 | rs4712261 | C | T | 4 | 0.02607 | 0.2823 | 0.8928 | 0.9024 | 0.0398 | 63.95 |
| 16 | 56846486 | rs11076230 | G | T | 4 | 0.8584 | 0.2827 | 0.9913 | 0.8773 | 0.0032 | 78.26 |
| 2 | 219081441 | rs636723 | A | G | 4 | 0.2037 | 0.2828 | 0.9556 | 0.9221 | 0.0167 | 70.69 |
| 2 | 219083955 | rs6717433 | C | G | 4 | 0.2037 | 0.2828 | 0.9556 | 0.9221 | 0.0167 | 70.69 |
| 3 | 102282360 | rs17219986 | A | G | 4 | 0.2524 | 0.2828 | 1.0598 | 1.1913 | 0 | 88.06 |
| 6 | 92320478 | rs9345149 | A | T | 4 | 0.5063 | 0.2828 | 0.9725 | 0.9008 | 0.007 | 75.24 |
| 2 | 38422331 | rs11679271 | C | T | 4 | 0.234 | 0.2832 | 1.0452 | 1.114 | 0.0007 | 82.39 |
| 2 | 219082361 | rs662250 | A | T | 4 | 0.2046 | 0.2832 | 1.0464 | 1.0844 | 0.0167 | 70.69 |
| 6 | 92321886 | rs9362888 | A | G | 4 | 0.5102 | 0.2834 | 1.028 | 1.1103 | 0.0068 | 75.38 |
| 6 | 94819838 | rs590701 | G | T | 4 | 0.009065 | 0.2834 | 1.0964 | 1.0658 | 0.0825 | 55.15 |
| 22 | 33864933 | rs4821368 | C | G | 4 | 0.03632 | 0.2835 | 1.0904 | 1.1105 | 0.0049 | 76.74 |
| 1 | 66624749 | rs6703929 | C | T | 4 | 0.02491 | 0.2836 | 0.854 | 0.8833 | 0.0907 | 53.65 |
| 8 | 127612296 | rs11990954 | A | C | 4 | 0.2465 | 0.284 | 1.057 | 1.1171 | 0.0123 | 72.49 |
| 2 | 5605816 | rs10929647 | A | C | 4 | 0.014 | 0.2841 | 0.9175 | 0.8963 | 0.0002 | 85.14 |
| 5 | 149561988 | rs2240787 | C | T | 4 | 0.01968 | 0.2845 | 0.7924 | 0.8181 | 0.0378 | 64.44 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 12 | 94742289 | rs10859960 | A | G | 4 | 0.02468 | 0.2845 | 1.0917 | 1.0734 | 0.0778 | 56.02 |
| 8 | 126997191 | rs2385503 | A | T | 4 | 0.3454 | 0.2846 | 1.0349 | 1.0877 | 0.0115 | 72.85 |
| 19 | 37368143 | rs12976005 | C | G | 4 | 0.7173 | 0.2846 | 1.013 | 1.1096 | 0.0005 | 83.23 |
| 9 | 10625232 | rs1322300 | C | T | 4 | 0.2058 | 0.2847 | 1.052 | 1.1052 | 0.0044 | 77.09 |
| 2 | 219141841 | rs526897 | A | G | 4 | 0.2052 | 0.2848 | 1.0464 | 1.084 | 0.0169 | 70.6 |
| 2 | 133486143 | rs4953868 | A | G | 4 | 0.6851 | 0.285 | 0.9853 | 0.8957 | 0.0003 | 84.18 |
| 11 | 106171269 | rs10890590 | A | G | 4 | 0.08405 | 0.2851 | 0.9327 | 0.904 | 0.0053 | 76.43 |
| 1 | 66625390 | rs6691740 | A | C | 4 | 0.02473 | 0.2852 | 0.8544 | 0.8833 | 0.0877 | 54.2 |
| 6 | 99797170 | rs12193060 | A | G | 4 | 0.1407 | 0.2853 | 0.9392 | 0.9062 | 0.0104 | 73.34 |
| 16 | 56846678 | rs12596498 | C | T | 4 | 0.8764 | 0.2853 | 1.0077 | 1.1396 | 0.003 | 78.42 |
| 5 | 93824426 | rs952663 | A | G | 4 | 0.5674 | 0.2857 | 1.0199 | 1.0908 | 0.0051 | 76.53 |
| 16 | 56842704 | rs1974876 | C | T | 4 | 0.876 | 0.2857 | 1.0077 | 1.1391 | 0.0031 | 78.31 |
| 2 | 219110935 | rs523305 | C | T | 4 | 0.2068 | 0.2858 | 1.0462 | 1.084 | 0.0167 | 70.69 |
| 2 | 219151961 | rs3770216 | A | G | 4 | 0.2112 | 0.2862 | 1.0457 | 1.0837 | 0.0171 | 70.54 |
| 8 | 126994033 | rs7007303 | A | G | 4 | 0.3604 | 0.2862 | 0.9672 | 0.9198 | 0.0119 | 72.64 |
| 21 | 33674908 | rs12329794 | A | G | 4 | 0.2243 | 0.2863 | 1.0611 | 1.1157 | 0.0141 | 71.72 |
| 2 | 219140813 | rs496674 | A | G | 4 | 0.2083 | 0.2864 | 1.046 | 1.0838 | 0.0167 | 70.67 |
| 2 | 219207003 | rs7574429 | G | T | 4 | 0.2259 | 0.2866 | 1.0443 | 1.0854 | 0.0142 | 71.66 |
| 15 | 60544836 | rs2940333 | A | G | 4 | 0.03284 | 0.2868 | 0.9109 | 0.9261 | 0.0931 | 53.22 |
| 2 | 219095517 | rs599973 | C | G | 4 | 0.2125 | 0.2871 | 0.9564 | 0.9226 | 0.0164 | 70.79 |
| 16 | 56847308 | rs16959980 | C | T | 4 | 0.889 | 0.2873 | 0.9932 | 0.8778 | 0.003 | 78.5 |
| 2 | 107784033 | rs13415031 | C | G | 3 | 0.01133 | 0.2875 | 0.9013 | 0.9212 | 0.053 | 65.95 |
| 2 | 219107871 | rs687747 | C | T | 4 | 0.2137 | 0.2878 | 1.0455 | 1.0836 | 0.0166 | 70.71 |
| 2 | 219111266 | rs7583449 | A | C | 4 | 0.2114 | 0.288 | 1.0457 | 1.0837 | 0.0165 | 70.76 |
| 22 | 33869717 | rs5755606 | C | T | 4 | 0.03066 | 0.288 | 0.9177 | 0.9072 | 0.0066 | 75.5 |
| 2 | 128371789 | rs7570249 | G | T | 4 | 0.02844 | 0.2881 | 1.0836 | 1.0685 | 0.0845 | 54.78 |
| 8 | 135101424 | rs1158934 | A | G | 4 | 0.01533 | 0.2881 | 0.9187 | 0.927 | 0.0214 | 69.05 |
| 2 | 30858916 | rs2030386 | A | G | 4 | 0.0001962 | 0.2883 | 0.8727 | 0.9216 | 0.0159 | 70.98 |
| 2 | 219137296 | rs490483 | A | T | 4 | 0.212 | 0.2883 | 0.9563 | 0.9229 | 0.0167 | 70.68 |
| 2 | 219145840 | rs523937 | C | G | 4 | 0.2129 | 0.2888 | 1.0456 | 1.0833 | 0.0169 | 70.62 |
| 3 | 102256173 | rs13060849 | A | C | 4 | 0.2369 | 0.2889 | 0.9417 | 0.8442 | 0 | 87.49 |
| 11 | 106227169 | rs10890611 | C | T | 4 | 0.1234 | 0.2889 | 0.9397 | 0.9099 | 0.0106 | 73.26 |
| 15 | 86273174 | rs879131 | A | G | 4 | 0.006504 | 0.2892 | 1.1299 | 1.0911 | 0.0438 | 63.01 |
| 2 | 219180978 | rs3731867 | A | G | 4 | 0.2166 | 0.2893 | 0.9567 | 0.9216 | 0.014 | 71.75 |
| 2 | 219128179 | rs12619347 | C | T | 4 | 0.2144 | 0.2894 | 0.9566 | 0.9229 | 0.0162 | 70.88 |
| 6 | 15935221 | rs13190874 | C | T | 4 | 0.0237 | 0.2896 | 1.1229 | 1.1074 | 0.042 | 63.42 |
| 2 | 38422312 | rs11679270 | A | C | 4 | 0.2432 | 0.2899 | 0.9576 | 0.8991 | 0.0007 | 82.41 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 2 | 219117933 | rs630858 | A | C | 4 | 0.2155 | 0.2901 | 1.0453 | 1.0833 | 0.0164 | 70.79 |
| 4 | 55661374 | rs17710298 | C | T | 3 | 0.04306 | 0.2903 | 0.7563 | 0.697 | 0.0086 | 78.96 |
| 6 | 94854362 | rs694170 | A | G | 4 | 0.01433 | 0.2903 | 1.0903 | 1.0638 | 0.0907 | 53.65 |
| 3 | 102253981 | rs1375513 | G | T | 4 | 0.3494 | 0.2908 | 1.0434 | 1.1678 | 0 | 88.19 |
| 2 | 107782134 | rs6542736 | A | G | 3 | 0.01208 | 0.291 | 0.9028 | 0.9229 | 0.056 | 65.31 |
| 6 | 94818161 | rs10944713 | A | T | 4 | 0.009731 | 0.291 | 1.0954 | 1.0649 | 0.081 | 55.43 |
| 4 | 116420192 | rs13123243 | A | T | 4 | 0.3629 | 0.2913 | 1.0334 | 1.1022 | 0.0014 | 80.74 |
| 10 | 48000055 | rs17457528 | A | G | 4 | 0.01197 | 0.2915 | 0.8746 | 0.9038 | 0.0513 | 61.34 |
| 12 | 94740811 | rs10859959 | C | T | 4 | 0.02535 | 0.292 | 1.0912 | 1.0724 | 0.0767 | 56.23 |
| 2 | 219173054 | rs832798 | A | G | 4 | 0.2211 | 0.2922 | 1.0448 | 1.0837 | 0.0155 | 71.14 |
| 3 | 102255525 | rs10511182 | C | G | 4 | 0.2501 | 0.2923 | 0.9433 | 0.8456 | 0 | 87.42 |
| 2 | 219132608 | rs576901 | A | G | 4 | 0.2204 | 0.2925 | 0.9571 | 0.9235 | 0.0165 | 70.74 |
| 3 | 102256428 | rs13065684 | C | T | 4 | 0.2517 | 0.2925 | 1.0599 | 1.183 | 0 | 87.49 |
| 6 | 15935963 | rs4712260 | A | G | 4 | 0.02572 | 0.2931 | 1.1208 | 1.1054 | 0.0433 | 63.13 |
| 2 | 219170663 | rs620596 | A | G | 4 | 0.2227 | 0.2933 | 1.0446 | 1.0831 | 0.0162 | 70.88 |
| 6 | 92326845 | rs9345152 | A | G | 4 | 0.5507 | 0.2933 | 0.9753 | 0.902 | 0.0064 | 75.63 |
| 2 | 30859375 | rs6548035 | A | G | 4 | 0.0002261 | 0.2934 | 1.1456 | 1.0851 | 0.0151 | 71.3 |
| 10 | 85953055 | rs7073756 | C | T | 4 | 0.039 | 0.2935 | 0.9185 | 0.9152 | 0.0207 | 69.28 |
| 4 | 116426743 | rs6813599 | A | T | 4 | 0.3613 | 0.2936 | 0.9676 | 0.9076 | 0.0013 | 80.88 |
| 5 | 13558432 | rs4463179 | A | G | 4 | 0.01894 | 0.2937 | 1.1471 | 1.1916 | 0.0002 | 84.93 |
| 19 | 37367247 | rs10411220 | A | G | 4 | 0.684 | 0.2939 | 1.0151 | 1.1102 | 0.0005 | 82.97 |
| 2 | 219151245 | rs562510 | A | C | 4 | 0.2272 | 0.2942 | 0.9577 | 0.9237 | 0.0165 | 70.75 |
| 16 | 56846460 | rs11076229 | A | G | 4 | 0.9318 | 0.2943 | 0.9958 | 0.8798 | 0.0029 | 78.54 |
| 16 | 53285438 | rs17205999 | A | G | 4 | 0.2805 | 0.2944 | 1.04 | 1.0855 | 0.0123 | 72.47 |
| 4 | 127224194 | rs11726082 | C | T | 4 | 0.1235 | 0.2946 | 0.9258 | 0.8984 | 0.0193 | 69.74 |
| 2 | 219150743 | rs3755041 | A | T | 4 | 0.2281 | 0.2947 | 1.0441 | 1.0824 | 0.0167 | 70.69 |
| 2 | 38411164 | rs1375010 | A | G | 4 | 0.2718 | 0.2949 | 0.96 | 0.9008 | 0.0008 | 82.19 |
| 13 | 85339936 | rs9547416 | A | T | 4 | 0.6442 | 0.295 | 0.9839 | 0.9134 | 0.0024 | 79.15 |
| 7 | 78883432 | rs2190179 | A | C | 4 | 0.4203 | 0.2951 | 1.0322 | 1.0989 | 0.0054 | 76.3 |
| 4 | 127248513 | rs17010704 | A | T | 4 | 0.1296 | 0.2953 | 1.0772 | 1.115 | 0.0136 | 71.9 |
| 2 | 38409334 | rs4589732 | C | G | 4 | 0.2879 | 0.2957 | 1.0402 | 1.1097 | 0.0008 | 82.13 |
| 2 | 219149672 | rs647990 | C | T | 4 | 0.2273 | 0.2959 | 1.0444 | 1.0823 | 0.0173 | 70.44 |
| 6 | 99799997 | rs1353588 | A | C | 4 | 0.1503 | 0.2959 | 1.0633 | 1.1023 | 0.0095 | 73.81 |
| 8 | 127608781 | rs6989132 | C | T | 4 | 0.2176 | 0.296 | 1.0606 | 1.1152 | 0.0118 | 72.68 |
| 12 | 104624562 | rs1962255 | A | C | 4 | 0.1494 | 0.2963 | 1.0574 | 1.0927 | 0.0099 | 73.62 |
| 21 | 33678481 | rs7280245 | A | G | 4 | 0.2274 | 0.2964 | 0.9429 | 0.8986 | 0.0137 | 71.87 |
| 13 | 21757174 | rs9510082 | A | G | 4 | 0.0402 | 0.2966 | 1.0781 | 1.0711 | 0.0562 | 60.29 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 13 | 84064321 | rs9546775 | G | T | 4 | 0.2116 | 0.2966 | 1.0663 | 1.1316 | 0.0044 | 77.13 |
| 2 | 219165985 | rs585185 | A | G | 4 | 0.2391 | 0.297 | 1.0442 | 1.086 | 0.0135 | 71.96 |
| 5 | 25914456 | rs6452297 | C | T | 4 | 0.62 | 0.2972 | 1.0187 | 1.1057 | 0.0011 | 81.3 |
| 19 | 40235596 | rs870379 | A | G | 4 | 0.00771 | 0.2974 | 0.9071 | 0.9158 | 0.0058 | 76.01 |
| 3 | 102265765 | rs16843198 | G | T | 4 | 0.2717 | 0.2976 | 0.9457 | 0.8461 | 0 | 87.61 |
| 3 | 124829191 | rs820450 | A | T | 4 | 0.0435 | 0.2978 | 0.9133 | 0.9053 | 0.012 | 72.61 |
| 2 | 172252159 | rs6721680 | G | T | 3 | 0.1964 | 0.298 | 1.0527 | 1.1362 | 0.0003 | 87.68 |
| 1 | 180325179 | rs7537211 | A | G | 4 | 0.3896 | 0.2981 | 1.0322 | 1.0984 | 0.0032 | 78.29 |
| 2 | 172376961 | rs3770451 | G | T | 3 | 0.2036 | 0.2982 | 1.0519 | 1.1309 | 0.0005 | 86.71 |
| 5 | 114734342 | rs7701924 | A | G | 4 | 0.2547 | 0.2982 | 1.0731 | 1.1349 | 0.0207 | 69.27 |
| 4 | 127243008 | rs17010686 | A | G | 4 | 0.1341 | 0.2989 | 0.9291 | 0.8975 | 0.0135 | 71.95 |
| 8 | 140499179 | rs2169623 | A | G | 4 | 0.5863 | 0.2992 | 0.9813 | 0.9211 | 0.0072 | 75.08 |
| 2 | 98867750 | rs1574516 | C | T | 4 | 0.0305 | 0.2995 | 0.8523 | 0.864 | 0.0271 | 67.29 |
| 8 | 127614227 | rs16901493 | G | T | 4 | 0.3054 | 0.2998 | 1.0501 | 1.1138 | 0.0117 | 72.73 |
| 2 | 30859637 | rs6710242 | C | T | 4 | 0.0002199 | 0.3 | 0.8717 | 0.921 | 0.013 | 72.16 |
| 15 | 90026124 | rs11852644 | A | T | 4 | 0.03111 | 0.3001 | 1.1445 | 1.1273 | 0.0425 | 63.3 |
| 22 | 33862734 | rs1473816 | A | G | 4 | 0.05074 | 0.3007 | 1.0848 | 1.1088 | 0.004 | 77.45 |
| 7 | 152433153 | rs760226 | A | G | 4 | 0.09139 | 0.3015 | 1.0652 | 1.099 | 0.0031 | 78.37 |
| 2 | 219018727 | rs4674308 | A | C | 4 | 0.1978 | 0.3016 | 0.955 | 0.924 | 0.0148 | 71.43 |
| 11 | 106197626 | rs1487892 | A | G | 4 | 0.1302 | 0.3019 | 0.9409 | 0.9098 | 0.0073 | 75.04 |
| 5 | 149543189 | rs2240782 | A | C | 3 | 0.004723 | 0.302 | 1.5267 | 1.3109 | 0.2045 | 36.99 |
| 22 | 36129946 | rs6000718 | A | G | 4 | 0.04014 | 0.3021 | 0.9173 | 0.9239 | 0.0495 | 61.73 |
| 2 | 172272168 | rs312925 | A | G | 3 | 0.2019 | 0.3022 | 1.0521 | 1.1354 | 0.0003 | 87.76 |
| 11 | 9802854 | rs360118 | C | G | 4 | 0.02166 | 0.3024 | 1.0906 | 1.0786 | 0.0309 | 66.23 |
| 4 | 10669107 | rs7698375 | A | G | 4 | 0.3893 | 0.3034 | 0.9646 | 0.91 | 0.009 | 74.1 |
| 6 | 94846081 | rs583000 | C | T | 4 | 0.01297 | 0.3035 | 1.0916 | 1.0629 | 0.0837 | 54.94 |
| 6 | 26652089 | rs9461270 | A | G | 4 | 0.01293 | 0.3037 | 0.9103 | 0.9336 | 0.061 | 59.29 |
| 2 | 219038063 | rs664514 | A | G | 4 | 0.2047 | 0.3038 | 0.9549 | 0.9233 | 0.0154 | 71.19 |
| 3 | 124828079 | rs820451 | C | T | 4 | 0.04541 | 0.3041 | 1.094 | 1.1039 | 0.0111 | 73 |
| 16 | 53292008 | rs8044591 | A | C | 4 | 0.2023 | 0.3041 | 1.0486 | 1.0882 | 0.0094 | 73.85 |
| 11 | 106221180 | rs7944123 | A | G | 4 | 0.1521 | 0.3043 | 1.0595 | 1.0954 | 0.011 | 73.07 |
| 19 | 33606816 | rs17685204 | C | T | 4 | 0.4731 | 0.3043 | 1.0422 | 1.1451 | 0.0045 | 77.02 |
| 13 | 43970674 | rs9533877 | A | G | 3 | 0.002112 | 0.3045 | 0.605 | 0.731 | 0.1264 | 51.66 |
| 2 | 219217232 | rs3770214 | C | T | 4 | 0.241 | 0.3046 | 1.0429 | 1.0827 | 0.0134 | 72 |
| 13 | 85345072 | rs366815 | A | G | 4 | 0.6826 | 0.3046 | 0.9857 | 0.9151 | 0.0025 | 79.1 |
| 6 | 30192566 | rs12181054 | G | T | 4 | 0.016 | 0.3047 | 1.1914 | 1.1608 | 0.0248 | 67.96 |
| 2 | 17253381 | rs1589272 | A | G | 4 | 0.4178 | 0.3048 | 1.0375 | 1.1112 | 0.0088 | 74.16 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 20 | 58938883 | rs725475 | C | T | 4 | 0.11 | 0.3052 | 1.0578 | 1.0794 | 0.0145 | 71.53 |
| 1 | 115171509 | rs17536161 | A | G | 4 | 0.09509 | 0.3053 | 1.1569 | 1.2286 | 0.005 | 76.62 |
| 9 | 10624079 | rs10738172 | A | G | 4 | 0.2249 | 0.3053 | 1.0499 | 1.0995 | 0.0051 | 76.52 |
| 7 | 78880949 | rs10238315 | G | T | 4 | 0.4426 | 0.3055 | 0.9701 | 0.9108 | 0.0049 | 76.71 |
| 2 | 219109481 | rs578450 | C | T | 4 | 0.2322 | 0.3056 | 0.9578 | 0.9252 | 0.0172 | 70.51 |
| 6 | 94838264 | rs2535660 | C | T | 4 | 0.01287 | 0.3056 | 0.916 | 0.9408 | 0.0815 | 55.34 |
| 19 | 13277170 | rs8182538 | A | G | 4 | 0.003375 | 0.3056 | 1.1088 | 1.0661 | 0.0606 | 59.36 |
| 4 | 127238127 | rs4530647 | C | T | 4 | 0.1492 | 0.306 | 1.0738 | 1.112 | 0.0147 | 71.44 |
| 16 | 8571064 | rs3924628 | A | G | 4 | 0.008019 | 0.306 | 1.1001 | 1.0753 | 0.0263 | 67.51 |
| 7 | 97262856 | rs13245026 | A | G | 4 | 0.3267 | 0.3061 | 0.9512 | 0.8851 | 0.0038 | 77.64 |
| 19 | 37368934 | rs7260436 | A | C | 4 | 0.799 | 0.3061 | 1.0091 | 1.102 | 0.0007 | 82.34 |
| 11 | 106210532 | rs10890604 | A | G | 4 | 0.1273 | 0.3063 | 0.9404 | 0.9131 | 0.0103 | 73.4 |
| 12 | 114341431 | rs12306540 | A | G | 4 | 0.01328 | 0.3073 | 1.1082 | 1.0805 | 0.0462 | 62.47 |
| 5 | 105619351 | rs13154869 | G | T | 4 | 0.508 | 0.3074 | 0.9703 | 0.8773 | 0.0003 | 84.3 |
| 16 | 53289736 | rs11647205 | A | G | 4 | 0.2081 | 0.3076 | 1.0474 | 1.0866 | 0.0096 | 73.78 |
| 9 | 10614494 | rs10733210 | A | C | 4 | 0.2557 | 0.3078 | 1.0466 | 1.0971 | 0.0063 | 75.72 |
| 7 | 97304570 | rs17344459 | C | T | 4 | 0.3479 | 0.3079 | 0.9541 | 0.8864 | 0.0033 | 78.11 |
| 11 | 106217194 | rs10890608 | A | T | 4 | 0.1301 | 0.308 | 0.9408 | 0.9086 | 0.0055 | 76.29 |
| 2 | 30854671 | rs1568403 | A | G | 4 | 0.0002204 | 0.3082 | 1.1447 | 1.0837 | 0.0124 | 72.4 |
| 2 | 219131764 | rs4674314 | C | T | 4 | 0.2017 | 0.3084 | 0.9553 | 0.9242 | 0.0138 | 71.8 |
| 12 | 130839269 | rs10751693 | A | G | 4 | 0.02008 | 0.3084 | 0.9207 | 0.9391 | 0.0693 | 57.65 |
| 13 | 84081505 | rs9575613 | A | C | 4 | 0.2372 | 0.3084 | 0.9367 | 0.8821 | 0.0063 | 75.71 |
| 10 | 30434183 | rs7915293 | A | G | 4 | 0.000902 | 0.3087 | 0.8829 | 0.9309 | 0.0471 | 62.26 |
| 5 | 25917816 | rs1428660 | C | T | 4 | 0.6387 | 0.3088 | 0.9826 | 0.9075 | 0.0013 | 80.83 |
| 2 | 17261376 | rs11674840 | A | G | 4 | 0.434 | 0.3094 | 0.9655 | 0.9016 | 0.0088 | 74.17 |
| 6 | 94775217 | rs2129857 | C | T | 4 | 0.006583 | 0.3097 | 1.1015 | 1.0673 | 0.0546 | 60.61 |
| 2 | 172315540 | rs10166005 | C | T | 3 | 0.2206 | 0.3099 | 0.9524 | 0.8832 | 0.0003 | 87.6 |
| 6 | 15938880 | rs13218971 | C | T | 4 | 0.02947 | 0.31 | 0.8949 | 0.9066 | 0.0378 | 64.45 |
| 8 | 5526530 | rs2725673 | A | G | 4 | 0.1022 | 0.3101 | 0.9315 | 0.9107 | 0.0134 | 72 |
| 22 | 23895420 | rs7285325 | A | G | 4 | 0.4638 | 0.3103 | 0.9707 | 0.9134 | 0.0111 | 73.02 |
| 3 | 124794918 | rs1268623 | G | T | 4 | 0.03575 | 0.3106 | 1.1009 | 1.1035 | 0.0121 | 72.54 |
| 7 | 97259519 | rs2058106 | A | T | 4 | 0.3251 | 0.3109 | 1.0518 | 1.1283 | 0.0041 | 77.36 |
| 7 | 97269283 | rs459 | C | T | 4 | 0.3306 | 0.3109 | 0.9516 | 0.8859 | 0.0036 | 77.83 |
| 19 | 13277350 | rs4499352 | G | T | 4 | 0.003605 | 0.311 | 1.108 | 1.0654 | 0.0603 | 59.43 |
| 6 | 6092415 | rs7748376 | C | G | 4 | 0.01504 | 0.3111 | 0.8904 | 0.9178 | 0.0602 | 59.46 |
| 20 | 927720 | rs6039433 | C | T | 4 | 0.253 | 0.3111 | 1.0604 | 1.1635 | 0.0001 | 85.25 |
| 21 | 40059369 | rs12626544 | A | G | 3 | 0.0239 | 0.3115 | 0.9162 | 0.9249 | 0.0348 | 70.21 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 2 | 229854835 | rs7579884 | A | G | 4 | 0.02336 | 0.312 | 0.8583 | 0.8717 | 0.0243 | 68.14 |
| 13 | 41469136 | rs7997862 | A | G | 4 | 0.1588 | 0.3125 | 1.0509 | 1.0818 | 0.01 | 73.54 |
| 13 | 84089937 | rs1446792 | A | G | 4 | 0.2502 | 0.3127 | 1.0663 | 1.1332 | 0.0062 | 75.74 |
| 7 | 97270302 | rs12669324 | C | T | 4 | 0.3394 | 0.313 | 1.0496 | 1.1285 | 0.0033 | 78.15 |
| 2 | 219104499 | rs7603816 | C | T | 4 | 0.2231 | 0.3137 | 1.0457 | 1.082 | 0.015 | 71.33 |
| 4 | 140857153 | rs11944843 | A | G | 4 | 0.5364 | 0.3144 | 1.0292 | 1.1164 | 0.0036 | 77.87 |
| 22 | 23885283 | rs16979674 | A | G | 4 | 0.4932 | 0.3144 | 0.9727 | 0.9144 | 0.0109 | 73.13 |
| 13 | 89218832 | rs7329978 | A | G | 4 | 0.2429 | 0.3146 | 0.8806 | 0.7875 | 0.007 | 75.23 |
| 18 | 8866666 | rs7236228 | T | C | 3 | 0.3781 | 0.3146 | 0.9588 | 0.865 | 0.0029 | 82.85 |
| 2 | 78149582 | rs17014922 | C | T | 4 | 0.009114 | 0.3152 | 1.1099 | 1.0963 | 0.0061 | 75.82 |
| 7 | 97262360 | rs993059 | C | T | 4 | 0.3417 | 0.3155 | 1.0497 | 1.1266 | 0.0041 | 77.38 |
| 12 | 130806294 | rs3741526 | C | T | 4 | 0.02228 | 0.3155 | 1.0847 | 1.0657 | 0.0591 | 59.68 |
| 9 | 2705284 | rs11793747 | C | G | 4 | 0.3608 | 0.3156 | 0.9662 | 0.9207 | 0.0116 | 72.77 |
| 5 | 114736927 | rs17137669 | A | G | 4 | 0.2912 | 0.3157 | 1.0669 | 1.1298 | 0.0194 | 69.7 |
| 2 | 184920491 | rs2198715 | C | T | 4 | 0.03017 | 0.3159 | 0.9079 | 0.9285 | 0.0879 | 54.17 |
| 7 | 97288397 | rs7808642 | G | T | 4 | 0.3593 | 0.3163 | 0.9551 | 0.8871 | 0.003 | 78.51 |
| 7 | 97274004 | rs7786920 | C | G | 4 | 0.3433 | 0.3164 | 0.9527 | 0.8862 | 0.0033 | 78.1 |
| 8 | 17547711 | rs1043883 | C | G | 4 | 0.191 | 0.3164 | 0.9532 | 0.9244 | 0.0124 | 72.44 |
| 8 | 14876643 | rs13261120 | C | T | 4 | 0.03261 | 0.3166 | 1.0815 | 1.0702 | 0.0429 | 63.22 |
| 18 | 57433136 | rs1377169 | A | G | 4 | 0.1951 | 0.3166 | 1.06 | 1.1038 | 0.0114 | 72.87 |
| 6 | 6090691 | rs1050783 | C | T | 4 | 0.02497 | 0.3167 | 0.902 | 0.9257 | 0.0859 | 54.52 |
| 5 | 105631852 | rs10479364 | C | T | 4 | 0.5491 | 0.3168 | 0.973 | 0.879 | 0.0002 | 84.47 |
| 1 | 199353517 | rs1536127 | A | C | 4 | 0.1668 | 0.317 | 1.0599 | 1.0919 | 0.0167 | 70.66 |
| 2 | 219242138 | rs2710246 | C | T | 4 | 0.2638 | 0.3173 | 0.9608 | 0.9237 | 0.0104 | 73.35 |
| 7 | 97259532 | rs2058105 | A | T | 4 | 0.3476 | 0.3175 | 0.9532 | 0.888 | 0.0041 | 77.41 |
| 7 | 97260570 | rs11764340 | A | C | 4 | 0.3476 | 0.3175 | 0.9532 | 0.888 | 0.0041 | 77.41 |
| 3 | 124821147 | rs820458 | C | T | 4 | 0.04824 | 0.3187 | 1.0927 | 1.1022 | 0.0096 | 73.76 |
| 7 | 97303824 | rs12668997 | C | T | 4 | 0.3858 | 0.3189 | 0.9578 | 0.889 | 0.0033 | 78.19 |
| 13 | 84102404 | rs9575621 | A | C | 4 | 0.2608 | 0.3194 | 1.0648 | 1.1318 | 0.006 | 75.92 |
| 7 | 97286690 | rs12704945 | A | T | 4 | 0.3605 | 0.3197 | 1.0468 | 1.1263 | 0.003 | 78.49 |
| 5 | 105504488 | rs4527577 | C | T | 4 | 0.6815 | 0.3199 | 1.0178 | 1.111 | 0.0022 | 79.41 |
| 2 | 5606908 | rs13390174 | C | T | 4 | 0.01699 | 0.3205 | 0.9204 | 0.9014 | 0.0001 | 85.93 |
| 15 | 86276360 | rs8041239 | A | G | 4 | 0.01394 | 0.3207 | 1.1154 | 1.0813 | 0.0565 | 60.21 |
| 1 | 75238998 | rs6693646 | G | T | 4 | 0.2424 | 0.321 | 1.0463 | 1.0942 | 0.0045 | 77.07 |
| 9 | 2705349 | rs11789876 | C | T | 4 | 0.3918 | 0.3212 | 1.0328 | 1.0885 | 0.0079 | 74.69 |
| 19 | 37369022 | rs7260548 | C | T | 4 | 0.8477 | 0.3213 | 0.9932 | 0.9124 | 0.0011 | 81.36 |
| 7 | 97297238 | rs2078467 | C | T | 4 | 0.3744 | 0.3215 | 1.0455 | 1.1258 | 0.003 | 78.52 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 16 | 53288365 | rs7206354 | A | C | 4 | 0.2519 | 0.3215 | 0.959 | 0.923 | 0.0098 | 73.64 |
| 5 | 105596842 | rs7705866 | C | T | 4 | 0.5881 | 0.3216 | 1.0249 | 1.1325 | 0.0003 | 83.86 |
| 5 | 114739103 | rs10060558 | C | T | 4 | 0.3037 | 0.3216 | 1.0652 | 1.1293 | 0.018 | 70.21 |
| 5 | 105488872 | rs9327956 | C | T | 4 | 0.6043 | 0.3222 | 1.0244 | 1.1293 | 0.0007 | 82.25 |
| 18 | 5585958 | rs1539811 | C | T | 4 | 0.3087 | 0.3228 | 1.0385 | 1.1134 | 0.0001 | 85.38 |
| 6 | 83341774 | rs9361943 | G | A | 3 | 0.09819 | 0.3234 | 1.2517 | 1.3851 | 0.0075 | 79.56 |
| 2 | 184938744 | rs10200357 | A | T | 4 | 0.03604 | 0.3236 | 1.098 | 1.0758 | 0.0874 | 54.25 |
| 3 | 124801210 | rs861890 | A | G | 4 | 0.04621 | 0.3237 | 0.914 | 0.9083 | 0.0101 | 73.48 |
| 2 | 6830471 | rs17650774 | A | G | 4 | 0.3537 | 0.3239 | 0.9637 | 0.9084 | 0.0022 | 79.39 |
| 16 | 8571128 | rs3924627 | A | G | 4 | 0.00747 | 0.3242 | 0.9081 | 0.9311 | 0.0227 | 68.64 |
| 2 | 184951945 | rs12693375 | C | T | 4 | 0.03536 | 0.3244 | 1.0984 | 1.0759 | 0.0857 | 54.57 |
| 2 | 5606432 | rs2882274 | C | T | 4 | 0.01839 | 0.3249 | 0.9206 | 0.9027 | 0.0001 | 85.62 |
| 7 | 152433675 | rs760228 | C | T | 4 | 0.1414 | 0.3249 | 1.0558 | 1.093 | 0.0034 | 78.07 |
| 7 | 26559015 | rs12672384 | C | T | 4 | 0.6486 | 0.325 | 1.0195 | 1.1125 | 0.0012 | 81.11 |
| 13 | 21757408 | rs2038711 | C | T | 4 | 0.03088 | 0.3251 | 0.9253 | 0.9339 | 0.0334 | 65.56 |
| 2 | 155411314 | rs1900132 | A | G | 4 | 0.02616 | 0.3253 | 1.0889 | 1.0702 | 0.0559 | 60.34 |
| 4 | 140897320 | rs3796632 | C | T | 4 | 0.06857 | 0.3254 | 1.2119 | 1.2609 | 0.0171 | 70.53 |
| 14 | 78058257 | rs11622407 | G | T | 4 | 0.2391 | 0.3254 | 1.0424 | 1.0751 | 0.0167 | 70.66 |
| 5 | 105575000 | rs10073985 | C | T | 4 | 0.5896 | 0.3258 | 0.9749 | 0.882 | 0.0004 | 83.33 |
| 20 | 58927301 | rs2426960 | A | G | 4 | 0.08209 | 0.3261 | 1.0627 | 1.0797 | 0.0086 | 74.28 |
| 6 | 99005968 | rs3123337 | C | T | 4 | 0.004916 | 0.3262 | 0.7623 | 0.8413 | 0.0372 | 64.58 |
| 6 | 117192477 | rs693602 | A | C | 4 | 0.04421 | 0.3262 | 0.9277 | 0.9271 | 0.0219 | 68.87 |
| 3 | 124810365 | rs4530474 | C | T | 4 | 0.04854 | 0.3264 | 1.0926 | 1.1011 | 0.009 | 74.07 |
| 5 | 105490206 | rs1435195 | C | G | 4 | 0.6615 | 0.3278 | 1.0203 | 1.134 | 0.0002 | 84.47 |
| 10 | 6544142 | rs678304 | C | G | 4 | 0.2883 | 0.3279 | 1.0423 | 1.0885 | 0.0086 | 74.28 |
| 3 | 124806457 | rs848146 | C | G | 4 | 0.05019 | 0.3284 | 1.092 | 1.1034 | 0.0068 | 75.37 |
| 1 | 205560841 | rs6685886 | A | C | 3 | 0.3779 | 0.3288 | 1.0334 | 1.1015 | 0.0027 | 83.12 |
| 16 | 7338583 | rs9936914 | A | T | 4 | 0.01453 | 0.3288 | 1.1536 | 1.1035 | 0.0753 | 56.49 |
| 3 | 102125413 | rs7431835 | A | T | 4 | 0.56 | 0.3294 | 1.0291 | 1.1895 | 0 | 90.69 |
| 3 | 124830480 | rs820448 | C | G | 4 | 0.05226 | 0.3298 | 0.9161 | 0.9072 | 0.0078 | 74.74 |
| 14 | 78048581 | rs11626916 | A | G | 4 | 0.2469 | 0.3298 | 0.96 | 0.9309 | 0.0172 | 70.49 |
| 7 | 152440071 | rs760229 | A | G | 4 | 0.1168 | 0.3301 | 0.9435 | 0.9184 | 0.0048 | 76.76 |
| 3 | 102252014 | rs13099753 | C | G | 4 | 0.44 | 0.3304 | 0.9653 | 0.8592 | 0 | 89.48 |
| 3 | 102130439 | rs2576377 | C | T | 4 | 0.5773 | 0.3305 | 1.0271 | 1.1938 | 0 | 91.5 |
| 5 | 175193656 | rs10061059 | A | G | 4 | 0.02279 | 0.3306 | 0.9077 | 0.9282 | 0.0565 | 60.23 |
| 14 | 94460547 | rs3861665 | A | G | 4 | 0.4271 | 0.3307 | 1.0373 | 1.1125 | 0.0066 | 75.51 |
| 22 | 33922689 | rs4821376 | A | G | 4 | 0.04027 | 0.3308 | 1.0822 | 1.0746 | 0.0351 | 65.12 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 14 | 78050487 | rs727208 | A | C | 4 | 0.2492 | 0.3311 | 1.0414 | 1.0744 | 0.0164 | 70.8 |
| 22 | 33934502 | rs3918439 | C | G | 4 | 0.04089 | 0.3311 | 0.9242 | 0.9311 | 0.0378 | 64.44 |
| 20 | 58941909 | rs6071442 | C | T | 4 | 0.1136 | 0.3312 | 0.9458 | 0.9288 | 0.0123 | 72.49 |
| 2 | 184931648 | rs17429535 | C | T | 4 | 0.03331 | 0.3314 | 0.91 | 0.9301 | 0.0814 | 55.35 |
| 22 | 33936111 | rs5999766 | C | T | 4 | 0.04101 | 0.3317 | 0.9242 | 0.9312 | 0.0379 | 64.42 |
| 2 | 184932641 | rs10203961 | C | T | 4 | 0.03302 | 0.3318 | 1.099 | 1.0752 | 0.0807 | 55.48 |
| 5 | 105596450 | rs10040995 | C | T | 4 | 0.6351 | 0.3318 | 0.9786 | 0.8848 | 0.0003 | 84.01 |
| 19 | 13277280 | rs4433935 | C | T | 4 | 0.004548 | 0.3319 | 0.9048 | 0.9409 | 0.0589 | 59.73 |
| 4 | 71017595 | rs1709257 | A | C | 4 | 0.1044 | 0.3321 | 1.1771 | 1.2549 | 0.003 | 78.44 |
| 1 | 199354868 | rs7547762 | A | G | 4 | 0.183 | 0.3325 | 0.9469 | 0.9141 | 0.0074 | 75.02 |
| 7 | 78868858 | rs4730806 | A | C | 4 | 0.5606 | 0.3326 | 0.9776 | 0.9187 | 0.0069 | 75.29 |
| 20 | 49473493 | rs6067766 | A | G | 4 | 0.5369 | 0.3328 | 0.9639 | 0.8808 | 0.0141 | 71.69 |
| 22 | 33922615 | rs4821375 | C | T | 4 | 0.04068 | 0.3328 | 1.0821 | 1.0742 | 0.0354 | 65.05 |
| 3 | 124812622 | rs2626028 | C | T | 4 | 0.05099 | 0.3329 | 1.0916 | 1.1009 | 0.008 | 74.66 |
| 3 | 102160572 | rs2595894 | C | G | 4 | 0.5532 | 0.3331 | 0.9713 | 0.8441 | 0 | 90.43 |
| 7 | 152436044 | rs498474 | A | G | 4 | 0.1104 | 0.3331 | 0.9408 | 0.9128 | 0.0029 | 78.58 |
| 7 | 152436388 | rs594243 | C | T | 4 | 0.1121 | 0.3333 | 1.0626 | 1.0953 | 0.0029 | 78.52 |
| 3 | 27918162 | rs2618115 | A | G | 4 | 0.04726 | 0.3336 | 0.8907 | 0.9051 | 0.0571 | 60.09 |
| 3 | 102159700 | rs2576391 | C | G | 4 | 0.5597 | 0.3341 | 1.029 | 1.1842 | 0 | 90.42 |
| 3 | 102172552 | rs10511181 | G | T | 4 | 0.5676 | 0.3341 | 1.0284 | 1.1843 | 0 | 90.43 |
| 7 | 152435872 | rs496724 | A | G | 4 | 0.1119 | 0.3342 | 1.0626 | 1.0954 | 0.0029 | 78.62 |
| 1 | 119091517 | rs2147780 | A | G | 3 | 0.03253 | 0.3343 | 1.2536 | 1.2369 | 0.0336 | 70.53 |
| 9 | 10654583 | rs10756092 | A | C | 4 | 0.3994 | 0.3344 | 0.9584 | 0.8818 | 0.001 | 81.67 |
| 22 | 33921035 | rs134434 | A | G | 4 | 0.04092 | 0.3345 | 1.082 | 1.074 | 0.0351 | 65.11 |
| 8 | 54439800 | rs7465458 | A | G | 4 | 0.01324 | 0.3346 | 1.1248 | 1.0914 | 0.0354 | 65.04 |
| 3 | 124805854 | rs820479 | A | G | 4 | 0.05159 | 0.3349 | 0.9163 | 0.9089 | 0.0081 | 74.58 |
| 7 | 152436337 | rs593874 | A | G | 4 | 0.1149 | 0.335 | 1.0621 | 1.095 | 0.0029 | 78.52 |
| 14 | 78048416 | rs11159368 | A | C | 4 | 0.2562 | 0.335 | 0.9608 | 0.9314 | 0.0167 | 70.67 |
| 3 | 102130617 | rs13060137 | A | G | 4 | 0.5982 | 0.3351 | 0.9744 | 0.8424 | 0 | 90.69 |
| 3 | 102127637 | rs17284842 | C | T | 4 | 0.5989 | 0.3353 | 1.0262 | 1.187 | 0 | 90.69 |
| 1 | 75241712 | rs12750340 | C | T | 4 | 0.2745 | 0.3355 | 0.958 | 0.9168 | 0.0055 | 76.27 |
| 3 | 102132997 | rs13077353 | G | T | 4 | 0.6001 | 0.3355 | 1.0261 | 1.1867 | 0 | 90.67 |
| 10 | 6544132 | rs604663 | C | T | 4 | 0.2729 | 0.3357 | 0.9624 | 0.9264 | 0.0073 | 75.07 |
| 7 | 26560257 | rs12670740 | C | T | 4 | 0.6474 | 0.3359 | 0.9808 | 0.904 | 0.0019 | 79.86 |
| 1 | 119091964 | rs6704254 | C | T | 3 | 0.03286 | 0.336 | 1.253 | 1.2364 | 0.0332 | 70.63 |
| 3 | 102125494 | rs1036467 | C | T | 4 | 0.6037 | 0.336 | 0.9748 | 0.8426 | 0 | 90.69 |
| 9 | 10655040 | rs4272438 | A | T | 4 | 0.4045 | 0.336 | 0.9588 | 0.882 | 0.0009 | 81.71 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 1 | 75235049 | rs3912426 | A | G | 4 | 0.2848 | 0.3362 | 1.0422 | 1.091 | 0.0045 | 77.01 |
| 6 | 94846661 | rs2535672 | A | G | 4 | 0.01335 | 0.3363 | 0.9162 | 0.943 | 0.0748 | 56.59 |
| 20 | 19705555 | rs6035436 | C | G | 4 | 0.227 | 0.3363 | 0.9297 | 0.8744 | 0.004 | 77.45 |
| 11 | 9273306 | rs4396289 | C | T | 4 | 0.04061 | 0.3365 | 1.1023 | 1.1032 | 0.0113 | 72.92 |
| 7 | 152436277 | rs593793 | A | G | 4 | 0.1159 | 0.3366 | 0.9417 | 0.9134 | 0.0029 | 78.58 |
| 3 | 102178032 | rs17398684 | A | G | 4 | 0.5843 | 0.3367 | 1.0272 | 1.1832 | 0 | 90.43 |
| 8 | 54436653 | rs7001769 | C | T | 4 | 0.01604 | 0.3367 | 0.892 | 0.9178 | 0.0397 | 63.96 |
| 3 | 29757722 | rs17024316 | C | G | 4 | 0.3014 | 0.3371 | 0.9628 | 0.9263 | 0.0105 | 73.31 |
| 3 | 102170772 | rs13088524 | A | C | 4 | 0.5878 | 0.3371 | 0.9737 | 0.8451 | 0 | 90.45 |
| 6 | 94798859 | rs2129859 | A | C | 4 | 0.01234 | 0.3373 | 1.0924 | 1.0604 | 0.0716 | 57.2 |
| 9 | 10654367 | rs4262363 | A | G | 4 | 0.3935 | 0.3373 | 1.044 | 1.1335 | 0.0009 | 81.84 |
| 16 | 26654324 | rs500285 | C | G | 4 | 0.03159 | 0.3373 | 0.8445 | 0.8646 | 0.0306 | 66.3 |
| 3 | 102155597 | rs17398421 | G | T | 4 | 0.581 | 0.3374 | 1.0275 | 1.1829 | 0 | 90.43 |
| 14 | 78048235 | rs10782463 | C | T | 4 | 0.2616 | 0.338 | 1.0404 | 1.073 | 0.0169 | 70.59 |
| 2 | 184940461 | rs13015290 | A | T | 4 | 0.03771 | 0.3382 | 0.9115 | 0.9307 | 0.0811 | 55.41 |
| 9 | 10651622 | rs7030381 | A | G | 4 | 0.3941 | 0.3382 | 1.0429 | 1.1305 | 0.0009 | 81.85 |
| 17 | 24496369 | rs12452739 | A | G | 4 | 0.3801 | 0.3384 | 0.9654 | 0.9194 | 0.0107 | 73.23 |
| 3 | 102150519 | rs2576382 | A | T | 4 | 0.5981 | 0.3385 | 0.9744 | 0.8437 | 0 | 90.67 |
| 14 | 78048326 | rs11159367 | A | G | 4 | 0.2626 | 0.3385 | 0.9613 | 0.932 | 0.017 | 70.55 |
| 3 | 144996927 | rs11706302 | A | G | 3 | 0.0004623 | 0.3386 | 0.8403 | 0.8993 | 0.0175 | 75.28 |
| 2 | 98846759 | rs4851164 | C | T | 4 | 0.0449 | 0.3388 | 0.8641 | 0.8687 | 0.0167 | 70.69 |
| 7 | 152434353 | rs672366 | C | G | 4 | 0.1097 | 0.3388 | 0.9407 | 0.9134 | 0.0027 | 78.81 |
| 9 | 10651798 | rs7030672 | C | G | 4 | 0.3997 | 0.3388 | 1.0426 | 1.1307 | 0.0009 | 81.75 |
| 1 | 75219251 | rs2346344 | G | T | 4 | 0.2872 | 0.3389 | 0.9597 | 0.9163 | 0.004 | 77.43 |
| 6 | 6092368 | rs7748218 | C | T | 4 | 0.02707 | 0.3389 | 0.9033 | 0.9281 | 0.0801 | 55.6 |
| 9 | 10652358 | rs7034568 | C | T | 4 | 0.4031 | 0.3389 | 1.0426 | 1.1317 | 0.0009 | 81.81 |
| 3 | 102160532 | rs2595893 | C | T | 4 | 0.5918 | 0.339 | 1.0267 | 1.1823 | 0 | 90.44 |
| 5 | 13541819 | rs3853117 | C | T | 4 | 0.007902 | 0.3391 | 0.8687 | 0.8631 | 0.0001 | 85.45 |
| 13 | 84112297 | rs13378761 | A | C | 4 | 0.2979 | 0.3391 | 1.0598 | 1.13 | 0.0042 | 77.25 |
| 3 | 178791718 | rs552757 | A | G | 4 | 0.03495 | 0.3393 | 0.9252 | 0.935 | 0.0371 | 64.61 |
| 9 | 10651370 | rs10756088 | A | G | 4 | 0.3986 | 0.3394 | 0.9593 | 0.8848 | 0.0009 | 81.84 |
| 9 | 10652166 | rs7019756 | C | T | 4 | 0.4095 | 0.3395 | 0.9599 | 0.8844 | 0.0009 | 81.76 |
| 2 | 105447653 | rs9989768 | C | T | 4 | 0.05253 | 0.3396 | 1.1438 | 1.1563 | 0.0099 | 73.63 |
| 6 | 6092904 | rs7772909 | C | T | 4 | 0.0267 | 0.3401 | 1.1073 | 1.0775 | 0.0788 | 55.84 |
| 2 | 78148150 | rs17014915 | C | T | 4 | 0.01122 | 0.3402 | 1.1068 | 1.0926 | 0.0053 | 76.41 |
| 12 | 104624341 | rs11833072 | C | T | 4 | 0.2203 | 0.3404 | 0.9532 | 0.9183 | 0.0061 | 75.82 |
| 18 | 57455551 | rs12457154 | A | G | 4 | 0.2524 | 0.3405 | 1.0532 | 1.0976 | 0.0138 | 71.81 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 75199985 | rs11162286 | A | G | 4 | 0.3131 | 0.3406 | 1.0398 | 1.0912 | 0.004 | 77.47 |
| 14 | 78085918 | rs10483907 | A | G | 4 | 0.2673 | 0.3406 | 1.0399 | 1.0735 | 0.0153 | 71.2 |
| 22 | 33926311 | rs4618151 | A | C | 4 | 0.04395 | 0.3406 | 0.9253 | 0.9326 | 0.0378 | 64.45 |
| 9 | 10649290 | rs4641116 | C | T | 4 | 0.3828 | 0.3407 | 0.9582 | 0.8857 | 0.0008 | 81.96 |
| 2 | 38204318 | rs3795980 | G | T | 4 | 0.009445 | 0.341 | 0.8745 | 0.897 | 0.0091 | 74 |
| 6 | 6089856 | rs3024466 | A | C | 4 | 0.02889 | 0.3412 | 1.1057 | 1.0767 | 0.0823 | 55.18 |
| 2 | 160112937 | rs6742654 | C | T | 4 | 0.01718 | 0.3414 | 1.1415 | 1.0995 | 0.0516 | 61.27 |
| 15 | 52099177 | rs12592703 | C | T | 4 | 0.6946 | 0.3414 | 0.9832 | 0.9014 | 0.0015 | 80.49 |
| 20 | 19724391 | rs16981125 | A | G | 4 | 0.2517 | 0.3414 | 0.9336 | 0.8748 | 0.0035 | 77.97 |
| 18 | 57455491 | rs12454424 | A | G | 4 | 0.2544 | 0.3418 | 0.9497 | 0.9113 | 0.0138 | 71.82 |
| 5 | 175189132 | rs1863931 | A | G | 4 | 0.02586 | 0.3419 | 0.9083 | 0.9289 | 0.0571 | 60.1 |
| 17 | 12110529 | rs16945798 | G | A | 3 | 0.7056 | 0.3425 | 0.9694 | 0.7524 | 0.0014 | 84.7 |
| 17 | 12103857 | rs714422 | A | G | 3 | 0.7377 | 0.3426 | 0.9729 | 0.7513 | 0.0013 | 84.94 |
| 3 | 102248274 | rs13074729 | G | T | 4 | 0.4108 | 0.3427 | 0.9595 | 0.8483 | 0 | 89.76 |
| 22 | 33933022 | rs738440 | C | T | 4 | 0.04414 | 0.3427 | 1.0807 | 1.0726 | 0.0358 | 64.94 |
| 4 | 116592228 | rs6533889 | G | T | 4 | 0.6026 | 0.3429 | 0.9811 | 0.9203 | 0.0037 | 77.8 |
| 18 | 57445327 | rs12454307 | C | T | 4 | 0.2412 | 0.343 | 0.9487 | 0.9093 | 0.0094 | 73.85 |
| 9 | 119033609 | rs12237890 | A | T | 4 | 0.009334 | 0.3434 | 1.2195 | 1.1463 | 0.0448 | 62.78 |
| 11 | 106389222 | rs11212007 | A | C | 4 | 0.146 | 0.3434 | 0.9404 | 0.9124 | 0.0069 | 75.31 |
| 4 | 114747468 | rs6857556 | A | G | 4 | 0.3487 | 0.3435 | 1.069 | 1.1506 | 0.0125 | 72.4 |
| 9 | 10658198 | rs7045753 | C | T | 4 | 0.4084 | 0.3438 | 0.958 | 0.8817 | 0.001 | 81.58 |
| 3 | 44994064 | rs4683014 | A | G | 4 | 0.2705 | 0.344 | 0.9624 | 0.9304 | 0.0115 | 72.82 |
| 4 | 13358506 | rs4698460 | G | T | 4 | 0.4235 | 0.3446 | 0.9674 | 0.9131 | 0.0063 | 75.66 |
| 8 | 17545472 | rs3817664 | G | T | 4 | 0.2276 | 0.3447 | 1.0459 | 1.0792 | 0.0106 | 73.24 |
| 1 | 75215582 | rs7522882 | A | T | 4 | 0.3053 | 0.3448 | 0.9611 | 0.9174 | 0.0041 | 77.36 |
| 18 | 57438389 | rs11876431 | A | G | 4 | 0.2409 | 0.3449 | 1.0541 | 1.097 | 0.0123 | 72.48 |
| 14 | 42258065 | rs10498375 | A | C | 4 | 0.1188 | 0.3454 | 0.8975 | 0.8597 | 0.0058 | 76.06 |
| 1 | 55469135 | rs7512894 | A | G | 4 | 0.007617 | 0.3456 | 0.8896 | 0.9272 | 0.0507 | 61.45 |
| 7 | 26566825 | rs12671326 | C | T | 4 | 0.6716 | 0.3461 | 0.9822 | 0.9087 | 0.003 | 78.5 |
| 10 | 85963395 | rs10887256 | C | G | 4 | 0.06447 | 0.3461 | 0.926 | 0.9213 | 0.0174 | 70.44 |
| 14 | 78086868 | rs1015964 | A | G | 4 | 0.2703 | 0.3461 | 0.9616 | 0.9317 | 0.0148 | 71.4 |
| 4 | 116462047 | rs1507942 | A | T | 4 | 0.3188 | 0.3463 | 1.039 | 1.0812 | 0.0111 | 73.03 |
| 22 | 33925331 | rs134442 | C | T | 4 | 0.04492 | 0.3467 | 1.0803 | 1.072 | 0.0352 | 65.09 |
| 14 | 78087589 | rs2098518 | C | G | 4 | 0.2496 | 0.347 | 0.9599 | 0.9273 | 0.0074 | 74.98 |
| 20 | 19708160 | rs17298185 | A | G | 4 | 0.2455 | 0.3471 | 1.0725 | 1.1413 | 0.0037 | 77.76 |
| 21 | 16556290 | rs2823718 | A | G | 4 | 0.03722 | 0.3471 | 1.0768 | 1.0892 | 0.0014 | 80.78 |
| 7 | 48310276 | rs6943725 | A | G | 4 | 0.3818 | 0.3475 | 1.0312 | 1.0764 | 0.0095 | 73.81 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 1 | 75222180 | rs3845358 | A | C | 4 | 0.3149 | 0.3479 | 1.0396 | 1.0892 | 0.0042 | 77.25 |
| 17 | 12108360 | rs12150546 | G | A | 3 | 0.7835 | 0.3482 | 0.9779 | 0.7535 | 0.0013 | 84.97 |
| 4 | 92459915 | rs6816636 | A | C | 4 | 0.3216 | 0.3488 | 1.0422 | 1.1062 | 0.0014 | 80.73 |
| 3 | 102108512 | rs13072000 | A | G | 4 | 0.5664 | 0.3489 | 0.9722 | 0.8452 | 0 | 90.85 |
| 8 | 32646497 | rs2919390 | A | C | 4 | 0.3037 | 0.3489 | 1.0375 | 1.0905 | 0.0014 | 80.65 |
| 10 | 125987432 | rs4303189 | A | G | 4 | 0.3745 | 0.3489 | 1.0874 | 1.2037 | 0.0111 | 73.02 |
| 18 | 5575158 | rs1719934 | A | G | 4 | 0.4445 | 0.349 | 1.0277 | 1.0983 | 0.0003 | 83.84 |
| 3 | 102102450 | rs4928096 | A | G | 4 | 0.5597 | 0.3494 | 0.9719 | 0.8456 | 0 | 90.91 |
| 3 | 102105082 | rs9832195 | A | C | 4 | 0.551 | 0.3494 | 1.0297 | 1.183 | 0 | 90.88 |
| 18 | 64661900 | rs9962491 | C | T | 4 | 0.02016 | 0.3495 | 0.9128 | 0.935 | 0.0503 | 61.54 |
| 5 | 16935090 | rs16869212 | A | G | 4 | 0.01498 | 0.3496 | 1.1789 | 1.1476 | 0.0117 | 72.75 |
| 5 | 105458740 | rs1991970 | A | C | 4 | 0.7043 | 0.3496 | 1.0179 | 1.1251 | 0.0005 | 83.05 |
| 3 | 102107128 | rs2713787 | C | G | 4 | 0.5546 | 0.3501 | 0.9714 | 0.8453 | 0 | 90.91 |
| 15 | 31694343 | rs11637847 | A | G | 4 | 0.6686 | 0.3501 | 0.9848 | 0.928 | 0.0087 | 74.25 |
| 4 | 116558768 | rs6847969 | A | G | 4 | 0.4548 | 0.3502 | 0.9734 | 0.9252 | 0.0058 | 76.04 |
| 6 | 94798998 | rs2171518 | C | T | 4 | 0.01296 | 0.3503 | 0.9161 | 0.9443 | 0.0684 | 57.82 |
| 7 | 152452942 | rs4726247 | A | G | 4 | 0.1055 | 0.3504 | 0.9418 | 0.9198 | 0.0035 | 77.91 |
| 5 | 105649426 | rs13361333 | C | T | 4 | 0.4767 | 0.3505 | 1.0342 | 1.1175 | 0.0017 | 80.22 |
| 3 | 102107251 | rs4060963 | A | G | 4 | 0.5573 | 0.3506 | 1.0293 | 1.1828 | 0 | 90.91 |
| 22 | 33903856 | rs134386 | C | T | 4 | 0.04541 | 0.3506 | 1.0801 | 1.0735 | 0.0285 | 66.89 |
| 5 | 105632419 | rs6883970 | C | T | 4 | 0.6594 | 0.3507 | 0.9809 | 0.903 | 0.0018 | 79.96 |
| 3 | 102101864 | rs2713793 | A | G | 4 | 0.5474 | 0.3508 | 1.0302 | 1.1822 | 0 | 90.75 |
| 3 | 102104116 | rs2576365 | A | C | 4 | 0.5598 | 0.3509 | 0.9718 | 0.8455 | 0 | 90.91 |
| 4 | 149810031 | rs2358469 | A | G | 4 | 0.03947 | 0.3509 | 0.9248 | 0.9358 | 0.0394 | 64.05 |
| 5 | 105644816 | rs6891526 | A | G | 4 | 0.6472 | 0.3513 | 1.0203 | 1.1086 | 0.0017 | 80.22 |
| 14 | 78053255 | rs11629123 | C | T | 4 | 0.266 | 0.3514 | 0.9615 | 0.928 | 0.0069 | 75.32 |
| 3 | 102112831 | rs13079002 | C | T | 4 | 0.5844 | 0.3515 | 0.9735 | 0.8455 | 0 | 90.9 |
| 6 | 6095762 | rs4960167 | C | T | 4 | 0.0255 | 0.3515 | 0.9024 | 0.9279 | 0.0675 | 58 |
| 2 | 98853280 | rs17022034 | A | T | 4 | 0.04659 | 0.3516 | 0.8646 | 0.8704 | 0.0152 | 71.26 |
| 13 | 84114641 | rs9602525 | A | T | 4 | 0.3113 | 0.3516 | 1.0582 | 1.1271 | 0.0041 | 77.35 |
| 2 | 83399672 | rs12232909 | A | G | 4 | 0.4005 | 0.3517 | 0.9709 | 0.9282 | 0.007 | 75.22 |
| 2 | 219004789 | rs17572485 | A | G | 4 | 0.2214 | 0.3517 | 0.9571 | 0.9289 | 0.0112 | 72.97 |
| 3 | 102100845 | rs2576369 | A | G | 4 | 0.5517 | 0.3517 | 0.971 | 0.8462 | 0 | 90.73 |
| 3 | 102101463 | rs2245266 | C | T | 4 | 0.5517 | 0.3517 | 0.971 | 0.8462 | 0 | 90.73 |
| 22 | 33870423 | rs5999742 | A | G | 4 | 0.02082 | 0.3523 | 1.0958 | 1.0886 | 0.0061 | 75.86 |
| 9 | 10647332 | rs4578000 | A | G | 4 | 0.3879 | 0.3526 | 0.9585 | 0.8879 | 0.0008 | 81.94 |
| 21 | 29968170 | rs363550 | C | G | 4 | 0.2645 | 0.3526 | 0.8985 | 0.834 | 0.0167 | 70.67 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 12 | 114335802 | rs768860 | G | T | 4 | 0.01217 | 0.3527 | 1.1104 | 1.0757 | 0.0373 | 64.57 |
| 3 | 102111994 | rs2713782 | A | G | 4 | 0.5822 | 0.3528 | 0.9732 | 0.8457 | 0 | 90.85 |
| 8 | 140497987 | rs9324508 | A | G | 4 | 0.5588 | 0.353 | 1.0246 | 1.0914 | 0.0066 | 75.52 |
| 20 | 58942206 | rs6128962 | A | G | 4 | 0.1338 | 0.353 | 0.9485 | 0.9314 | 0.0115 | 72.84 |
| 5 | 105507616 | rs12719550 | A | T | 4 | 0.6796 | 0.3531 | 0.9807 | 0.889 | 0.0005 | 82.93 |
| 20 | 58926954 | rs2024676 | A | G | 4 | 0.1149 | 0.3531 | 1.0571 | 1.0754 | 0.0089 | 74.13 |
| 4 | 116502459 | rs10000358 | A | G | 4 | 0.446 | 0.3532 | 1.0281 | 1.0796 | 0.0069 | 75.32 |
| 12 | 114336692 | rs7964025 | A | G | 4 | 0.01256 | 0.3534 | 0.901 | 0.9299 | 0.038 | 64.39 |
| 9 | 10645642 | rs10756076 | A | G | 4 | 0.3915 | 0.3535 | 1.043 | 1.1254 | 0.0009 | 81.77 |
| 6 | 30203582 | rs10947056 | C | G | 4 | 0.01694 | 0.3536 | 0.8409 | 0.8729 | 0.0218 | 68.91 |
| 9 | 10645189 | rs10809145 | A | G | 4 | 0.3913 | 0.3541 | 1.0433 | 1.1253 | 0.001 | 81.65 |
| 20 | 19730288 | rs17298654 | G | T | 4 | 0.265 | 0.3542 | 1.0689 | 1.1371 | 0.0041 | 77.34 |
| 2 | 98860167 | rs4851166 | C | T | 4 | 0.03914 | 0.3546 | 0.858 | 0.8722 | 0.0185 | 70.04 |
| 6 | 25280013 | rs6910965 | C | G | 4 | 0.003173 | 0.3547 | 0.8749 | 0.9208 | 0.0265 | 67.47 |
| 6 | 30134215 | rs12208867 | A | G | 4 | 0.005102 | 0.3547 | 1.2336 | 1.1631 | 0.0099 | 73.61 |
| 12 | 130809881 | rs10751692 | C | T | 4 | 0.02612 | 0.3547 | 0.924 | 0.9423 | 0.0538 | 60.8 |
| 4 | 116514942 | rs7436414 | A | G | 4 | 0.4544 | 0.3553 | 0.9732 | 0.9266 | 0.0068 | 75.33 |
| 7 | 152436269 | rs521309 | A | G | 4 | 0.1048 | 0.3553 | 0.9369 | 0.9141 | 0.004 | 77.51 |
| 9 | 10629445 | rs4741044 | A | G | 4 | 0.3948 | 0.3553 | 0.9588 | 0.8915 | 0.0014 | 80.65 |
| 21 | 16557827 | rs2823722 | C | T | 4 | 0.05508 | 0.3554 | 0.9314 | 0.9149 | 0.001 | 81.54 |
| 2 | 30848531 | rs4952179 | C | T | 4 | 0.003139 | 0.3558 | 0.8925 | 0.9317 | 0.0272 | 67.26 |
| 1 | 48877073 | rs12562662 | C | T | 4 | 0.5069 | 0.3559 | 1.0493 | 1.1632 | 0.0054 | 76.33 |
| 4 | 116481279 | rs12650886 | C | T | 4 | 0.4281 | 0.3563 | 1.0292 | 1.0772 | 0.0088 | 74.16 |
| 7 | 26562895 | rs2286180 | C | G | 4 | 0.7205 | 0.3565 | 1.0152 | 1.0993 | 0.0026 | 78.95 |
| 13 | 84121490 | rs9565956 | C | T | 4 | 0.3346 | 0.3567 | 1.0554 | 1.127 | 0.0037 | 77.78 |
| 1 | 48896154 | rs7556311 | A | G | 4 | 0.2484 | 0.3568 | 1.092 | 1.1679 | 0.0075 | 74.95 |
| 20 | 19725525 | rs6136836 | C | T | 4 | 0.281 | 0.3571 | 1.0667 | 1.1391 | 0.0031 | 78.31 |
| 4 | 92459825 | rs6532289 | C | T | 4 | 0.3147 | 0.3575 | 0.9612 | 0.9118 | 0.0018 | 80.01 |
| 4 | 116537368 | rs6533870 | A | G | 4 | 0.4801 | 0.3575 | 1.0258 | 1.0801 | 0.0054 | 76.34 |
| 7 | 152437650 | rs2018083 | A | G | 4 | 0.1222 | 0.3576 | 1.059 | 1.0852 | 0.0039 | 77.54 |
| 12 | 51731549 | rs10747658 | A | G | 4 | 0.09068 | 0.3576 | 0.9393 | 0.921 | 0.0064 | 75.64 |
| 12 | 128847165 | rs10773708 | A | G | 4 | 0.04136 | 0.3576 | 0.925 | 0.934 | 0.0331 | 65.63 |
| 4 | 116501880 | rs7437909 | C | T | 4 | 0.4589 | 0.3577 | 0.9734 | 0.9268 | 0.0067 | 75.43 |
| 9 | 10647075 | rs4587381 | G | T | 4 | 0.4029 | 0.3578 | 1.042 | 1.1252 | 0.0008 | 82.06 |
| 14 | 78035507 | rs1122840 | A | G | 4 | 0.2696 | 0.3583 | 1.0399 | 1.0754 | 0.0084 | 74.41 |
| 22 | 33932582 | rs7284380 | A | G | 4 | 0.04899 | 0.3583 | 1.0788 | 1.0708 | 0.0334 | 65.55 |
| 2 | 38406957 | rs6745929 | C | T | 4 | 0.4742 | 0.3584 | 1.0295 | 1.1146 | 0.0002 | 84.93 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 5 | 105495362 | rs972529 | A | C | 4 | 0.7036 | 0.3587 | 0.9822 | 0.8896 | 0.0005 | 83.16 |
| 13 | 89217299 | rs10851281 | A | G | 4 | 0.2728 | 0.3588 | 0.8876 | 0.8041 | 0.0068 | 75.36 |
| 9 | 10645366 | rs10809147 | C | T | 4 | 0.4054 | 0.359 | 0.9597 | 0.8894 | 0.0009 | 81.77 |
| 13 | 89220997 | rs6492451 | C | T | 4 | 0.2852 | 0.359 | 1.1235 | 1.2432 | 0.0072 | 75.11 |
| 3 | 102098826 | rs2245473 | A | G | 4 | 0.5735 | 0.3595 | 0.9724 | 0.8481 | 0 | 90.72 |
| 14 | 78084707 | rs11844960 | A | C | 4 | 0.3041 | 0.3595 | 1.0369 | 1.0713 | 0.0139 | 71.77 |
| 4 | 116508739 | rs7685112 | C | T | 4 | 0.4675 | 0.3598 | 0.9739 | 0.927 | 0.0067 | 75.46 |
| 9 | 10646211 | rs10756079 | C | T | 4 | 0.4098 | 0.3598 | 1.0413 | 1.1244 | 0.0008 | 81.98 |
| 21 | 16557703 | rs2823721 | A | G | 4 | 0.04666 | 0.3599 | 1.0747 | 1.0892 | 0.0012 | 81.1 |
| 5 | 13544938 | rs11952402 | C | T | 4 | 0.02316 | 0.3601 | 1.1548 | 1.1704 | 0.0005 | 83.03 |
| 21 | 40106968 | rs9305680 | C | G | 4 | 0.04922 | 0.3601 | 0.9285 | 0.9404 | 0.0588 | 59.75 |
| 14 | 78085602 | rs2193670 | A | G | 4 | 0.276 | 0.3605 | 1.0395 | 1.0768 | 0.0067 | 75.41 |
| 6 | 30221529 | rs12202131 | A | T | 4 | 0.01626 | 0.3606 | 1.1926 | 1.1446 | 0.0223 | 68.73 |
| 13 | 89121163 | rs1327342 | C | G | 3 | 0.09914 | 0.3606 | 0.7815 | 0.6793 | 0.0015 | 84.58 |
| 4 | 8400638 | rs1678305 | C | T | 4 | 0.4285 | 0.3612 | 1.0296 | 1.0815 | 0.0057 | 76.13 |
| 4 | 92459054 | rs9999729 | C | G | 4 | 0.2904 | 0.3614 | 0.9589 | 0.9117 | 0.0017 | 80.11 |
| 21 | 16557408 | rs238964 | C | G | 4 | 0.04419 | 0.3614 | 0.9303 | 0.9192 | 0.0013 | 80.93 |
| 4 | 116548408 | rs6814621 | A | C | 4 | 0.4794 | 0.3615 | 0.9746 | 0.9261 | 0.0055 | 76.28 |
| 4 | 116554439 | rs7440324 | A | T | 4 | 0.4794 | 0.3615 | 0.9746 | 0.9261 | 0.0055 | 76.28 |
| 4 | 92459103 | rs9999885 | A | G | 4 | 0.29 | 0.3617 | 1.0429 | 1.0971 | 0.0017 | 80.27 |
| 2 | 83407484 | rs7425554 | C | T | 4 | 0.4136 | 0.362 | 0.9714 | 0.9301 | 0.0081 | 74.59 |
| 4 | 116495156 | rs6533856 | G | T | 4 | 0.3839 | 0.3624 | 1.0333 | 1.0762 | 0.0127 | 72.3 |
| 18 | 5569427 | rs1785427 | A | G | 4 | 0.3843 | 0.3624 | 1.0306 | 1.0948 | 0.0002 | 84.64 |
| 21 | 29945121 | rs2832424 | A | C | 4 | 0.2808 | 0.3625 | 0.902 | 0.8361 | 0.0155 | 71.15 |
| 21 | 16557390 | rs6517695 | G | T | 4 | 0.03926 | 0.3626 | 1.0761 | 1.0871 | 0.0012 | 81.04 |
| 21 | 16556577 | rs2823720 | A | C | 4 | 0.04037 | 0.3627 | 0.9297 | 0.9202 | 0.0013 | 80.96 |
| 22 | 33925528 | rs134443 | C | T | 4 | 0.04871 | 0.3627 | 0.9269 | 0.9339 | 0.031 | 66.19 |
| 8 | 14884317 | rs10109779 | A | G | 4 | 0.057 | 0.3628 | 0.9325 | 0.9385 | 0.0353 | 65.06 |
| 14 | 78067940 | rs4243660 | C | T | 4 | 0.2764 | 0.3629 | 1.0394 | 1.0765 | 0.0065 | 75.55 |
| 18 | 5570911 | rs1719933 | C | T | 4 | 0.3884 | 0.3629 | 0.9705 | 0.9136 | 0.0002 | 84.63 |
| 21 | 40073319 | rs7278733 | A | G | 4 | 0.03275 | 0.3629 | 0.9226 | 0.9374 | 0.0397 | 63.97 |
| 6 | 94814379 | rs9363138 | G | T | 4 | 0.01425 | 0.3633 | 1.0903 | 1.0572 | 0.07 | 57.5 |
| 4 | 116542863 | rs11933617 | A | G | 4 | 0.4857 | 0.3635 | 1.0257 | 1.0797 | 0.0053 | 76.41 |
| 4 | 116540440 | rs7687193 | A | G | 4 | 0.4861 | 0.3638 | 0.975 | 0.9264 | 0.0054 | 76.34 |
| 4 | 116548085 | rs11947264 | C | T | 4 | 0.4861 | 0.3638 | 0.975 | 0.9264 | 0.0054 | 76.34 |
| 2 | 83404583 | rs6745924 | C | G | 4 | 0.441 | 0.3646 | 1.0273 | 1.0752 | 0.0067 | 75.44 |
| 2 | 107783958 | rs13414755 | A | C | 3 | 0.01367 | 0.3648 | 0.9044 | 0.9299 | 0.0408 | 68.73 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 14 | 78060216 | rs1030124 | G | T | 4 | 0.2792 | 0.3648 | 0.9623 | 0.9291 | 0.0065 | 75.59 |
| 21 | 29954574 | rs363569 | C | T | 4 | 0.277 | 0.3648 | 0.9011 | 0.8355 | 0.0144 | 71.58 |
| 12 | 119024673 | rs3852587 | A | C | 3 | 0.3818 | 0.3654 | 1.0516 | 1.17 | 0.0027 | 83.1 |
| 18 | 64690810 | rs2051303 | A | T | 4 | 0.01313 | 0.3655 | 1.1005 | 1.0693 | 0.0361 | 64.87 |
| 18 | 64691203 | rs2051301 | C | T | 4 | 0.01313 | 0.3655 | 1.1005 | 1.0693 | 0.0361 | 64.87 |
| 18 | 64693088 | rs2004027 | A | T | 4 | 0.01313 | 0.3655 | 1.1005 | 1.0693 | 0.0361 | 64.87 |
| 4 | 116540808 | rs12233647 | A | G | 4 | 0.4925 | 0.3657 | 1.0253 | 1.0794 | 0.0052 | 76.47 |
| 4 | 116549189 | rs4833478 | A | G | 4 | 0.4925 | 0.3657 | 1.0253 | 1.0794 | 0.0052 | 76.47 |
| 3 | 102098240 | rs2245556 | C | T | 4 | 0.5865 | 0.3658 | 0.9732 | 0.8495 | 0 | 90.69 |
| 8 | 17655354 | rs6586642 | C | T | 4 | 0.01312 | 0.3658 | 0.8887 | 0.9203 | 0.0357 | 64.96 |
| 5 | 13541800 | rs151152 | C | T | 4 | 0.0113 | 0.3659 | 0.8757 | 0.8698 | 0.0001 | 85.86 |
| 18 | 5591403 | rs1785418 | A | G | 4 | 0.3897 | 0.3662 | 0.9703 | 0.9156 | 0.0004 | 83.6 |
| 6 | 51884494 | rs12196767 | C | T | 4 | 0.05242 | 0.3666 | 0.9143 | 0.9168 | 0.0168 | 70.64 |
| 18 | 44764374 | rs8089910 | C | G | 4 | 0.4278 | 0.3669 | 1.0291 | 1.0818 | 0.0034 | 78.05 |
| 21 | 16555965 | rs1492957 | C | T | 4 | 0.0429 | 0.367 | 1.0745 | 1.0859 | 0.0012 | 81.02 |
| 2 | 29149180 | rs13385188 | A | G | 3 | 0.04633 | 0.3672 | 1.0901 | 1.0877 | 0.0234 | 73.36 |
| 14 | 78060082 | rs1030123 | A | G | 4 | 0.2831 | 0.3673 | 1.0388 | 1.0758 | 0.0064 | 75.59 |
| 21 | 16553084 | rs2823705 | A | G | 4 | 0.04974 | 0.3675 | 0.9326 | 0.9231 | 0.002 | 79.75 |
| 7 | 26553081 | rs17153906 | C | T | 4 | 0.9687 | 0.3677 | 0.9983 | 0.8974 | 0.0002 | 84.74 |
| 4 | 116523298 | rs4834470 | C | T | 4 | 0.4922 | 0.3679 | 1.0253 | 1.078 | 0.006 | 75.88 |
| 4 | 92462703 | rs6532292 | C | T | 4 | 0.3074 | 0.3681 | 1.041 | 1.0939 | 0.0019 | 79.94 |
| 5 | 105493632 | rs974073 | G | T | 4 | 0.7616 | 0.3685 | 1.0144 | 1.1222 | 0.0004 | 83.49 |
| 12 | 114337140 | rs11067584 | C | T | 4 | 0.01393 | 0.3686 | 1.1074 | 1.0732 | 0.0355 | 65.01 |
| 2 | 30841879 | rs6548032 | A | G | 4 | 0.003583 | 0.3691 | 1.1157 | 1.0711 | 0.0223 | 68.76 |
| 10 | 30461295 | rs11007912 | C | G | 4 | 0.003634 | 0.3692 | 1.1244 | 1.0686 | 0.0522 | 61.12 |
| 1 | 75106090 | rs12743570 | C | G | 4 | 0.2548 | 0.3693 | 1.0466 | 1.091 | 0.0029 | 78.58 |
| 5 | 114715541 | rs1455845 | A | G | 4 | 0.361 | 0.3693 | 1.0612 | 1.1244 | 0.0157 | 71.05 |
| 8 | 140497072 | rs10104031 | C | T | 4 | 0.5482 | 0.3693 | 1.0253 | 1.0845 | 0.0102 | 73.47 |
| 3 | 102089971 | rs17338506 | C | T | 4 | 0.7621 | 0.3698 | 1.0155 | 1.1335 | 0.0004 | 83.71 |
| 6 | 130362937 | rs945889 | C | T | 4 | 0.3274 | 0.3699 | 0.9375 | 0.8432 | 0.0005 | 82.91 |
| 21 | 16555455 | rs4465860 | C | T | 4 | 0.04462 | 0.3699 | 0.9312 | 0.9212 | 0.0012 | 81.09 |
| 21 | 16555664 | rs2823716 | A | G | 4 | 0.04462 | 0.3699 | 0.9312 | 0.9212 | 0.0012 | 81.09 |
| 4 | 116518282 | rs7663921 | C | T | 4 | 0.4985 | 0.37 | 0.9757 | 0.9278 | 0.0059 | 75.95 |
| 21 | 40129825 | rs741866 | C | T | 4 | 0.05081 | 0.3705 | 0.9289 | 0.9388 | 0.0429 | 63.21 |
| 4 | 92459702 | rs7659326 | A | T | 4 | 0.3497 | 0.3706 | 0.9618 | 0.9073 | 0.0012 | 81.2 |
| 21 | 16555396 | rs2251006 | C | T | 4 | 0.04524 | 0.3706 | 1.0737 | 1.0853 | 0.0012 | 81.06 |
| 4 | 116558804 | rs6847471 | A | G | 4 | 0.5062 | 0.3708 | 1.0245 | 1.0786 | 0.0051 | 76.55 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 18 | 64676889 | rs9948116 | A | G | 4 | 0.01771 | 0.3708 | 0.9125 | 0.9372 | 0.0423 | 63.35 |
| 9 | 10647559 | rs10756080 | C | T | 4 | 0.4409 | 0.3709 | 1.0386 | 1.1232 | 0.0007 | 82.5 |
| 2 | 105447178 | rs6711988 | C | T | 4 | 0.05667 | 0.371 | 1.1415 | 1.1465 | 0.0099 | 73.63 |
| 5 | 105642920 | rs10068181 | A | G | 4 | 0.6174 | 0.3711 | 1.0238 | 1.1159 | 0.0009 | 81.76 |
| 21 | 16554963 | rs2823712 | A | G | 4 | 0.04632 | 0.3712 | 1.0733 | 1.085 | 0.0013 | 80.97 |
| 6 | 130363872 | rs2876066 | A | C | 4 | 0.3485 | 0.3716 | 0.9403 | 0.8435 | 0.0005 | 82.99 |
| 15 | 52109020 | rs12917513 | A | T | 4 | 0.4267 | 0.3721 | 0.9629 | 0.8981 | 0.0018 | 79.98 |
| 4 | 92463052 | rs6532293 | A | G | 4 | 0.321 | 0.3726 | 1.0395 | 1.0925 | 0.0018 | 79.97 |
| 22 | 33929534 | rs5999761 | C | G | 4 | 0.05311 | 0.3726 | 1.0773 | 1.0694 | 0.0304 | 66.35 |
| 4 | 116559642 | rs6854632 | A | G | 4 | 0.5135 | 0.3728 | 0.9765 | 0.9273 | 0.0051 | 76.59 |
| 2 | 113527418 | rs9678578 | A | T | 4 | 0.01966 | 0.3731 | 0.9154 | 0.9352 | 0.0267 | 67.42 |
| 1 | 75112763 | rs7552148 | C | T | 4 | 0.2608 | 0.3732 | 0.956 | 0.9171 | 0.0028 | 78.73 |
| 16 | 7338453 | rs9934586 | A | G | 4 | 0.01848 | 0.3733 | 0.8704 | 0.912 | 0.0673 | 58.04 |
| 21 | 40071834 | rs2205205 | A | G | 4 | 0.03375 | 0.3735 | 1.0834 | 1.0661 | 0.0364 | 64.79 |
| 20 | 19711787 | rs17370440 | A | T | 4 | 0.3131 | 0.3736 | 1.0621 | 1.136 | 0.0026 | 78.94 |
| 6 | 51868413 | rs12206267 | C | T | 4 | 0.05838 | 0.3741 | 1.0929 | 1.0872 | 0.0248 | 67.97 |
| 18 | 5584739 | rs1785409 | C | T | 4 | 0.37 | 0.3741 | 0.9694 | 0.9163 | 0.0003 | 84.26 |
| 21 | 16553507 | rs1389073 | G | T | 4 | 0.05162 | 0.3744 | 0.9332 | 0.9229 | 0.0015 | 80.58 |
| 4 | 92466196 | rs1528578 | C | G | 4 | 0.3195 | 0.3745 | 1.0396 | 1.0898 | 0.0026 | 78.9 |
| 4 | 92462591 | rs1919227 | G | T | 4 | 0.3275 | 0.3746 | 1.0393 | 1.0928 | 0.0018 | 80.04 |
| 6 | 83346508 | rs9443987 | C | T | 3 | 0.1804 | 0.3751 | 1.1927 | 1.3589 | 0.004 | 81.88 |
| 15 | 89951919 | rs7495265 | C | T | 4 | 0.1974 | 0.3751 | 0.9484 | 0.9085 | 0.0009 | 81.79 |
| 3 | 102218829 | rs17399603 | A | G | 4 | 0.6454 | 0.3752 | 0.9777 | 0.8589 | 0 | 89.97 |
| 10 | 129849048 | rs6482660 | A | G | 4 | 0.3217 | 0.3753 | 1.0384 | 1.0962 | 0.0004 | 83.3 |
| 6 | 83349658 | rs6939695 | C | A | 3 | 0.1966 | 0.3754 | 1.1831 | 1.3566 | 0.0041 | 81.81 |
| 21 | 16549874 | rs239009 | A | G | 4 | 0.05571 | 0.3756 | 1.0716 | 1.0856 | 0.0013 | 80.93 |
| 21 | 16551609 | rs2823702 | A | G | 4 | 0.05198 | 0.3757 | 0.9333 | 0.9242 | 0.0019 | 79.93 |
| 6 | 55494436 | rs9357865 | A | G | 4 | 0.9375 | 0.376 | 1.0042 | 0.8874 | 0.0013 | 80.83 |
| 2 | 83410251 | rs6760584 | G | T | 4 | 0.4328 | 0.3762 | 1.0285 | 1.0699 | 0.0134 | 71.99 |
| 21 | 16555717 | rs2823717 | A | T | 4 | 0.04731 | 0.3763 | 0.932 | 0.9217 | 0.0011 | 81.35 |
| 1 | 95591184 | rs11590181 | G | T | 4 | 0.1787 | 0.3764 | 1.075 | 1.1163 | 0.005 | 76.61 |
| 18 | 5577607 | rs1719937 | A | G | 4 | 0.507 | 0.3764 | 1.0242 | 1.0925 | 0.0004 | 83.44 |
| 7 | 97308426 | rs6465629 | C | T | 4 | 0.5366 | 0.3765 | 0.9697 | 0.8983 | 0.0022 | 79.44 |
| 10 | 30470812 | rs10508745 | C | T | 4 | 0.004977 | 0.3766 | 1.1198 | 1.0666 | 0.0554 | 60.44 |
| 21 | 16553692 | rs4381854 | C | T | 4 | 0.05132 | 0.3768 | 0.9331 | 0.9227 | 0.0013 | 80.85 |
| 18 | 5584350 | rs1785407 | A | G | 4 | 0.3767 | 0.3771 | 1.0311 | 1.0913 | 0.0002 | 84.45 |
| 18 | 5584648 | rs1785408 | A | G | 4 | 0.3767 | 0.3771 | 1.0311 | 1.0913 | 0.0002 | 84.45 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 18 | 5584667 | rs1719943 | C | T | 4 | 0.3767 | 0.3771 | 1.0311 | 1.0913 | 0.0002 | 84.45 |
| 3 | 44998914 | rs6441875 | C | T | 4 | 0.366 | 0.3774 | 1.0317 | 1.0714 | 0.0084 | 74.43 |
| 3 | 45005286 | rs4683016 | A | G | 4 | 0.3686 | 0.3774 | 0.9695 | 0.9332 | 0.0082 | 74.54 |
| 20 | 19731315 | rs17370886 | G | T | 4 | 0.3026 | 0.3774 | 0.9405 | 0.8832 | 0.0032 | 78.23 |
| 10 | 30470483 | rs7896890 | C | T | 4 | 0.004957 | 0.3775 | 0.893 | 0.9376 | 0.0553 | 60.47 |
| 21 | 16554814 | rs238962 | C | T | 4 | 0.08243 | 0.3775 | 0.9385 | 0.9235 | 0.0024 | 79.18 |
| 11 | 80661677 | rs17141854 | A | G | 4 | 0.243 | 0.3778 | 0.9047 | 0.8479 | 0.0106 | 73.25 |
| 21 | 16553672 | rs1389071 | A | T | 4 | 0.05267 | 0.3779 | 1.0712 | 1.0833 | 0.0014 | 80.76 |
| 6 | 130357104 | rs1415699 | A | G | 4 | 0.3443 | 0.3783 | 0.9405 | 0.845 | 0.0004 | 83.46 |
| 3 | 45011179 | rs9835136 | A | G | 4 | 0.3714 | 0.3784 | 1.0313 | 1.0715 | 0.0081 | 74.6 |
| 22 | 33926150 | rs134445 | C | T | 4 | 0.05342 | 0.3784 | 0.9283 | 0.9351 | 0.0278 | 67.1 |
| 15 | 84618315 | rs1159895 | A | G | 4 | 0.01073 | 0.3785 | 1.103 | 1.0613 | 0.0639 | 58.71 |
| 8 | 6812946 | rs4543566 | C | G | 4 | 0.02429 | 0.3789 | 1.1288 | 1.0847 | 0.0671 | 58.07 |
| 21 | 16554235 | rs2823709 | A | G | 4 | 0.05264 | 0.3791 | 1.0712 | 1.0836 | 0.0013 | 80.96 |
| 2 | 70819307 | rs11126291 | G | T | 4 | 0.08318 | 0.3798 | 0.8722 | 0.8459 | 0.0047 | 76.89 |
| 5 | 105638139 | rs10063657 | C | T | 4 | 0.738 | 0.3798 | 1.0154 | 1.1183 | 0.0003 | 84.17 |
| 21 | 16555037 | rs2823713 | A | T | 4 | 0.05033 | 0.38 | 1.072 | 1.0843 | 0.0011 | 81.37 |
| 4 | 21227279 | rs6848248 | A | G | 4 | 0.005428 | 0.3811 | 0.9073 | 0.9349 | 0.0102 | 73.47 |
| 18 | 5577094 | rs1785378 | A | G | 4 | 0.4601 | 0.3818 | 0.9738 | 0.9161 | 0.0004 | 83.72 |
| 7 | 157015643 | rs221238 | C | T | 4 | 0.04006 | 0.3821 | 0.8904 | 0.8947 | 0.0085 | 74.34 |
| 11 | 131494847 | rs3925045 | C | G | 4 | 0.4078 | 0.3821 | 1.0387 | 1.1062 | 0.0026 | 78.94 |
| 11 | 80661868 | rs10897779 | G | T | 4 | 0.3454 | 0.3825 | 1.0397 | 1.0871 | 0.0068 | 75.38 |
| 21 | 16554494 | rs2823710 | A | G | 4 | 0.0525 | 0.3825 | 0.9335 | 0.9229 | 0.0011 | 81.23 |
| 21 | 40081847 | rs2837218 | C | G | 4 | 0.05128 | 0.3825 | 1.0762 | 1.0626 | 0.0458 | 62.54 |
| 4 | 89068576 | rs17842205 | A | C | 4 | 0.2519 | 0.3828 | 1.0756 | 1.142 | 0.0036 | 77.83 |
| 8 | 14879068 | rs9650382 | A | G | 4 | 0.04802 | 0.3828 | 1.0758 | 1.0607 | 0.046 | 62.51 |
| 21 | 16553023 | rs2823704 | C | T | 4 | 0.05494 | 0.3829 | 1.0706 | 1.0821 | 0.0015 | 80.52 |
| 2 | 17222881 | rs484687 | C | T | 4 | 0.4947 | 0.3831 | 1.0351 | 1.1027 | 0.0113 | 72.91 |
| 4 | 116552171 | rs6836582 | A | G | 4 | 0.5133 | 0.3831 | 1.0241 | 1.0765 | 0.0052 | 76.46 |
| 6 | 83342419 | rs6904410 | C | T | 3 | 0.2069 | 0.3831 | 1.1777 | 1.3556 | 0.0034 | 82.41 |
| 21 | 16551998 | rs239010 | A | G | 4 | 0.05474 | 0.3832 | 1.0706 | 1.0813 | 0.0017 | 80.25 |
| 16 | 47680675 | rs1345408 | C | G | 4 | 0.02401 | 0.3835 | 0.9236 | 0.9406 | 0.0254 | 67.77 |
| 16 | 74938492 | rs17698989 | A | G | 4 | 0.5793 | 0.3835 | 1.026 | 1.1017 | 0.003 | 78.45 |
| 14 | 78030008 | rs1544623 | A | G | 4 | 0.326 | 0.3836 | 0.966 | 0.9351 | 0.0106 | 73.24 |
| 21 | 16558862 | rs2823725 | A | T | 4 | 0.06447 | 0.384 | 1.0727 | 1.0859 | 0.0018 | 80 |
| 3 | 29736510 | rs1371844 | C | T | 4 | 0.4312 | 0.3843 | 0.971 | 0.9318 | 0.0108 | 73.17 |
| 2 | 38439578 | rs6716350 | C | T | 4 | 0.4079 | 0.3844 | 1.0329 | 1.109 | 0.0001 | 86.21 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 2 | 51647831 | rs1406429 | C | T | 4 | 0.03556 | 0.3846 | 0.9292 | 0.9444 | 0.0394 | 64.06 |
| 4 | 116456988 | rs17686110 | A | C | 4 | 0.3836 | 0.3848 | 1.0331 | 1.0748 | 0.0088 | 74.21 |
| 21 | 40085103 | rs2837223 | C | T | 4 | 0.04882 | 0.3848 | 1.0772 | 1.0625 | 0.0455 | 62.61 |
| 18 | 5582779 | rs1719939 | C | T | 4 | 0.3979 | 0.3854 | 0.9711 | 0.9171 | 0.0002 | 84.68 |
| 21 | 16550664 | rs2823700 | C | G | 4 | 0.05727 | 0.3855 | 1.0698 | 1.0809 | 0.0016 | 80.27 |
| 3 | 45009415 | rs4683017 | C | T | 4 | 0.3947 | 0.3859 | 0.9711 | 0.9345 | 0.0084 | 74.43 |
| 3 | 29738242 | rs6783723 | A | G | 4 | 0.4344 | 0.3863 | 1.0296 | 1.0727 | 0.0109 | 73.11 |
| 4 | 92527407 | rs7668527 | A | T | 4 | 0.486 | 0.3864 | 1.0274 | 1.0826 | 0.0051 | 76.57 |
| 10 | 30463891 | rs11007913 | A | G | 4 | 0.004028 | 0.3865 | 1.1228 | 1.0664 | 0.0493 | 61.77 |
| 18 | 5579721 | rs1785381 | C | T | 4 | 0.4758 | 0.3871 | 1.0263 | 1.091 | 0.0004 | 83.4 |
| 2 | 113532952 | rs990524 | C | T | 4 | 0.02254 | 0.3872 | 1.0902 | 1.068 | 0.0241 | 68.19 |
| 2 | 105446439 | rs13385109 | A | T | 4 | 0.06265 | 0.3877 | 0.8778 | 0.8732 | 0.0079 | 74.69 |
| 5 | 30094872 | rs11743490 | A | G | 4 | 0.02077 | 0.3878 | 0.8675 | 0.9118 | 0.0655 | 58.38 |
| 6 | 30201343 | rs10947055 | C | T | 4 | 0.02305 | 0.3881 | 1.1767 | 1.1393 | 0.0152 | 71.24 |
| 21 | 16549688 | rs2823696 | A | T | 4 | 0.05844 | 0.3882 | 1.0696 | 1.082 | 0.0013 | 80.85 |
| 21 | 16550560 | rs2823699 | C | T | 4 | 0.05984 | 0.3882 | 0.9354 | 0.9255 | 0.0016 | 80.31 |
| 21 | 17225906 | rs7282020 | A | C | 4 | 0.006503 | 0.3883 | 1.1145 | 1.0652 | 0.0496 | 61.69 |
| 9 | 119032843 | rs1335405 | C | T | 4 | 0.01042 | 0.3884 | 0.8211 | 0.8797 | 0.038 | 64.39 |
| 21 | 16552797 | rs2823703 | C | G | 4 | 0.05723 | 0.3884 | 0.9347 | 0.9254 | 0.0016 | 80.37 |
| 3 | 29737133 | rs6780134 | A | G | 4 | 0.4407 | 0.3886 | 1.0292 | 1.0724 | 0.0108 | 73.16 |
| 3 | 29736653 | rs1371846 | A | C | 4 | 0.4439 | 0.3889 | 0.9718 | 0.9324 | 0.0106 | 73.27 |
| 2 | 51632332 | rs2715088 | C | T | 4 | 0.02478 | 0.389 | 1.0815 | 1.0609 | 0.0279 | 67.05 |
| 1 | 199359602 | rs942703 | C | T | 4 | 0.2653 | 0.3893 | 0.9553 | 0.9205 | 0.0048 | 76.77 |
| 7 | 97309563 | rs13223125 | A | T | 4 | 0.5874 | 0.3895 | 0.9734 | 0.9003 | 0.002 | 79.71 |
| 8 | 60881049 | rs10101487 | A | G | 4 | 0.5974 | 0.3895 | 0.98 | 0.9275 | 0.0068 | 75.37 |
| 21 | 16550037 | rs2823697 | C | T | 4 | 0.05909 | 0.3898 | 1.0694 | 1.0816 | 0.0013 | 80.88 |
| 4 | 21227268 | rs6824942 | C | T | 4 | 0.005719 | 0.3899 | 0.908 | 0.9358 | 0.0094 | 73.87 |
| 2 | 30844445 | rs7592480 | A | G | 4 | 0.003978 | 0.3902 | 1.1133 | 1.0663 | 0.0248 | 67.96 |
| 18 | 5586091 | rs1539812 | C | T | 4 | 0.4149 | 0.3906 | 0.9721 | 0.9176 | 0.0002 | 84.82 |
| 18 | 5586603 | rs1719944 | C | T | 4 | 0.4149 | 0.3906 | 0.9721 | 0.9176 | 0.0002 | 84.82 |
| 4 | 92461122 | rs1528581 | C | T | 4 | 0.3549 | 0.3908 | 1.0374 | 1.0897 | 0.002 | 79.74 |
| 2 | 70823291 | rs3755352 | A | T | 4 | 0.08748 | 0.3909 | 1.1449 | 1.1801 | 0.0041 | 77.4 |
| 21 | 40083524 | rs760285 | A | G | 4 | 0.04935 | 0.391 | 0.9285 | 0.9415 | 0.0433 | 63.13 |
| 7 | 157017352 | rs221242 | A | C | 4 | 0.04297 | 0.3915 | 0.8919 | 0.8969 | 0.0088 | 74.16 |
| 18 | 5584917 | rs1785410 | C | T | 4 | 0.4162 | 0.3915 | 1.0286 | 1.0899 | 0.0002 | 84.94 |
| 5 | 105650703 | rs13185392 | C | T | 4 | 0.653 | 0.3916 | 1.0214 | 1.1108 | 0.001 | 81.64 |
| 21 | 16550380 | rs9808741 | G | T | 4 | 0.06359 | 0.3917 | 1.0681 | 1.0806 | 0.0014 | 80.63 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 6 | 52615564 | rs9463810 | T | G | 3 | 0.042 | 0.3919 | 1.3047 | 1.3099 | 0.0104 | 78.09 |
| 18 | 5580926 | rs1785382 | C | T | 4 | 0.4079 | 0.3919 | 1.0292 | 1.0868 | 0.0004 | 83.74 |
| 11 | 131483057 | rs11605616 | C | G | 2 | 0.002447 | 0.3923 | 0.3069 | 0.4345 | 0.0245 | 80.22 |
| 4 | 21227551 | rs13117892 | A | T | 4 | 0.00593 | 0.3936 | 0.9083 | 0.9361 | 0.0092 | 73.98 |
| 4 | 92472949 | rs1406316 | C | T | 4 | 0.3945 | 0.3939 | 0.9673 | 0.9206 | 0.0026 | 78.99 |
| 4 | 116441466 | rs10434023 | C | T | 4 | 0.405 | 0.3939 | 1.0316 | 1.0731 | 0.009 | 74.07 |
| 4 | 116472360 | rs7655124 | C | T | 4 | 0.4088 | 0.3939 | 1.0313 | 1.0743 | 0.0076 | 74.87 |
| 7 | 97313206 | rs17131831 | A | G | 4 | 0.6003 | 0.3941 | 0.9743 | 0.901 | 0.002 | 79.77 |
| 3 | 29753247 | rs1866773 | C | T | 4 | 0.3816 | 0.3943 | 1.0315 | 1.0688 | 0.009 | 74.06 |
| 15 | 86281541 | rs1435399 | A | T | 4 | 0.01064 | 0.3944 | 0.8878 | 0.9281 | 0.0373 | 64.55 |
| 16 | 50054960 | rs13338826 | C | G | 4 | 0.1374 | 0.3945 | 0.9377 | 0.9205 | 0.0077 | 74.8 |
| 21 | 40114073 | rs1984023 | A | G | 4 | 0.05661 | 0.3946 | 1.0746 | 1.0609 | 0.0467 | 62.34 |
| 4 | 92471115 | rs6833290 | C | T | 4 | 0.4025 | 0.3948 | 1.0332 | 1.086 | 0.0026 | 78.96 |
| 15 | 89900920 | rs11637543 | C | T | 4 | 0.2726 | 0.3948 | 0.9564 | 0.9131 | 0.0008 | 81.98 |
| 7 | 157023027 | rs221250 | A | G | 4 | 0.04365 | 0.395 | 1.1208 | 1.1145 | 0.0084 | 74.39 |
| 17 | 51880345 | rs7224952 | C | T | 4 | 0.005472 | 0.395 | 0.8983 | 0.9352 | 0.0227 | 68.61 |
| 2 | 30858582 | rs2030383 | G | T | 4 | 0.001234 | 0.3958 | 0.8849 | 0.9339 | 0.0143 | 71.63 |
| 2 | 55796721 | rs12474717 | G | T | 4 | 0.007739 | 0.3961 | 0.8431 | 0.883 | 0.0061 | 75.8 |
| 4 | 116485614 | rs6828907 | C | G | 4 | 0.4087 | 0.3961 | 0.9694 | 0.9304 | 0.0071 | 75.17 |
| 18 | 5579629 | rs1785380 | A | C | 4 | 0.5253 | 0.3961 | 1.0232 | 1.0882 | 0.0004 | 83.4 |
| 2 | 51629015 | rs1528814 | C | T | 4 | 0.02574 | 0.3962 | 1.0816 | 1.0595 | 0.0318 | 65.99 |
| 2 | 30843832 | rs13003439 | G | T | 4 | 0.004369 | 0.3963 | 1.112 | 1.0654 | 0.0247 | 68 |
| 2 | 51641486 | rs2698022 | A | C | 4 | 0.03105 | 0.3968 | 1.0782 | 1.0599 | 0.0288 | 66.81 |
| 4 | 92459301 | rs7653977 | A | T | 4 | 0.3215 | 0.3969 | 0.9617 | 0.9165 | 0.0013 | 80.96 |
| 22 | 33897413 | rs134370 | C | G | 4 | 0.05943 | 0.397 | 1.0753 | 1.0692 | 0.0204 | 69.37 |
| 4 | 21227772 | rs10000010 | C | T | 4 | 0.006148 | 0.3972 | 0.9087 | 0.9365 | 0.009 | 74.08 |
| 4 | 58782188 | rs2570073 | A | C | 4 | 0.01138 | 0.3975 | 1.1032 | 1.0692 | 0.0211 | 69.12 |
| 2 | 30858583 | rs2030384 | G | T | 4 | 0.001245 | 0.3977 | 0.885 | 0.9342 | 0.0142 | 71.67 |
| 5 | 105650965 | rs13185419 | A | C | 4 | 0.6784 | 0.3979 | 0.9806 | 0.9011 | 0.0009 | 81.8 |
| 21 | 40101083 | rs2837232 | A | G | 4 | 0.04679 | 0.398 | 1.0779 | 1.0621 | 0.0392 | 64.1 |
| 4 | 116438169 | rs6853566 | C | T | 4 | 0.4172 | 0.3983 | 0.9701 | 0.9323 | 0.0087 | 74.22 |
| 8 | 17542512 | rs6981782 | C | T | 2 | 0.0116 | 0.3983 | 2.0451 | 1.8516 | 0.0111 | 84.5 |
| 3 | 151370478 | rs16862540 | C | G | 4 | 0.6685 | 0.3988 | 1.0192 | 1.0892 | 0.0078 | 74.75 |
| 8 | 12893231 | rs1519150 | A | T | 4 | 0.001942 | 0.3988 | 0.8831 | 0.936 | 0.0281 | 67 |
| 2 | 38431205 | rs6737169 | C | T | 4 | 0.4515 | 0.3989 | 0.971 | 0.9032 | 0.0001 | 86.56 |
| 12 | 119031310 | rs3936255 | T | G | 3 | 0.4106 | 0.3989 | 1.0485 | 1.1586 | 0.0027 | 83.07 |
| 12 | 128846223 | rs1376795 | C | T | 4 | 0.04818 | 0.3989 | 1.0784 | 1.0657 | 0.0288 | 66.81 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 5 | 105608827 | rs6878200 | C | T | 4 | 0.7587 | 0.3992 | 0.9868 | 0.9148 | 0.0026 | 78.91 |
| 12 | 118998008 | rs3852585 | T | C | 3 | 0.4667 | 0.3992 | 1.0428 | 1.1589 | 0.0024 | 83.46 |
| 21 | 17222789 | rs17210470 | C | T | 4 | 0.01289 | 0.3995 | 1.1066 | 1.0624 | 0.0629 | 58.9 |
| 3 | 151376909 | rs1386291 | C | T | 4 | 0.6559 | 0.3998 | 1.02 | 1.0888 | 0.0078 | 74.74 |
| 1 | 48896205 | rs7556329 | C | G | 4 | 0.3259 | 0.4001 | 1.0776 | 1.1563 | 0.0055 | 76.28 |
| 2 | 17296529 | rs6712339 | C | T | 4 | 0.7084 | 0.4004 | 1.0183 | 1.0947 | 0.0111 | 73.02 |
| 12 | 17575942 | rs11043491 | G | T | 4 | 0.4006 | 0.4005 | 0.9627 | 0.9119 | 0.0038 | 77.67 |
| 12 | 128845279 | rs1031400 | A | G | 4 | 0.04867 | 0.4005 | 0.9274 | 0.9383 | 0.0277 | 67.11 |
| 9 | 4855256 | rs12554461 | A | G | 4 | 0.8339 | 0.4009 | 0.9922 | 0.9316 | 0.0088 | 74.2 |
| 18 | 5588976 | rs1785415 | A | G | 4 | 0.4444 | 0.4009 | 0.9738 | 0.9185 | 0.0002 | 85.16 |
| 11 | 131489477 | rs12223742 | C | T | 4 | 0.4171 | 0.401 | 0.9635 | 0.9078 | 0.0026 | 78.96 |
| 21 | 40083878 | rs11701338 | C | T | 4 | 0.05186 | 0.4012 | 0.9293 | 0.9423 | 0.0407 | 63.73 |
| 18 | 5586929 | rs1785413 | A | G | 4 | 0.4477 | 0.4013 | 1.0267 | 1.0886 | 0.0002 | 85.15 |
| 2 | 51644884 | rs1919433 | C | G | 4 | 0.03563 | 0.4017 | 1.0767 | 1.0581 | 0.0347 | 65.23 |
| 1 | 108005170 | rs17479604 | A | C | 4 | 0.09217 | 0.402 | 1.0898 | 1.1067 | 0.0046 | 76.96 |
| 4 | 116498891 | rs12651062 | A | G | 4 | 0.4256 | 0.402 | 1.0304 | 1.0743 | 0.0066 | 75.47 |
| 16 | 7375184 | rs7202219 | A | T | 4 | 0.00784 | 0.402 | 0.8517 | 0.91 | 0.0458 | 62.55 |
| 22 | 33870522 | rs5750066 | G | T | 4 | 0.03148 | 0.402 | 1.0909 | 1.0852 | 0.0034 | 78.04 |
| 14 | 94397359 | rs7157782 | C | T | 4 | 0.05314 | 0.4024 | 0.861 | 0.8622 | 0.0074 | 74.99 |
| 18 | 5587676 | rs1785414 | G | T | 4 | 0.4666 | 0.4024 | 0.9748 | 0.9176 | 0.0001 | 85.36 |
| 22 | 33899690 | rs134378 | G | T | 4 | 0.06248 | 0.4028 | 1.0744 | 1.0689 | 0.019 | 69.85 |
| 1 | 75084050 | rs12747472 | C | T | 4 | 0.3054 | 0.4029 | 1.0424 | 1.0848 | 0.0032 | 78.23 |
| 6 | 30227869 | rs9468692 | G | T | 4 | 0.02192 | 0.4029 | 0.8457 | 0.8841 | 0.0231 | 68.51 |
| 10 | 110674541 | rs3934875 | A | G | 4 | 0.01789 | 0.4034 | 1.1136 | 1.0702 | 0.0558 | 60.38 |
| 18 | 5586822 | rs1719983 | C | T | 4 | 0.4537 | 0.4034 | 1.0263 | 1.0884 | 0.0001 | 85.22 |
| 4 | 92477494 | rs1528564 | C | T | 4 | 0.3559 | 0.4037 | 0.9645 | 0.9251 | 0.0042 | 77.33 |
| 12 | 10711189 | rs10743918 | A | C | 4 | 0.01125 | 0.4038 | 1.096 | 1.0551 | 0.0578 | 59.96 |
| 10 | 110505088 | rs17769395 | C | T | 4 | 0.03553 | 0.4039 | 1.1022 | 1.0694 | 0.0652 | 58.46 |
| 5 | 13551578 | rs6874889 | A | G | 4 | 0.0369 | 0.4042 | 1.1401 | 1.1596 | 0.0002 | 84.39 |
| 2 | 51644950 | rs1919432 | C | T | 4 | 0.03365 | 0.4046 | 0.928 | 0.9443 | 0.0298 | 66.53 |
| 13 | 84181912 | rs7319590 | C | T | 4 | 0.5195 | 0.4054 | 1.0365 | 1.1175 | 0.0021 | 79.62 |
| 18 | 5588554 | rs1719985 | C | T | 4 | 0.4678 | 0.4054 | 1.0255 | 1.0859 | 0.0002 | 84.52 |
| 3 | 151371682 | rs1486796 | C | T | 4 | 0.6931 | 0.4055 | 0.9826 | 0.9189 | 0.0075 | 74.93 |
| 18 | 44767911 | rs12962825 | A | G | 4 | 0.494 | 0.4066 | 0.975 | 0.9286 | 0.0032 | 78.23 |
| 2 | 51635788 | rs2715077 | A | C | 4 | 0.02855 | 0.4067 | 1.0801 | 1.0599 | 0.0254 | 67.79 |
| 10 | 30332603 | rs11007851 | C | T | 4 | 0.05099 | 0.4067 | 0.9328 | 0.9457 | 0.0394 | 64.05 |
| 21 | 29943925 | rs363586 | G | T | 4 | 0.3528 | 0.4069 | 1.0936 | 1.1783 | 0.0154 | 71.18 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 14 | 32680251 | rs6571583 | C | T | 4 | 0.05364 | 0.4073 | 1.0782 | 1.0629 | 0.0393 | 64.08 |
| 16 | 45361965 | rs11247495 | C | T | 4 | 0.656 | 0.408 | 0.9767 | 0.8981 | 0.0019 | 79.85 |
| 7 | 97314777 | rs6966699 | C | T | 4 | 0.6558 | 0.4089 | 0.9781 | 0.9033 | 0.0018 | 80.08 |
| 9 | 10622596 | rs2890924 | G | T | 4 | 0.588 | 0.4089 | 0.9735 | 0.9021 | 0.0014 | 80.79 |
| 12 | 118973019 | rs5028648 | G | A | 3 | 0.4344 | 0.4094 | 1.0466 | 1.1547 | 0.0027 | 83.04 |
| 16 | 7371378 | rs8057663 | A | G | 4 | 0.01152 | 0.41 | 0.8585 | 0.9128 | 0.0513 | 61.32 |
| 14 | 94397102 | rs7157079 | A | G | 4 | 0.06065 | 0.4101 | 0.8676 | 0.8657 | 0.0069 | 75.28 |
| 22 | 33890448 | rs134318 | C | T | 4 | 0.06398 | 0.4103 | 1.074 | 1.0679 | 0.0186 | 70 |
| 2 | 219002502 | rs6720403 | A | C | 4 | 0.3509 | 0.4104 | 1.0342 | 1.0691 | 0.009 | 74.09 |
| 2 | 219003493 | rs3821031 | C | T | 4 | 0.3509 | 0.4104 | 1.0342 | 1.0691 | 0.009 | 74.09 |
| 21 | 40094036 | rs2837227 | C | T | 4 | 0.05022 | 0.4105 | 0.9288 | 0.9434 | 0.0412 | 63.62 |
| 7 | 157012904 | rs6944484 | A | C | 4 | 0.05095 | 0.4109 | 1.1173 | 1.1131 | 0.0068 | 75.35 |
| 1 | 48894788 | rs6674328 | C | T | 4 | 0.3474 | 0.411 | 0.9309 | 0.8655 | 0.0044 | 77.09 |
| 4 | 92459340 | rs7683541 | C | T | 4 | 0.4201 | 0.4111 | 1.0325 | 1.0809 | 0.0043 | 77.23 |
| 17 | 68393833 | rs4969122 | A | C | 4 | 0.01896 | 0.4111 | 0.9205 | 0.9499 | 0.062 | 59.08 |
| 17 | 68393953 | rs4969123 | A | G | 4 | 0.01896 | 0.4111 | 0.9205 | 0.9499 | 0.062 | 59.08 |
| 6 | 117190939 | rs603540 | C | T | 4 | 0.05399 | 0.4113 | 1.0748 | 1.0695 | 0.0143 | 71.62 |
| 2 | 51633763 | rs2698029 | G | T | 4 | 0.02185 | 0.4114 | 0.9225 | 0.9434 | 0.0229 | 68.55 |
| 7 | 152454977 | rs1107875 | A | G | 4 | 0.1623 | 0.4117 | 1.0536 | 1.0768 | 0.0036 | 77.85 |
| 11 | 18858429 | rs4757732 | C | T | 4 | 0.0247 | 0.4122 | 0.8812 | 0.9125 | 0.0269 | 67.33 |
| 9 | 10614748 | rs2146089 | A | G | 4 | 0.5481 | 0.4124 | 0.9708 | 0.9079 | 0.003 | 78.5 |
| 21 | 40095584 | rs2837229 | C | T | 4 | 0.04883 | 0.4124 | 0.9284 | 0.9433 | 0.0395 | 64.04 |
| 9 | 10616033 | rs7030993 | A | G | 4 | 0.5557 | 0.413 | 1.0294 | 1.1012 | 0.0029 | 78.63 |
| 14 | 94396959 | rs7156858 | A | C | 4 | 0.06379 | 0.4132 | 0.8686 | 0.8664 | 0.0071 | 75.17 |
| 7 | 152455222 | rs1107874 | A | T | 4 | 0.1663 | 0.4138 | 0.9493 | 0.9284 | 0.0035 | 77.96 |
| 22 | 33928993 | rs713969 | A | C | 4 | 0.06868 | 0.4139 | 0.9323 | 0.9386 | 0.0236 | 68.33 |
| 12 | 97075690 | rs10860299 | A | G | 4 | 0.8371 | 0.414 | 1.0077 | 0.9269 | 0.0025 | 79.03 |
| 17 | 68392507 | rs4494615 | C | T | 4 | 0.02068 | 0.4141 | 0.9216 | 0.9504 | 0.0638 | 58.74 |
| 22 | 33909346 | rs134406 | C | T | 4 | 0.06423 | 0.4143 | 0.9312 | 0.9373 | 0.0196 | 69.65 |
| 4 | 72311240 | rs7655668 | C | G | 4 | 0.1557 | 0.4144 | 0.9272 | 0.8795 | 0.0001 | 85.63 |
| 6 | 83348993 | rs1999412 | C | A | 3 | 0.2742 | 0.4147 | 1.1516 | 1.3396 | 0.0024 | 83.4 |
| 2 | 51640024 | rs2698024 | A | G | 4 | 0.03704 | 0.4149 | 1.0755 | 1.0571 | 0.03 | 66.48 |
| 7 | 97316047 | rs10486009 | C | G | 4 | 0.6857 | 0.415 | 0.9799 | 0.9036 | 0.0017 | 80.21 |
| 3 | 24755270 | rs4075988 | A | G | 4 | 0.02447 | 0.4151 | 1.118 | 1.0823 | 0.0279 | 67.06 |
| 4 | 40505735 | rs882733 | A | G | 4 | 0.742 | 0.4151 | 0.9841 | 0.9073 | 0.0033 | 78.18 |
| 2 | 51646842 | rs1528812 | C | G | 4 | 0.0383 | 0.4152 | 1.0751 | 1.0576 | 0.0286 | 66.86 |
| 2 | 38424759 | rs10198323 | C | T | 4 | 0.5298 | 0.4155 | 0.9757 | 0.9066 | 0.0001 | 86.51 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 3 | 117034860 | rs2944404 | A | G | 4 | 0.01331 | 0.4155 | 1.1856 | 1.1068 | 0.0552 | 60.5 |
| 4 | 72302238 | rs7689609 | C | T | 4 | 0.1174 | 0.4156 | 1.0834 | 1.126 | 0.0002 | 84.61 |
| 4 | 13326569 | rs13120921 | C | T | 4 | 0.2491 | 0.4159 | 1.0422 | 1.0705 | 0.0054 | 76.33 |
| 15 | 58093606 | rs12595222 | A | G | 4 | 0.9554 | 0.416 | 1.0028 | 1.1091 | 0.001 | 81.59 |
| 12 | 126490843 | rs4761007 | C | T | 4 | 0.04038 | 0.4163 | 0.9204 | 0.9297 | 0.0094 | 73.84 |
| 21 | 40127381 | rs9980807 | C | T | 4 | 0.06215 | 0.4163 | 0.9321 | 0.9441 | 0.0409 | 63.69 |
| 17 | 68391508 | rs4476236 | A | G | 4 | 0.02096 | 0.4165 | 1.0849 | 1.0519 | 0.0631 | 58.86 |
| 18 | 5589104 | rs1785416 | C | T | 4 | 0.5197 | 0.4166 | 0.9777 | 0.9189 | 0.0001 | 85.78 |
| 17 | 68393030 | rs4969120 | C | T | 4 | 0.01995 | 0.4173 | 0.9211 | 0.9504 | 0.0611 | 59.28 |
| 4 | 40498127 | rs17441923 | C | T | 4 | 0.709 | 0.4174 | 0.982 | 0.9091 | 0.004 | 77.48 |
| 4 | 115536217 | rs11935578 | G | T | 4 | 0.2529 | 0.4174 | 0.9595 | 0.9334 | 0.0047 | 76.84 |
| 10 | 110629257 | rs12258374 | C | T | 4 | 0.03993 | 0.4177 | 1.0862 | 1.0587 | 0.0638 | 58.73 |
| 5 | 64329326 | rs1309540 | A | G | 4 | 0.01347 | 0.418 | 1.1272 | 1.0831 | 0.0222 | 68.78 |
| 12 | 68680548 | rs11178026 | C | T | 4 | 0.3003 | 0.4181 | 0.9599 | 0.9266 | 0.0045 | 77.02 |
| 16 | 29922065 | rs11150580 | C | T | 3 | 0.8991 | 0.4182 | 0.9953 | 0.9166 | 0.001 | 85.61 |
| 21 | 40087332 | rs2837225 | A | C | 4 | 0.06791 | 0.4182 | 1.074 | 1.064 | 0.0291 | 66.73 |
| 16 | 7375166 | rs7202208 | A | G | 4 | 0.008576 | 0.4183 | 0.8532 | 0.9123 | 0.0437 | 63.04 |
| 13 | 89221294 | rs7984054 | A | C | 4 | 0.3378 | 0.4185 | 1.1104 | 1.2165 | 0.0064 | 75.6 |
| 11 | 18846017 | rs1384642 | A | G | 4 | 0.02361 | 0.4187 | 1.1365 | 1.095 | 0.0265 | 67.46 |
| 17 | 68394861 | rs4570929 | A | C | 4 | 0.02031 | 0.4194 | 1.0854 | 1.0519 | 0.0613 | 59.23 |
| 17 | 68392999 | rs4969119 | C | T | 4 | 0.02092 | 0.4195 | 0.9217 | 0.9509 | 0.0626 | 58.96 |
| 10 | 110714483 | rs11599609 | C | T | 4 | 0.02777 | 0.4197 | 1.1059 | 1.0665 | 0.0646 | 58.58 |
| 2 | 51639121 | rs2950942 | C | T | 4 | 0.03214 | 0.4198 | 0.9279 | 0.9447 | 0.0228 | 68.59 |
| 4 | 116428916 | rs2135965 | A | G | 4 | 0.4708 | 0.4199 | 0.973 | 0.9323 | 0.006 | 75.87 |
| 5 | 105416189 | rs10056331 | C | T | 4 | 0.858 | 0.4199 | 1.0067 | 1.0768 | 0.0027 | 78.8 |
| 13 | 84142066 | rs9575636 | A | G | 4 | 0.5383 | 0.4201 | 1.0335 | 1.1096 | 0.0021 | 79.52 |
| 2 | 113543867 | rs1446521 | A | G | 4 | 0.0176 | 0.4203 | 0.9117 | 0.9364 | 0.0167 | 70.69 |
| 2 | 51646400 | rs1528813 | A | T | 4 | 0.04125 | 0.4205 | 0.9307 | 0.9471 | 0.034 | 65.42 |
| 10 | 110748773 | rs11592575 | C | T | 4 | 0.02522 | 0.4205 | 0.9037 | 0.9387 | 0.0683 | 57.84 |
| 4 | 92469018 | rs6532296 | A | G | 4 | 0.382 | 0.4207 | 1.0335 | 1.073 | 0.0059 | 75.97 |
| 2 | 64135002 | rs7560803 | A | G | 4 | 0.03192 | 0.4212 | 1.1651 | 1.1118 | 0.0474 | 62.18 |
| 2 | 172243583 | rs10803863 | C | T | 4 | 0.2684 | 0.4212 | 0.9584 | 0.9219 | 0.0009 | 81.86 |
| 17 | 68394639 | rs8078727 | C | T | 4 | 0.0201 | 0.4213 | 0.9212 | 0.9508 | 0.0603 | 59.44 |
| 4 | 92462653 | rs6532291 | A | G | 4 | 0.3549 | 0.4218 | 1.0376 | 1.086 | 0.0014 | 80.64 |
| 8 | 112148387 | rs1896238 | A | G | 4 | 0.2794 | 0.4219 | 0.9572 | 0.9205 | 0.0018 | 80.02 |
| 5 | 115858991 | rs32972 | C | T | 4 | 0.7182 | 0.422 | 1.013 | 1.0891 | 0.0001 | 85.8 |
| 21 | 16548642 | rs2823692 | A | C | 4 | 0.06726 | 0.422 | 0.935 | 0.9266 | 0.0011 | 81.29 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 13 | 43932814 | rs9533862 | C | G | 3 | 0.002227 | 0.4221 | 0.6063 | 0.7634 | 0.0872 | 59.01 |
| 4 | 72340320 | rs12650549 | G | T | 4 | 0.1562 | 0.4224 | 0.9295 | 0.8888 | 0.0002 | 84.39 |
| 11 | 18845442 | rs1384641 | C | G | 4 | 0.02531 | 0.4228 | 0.8822 | 0.9138 | 0.0247 | 68 |
| 2 | 51639646 | rs2715062 | A | G | 4 | 0.03668 | 0.423 | 1.0757 | 1.0567 | 0.0275 | 67.18 |
| 4 | 72342980 | rs2363717 | G | T | 4 | 0.1573 | 0.423 | 1.0756 | 1.1247 | 0.0003 | 84.32 |
| 2 | 51632225 | rs2715086 | A | T | 4 | 0.02663 | 0.4233 | 1.0804 | 1.0575 | 0.0242 | 68.15 |
| 4 | 72339473 | rs10938138 | C | G | 4 | 0.1576 | 0.4233 | 1.0756 | 1.1253 | 0.0002 | 84.49 |
| 15 | 89910099 | rs6496832 | A | G | 4 | 0.2518 | 0.4235 | 1.0453 | 1.0749 | 0.0045 | 77.04 |
| 1 | 48893107 | rs973886 | G | T | 4 | 0.356 | 0.4236 | 1.0734 | 1.1537 | 0.0039 | 77.54 |
| 2 | 51635357 | rs2698028 | C | T | 4 | 0.02469 | 0.424 | 0.924 | 0.9446 | 0.022 | 68.85 |
| 17 | 68389374 | rs4575596 | C | T | 4 | 0.02128 | 0.4242 | 1.0847 | 1.0512 | 0.0616 | 59.18 |
| 4 | 40496876 | rs17513709 | G | T | 4 | 0.7313 | 0.4245 | 0.9834 | 0.91 | 0.0039 | 77.53 |
| 6 | 83348901 | rs1999411 | T | C | 3 | 0.2847 | 0.4245 | 1.1494 | 1.3351 | 0.0022 | 83.62 |
| 7 | 97316254 | rs10486010 | C | T | 4 | 0.6903 | 0.4249 | 1.0202 | 1.105 | 0.0016 | 80.36 |
| 9 | 71237455 | rs3737172 | C | T | 4 | 0.03508 | 0.425 | 1.0993 | 1.0697 | 0.0406 | 63.75 |
| 11 | 2794317 | rs12285496 | C | G | 4 | 0.05793 | 0.4253 | 1.0887 | 1.0721 | 0.03 | 66.48 |
| 7 | 97319748 | rs10486011 | C | T | 4 | 0.6963 | 0.4257 | 0.9805 | 0.9049 | 0.0017 | 80.24 |
| 17 | 787555 | rs7222776 | G | T | 4 | 0.02682 | 0.4259 | 0.9188 | 0.9185 | 0.0003 | 83.95 |
| 2 | 172266418 | rs2138348 | G | T | 4 | 0.27 | 0.426 | 0.9586 | 0.9219 | 0.0007 | 82.32 |
| 14 | 42261110 | rs17633001 | A | G | 4 | 0.1912 | 0.426 | 0.9038 | 0.8656 | 0.0037 | 77.77 |
| 17 | 68395088 | rs4503863 | C | T | 4 | 0.02069 | 0.4261 | 0.9216 | 0.9512 | 0.0595 | 59.61 |
| 4 | 72334532 | rs1563045 | C | T | 4 | 0.1181 | 0.4272 | 0.9262 | 0.894 | 0.0002 | 84.71 |
| 4 | 92464469 | rs955500 | C | T | 4 | 0.4043 | 0.4274 | 0.9691 | 0.9309 | 0.004 | 77.49 |
| 2 | 38427194 | rs11687138 | A | G | 4 | 0.751 | 0.4278 | 0.9872 | 0.908 | 0.0001 | 85.68 |
| 21 | 40131660 | rs1004663 | C | G | 4 | 0.06463 | 0.428 | 1.0722 | 1.0584 | 0.0377 | 64.46 |
| 2 | 51632624 | rs2715089 | A | C | 4 | 0.02744 | 0.4283 | 1.08 | 1.057 | 0.0235 | 68.36 |
| 2 | 17263732 | rs287300 | A | G | 4 | 0.716 | 0.4287 | 1.0178 | 1.0884 | 0.0111 | 73 |
| 4 | 72340027 | rs4694388 | A | G | 4 | 0.1647 | 0.4292 | 0.9306 | 0.8897 | 0.0002 | 84.44 |
| 17 | 9717196 | rs12953287 | C | T | 4 | 0.1281 | 0.4293 | 0.9298 | 0.9172 | 0.0065 | 75.57 |
| 4 | 72341689 | rs2016353 | A | G | 4 | 0.1622 | 0.4296 | 1.0754 | 1.124 | 0.0002 | 84.37 |
| 5 | 64346595 | rs266581 | A | T | 4 | 0.008977 | 0.4297 | 0.8811 | 0.9224 | 0.0156 | 71.09 |
| 17 | 68393965 | rs4969124 | C | T | 4 | 0.02152 | 0.4297 | 1.0846 | 1.0509 | 0.0595 | 59.59 |
| 4 | 72327457 | rs12506660 | C | T | 4 | 0.1132 | 0.43 | 1.0807 | 1.1198 | 0.0001 | 85.27 |
| 10 | 110747661 | rs11194333 | C | T | 4 | 0.02777 | 0.43 | 0.9053 | 0.9399 | 0.0684 | 57.83 |
| 3 | 106367794 | rs884477 | A | G | 3 | 0.0102 | 0.4301 | 0.8757 | 0.919 | 0.0309 | 71.25 |
| 7 | 97318328 | rs13224424 | C | T | 4 | 0.7163 | 0.4305 | 1.0186 | 1.1039 | 0.0017 | 80.21 |
| 2 | 134741150 | rs3791275 | A | G | 3 | 0.03556 | 0.4309 | 0.8273 | 0.8548 | 0.0156 | 75.95 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 2 | 51645727 | rs1609361 | A | G | 4 | 0.03475 | 0.431 | 0.9295 | 0.9465 | 0.0238 | 68.28 |
| 11 | 18844035 | rs4325289 | C | G | 4 | 0.02961 | 0.4311 | 1.1302 | 1.0931 | 0.024 | 68.2 |
| 11 | 13577497 | rs11022897 | C | T | 4 | 0.7545 | 0.4315 | 0.9885 | 0.9357 | 0.0063 | 75.71 |
| 14 | 42258562 | rs1712699 | A | C | 4 | 0.1838 | 0.4315 | 0.9094 | 0.8734 | 0.0032 | 78.25 |
| 17 | 68394559 | rs8078564 | C | G | 4 | 0.0213 | 0.4316 | 0.9219 | 0.9516 | 0.0585 | 59.8 |
| 2 | 172249855 | rs1554166 | G | T | 4 | 0.2922 | 0.4318 | 0.9604 | 0.9229 | 0.0007 | 82.23 |
| 4 | 92460094 | rs6816883 | A | G | 4 | 0.4038 | 0.4323 | 0.9688 | 0.9311 | 0.004 | 77.51 |
| 15 | 58091041 | rs4775230 | C | T | 4 | 0.8928 | 0.4323 | 0.9933 | 1.1102 | 0.0005 | 83.19 |
| 2 | 17251821 | rs287293 | C | T | 4 | 0.7274 | 0.4325 | 1.0171 | 1.0876 | 0.0111 | 73 |
| 2 | 172257876 | rs6757773 | A | T | 4 | 0.2831 | 0.4326 | 0.9597 | 0.9223 | 0.0006 | 82.64 |
| 6 | 52586483 | rs9474254 | G | A | 3 | 0.04517 | 0.4326 | 1.303 | 1.2947 | 0.0074 | 79.62 |
| 8 | 54337603 | rs16918960 | A | T | 4 | 0.02021 | 0.4327 | 0.8753 | 0.9085 | 0.0128 | 72.23 |
| 7 | 44209963 | rs2971668 | C | G | 3 | 0.03591 | 0.4329 | 1.1048 | 1.0785 | 0.0348 | 70.21 |
| 2 | 113541857 | rs2100071 | A | C | 4 | 0.02845 | 0.433 | 0.9203 | 0.9411 | 0.0208 | 69.24 |
| 8 | 129304629 | rs16902742 | A | G | 4 | 0.3538 | 0.4337 | 1.0804 | 1.1508 | 0.0099 | 73.62 |
| 11 | 18877606 | rs2200174 | A | G | 4 | 0.02154 | 0.4338 | 1.1417 | 1.0948 | 0.0246 | 68.04 |
| 4 | 92491016 | rs6532301 | A | G | 4 | 0.4781 | 0.434 | 0.9725 | 0.9272 | 0.003 | 78.44 |
| 2 | 38417031 | rs10177042 | C | G | 4 | 0.6705 | 0.4341 | 1.0165 | 1.0937 | 0.0001 | 85.55 |
| 1 | 95558817 | rs17113368 | C | T | 4 | 0.267 | 0.4342 | 0.935 | 0.8909 | 0.0035 | 77.91 |
| 1 | 199367062 | rs10800760 | A | G | 4 | 0.302 | 0.4343 | 1.0451 | 1.0843 | 0.0031 | 78.31 |
| 4 | 72332316 | rs2045012 | G | T | 4 | 0.1206 | 0.4343 | 1.079 | 1.119 | 0.0001 | 85.34 |
| 2 | 29148258 | rs17744093 | C | G | 4 | 0.02975 | 0.4344 | 1.0955 | 1.0623 | 0.0496 | 61.71 |
| 2 | 51630745 | rs11563043 | C | G | 4 | 0.02832 | 0.4344 | 0.9264 | 0.9465 | 0.0228 | 68.6 |
| 14 | 78027611 | rs11622766 | A | G | 4 | 0.3282 | 0.4344 | 0.9655 | 0.9361 | 0.0046 | 76.94 |
| 2 | 51632158 | rs2715084 | C | T | 4 | 0.02845 | 0.4347 | 1.0794 | 1.0564 | 0.0228 | 68.57 |
| 9 | 71237419 | rs1217339 | A | G | 4 | 0.03743 | 0.4351 | 0.9107 | 0.9359 | 0.039 | 64.15 |
| 3 | 178807690 | rs9855198 | A | G | 4 | 0.01877 | 0.4353 | 1.0967 | 1.0577 | 0.0524 | 61.09 |
| 9 | 71237918 | rs1217338 | C | T | 4 | 0.03861 | 0.4355 | 0.9117 | 0.936 | 0.0381 | 64.38 |
| 12 | 65462660 | rs994302 | C | G | 4 | 0.06695 | 0.4357 | 1.0664 | 1.0535 | 0.0349 | 65.18 |
| 2 | 29142915 | rs17744052 | A | G | 4 | 0.03704 | 0.4358 | 0.9178 | 0.9422 | 0.0456 | 62.6 |
| 10 | 122962348 | rs11593067 | C | T | 4 | 0.5445 | 0.436 | 0.9792 | 0.9429 | 0.0114 | 72.87 |
| 2 | 172300209 | rs6722757 | A | G | 4 | 0.3003 | 0.4361 | 0.961 | 0.9238 | 0.0008 | 82.13 |
| 17 | 68395153 | rs7223107 | C | T | 4 | 0.02192 | 0.4364 | 0.9223 | 0.952 | 0.0577 | 59.97 |
| 10 | 110697815 | rs7070406 | A | T | 4 | 0.02396 | 0.4368 | 1.1081 | 1.0653 | 0.0552 | 60.5 |
| 10 | 110747675 | rs11194334 | A | C | 4 | 0.03026 | 0.4369 | 0.8982 | 0.935 | 0.0668 | 58.14 |
| 1 | 75124915 | rs6664850 | A | G | 4 | 0.3835 | 0.4373 | 1.0346 | 1.0768 | 0.0027 | 78.77 |
| 7 | 125563862 | rs626762 | A | C | 4 | 0.05575 | 0.4376 | 0.902 | 0.9206 | 0.023 | 68.53 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 4 | 92478508 | rs1534556 | A | G | 4 | 0.6293 | 0.4377 | 1.019 | 1.081 | 0.0016 | 80.4 |
| 4 | 72334992 | rs1319630 | C | T | 4 | 0.1327 | 0.4379 | 1.0765 | 1.1161 | 0.0002 | 84.84 |
| 12 | 68683295 | rs1565723 | C | T | 4 | 0.3361 | 0.438 | 0.9628 | 0.9287 | 0.0038 | 77.68 |
| 2 | 113537588 | rs2515404 | C | T | 4 | 0.02926 | 0.4384 | 1.0861 | 1.0618 | 0.021 | 69.18 |
| 4 | 92459948 | rs6532290 | G | T | 4 | 0.4311 | 0.439 | 1.0304 | 1.0734 | 0.0037 | 77.73 |
| 8 | 4083982 | rs17069682 | A | C | 4 | 0.2449 | 0.439 | 1.1054 | 1.1976 | 0.0004 | 83.73 |
| 6 | 117190566 | rs682747 | A | C | 4 | 0.05519 | 0.4393 | 0.9307 | 0.9378 | 0.0126 | 72.34 |
| 4 | 72328528 | rs3907208 | A | T | 4 | 0.1194 | 0.4394 | 1.0797 | 1.118 | 0.0001 | 85.35 |
| 2 | 172294897 | rs2292815 | C | G | 4 | 0.3027 | 0.44 | 0.9612 | 0.9238 | 0.0007 | 82.47 |
| 1 | 75146613 | rs17562236 | A | G | 4 | 0.3894 | 0.4404 | 0.967 | 0.9294 | 0.0028 | 78.68 |
| 10 | 110679319 | rs17700354 | C | T | 4 | 0.02168 | 0.4404 | 1.11 | 1.0657 | 0.0499 | 61.64 |
| 6 | 1653870 | rs9405506 | C | T | 4 | 0.7647 | 0.4407 | 1.0125 | 1.0837 | 0.0017 | 80.15 |
| 2 | 51649917 | rs1528809 | A | G | 4 | 0.03847 | 0.4408 | 1.0755 | 1.0551 | 0.0267 | 67.42 |
| 6 | 51283445 | rs13211684 | C | T | 4 | 0.3399 | 0.4409 | 0.9656 | 0.9359 | 0.0049 | 76.74 |
| 1 | 199367119 | rs12025414 | A | G | 4 | 0.2923 | 0.4411 | 0.956 | 0.923 | 0.003 | 78.51 |
| 2 | 172268975 | rs12185567 | A | C | 4 | 0.2998 | 0.4412 | 1.0406 | 1.083 | 0.0006 | 82.79 |
| 3 | 29735511 | rs1440524 | C | T | 4 | 0.4363 | 0.4415 | 1.0286 | 1.0666 | 0.0055 | 76.23 |
| 12 | 128846311 | rs1376796 | G | T | 4 | 0.05853 | 0.4416 | 0.9302 | 0.9418 | 0.0221 | 68.83 |
| 2 | 172244094 | rs11678984 | G | T | 4 | 0.3092 | 0.4417 | 0.9617 | 0.924 | 0.0007 | 82.49 |
| 4 | 92530648 | rs6820807 | A | T | 4 | 0.4518 | 0.4419 | 0.9713 | 0.9332 | 0.006 | 75.86 |
| 1 | 75147442 | rs12755578 | C | G | 4 | 0.4025 | 0.4422 | 0.9676 | 0.9292 | 0.0027 | 78.76 |
| 10 | 110680293 | rs17700389 | G | T | 4 | 0.0218 | 0.4426 | 1.1099 | 1.0655 | 0.0495 | 61.71 |
| 2 | 113503827 | rs4849143 | C | G | 4 | 0.01677 | 0.4427 | 0.9132 | 0.9445 | 0.0309 | 66.22 |
| 5 | 115859204 | rs32973 | A | G | 3 | 0.1932 | 0.4429 | 0.9408 | 0.8942 | 0.0021 | 83.81 |
| 18 | 40396618 | rs9949152 | C | T | 4 | 0.03277 | 0.4431 | 1.1026 | 1.0647 | 0.0582 | 59.86 |
| 16 | 7375151 | rs7202052 | A | G | 4 | 0.01073 | 0.4432 | 0.8578 | 0.9162 | 0.0407 | 63.73 |
| 4 | 92528251 | rs1528579 | A | T | 4 | 0.4614 | 0.4433 | 0.9719 | 0.933 | 0.0056 | 76.21 |
| 3 | 8907353 | rs658339 | A | G | 3 | 0.007626 | 0.4436 | 0.7163 | 0.819 | 0.0568 | 65.12 |
| 5 | 104055382 | rs17350038 | C | G | 4 | 0.07337 | 0.4437 | 1.0855 | 1.0868 | 0.0035 | 77.92 |
| 2 | 38443251 | rs11687878 | G | T | 4 | 0.7705 | 0.444 | 1.012 | 1.0984 | 0.0001 | 85.75 |
| 4 | 92528566 | rs10856885 | C | T | 4 | 0.459 | 0.4441 | 0.9718 | 0.9335 | 0.006 | 75.9 |
| 5 | 13526523 | rs16902590 | C | T | 4 | 0.02897 | 0.4442 | 0.8628 | 0.8649 | 0.0003 | 83.91 |
| 8 | 4084387 | rs17069688 | C | G | 4 | 0.242 | 0.4443 | 1.1062 | 1.196 | 0.0003 | 83.8 |
| 4 | 92524147 | rs6844256 | C | G | 4 | 0.5708 | 0.4447 | 0.9785 | 0.932 | 0.0041 | 77.38 |
| 4 | 92484643 | rs1881454 | C | G | 4 | 0.4221 | 0.4448 | 1.0307 | 1.0697 | 0.0054 | 76.33 |
| 2 | 38441642 | rs11900967 | A | T | 4 | 0.7831 | 0.4455 | 0.9888 | 0.9107 | 0.0001 | 85.75 |
| 6 | 30248519 | rs13212414 | A | T | 4 | 0.01899 | 0.4456 | 0.838 | 0.8901 | 0.0237 | 68.32 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 5 | 178244599 | rs6894878 | A | G | 3 | 0.3075 | 0.4458 | 1.0578 | 1.1499 | 0.0001 | 89.61 |
| 17 | 9717002 | rs12936268 | A | T | 4 | 0.1489 | 0.4459 | 0.9332 | 0.9197 | 0.0062 | 75.79 |
| 22 | 23839747 | rs713876 | A | G | 4 | 0.534 | 0.4459 | 1.0239 | 1.0666 | 0.0086 | 74.29 |
| 5 | 105465931 | rs10066864 | C | T | 4 | 0.9529 | 0.4462 | 1.003 | 0.9099 | 0.002 | 79.79 |
| 4 | 92489733 | rs6841781 | C | T | 4 | 0.432 | 0.4463 | 1.0301 | 1.0692 | 0.0056 | 76.16 |
| 6 | 94859869 | rs2787950 | A | C | 4 | 0.01482 | 0.4464 | 0.9162 | 0.9513 | 0.05 | 61.6 |
| 6 | 94782808 | rs1352380 | C | T | 4 | 0.02624 | 0.4465 | 1.0801 | 1.0488 | 0.0551 | 60.52 |
| 9 | 71238297 | rs2991695 | A | G | 4 | 0.04307 | 0.4473 | 0.9136 | 0.938 | 0.0397 | 63.98 |
| 4 | 92521289 | rs2178221 | C | T | 4 | 0.5843 | 0.4475 | 0.9792 | 0.9323 | 0.0041 | 77.42 |
| 2 | 51648256 | rs1581667 | C | T | 4 | 0.04171 | 0.4481 | 0.9313 | 0.9483 | 0.0243 | 68.13 |
| 2 | 51649426 | rs2698014 | G | T | 4 | 0.04211 | 0.4482 | 1.0736 | 1.0545 | 0.0246 | 68.04 |
| 5 | 104037774 | rs17415237 | A | C | 4 | 0.07398 | 0.4483 | 1.0853 | 1.0839 | 0.0047 | 76.86 |
| 5 | 64338340 | rs1309534 | A | G | 4 | 0.01434 | 0.4484 | 1.126 | 1.0798 | 0.0172 | 70.48 |
| 7 | 152454874 | rs2311855 | G | T | 4 | 0.279 | 0.4484 | 0.9623 | 0.9341 | 0.002 | 79.66 |
| 10 | 110692416 | rs11596345 | A | G | 4 | 0.02621 | 0.4485 | 1.1063 | 1.0637 | 0.0542 | 60.7 |
| 10 | 110687958 | rs11595032 | A | T | 4 | 0.0251 | 0.4486 | 0.9032 | 0.9398 | 0.0523 | 61.12 |
| 2 | 172277833 | rs312918 | C | G | 4 | 0.3307 | 0.4487 | 1.0378 | 1.082 | 0.0005 | 83.16 |
| 2 | 38418894 | rs11884107 | C | T | 4 | 0.7933 | 0.4491 | 1.0106 | 1.0939 | 0.0002 | 85.17 |
| 2 | 64137490 | rs13429819 | A | G | 4 | 0.03418 | 0.4491 | 0.8592 | 0.903 | 0.0418 | 63.47 |
| 4 | 72345306 | rs2579331 | A | G | 4 | 0.1508 | 0.4496 | 1.0739 | 1.1091 | 0.0004 | 83.41 |
| 16 | 45321875 | rs2075157 | C | T | 4 | 0.7554 | 0.4497 | 0.9838 | 0.9063 | 0.0015 | 80.49 |
| 2 | 172285522 | rs10206062 | A | T | 4 | 0.3184 | 0.4503 | 0.9625 | 0.9246 | 0.0005 | 82.92 |
| 2 | 64129701 | rs17028360 | A | G | 4 | 0.002292 | 0.4507 | 0.7867 | 0.8871 | 0.0285 | 66.88 |
| 11 | 83240882 | rs7943773 | C | T | 4 | 0.5211 | 0.4508 | 1.0659 | 1.1852 | 0.0059 | 75.94 |
| 15 | 36730429 | rs10852029 | A | G | 4 | 0.04543 | 0.4508 | 1.0741 | 1.0598 | 0.0128 | 72.26 |
| 3 | 117050666 | rs3772968 | A | G | 4 | 0.02711 | 0.4509 | 1.165 | 1.0952 | 0.0688 | 57.75 |
| 4 | 92523247 | rs6837355 | A | G | 4 | 0.5929 | 0.4509 | 0.9797 | 0.9327 | 0.004 | 77.46 |
| 8 | 54348944 | rs9792157 | A | C | 4 | 0.01968 | 0.4509 | 0.8736 | 0.9093 | 0.0102 | 73.45 |
| 16 | 70564733 | rs7197967 | A | G | 4 | 0.01981 | 0.4509 | 1.1369 | 1.099 | 0.0049 | 76.73 |
| 12 | 68683857 | rs1565725 | C | T | 4 | 0.3504 | 0.4511 | 1.0381 | 1.0757 | 0.0036 | 77.81 |
| 13 | 89487776 | rs1491005 | C | T | 4 | 0.03891 | 0.4512 | 1.0955 | 1.0634 | 0.0448 | 62.77 |
| 17 | 68396477 | rs8069336 | A | G | 4 | 0.02378 | 0.4515 | 1.0831 | 1.0492 | 0.0548 | 60.58 |
| 6 | 116133539 | rs9400871 | T | A | 3 | 0.01413 | 0.4516 | 1.1558 | 1.1375 | 0.0029 | 82.88 |
| 13 | 76023588 | rs285669 | A | G | 4 | 0.01406 | 0.452 | 0.9103 | 0.9423 | 0.0193 | 69.75 |
| 2 | 51633654 | rs2222779 | A | G | 4 | 0.04528 | 0.4521 | 0.9319 | 0.9494 | 0.0297 | 66.55 |
| 7 | 152443576 | rs607348 | C | T | 4 | 0.3239 | 0.4525 | 1.0381 | 1.0723 | 0.0027 | 78.86 |
| 10 | 110687591 | rs6584909 | A | G | 4 | 0.02482 | 0.4527 | 1.1074 | 1.0638 | 0.0507 | 61.46 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 1 | 75159525 | rs12121720 | A | G | 4 | 0.4067 | 0.4528 | 1.033 | 1.0749 | 0.0024 | 79.15 |
| 13 | 84143232 | rs12100200 | A | G | 4 | 0.6796 | 0.4528 | 1.0222 | 1.101 | 0.0021 | 79.53 |
| 2 | 172285362 | rs7597387 | C | T | 4 | 0.3237 | 0.453 | 1.0386 | 1.0812 | 0.0005 | 82.99 |
| 4 | 72336555 | rs2060903 | A | G | 4 | 0.1483 | 0.453 | 0.9308 | 0.8983 | 0.0002 | 84.88 |
| 2 | 172288200 | rs973889 | A | G | 4 | 0.3265 | 0.4531 | 0.9631 | 0.9253 | 0.0006 | 82.81 |
| 2 | 51649455 | rs2715057 | C | T | 4 | 0.04291 | 0.4532 | 0.9317 | 0.9487 | 0.0235 | 68.35 |
| 2 | 51649652 | rs1528811 | C | T | 4 | 0.04447 | 0.4532 | 0.9322 | 0.9489 | 0.0246 | 68.02 |
| 2 | 51652775 | rs2715076 | A | C | 4 | 0.04441 | 0.4533 | 1.0727 | 1.0538 | 0.0246 | 68.04 |
| 2 | 172294131 | rs10207085 | G | T | 4 | 0.3216 | 0.4534 | 1.0388 | 1.0807 | 0.0006 | 82.77 |
| 12 | 10712107 | rs7297205 | C | T | 4 | 0.0131 | 0.4534 | 1.0957 | 1.0524 | 0.0449 | 62.75 |
| 12 | 68683835 | rs1565724 | A | C | 4 | 0.3583 | 0.4534 | 0.9639 | 0.9302 | 0.0038 | 77.65 |
| 7 | 152475034 | rs7810943 | A | G | 4 | 0.4006 | 0.4535 | 1.0303 | 1.0656 | 0.0044 | 77.1 |
| 2 | 172488378 | rs10202823 | C | T | 3 | 0.6502 | 0.4536 | 1.0178 | 1.1023 | 0.0001 | 89.47 |
| 4 | 72337409 | rs10470737 | A | G | 4 | 0.1495 | 0.4537 | 0.931 | 0.8987 | 0.0002 | 84.8 |
| 11 | 86022325 | rs1938928 | C | T | 4 | 0.441 | 0.4537 | 1.0493 | 1.1049 | 0.0122 | 72.53 |
| 5 | 104047674 | rs12516369 | A | G | 4 | 0.0776 | 0.454 | 1.0842 | 1.0827 | 0.0047 | 76.84 |
| 13 | 84147159 | rs9575638 | G | T | 4 | 0.6861 | 0.454 | 0.9787 | 0.9081 | 0.0021 | 79.57 |
| 5 | 168144746 | rs11134531 | A | G | 4 | 0.06997 | 0.4541 | 0.9356 | 0.9422 | 0.0111 | 73.03 |
| 10 | 110686488 | rs12258030 | A | G | 4 | 0.02387 | 0.4541 | 1.1082 | 1.064 | 0.0487 | 61.9 |
| 8 | 5510132 | rs10100498 | A | C | 4 | 0.6486 | 0.4544 | 0.9817 | 0.9329 | 0.006 | 75.91 |
| 10 | 110734026 | rs11596046 | A | G | 4 | 0.029 | 0.4544 | 0.9054 | 0.9408 | 0.0548 | 60.58 |
| 10 | 110734457 | rs17701356 | A | G | 4 | 0.029 | 0.4544 | 0.9054 | 0.9408 | 0.0548 | 60.58 |
| 10 | 110734927 | rs17779611 | C | T | 4 | 0.029 | 0.4544 | 0.9054 | 0.9408 | 0.0548 | 60.58 |
| 1 | 75134581 | rs1327098 | A | G | 4 | 0.4748 | 0.4546 | 1.0289 | 1.0733 | 0.0038 | 77.68 |
| 2 | 172350303 | rs12692973 | C | T | 4 | 0.3212 | 0.4547 | 0.9626 | 0.9273 | 0.0009 | 81.83 |
| 8 | 17651768 | rs3862101 | C | T | 4 | 0.02903 | 0.4548 | 1.1132 | 1.0699 | 0.0458 | 62.54 |
| 13 | 53936097 | rs9536735 | A | G | 4 | 0.9194 | 0.4553 | 1.0059 | 1.1064 | 0.0074 | 74.96 |
| 4 | 183403463 | rs7696796 | A | G | 4 | 0.09072 | 0.4554 | 0.9347 | 0.9333 | 0.0058 | 76.04 |
| 11 | 83252000 | rs2037194 | A | G | 4 | 0.5197 | 0.4557 | 0.9357 | 0.8385 | 0.0051 | 76.56 |
| 17 | 68395857 | rs6501572 | G | T | 4 | 0.02515 | 0.4557 | 1.0823 | 1.0487 | 0.0554 | 60.45 |
| 2 | 38366214 | rs875654 | C | T | 4 | 0.7735 | 0.4566 | 0.9861 | 0.9183 | 0.0051 | 76.56 |
| 8 | 135092098 | rs11998159 | A | G | 4 | 0.06789 | 0.4566 | 0.9386 | 0.9484 | 0.0209 | 69.2 |
| 8 | 54346783 | rs2162181 | C | T | 4 | 0.02256 | 0.4568 | 1.1411 | 1.0987 | 0.0097 | 73.72 |
| 10 | 110740736 | rs11593939 | C | T | 4 | 0.02978 | 0.4568 | 0.9059 | 0.9413 | 0.0561 | 60.31 |
| 2 | 134738798 | rs3828176 | A | T | 4 | 0.01862 | 0.4572 | 0.8165 | 0.8702 | 0.0218 | 68.92 |
| 21 | 32946315 | rs2833934 | C | T | 4 | 0.04252 | 0.4574 | 1.2192 | 1.1375 | 0.0565 | 60.23 |
| 4 | 92514491 | rs7672780 | A | G | 4 | 0.5717 | 0.4575 | 1.022 | 1.0713 | 0.0039 | 77.6 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 8 | 54355648 | rs2059547 | C | T | 4 | 0.02239 | 0.4577 | 0.8766 | 0.9097 | 0.0089 | 74.11 |
| 18 | 6397483 | rs4797242 | A | C | 4 | 0.01784 | 0.4578 | 0.9124 | 0.9414 | 0.0151 | 71.3 |
| 2 | 38418548 | rs13431831 | C | G | 4 | 0.8395 | 0.4579 | 0.9919 | 0.9159 | 0.0002 | 85.1 |
| 13 | 39443193 | rs7338145 | A | G | 4 | 0.5714 | 0.458 | 0.9791 | 0.9346 | 0.0026 | 78.89 |
| 2 | 51649771 | rs1528810 | C | T | 4 | 0.04575 | 0.4583 | 0.9326 | 0.9493 | 0.0239 | 68.25 |
| 6 | 121666786 | rs9320803 | C | T | 4 | 0.01097 | 0.4583 | 0.8903 | 0.9396 | 0.0514 | 61.32 |
| 6 | 94777061 | rs10806484 | A | C | 4 | 0.03018 | 0.4592 | 1.078 | 1.0478 | 0.0517 | 61.24 |
| 2 | 172313645 | rs4667694 | A | G | 4 | 0.3244 | 0.4594 | 1.0386 | 1.0794 | 0.0006 | 82.56 |
| 5 | 104020427 | rs7445539 | A | G | 4 | 0.07995 | 0.4595 | 1.0835 | 1.0834 | 0.0036 | 77.84 |
| 10 | 110740500 | rs11593900 | C | T | 4 | 0.03027 | 0.4603 | 0.9057 | 0.9416 | 0.0563 | 60.26 |
| 10 | 110736026 | rs11597293 | A | C | 4 | 0.0298 | 0.4606 | 0.9059 | 0.9415 | 0.0538 | 60.79 |
| 8 | 54352873 | rs9792266 | A | T | 4 | 0.0202 | 0.4609 | 0.8741 | 0.9104 | 0.0093 | 73.93 |
| 2 | 172343943 | rs10174525 | C | T | 4 | 0.3308 | 0.4615 | 1.038 | 1.0781 | 0.0007 | 82.25 |
| 12 | 10711585 | rs10845199 | C | T | 4 | 0.01318 | 0.4616 | 0.9143 | 0.9524 | 0.0472 | 62.23 |
| 6 | 99031254 | rs6941388 | A | T | 4 | 0.01657 | 0.4617 | 0.8071 | 0.8735 | 0.0154 | 71.17 |
| 2 | 172345846 | rs6705200 | A | G | 4 | 0.3312 | 0.462 | 0.9634 | 0.9277 | 0.0008 | 82.21 |
| 2 | 172348869 | rs10497374 | A | G | 4 | 0.3312 | 0.462 | 0.9634 | 0.9277 | 0.0008 | 82.21 |
| 9 | 10616389 | rs1322294 | A | G | 4 | 0.6119 | 0.462 | 1.0254 | 1.0888 | 0.0038 | 77.67 |
| 10 | 124859893 | rs17104648 | C | G | 4 | 0.05971 | 0.462 | 1.1788 | 1.133 | 0.0276 | 67.15 |
| 11 | 115309136 | rs427875 | A | C | 4 | 0.02528 | 0.4621 | 1.0939 | 1.0658 | 0.0118 | 72.68 |
| 2 | 172317202 | rs10184866 | G | T | 4 | 0.3292 | 0.4625 | 1.0382 | 1.0786 | 0.0006 | 82.57 |
| 5 | 104050721 | rs12513560 | C | T | 4 | 0.08427 | 0.4625 | 0.9239 | 0.925 | 0.0047 | 76.84 |
| 2 | 172349291 | rs11757 | C | G | 4 | 0.338 | 0.4626 | 0.9639 | 0.9281 | 0.0008 | 82.06 |
| 8 | 140500127 | rs12680834 | C | T | 4 | 0.8782 | 0.4626 | 0.993 | 0.9254 | 0.0045 | 77.03 |
| 5 | 104017956 | rs12189083 | C | T | 4 | 0.08162 | 0.4627 | 0.9234 | 0.9234 | 0.0035 | 77.96 |
| 4 | 72333961 | rs9790757 | C | T | 4 | 0.1519 | 0.4631 | 1.0768 | 1.12 | 0.0001 | 85.79 |
| 4 | 187045575 | rs13110782 | A | G | 4 | 0.7749 | 0.4634 | 0.9897 | 0.9362 | 0.0022 | 79.41 |
| 8 | 135211030 | rs1446995 | G | T | 4 | 0.01684 | 0.4635 | 1.0854 | 1.0566 | 0.0109 | 73.1 |
| 6 | 116137208 | rs9320546 | T | C | 3 | 0.01723 | 0.4639 | 1.1525 | 1.1346 | 0.0027 | 83.04 |
| 12 | 126490295 | rs10847348 | C | T | 4 | 0.05551 | 0.464 | 1.0793 | 1.0709 | 0.005 | 76.66 |
| 1 | 65085401 | rs10789166 | A | G | 4 | 0.07323 | 0.4641 | 1.0972 | 1.0875 | 0.0085 | 74.36 |
| 3 | 117048717 | rs2972479 | C | T | 4 | 0.02899 | 0.4641 | 1.1621 | 1.0928 | 0.0651 | 58.47 |
| 12 | 97094264 | rs1847534 | A | C | 4 | 0.5715 | 0.4641 | 1.0225 | 0.9272 | 0.0011 | 81.24 |
| 2 | 172334389 | rs10194102 | C | G | 4 | 0.3352 | 0.4643 | 1.0377 | 1.0781 | 0.0007 | 82.5 |
| 6 | 136476887 | rs3757154 | C | G | 4 | 0.4631 | 0.4643 | 0.9739 | 0.939 | 0.0039 | 77.56 |
| 9 | 10573907 | rs4741038 | A | T | 3 | 0.2101 | 0.4643 | 1.0993 | 1.1673 | 0.0041 | 81.85 |
| 11 | 2799123 | rs12294675 | A | G | 4 | 0.07443 | 0.4644 | 1.0905 | 1.0729 | 0.0256 | 67.74 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 7 | 52155467 | rs2953431 | A | G | 4 | 0.0461 | 0.4646 | 1.0723 | 1.059 | 0.0087 | 74.26 |
| 12 | 68673713 | rs7134411 | C | T | 4 | 0.3401 | 0.4651 | 1.038 | 1.0724 | 0.0033 | 78.19 |
| 1 | 75167786 | rs12127639 | C | G | 4 | 0.4555 | 0.4655 | 0.9711 | 0.9321 | 0.0025 | 79.03 |
| 1 | 75176175 | rs10782637 | A | C | 4 | 0.4603 | 0.4657 | 0.9714 | 0.9322 | 0.0026 | 78.98 |
| 2 | 172328016 | rs4668412 | A | G | 4 | 0.338 | 0.4658 | 0.9639 | 0.9275 | 0.0006 | 82.64 |
| 4 | 92480699 | rs4593093 | G | T | 4 | 0.4898 | 0.4658 | 0.9743 | 0.9374 | 0.0051 | 76.58 |
| 8 | 54352922 | rs9792384 | A | G | 4 | 0.02096 | 0.4658 | 0.8748 | 0.911 | 0.009 | 74.1 |
| 2 | 172335589 | rs11904009 | G | T | 4 | 0.3413 | 0.4662 | 1.0372 | 1.0777 | 0.0007 | 82.44 |
| 2 | 98851853 | rs4851165 | C | T | 4 | 0.06327 | 0.4664 | 0.879 | 0.8941 | 0.0071 | 75.16 |
| 8 | 54353550 | rs16918988 | C | T | 4 | 0.02256 | 0.4669 | 1.1437 | 1.0996 | 0.0083 | 74.46 |
| 2 | 51624921 | rs1919434 | C | T | 4 | 0.02726 | 0.467 | 1.0793 | 1.0521 | 0.023 | 68.51 |
| 6 | 121445811 | rs9401367 | C | T | 4 | 0.01803 | 0.4676 | 0.9005 | 0.9416 | 0.0437 | 63.02 |
| 10 | 128737210 | rs7092964 | C | T | 4 | 0.9677 | 0.4676 | 1.0025 | 0.8949 | 0.0015 | 80.55 |
| 16 | 6838730 | rs8054432 | C | T | 4 | 0.02865 | 0.4676 | 1.0872 | 1.0699 | 0.0029 | 78.56 |
| 8 | 129307851 | rs7812998 | A | G | 4 | 0.3878 | 0.468 | 1.0746 | 1.1408 | 0.0086 | 74.28 |
| 2 | 51645271 | rs1569190 | G | T | 4 | 0.0614 | 0.4681 | 0.9344 | 0.9476 | 0.021 | 69.16 |
| 4 | 149818435 | rs4435727 | C | G | 4 | 0.0718 | 0.4685 | 0.9283 | 0.9376 | 0.0123 | 72.47 |
| 8 | 54356785 | rs2376422 | A | G | 4 | 0.02068 | 0.4685 | 1.1436 | 1.0969 | 0.0093 | 73.92 |
| 1 | 48859991 | rs12566140 | A | G | 4 | 0.8444 | 0.4686 | 1.0143 | 1.1317 | 0.0032 | 78.24 |
| 3 | 29756855 | rs1866774 | A | G | 4 | 0.4522 | 0.4689 | 1.0271 | 1.06 | 0.0071 | 75.2 |
| 5 | 104018213 | rs12189097 | C | T | 4 | 0.08501 | 0.4689 | 0.9242 | 0.924 | 0.0032 | 78.2 |
| 8 | 129311457 | rs7840538 | C | G | 4 | 0.3899 | 0.4689 | 1.0743 | 1.1406 | 0.0085 | 74.33 |
| 2 | 51628777 | rs1528815 | C | G | 4 | 0.02698 | 0.469 | 1.0795 | 1.0522 | 0.0217 | 68.93 |
| 5 | 104028035 | rs6892501 | A | C | 4 | 0.08634 | 0.4693 | 1.0817 | 1.082 | 0.0033 | 78.13 |
| 3 | 151327125 | rs12485454 | C | T | 4 | 0.8877 | 0.4694 | 1.0054 | 1.067 | 0.0046 | 76.91 |
| 6 | 94788810 | rs10944710 | C | T | 4 | 0.02729 | 0.4696 | 1.0795 | 1.0467 | 0.0518 | 61.21 |
| 6 | 136508827 | rs2170231 | C | T | 4 | 0.5469 | 0.4696 | 0.9786 | 0.9336 | 0.0008 | 82.04 |
| 4 | 92539047 | rs2904382 | A | G | 4 | 0.5694 | 0.4698 | 1.0221 | 1.0684 | 0.0044 | 77.13 |
| 10 | 110709762 | rs11593385 | C | T | 4 | 0.02915 | 0.4701 | 0.9056 | 0.9427 | 0.0535 | 60.86 |
| 8 | 135210399 | rs7011020 | A | G | 4 | 0.02149 | 0.4704 | 0.9235 | 0.947 | 0.0109 | 73.09 |
| 2 | 51628765 | rs1528816 | A | G | 4 | 0.02716 | 0.4706 | 1.0794 | 1.052 | 0.0217 | 68.93 |
| 2 | 113541556 | rs7599662 | C | T | 4 | 0.0325 | 0.4707 | 0.9207 | 0.9442 | 0.0187 | 69.97 |
| 12 | 126488790 | rs11059127 | G | T | 4 | 0.06791 | 0.4708 | 1.0762 | 1.07 | 0.0054 | 76.31 |
| 6 | 20974836 | rs9368246 | C | T | 4 | 0.7403 | 0.4709 | 1.0123 | 1.061 | 0.0088 | 74.17 |
| 6 | 136500942 | rs2046091 | A | G | 4 | 0.5343 | 0.4709 | 0.9778 | 0.9361 | 0.0016 | 80.27 |
| 13 | 54051478 | rs9597010 | A | T | 4 | 0.3578 | 0.4709 | 1.0466 | 0.9041 | 0.0004 | 83.43 |
| 8 | 129311983 | rs10505507 | C | T | 4 | 0.3946 | 0.4711 | 1.0735 | 1.1401 | 0.0084 | 74.39 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 13 | 39470053 | rs7339164 | A | G | 4 | 0.4594 | 0.4712 | 1.0268 | 1.0693 | 0.0011 | 81.41 |
| 2 | 51636011 | rs2698026 | A | G | 4 | 0.04094 | 0.4713 | 1.0746 | 1.0542 | 0.0169 | 70.59 |
| 8 | 129316558 | rs9693045 | C | T | 4 | 0.3951 | 0.4714 | 1.0735 | 1.1405 | 0.0081 | 74.55 |
| 2 | 51651289 | rs2698011 | G | T | 4 | 0.04472 | 0.4719 | 0.9323 | 0.9506 | 0.0232 | 68.47 |
| 2 | 51626532 | rs1358580 | A | G | 4 | 0.02751 | 0.472 | 0.9266 | 0.9508 | 0.0219 | 68.87 |
| 13 | 104284662 | rs9519490 | C | T | 4 | 0.4922 | 0.472 | 1.0308 | 1.0725 | 0.0092 | 73.97 |
| 2 | 172272267 | rs312924 | A | T | 4 | 0.3685 | 0.4724 | 0.9661 | 0.9265 | 0.0004 | 83.68 |
| 7 | 26555282 | rs4140898 | A | G | 3 | 0.9362 | 0.4724 | 1.0033 | 1.0817 | 0.0025 | 83.32 |
| 4 | 92512505 | rs1358554 | C | T | 4 | 0.6318 | 0.473 | 0.9818 | 0.9356 | 0.0038 | 77.64 |
| 6 | 124511753 | rs9388306 | C | G | 4 | 0.0146 | 0.473 | 1.1414 | 1.0743 | 0.042 | 63.42 |
| 1 | 75170858 | rs12732265 | C | T | 4 | 0.4863 | 0.4734 | 1.0278 | 1.0712 | 0.0027 | 78.83 |
| 5 | 64299723 | rs13178969 | C | T | 4 | 0.01454 | 0.4734 | 1.125 | 1.0756 | 0.0163 | 70.83 |
| 12 | 126488548 | rs11059124 | A | G | 4 | 0.06936 | 0.4737 | 1.0758 | 1.0697 | 0.0053 | 76.43 |
| 6 | 136500931 | rs2046092 | A | G | 4 | 0.5482 | 0.474 | 0.9785 | 0.9364 | 0.0016 | 80.37 |
| 21 | 40088875 | rs2837226 | A | C | 4 | 0.06928 | 0.4746 | 1.071 | 1.0554 | 0.025 | 67.92 |
| 2 | 172376928 | rs3770452 | A | G | 4 | 0.3206 | 0.4747 | 0.9626 | 0.9305 | 0.0009 | 81.77 |
| 13 | 89159717 | rs9560417 | A | G | 4 | 0.4054 | 0.4747 | 0.9044 | 0.8194 | 0.0028 | 78.68 |
| 21 | 40145943 | rs2837258 | A | C | 4 | 0.07279 | 0.4748 | 1.0706 | 1.0566 | 0.0227 | 68.63 |
| 4 | 92510260 | rs7654013 | G | T | 4 | 0.5467 | 0.475 | 1.0243 | 1.069 | 0.0055 | 76.22 |
| 1 | 75167915 | rs12129191 | A | G | 4 | 0.4911 | 0.4752 | 0.9733 | 0.9337 | 0.0026 | 78.88 |
| 8 | 135214566 | rs6994801 | C | G | 4 | 0.0174 | 0.4754 | 0.9211 | 0.9475 | 0.0108 | 73.18 |
| 8 | 135212703 | rs4897681 | C | T | 4 | 0.01746 | 0.4758 | 1.0855 | 1.0555 | 0.0104 | 73.34 |
| 10 | 110707237 | rs17778715 | C | T | 4 | 0.03052 | 0.4763 | 0.9063 | 0.9431 | 0.0509 | 61.42 |
| 6 | 116136091 | rs9372449 | G | C | 3 | 0.01536 | 0.4767 | 1.1606 | 1.1351 | 0.0022 | 83.61 |
| 2 | 51625061 | rs1528817 | A | G | 4 | 0.02947 | 0.4768 | 0.9275 | 0.9514 | 0.0223 | 68.74 |
| 22 | 33870650 | rs9610223 | C | T | 4 | 0.05452 | 0.4769 | 0.9248 | 0.9339 | 0.0042 | 77.33 |
| 2 | 51626312 | rs2698031 | A | G | 4 | 0.02834 | 0.477 | 0.927 | 0.9512 | 0.0213 | 69.07 |
| 12 | 97094459 | rs1354486 | A | G | 4 | 0.6219 | 0.4772 | 1.0203 | 0.9303 | 0.0023 | 79.36 |
| 5 | 178226479 | rs11948690 | C | G | 4 | 0.3698 | 0.4775 | 0.9521 | 0.8969 | 0.0002 | 84.43 |
| 13 | 84157238 | rs9319065 | A | G | 4 | 0.7254 | 0.4776 | 0.9815 | 0.9129 | 0.0022 | 79.5 |
| 2 | 172379340 | rs7586207 | A | G | 4 | 0.3226 | 0.4778 | 0.9627 | 0.9309 | 0.0009 | 81.81 |
| 14 | 77999119 | rs11625200 | A | C | 4 | 0.3339 | 0.478 | 1.0354 | 1.06 | 0.0072 | 75.12 |
| 6 | 121698543 | rs9320809 | A | G | 4 | 0.009762 | 0.4781 | 0.8886 | 0.9414 | 0.0469 | 62.3 |
| 1 | 199367371 | rs11589642 | A | G | 4 | 0.3166 | 0.4782 | 1.0438 | 1.078 | 0.0024 | 79.15 |
| 16 | 47669016 | rs2967255 | A | C | 4 | 0.03756 | 0.4783 | 0.9284 | 0.9495 | 0.0219 | 68.88 |
| 10 | 110729755 | rs10509885 | C | T | 4 | 0.03057 | 0.4784 | 1.1034 | 1.0602 | 0.051 | 61.39 |
| 14 | 32679948 | rs8013167 | A | G | 4 | 0.07291 | 0.4786 | 1.0725 | 1.0579 | 0.0211 | 69.12 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 1 | 51248076 | rs3813634 | A | G | 4 | 0.08214 | 0.4788 | 0.9406 | 0.9482 | 0.0135 | 71.96 |
| 8 | 135092082 | rs11990927 | A | G | 4 | 0.07679 | 0.479 | 1.0633 | 1.0526 | 0.0177 | 70.29 |
| 5 | 178229382 | rs11958941 | C | T | 4 | 0.3509 | 0.4791 | 0.9506 | 0.8978 | 0.0002 | 84.43 |
| 16 | 47674551 | rs2908915 | C | T | 4 | 0.03697 | 0.4791 | 0.929 | 0.95 | 0.0202 | 69.42 |
| 6 | 94860568 | rs546226 | A | G | 4 | 0.01892 | 0.4796 | 0.9198 | 0.9546 | 0.0468 | 62.32 |
| 13 | 39474064 | rs12873354 | C | T | 4 | 0.4934 | 0.4797 | 0.9758 | 0.9365 | 0.0011 | 81.35 |
| 6 | 94860527 | rs546100 | A | C | 4 | 0.01865 | 0.4798 | 1.0874 | 1.0476 | 0.0462 | 62.46 |
| 5 | 104064571 | rs17416034 | C | T | 4 | 0.07673 | 0.48 | 0.9216 | 0.923 | 0.0022 | 79.43 |
| 7 | 52158227 | rs2465796 | C | T | 4 | 0.04989 | 0.48 | 1.071 | 1.0565 | 0.0092 | 73.98 |
| 16 | 47669641 | rs2967254 | C | T | 4 | 0.03854 | 0.4802 | 1.0767 | 1.0528 | 0.0225 | 68.68 |
| 5 | 178257390 | rs6895371 | C | T | 4 | 0.3312 | 0.4803 | 0.9496 | 0.8994 | 0.0002 | 84.43 |
| 8 | 135092194 | rs11998140 | A | C | 4 | 0.08507 | 0.4804 | 0.9415 | 0.9496 | 0.0171 | 70.54 |
| 3 | 113072462 | rs1282932 | A | C | 4 | 0.9153 | 0.4811 | 1.004 | 0.9369 | 0.0022 | 79.41 |
| 6 | 157077339 | rs6913743 | A | G | 4 | 0.02728 | 0.4813 | 0.8432 | 0.8937 | 0.0232 | 68.45 |
| 2 | 115868314 | rs17453131 | A | G | 4 | 0.8106 | 0.4818 | 0.9869 | 0.9171 | 0.0063 | 75.69 |
| 11 | 3638426 | rs10834744 | A | G | 4 | 0.03919 | 0.4818 | 0.9076 | 0.9422 | 0.0598 | 59.54 |
| 8 | 135219115 | rs7012406 | A | T | 4 | 0.03901 | 0.4819 | 0.9306 | 0.9517 | 0.0226 | 68.66 |
| 6 | 52591585 | rs9463804 | T | A | 3 | 0.04019 | 0.4823 | 1.3162 | 1.2773 | 0.0051 | 81.05 |
| 8 | 54356965 | rs2376420 | A | T | 4 | 0.02255 | 0.4823 | 0.8761 | 0.9134 | 0.0083 | 74.46 |
| 5 | 178239194 | rs6862829 | C | T | 4 | 0.3418 | 0.4824 | 0.9507 | 0.8996 | 0.0002 | 84.55 |
| 5 | 178239195 | rs6883566 | A | G | 4 | 0.3418 | 0.4824 | 0.9507 | 0.8996 | 0.0002 | 84.55 |
| 5 | 178253452 | rs11954382 | C | T | 4 | 0.3353 | 0.4824 | 0.9501 | 0.8997 | 0.0002 | 84.49 |
| 7 | 121757354 | rs920802 | A | G | 4 | 0.01393 | 0.4824 | 0.9127 | 0.9497 | 0.0267 | 67.4 |
| 16 | 6838963 | rs8054809 | C | G | 4 | 0.03317 | 0.483 | 1.0848 | 1.0685 | 0.0024 | 79.14 |
| 10 | 36634477 | rs4934805 | A | G | 4 | 0.4213 | 0.4831 | 1.0494 | 1.1009 | 0.0061 | 75.86 |
| 11 | 13470839 | rs6254 | C | T | 4 | 0.9695 | 0.4831 | 1.0014 | 0.9413 | 0.0043 | 77.19 |
| 6 | 20964682 | rs4712556 | A | G | 4 | 0.7888 | 0.4833 | 1.0099 | 1.0598 | 0.0081 | 74.6 |
| 11 | 13531228 | rs1903102 | A | C | 4 | 0.9535 | 0.4834 | 1.0021 | 1.0611 | 0.0053 | 76.41 |
| 1 | 81205753 | rs7537835 | A | G | 4 | 0.0184 | 0.4836 | 1.0888 | 1.0534 | 0.0203 | 69.4 |
| 5 | 178232797 | rs6870926 | C | T | 4 | 0.348 | 0.4838 | 1.0512 | 1.1113 | 0.0002 | 84.55 |
| 5 | 178229129 | rs11949892 | C | T | 4 | 0.3668 | 0.4839 | 1.0503 | 1.1134 | 0.0002 | 84.63 |
| 22 | 23850095 | rs5752064 | C | T | 4 | 0.6137 | 0.4839 | 0.981 | 0.9423 | 0.0081 | 74.58 |
| 5 | 178229142 | rs11949180 | A | G | 4 | 0.3674 | 0.484 | 0.9522 | 0.8982 | 0.0002 | 84.63 |
| 6 | 136516487 | rs9494457 | A | T | 4 | 0.599 | 0.4842 | 1.019 | 1.0694 | 0.0007 | 82.35 |
| 10 | 110724687 | rs4314990 | C | T | 4 | 0.03152 | 0.4846 | 0.9068 | 0.9439 | 0.0502 | 61.56 |
| 5 | 178227589 | rs11948175 | A | C | 4 | 0.3853 | 0.4848 | 0.9536 | 0.8981 | 0.0002 | 84.56 |
| 10 | 110722721 | rs11596823 | A | G | 4 | 0.03143 | 0.4849 | 1.1028 | 1.0594 | 0.05 | 61.61 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 10 | 110723326 | rs17779320 | A | G | 4 | 0.03143 | 0.4849 | 1.1028 | 1.0594 | 0.05 | 61.61 |
| 4 | 58802595 | rs2553316 | C | G | 4 | 0.01156 | 0.4851 | 1.1009 | 1.0605 | 0.009 | 74.07 |
| 8 | 12887282 | rs13281642 | A | T | 4 | 0.002589 | 0.4853 | 1.2486 | 1.117 | 0.0102 | 73.45 |
| 6 | 33235965 | rs4713614 | A | C | 4 | 0.0859 | 0.4854 | 0.9401 | 0.9509 | 0.0243 | 68.12 |
| 10 | 110707994 | rs17700585 | C | T | 4 | 0.03066 | 0.4854 | 1.1033 | 1.0594 | 0.0495 | 61.73 |
| 10 | 122674538 | rs11199656 | C | T | 4 | 0.2791 | 0.4866 | 1.1058 | 1.1627 | 0.0057 | 76.12 |
| 6 | 52589637 | rs9474257 | G | T | 3 | 0.04217 | 0.4867 | 1.3127 | 1.275 | 0.005 | 81.16 |
| 16 | 7375088 | rs7184072 | C | T | 4 | 0.01422 | 0.4873 | 1.1595 | 1.084 | 0.0365 | 64.76 |
| 3 | 113073512 | rs1282931 | A | T | 4 | 0.8927 | 0.4877 | 0.995 | 1.0673 | 0.0018 | 80.02 |
| 11 | 13516530 | rs11608098 | C | T | 4 | 0.9791 | 0.4879 | 1.001 | 1.0606 | 0.0053 | 76.39 |
| 5 | 104073920 | rs325524 | C | G | 4 | 0.08364 | 0.4881 | 1.0835 | 1.0815 | 0.0024 | 79.23 |
| 5 | 104081546 | rs325538 | A | G | 4 | 0.05901 | 0.4882 | 0.9158 | 0.9192 | 0.0008 | 81.96 |
| 15 | 89915807 | rs7174086 | C | G | 4 | 0.3129 | 0.4883 | 0.9618 | 0.937 | 0.0027 | 78.85 |
| 8 | 135164118 | rs6981423 | C | T | 4 | 0.07501 | 0.4884 | 1.0641 | 1.0497 | 0.0246 | 68.03 |
| 2 | 51634538 | rs2715079 | A | G | 4 | 0.02955 | 0.4887 | 1.0789 | 1.0532 | 0.0131 | 72.11 |
| 3 | 56421736 | rs931461 | G | T | 4 | 0.7279 | 0.4887 | 0.9874 | 1.0643 | 0.0025 | 79.01 |
| 5 | 104016997 | rs6859797 | A | C | 4 | 0.06995 | 0.4888 | 1.0895 | 1.0839 | 0.0021 | 79.64 |
| 10 | 30332299 | rs12779954 | A | T | 4 | 0.0674 | 0.4888 | 0.9363 | 0.9521 | 0.0285 | 66.9 |
| 2 | 51626897 | rs1358578 | A | G | 4 | 0.06823 | 0.4892 | 1.0658 | 1.0484 | 0.0296 | 66.59 |
| 2 | 51629318 | rs2715081 | C | T | 4 | 0.03091 | 0.4893 | 0.9274 | 0.9512 | 0.0177 | 70.31 |
| 5 | 178229183 | rs11958887 | C | T | 4 | 0.3783 | 0.4893 | 0.9532 | 0.8991 | 0.0002 | 84.7 |
| 5 | 104076454 | rs325527 | C | T | 4 | 0.07788 | 0.4894 | 0.9218 | 0.9236 | 0.0018 | 80.01 |
| 8 | 129318285 | rs16902754 | A | C | 4 | 0.4142 | 0.49 | 1.0725 | 1.1381 | 0.0079 | 74.71 |
| 2 | 172363343 | rs6758704 | C | T | 4 | 0.3574 | 0.4902 | 1.036 | 1.0723 | 0.0009 | 81.9 |
| 2 | 172304324 | rs6710698 | C | G | 4 | 0.4661 | 0.4905 | 1.0286 | 1.0735 | 0.0008 | 82.17 |
| 3 | 29734340 | rs17550007 | G | T | 4 | 0.5486 | 0.4907 | 0.9783 | 0.9445 | 0.0069 | 75.29 |
| 6 | 30245628 | rs1018846 | A | G | 4 | 0.01707 | 0.4909 | 1.1945 | 1.1142 | 0.0169 | 70.62 |
| 7 | 125587676 | rs593517 | A | C | 4 | 0.06335 | 0.4911 | 1.1036 | 1.0686 | 0.0488 | 61.87 |
| 3 | 113072652 | rs1913494 | A | G | 4 | 0.8748 | 0.4912 | 1.0059 | 0.9376 | 0.0019 | 79.89 |
| 7 | 125587627 | rs593446 | C | T | 4 | 0.06248 | 0.4912 | 1.1039 | 1.0688 | 0.048 | 62.06 |
| 6 | 136506453 | rs7770469 | A | G | 4 | 0.6854 | 0.4917 | 1.0149 | 1.0648 | 0.002 | 79.75 |
| 2 | 17289256 | rs1983375 | C | T | 4 | 0.925 | 0.4918 | 0.9954 | 0.9278 | 0.0096 | 73.78 |
| 2 | 29140696 | rs10495767 | A | G | 4 | 0.06786 | 0.4921 | 1.08 | 1.0548 | 0.0474 | 62.18 |
| 5 | 104080504 | rs325533 | A | G | 4 | 0.08266 | 0.4923 | 1.0835 | 1.0837 | 0.0015 | 80.61 |
| 5 | 104073206 | rs325522 | C | G | 4 | 0.08122 | 0.4925 | 1.0838 | 1.082 | 0.0018 | 79.98 |
| 14 | 39252820 | rs12147244 | A | G | 4 | 0.03142 | 0.4928 | 1.1323 | 1.0731 | 0.0619 | 59.12 |
| 2 | 134734676 | rs3791261 | G | T | 4 | 0.0281 | 0.4934 | 1.2171 | 1.1398 | 0.0207 | 69.26 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 5 | 62562511 | rs347670 | C | T | 4 | 0.8218 | 0.4934 | 0.9875 | 0.9086 | 0.0023 | 79.31 |
| 2 | 60183809 | rs6726368 | C | G | 4 | 0.9947 | 0.4935 | 1.0003 | 1.0642 | 0.0042 | 77.25 |
| 20 | 39604287 | rs2866743 | A | G | 4 | 0.1618 | 0.4936 | 0.8337 | 0.805 | 0.0055 | 76.27 |
| 14 | 39253036 | rs10483520 | A | G | 4 | 0.0318 | 0.4937 | 1.132 | 1.0733 | 0.0604 | 59.42 |
| 10 | 30332480 | rs12780390 | C | T | 4 | 0.07301 | 0.4938 | 0.9376 | 0.9521 | 0.0255 | 67.76 |
| 10 | 32470365 | rs2998089 | G | T | 4 | 0.04543 | 0.4941 | 0.8241 | 0.8814 | 0.0359 | 64.9 |
| 5 | 104092841 | rs161785 | A | C | 4 | 0.09343 | 0.4946 | 0.9249 | 0.9229 | 0.0015 | 80.59 |
| 2 | 172443575 | rs6724337 | C | T | 4 | 0.3491 | 0.4949 | 0.9647 | 0.9333 | 0.0009 | 81.87 |
| 2 | 113545707 | rs4849147 | A | T | 4 | 0.02824 | 0.4952 | 1.0899 | 1.0605 | 0.0103 | 73.38 |
| 10 | 110687487 | rs11592721 | A | G | 4 | 0.03214 | 0.4954 | 0.9 | 0.9393 | 0.042 | 63.44 |
| 4 | 92549226 | rs4301075 | A | T | 4 | 0.5463 | 0.4955 | 0.9768 | 0.9408 | 0.0066 | 75.5 |
| 4 | 92515582 | rs1554850 | A | C | 4 | 0.699 | 0.496 | 1.0163 | 1.0697 | 0.0043 | 77.23 |
| 5 | 104072799 | rs12514766 | A | T | 4 | 0.08353 | 0.496 | 1.0831 | 1.0813 | 0.0018 | 80.02 |
| 3 | 56416017 | rs9817231 | A | T | 4 | 0.6972 | 0.4966 | 1.014 | 0.941 | 0.002 | 79.7 |
| 5 | 104076769 | rs106451 | A | C | 4 | 0.0824 | 0.4966 | 1.0835 | 1.082 | 0.0016 | 80.35 |
| 15 | 52090751 | rs1897042 | A | T | 4 | 0.8712 | 0.4966 | 0.9939 | 1.0656 | 0.0024 | 79.14 |
| 6 | 116136871 | rs9374567 | T | C | 3 | 0.01385 | 0.4968 | 1.1585 | 1.1286 | 0.0021 | 83.82 |
| 5 | 104093326 | rs161787 | C | T | 4 | 0.09532 | 0.4975 | 0.9254 | 0.9232 | 0.0014 | 80.69 |
| 1 | 48880413 | rs12058997 | C | T | 4 | 0.7262 | 0.4978 | 1.0222 | 1.0985 | 0.0082 | 74.55 |
| 7 | 125586751 | rs473762 | A | T | 4 | 0.06362 | 0.4981 | 1.1034 | 1.0677 | 0.0475 | 62.16 |
| 8 | 135092624 | rs1379440 | C | T | 4 | 0.08813 | 0.4985 | 1.0615 | 1.0521 | 0.0135 | 71.96 |
| 21 | 16544957 | rs238946 | A | G | 4 | 0.09625 | 0.4985 | 0.9396 | 0.9338 | 0.0006 | 82.82 |
| 20 | 55497673 | rs6099656 | C | T | 4 | 0.05536 | 0.4988 | 0.9318 | 0.9527 | 0.0317 | 66.02 |
| 2 | 172371640 | rs6754817 | C | T | 4 | 0.3797 | 0.4994 | 0.9668 | 0.9332 | 0.0007 | 82.32 |
| 5 | 104074988 | rs325526 | A | G | 4 | 0.0833 | 0.4995 | 0.9232 | 0.9248 | 0.0016 | 80.3 |
| 9 | 82311365 | rs11138705 | C | G | 4 | 0.01825 | 0.4995 | 0.9042 | 0.9472 | 0.0432 | 63.15 |
| 2 | 172398426 | rs908670 | C | T | 4 | 0.3378 | 0.4997 | 1.0375 | 1.0718 | 0.0007 | 82.49 |
| 6 | 52612989 | rs1884456 | A | G | 3 | 0.05879 | 0.4998 | 1.2863 | 1.2695 | 0.0042 | 81.75 |
| 2 | 51632112 | rs11563162 | A | G | 4 | 0.03248 | 0.5003 | 1.082 | 1.0524 | 0.0178 | 70.27 |
| 8 | 135192071 | rs1124525 | A | G | 4 | 0.02454 | 0.5003 | 0.9246 | 0.9493 | 0.0094 | 73.89 |
| 5 | 104095776 | rs161788 | C | T | 4 | 0.09764 | 0.5004 | 1.0801 | 1.0828 | 0.0014 | 80.77 |
| 11 | 13530401 | rs10500784 | A | C | 4 | 0.9935 | 0.5006 | 1.0003 | 0.9447 | 0.0052 | 76.47 |
| 2 | 172358072 | rs10167419 | A | G | 4 | 0.3818 | 0.5007 | 0.967 | 0.9336 | 0.0007 | 82.24 |
| 21 | 17228121 | rs2824148 | A | G | 4 | 0.007378 | 0.5011 | 1.1099 | 1.0529 | 0.0301 | 66.43 |
| 2 | 51622700 | rs1997326 | G | T | 4 | 0.06504 | 0.5015 | 0.936 | 0.9522 | 0.0211 | 69.13 |
| 4 | 92549378 | rs7672281 | A | C | 4 | 0.5452 | 0.5016 | 0.9767 | 0.9413 | 0.0063 | 75.68 |
| 7 | 44215353 | rs2908282 | A | G | 4 | 0.04651 | 0.5018 | 1.0956 | 1.0567 | 0.0614 | 59.21 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 2 | 172355011 | rs7608403 | A | C | 4 | 0.3858 | 0.502 | 0.9673 | 0.9335 | 0.0007 | 82.4 |
| 11 | 86021251 | rs2155035 | A | G | 4 | 0.5056 | 0.503 | 1.0426 | 1.0949 | 0.0105 | 73.3 |
| 11 | 86018768 | rs10898515 | C | T | 4 | 0.5012 | 0.5031 | 0.9586 | 0.913 | 0.0104 | 73.36 |
| 5 | 104090924 | rs161456 | C | T | 4 | 0.09919 | 0.5032 | 0.9262 | 0.9238 | 0.0013 | 80.89 |
| 5 | 104091863 | rs161783 | C | T | 4 | 0.09919 | 0.5032 | 0.9262 | 0.9238 | 0.0013 | 80.89 |
| 7 | 52238030 | rs10250470 | A | G | 4 | 0.03225 | 0.5032 | 0.9226 | 0.9542 | 0.0449 | 62.76 |
| 5 | 104093239 | rs161786 | C | T | 4 | 0.09962 | 0.5034 | 1.0796 | 1.0824 | 0.0013 | 80.87 |
| 8 | 135216479 | rs992526 | C | T | 4 | 0.02154 | 0.5034 | 0.9242 | 0.9499 | 0.0085 | 74.34 |
| 2 | 172412537 | rs4668414 | A | C | 4 | 0.3717 | 0.504 | 0.9663 | 0.9342 | 0.0008 | 82.15 |
| 5 | 104090937 | rs161457 | C | T | 4 | 0.09995 | 0.5041 | 1.0795 | 1.0822 | 0.0013 | 80.86 |
| 5 | 104091358 | rs161782 | A | G | 4 | 0.09995 | 0.5041 | 1.0795 | 1.0822 | 0.0013 | 80.86 |
| 2 | 134734535 | rs3791259 | C | T | 4 | 0.0218 | 0.5042 | 0.818 | 0.8752 | 0.0133 | 72.05 |
| 10 | 110717700 | rs17779136 | C | T | 4 | 0.03347 | 0.5048 | 0.9079 | 0.946 | 0.0468 | 62.31 |
| 13 | 89055707 | rs7994475 | A | G | 4 | 0.504 | 0.5052 | 1.0853 | 1.2112 | 0.0022 | 79.45 |
| 3 | 56416159 | rs11130520 | G | T | 4 | 0.6658 | 0.5055 | 0.9847 | 1.0618 | 0.0018 | 79.98 |
| 3 | 56418235 | rs6445788 | C | G | 4 | 0.6029 | 0.5055 | 0.9813 | 1.0631 | 0.0017 | 80.19 |
| 7 | 125587892 | rs526981 | C | T | 4 | 0.06741 | 0.5056 | 1.1019 | 1.0667 | 0.046 | 62.5 |
| 15 | 91523799 | rs17539990 | C | G | 3 | 0.7869 | 0.5056 | 0.9861 | 0.8982 | 0.0019 | 84.11 |
| 21 | 40141997 | rs2837249 | A | G | 4 | 0.08568 | 0.5057 | 1.0675 | 1.0528 | 0.0211 | 69.12 |
| 4 | 57460303 | rs4865165 | C | T | 4 | 0.0525 | 0.5059 | 1.0694 | 1.0454 | 0.0335 | 65.53 |
| 2 | 172398511 | rs908671 | C | G | 4 | 0.3498 | 0.5061 | 0.9647 | 0.9335 | 0.0006 | 82.75 |
| 3 | 56415469 | rs6763636 | G | T | 4 | 0.6638 | 0.5063 | 0.9846 | 1.0615 | 0.0019 | 79.88 |
| 5 | 104087924 | rs325565 | G | T | 4 | 0.09119 | 0.5063 | 1.0812 | 1.082 | 0.0012 | 81.14 |
| 1 | 48878877 | rs7535727 | G | T | 4 | 0.7618 | 0.5068 | 0.9813 | 0.912 | 0.0077 | 74.8 |
| 6 | 136507734 | rs1600620 | A | T | 4 | 0.7212 | 0.5068 | 0.9874 | 0.9391 | 0.0008 | 82.05 |
| 4 | 92557826 | rs2091765 | A | G | 4 | 0.587 | 0.5073 | 0.9789 | 0.9418 | 0.0062 | 75.73 |
| 6 | 136507868 | rs1600619 | A | T | 4 | 0.7101 | 0.5074 | 1.0133 | 1.0652 | 0.0007 | 82.31 |
| 8 | 135205190 | rs765847 | A | G | 4 | 0.0258 | 0.5074 | 1.0808 | 1.0527 | 0.0088 | 74.2 |
| 12 | 97093097 | rs1504558 | C | G | 4 | 0.3765 | 0.5075 | 0.9665 | 1.0708 | 0.0008 | 81.97 |
| 2 | 172417165 | rs3770445 | C | T | 4 | 0.3518 | 0.5076 | 1.0364 | 1.0706 | 0.0006 | 82.54 |
| 14 | 78012231 | rs10431730 | A | G | 4 | 0.3828 | 0.5078 | 0.9688 | 0.9454 | 0.0055 | 76.28 |
| 4 | 21477856 | rs2063658 | A | T | 4 | 0.7696 | 0.5085 | 0.9896 | 0.9375 | 0.0005 | 83.1 |
| 7 | 9678156 | rs6973468 | G | T | 4 | 0.05025 | 0.5086 | 1.0927 | 1.0663 | 0.0131 | 72.1 |
| 14 | 78016834 | rs1990531 | A | G | 4 | 0.4251 | 0.5087 | 1.0291 | 1.0591 | 0.0036 | 77.86 |
| 21 | 40139786 | rs9982859 | C | T | 4 | 0.08585 | 0.5088 | 1.0674 | 1.0521 | 0.0218 | 68.9 |
| 8 | 12906017 | rs13252623 | G | T | 4 | 0.0034 | 0.5089 | 1.2447 | 1.1134 | 0.0087 | 74.26 |
| 4 | 171427766 | rs2030549 | A | T | 4 | 0.02425 | 0.509 | 0.7818 | 0.862 | 0.0277 | 67.11 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 65081975 | rs4916005 | C | T | 4 | 0.07889 | 0.5093 | 0.913 | 0.926 | 0.007 | 75.25 |
| 1 | 51252846 | rs7555006 | A | G | 4 | 0.04457 | 0.5094 | 1.0769 | 1.0535 | 0.012 | 72.58 |
| 5 | 104119377 | rs161776 | C | G | 4 | 0.1032 | 0.5097 | 1.0795 | 1.081 | 0.0016 | 80.34 |
| 8 | 12897996 | rs12375378 | A | C | 4 | 0.003632 | 0.5097 | 1.24 | 1.1108 | 0.0099 | 73.6 |
| 10 | 32469248 | rs3006662 | A | C | 4 | 0.04317 | 0.5098 | 1.2164 | 1.1301 | 0.0349 | 65.17 |
| 5 | 104118535 | rs325492 | C | T | 4 | 0.1029 | 0.5099 | 0.9263 | 0.9251 | 0.0016 | 80.35 |
| 5 | 104077349 | rs325530 | G | T | 4 | 0.09045 | 0.5103 | 0.9248 | 0.9255 | 0.0013 | 80.9 |
| 5 | 104077611 | rs325531 | A | G | 4 | 0.09045 | 0.5103 | 0.9248 | 0.9255 | 0.0013 | 80.9 |
| 5 | 104077750 | rs325532 | C | T | 4 | 0.09082 | 0.5105 | 1.0812 | 1.0804 | 0.0013 | 80.88 |
| 6 | 136506228 | rs7748159 | G | T | 4 | 0.7251 | 0.5107 | 1.0126 | 1.0643 | 0.0008 | 82.06 |
| 21 | 37142961 | rs17192962 | A | G | 4 | 0.793 | 0.5109 | 0.9776 | 0.8804 | 0.0071 | 75.2 |
| 2 | 115870472 | rs13022199 | A | G | 4 | 0.8574 | 0.511 | 1.0099 | 1.0839 | 0.0061 | 75.81 |
| 2 | 184952504 | rs13036001 | C | T | 4 | 0.05351 | 0.5114 | 1.0946 | 1.057 | 0.0508 | 61.44 |
| 6 | 136508312 | rs12662330 | A | C | 4 | 0.7267 | 0.5116 | 0.9876 | 0.9392 | 0.0007 | 82.41 |
| 2 | 51618222 | rs3915321 | C | T | 4 | 0.06664 | 0.5124 | 0.9343 | 0.95 | 0.014 | 71.75 |
| 5 | 104119936 | rs161777 | C | T | 4 | 0.1052 | 0.5126 | 1.079 | 1.0806 | 0.0016 | 80.44 |
| 2 | 51618920 | rs2354378 | C | T | 4 | 0.0688 | 0.513 | 0.9348 | 0.9503 | 0.0146 | 71.48 |
| 6 | 136507265 | rs4896199 | A | C | 4 | 0.7354 | 0.5131 | 0.988 | 0.94 | 0.0008 | 82 |
| 4 | 57460809 | rs9998008 | A | G | 4 | 0.05501 | 0.5132 | 1.0687 | 1.0448 | 0.0323 | 65.84 |
| 2 | 51618512 | rs3915322 | A | G | 4 | 0.06824 | 0.5133 | 1.0699 | 1.0524 | 0.0144 | 71.56 |
| 3 | 56416835 | rs9880091 | C | T | 4 | 0.6173 | 0.5133 | 0.9821 | 1.061 | 0.0021 | 79.63 |
| 7 | 52237378 | rs11238186 | A | C | 4 | 0.03263 | 0.5134 | 1.0837 | 1.0468 | 0.0446 | 62.82 |
| 5 | 104089373 | rs325569 | A | T | 4 | 0.09607 | 0.514 | 0.926 | 0.9249 | 0.001 | 81.46 |
| 5 | 104077128 | rs325529 | C | T | 4 | 0.09298 | 0.5141 | 1.0806 | 1.0799 | 0.0013 | 80.97 |
| 4 | 58794368 | rs2570089 | C | T | 4 | 0.009541 | 0.5147 | 1.1049 | 1.0591 | 0.0063 | 75.72 |
| 5 | 104088490 | rs325567 | C | T | 4 | 0.09664 | 0.5152 | 0.9261 | 0.9252 | 0.0011 | 81.43 |
| 12 | 51736002 | rs2364153 | C | T | 4 | 0.1417 | 0.5152 | 0.9476 | 0.9384 | 0.0017 | 80.15 |
| 6 | 30235852 | rs1318638 | C | T | 4 | 0.01902 | 0.5153 | 0.8402 | 0.9024 | 0.0155 | 71.15 |
| 10 | 110714051 | rs17779016 | A | G | 4 | 0.03809 | 0.5154 | 1.0989 | 1.0555 | 0.0477 | 62.11 |
| 13 | 89054175 | rs9634611 | G | T | 4 | 0.5206 | 0.5156 | 0.9241 | 0.8282 | 0.002 | 79.7 |
| 1 | 66960695 | rs11208951 | C | T | 4 | 0.07328 | 0.5157 | 0.9346 | 0.9548 | 0.0386 | 64.25 |
| 8 | 54357042 | rs2376419 | A | G | 4 | 0.02546 | 0.5159 | 0.8784 | 0.9191 | 0.0077 | 74.78 |
| 6 | 54711017 | rs4715472 | A | G | 4 | 0.08098 | 0.5162 | 0.9076 | 0.9337 | 0.0352 | 65.1 |
| 3 | 151314149 | rs9844449 | C | T | 4 | 0.7087 | 0.5163 | 0.9823 | 1.0776 | 0.004 | 77.51 |
| 21 | 40136888 | rs2837246 | C | T | 4 | 0.08425 | 0.5165 | 1.0677 | 1.0521 | 0.0186 | 69.98 |
| 10 | 36637209 | rs12571128 | A | G | 4 | 0.4784 | 0.5169 | 0.9583 | 0.9139 | 0.0056 | 76.19 |
| 6 | 121702869 | rs9398632 | A | C | 4 | 0.01233 | 0.517 | 0.8919 | 0.9457 | 0.0431 | 63.16 |

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|----|-----------|-------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 21 | 37142296 | rs8134687 | C | T | 4 | 0.806 | 0.5172 | 1.0213 | 1.1329 | 0.0072 | 75.12 |
| 5 | 104115918 | rs17351308 | A | G | 4 | 0.1098 | 0.5174 | 1.0779 | 1.08 | 0.0014 | 80.66 |
| 9 | 7514847 | rs10124892 | C | T | 4 | 0.07871 | 0.5175 | 1.0635 | 1.046 | 0.028 | 67.02 |
| 5 | 104086941 | rs325563 | A | G | 4 | 0.09876 | 0.5177 | 1.0793 | 1.0806 | 0.001 | 81.53 |
| 4 | 65093689 | rs4434285 | A | T | 4 | 0.03962 | 0.5181 | 0.9124 | 0.9451 | 0.0304 | 66.35 |
| 5 | 104087577 | rs325564 | C | G | 4 | 0.09858 | 0.5181 | 0.9265 | 0.9255 | 0.001 | 81.53 |
| 5 | 104015822 | rs12522864 | A | G | 4 | 0.09572 | 0.5184 | 0.9264 | 0.9306 | 0.0026 | 78.94 |
| 5 | 104090901 | rs12520736 | C | T | 4 | 0.1103 | 0.5184 | 1.0771 | 1.0804 | 0.0011 | 81.35 |
| 13 | 89086817 | rs9560407 | A | G | 4 | 0.4743 | 0.5184 | 0.916 | 0.8269 | 0.0016 | 80.39 |
| 13 | 72776677 | rs9318155 | A | C | 4 | 0.01838 | 0.5185 | 1.0877 | 1.0456 | 0.0325 | 65.79 |
| 9 | 2690620 | rs1454629 | C | T | 4 | 0.7239 | 0.5191 | 1.0137 | 1.0576 | 0.0078 | 74.77 |
| 2 | 172397314 | rs6759575 | C | T | 4 | 0.3171 | 0.5193 | 0.9612 | 0.935 | 0.0008 | 82.13 |
| 21 | 37142992 | rs2835491 | G | T | 4 | 0.821 | 0.5196 | 1.0197 | 1.1334 | 0.0068 | 75.37 |
| 13 | 89050456 | rs12561049 | A | G | 4 | 0.5325 | 0.5197 | 1.08 | 1.2057 | 0.002 | 79.67 |
| 6 | 136507126 | rs4896198 | C | T | 4 | 0.7614 | 0.5198 | 1.0109 | 1.0631 | 0.0008 | 82.2 |
| 7 | 49031338 | rs10258925 | A | G | 4 | 0.5669 | 0.5202 | 1.0241 | 1.0655 | 0.0036 | 77.82 |
| 1 | 51249676 | rs12092511 | A | G | 4 | 0.09512 | 0.5203 | 0.9429 | 0.9523 | 0.0122 | 72.52 |
| 8 | 135087684 | rs1379435 | C | T | 4 | 0.1041 | 0.5204 | 1.0585 | 1.0495 | 0.013 | 72.16 |
| 3 | 56410015 | rs9851360 | C | T | 4 | 0.6172 | 0.5206 | 1.0179 | 0.9435 | 0.0016 | 80.32 |
| 6 | 30236421 | rs12212092 | C | T | 4 | 0.01963 | 0.5207 | 0.841 | 0.9033 | 0.0151 | 71.29 |
| 19 | 61182755 | rs11084419 | C | T | 4 | 0.9227 | 0.5207 | 1.0046 | 1.0854 | 0.0011 | 81.41 |
| 3 | 176307233 | rs4894477 | A | G | 4 | 0.6722 | 0.5211 | 1.0158 | 1.0587 | 0.0032 | 78.21 |
| 10 | 124863434 | rs17104653 | C | G | 4 | 0.07622 | 0.5212 | 1.1726 | 1.1235 | 0.0191 | 69.83 |
| 6 | 124523218 | rs802272 | C | T | 4 | 0.0142 | 0.5213 | 1.1392 | 1.066 | 0.036 | 64.9 |
| 2 | 38369932 | rs13417898 | C | T | 4 | 0.4222 | 0.522 | 0.9712 | 0.9466 | 0.0047 | 76.85 |
| 3 | 56410435 | rs1546060 | A | C | 4 | 0.5947 | 0.5224 | 1.0191 | 0.9436 | 0.0016 | 80.36 |
| 3 | 56411201 | rs1491158 | A | G | 4 | 0.6284 | 0.523 | 0.9829 | 1.0593 | 0.0017 | 80.15 |
| 3 | 56412896 | rs111130518 | C | T | 4 | 0.6216 | 0.5239 | 0.9826 | 1.0591 | 0.0018 | 80.07 |
| 8 | 54357197 | rs4565474 | A | G | 4 | 0.0252 | 0.524 | 1.138 | 1.0866 | 0.0071 | 75.17 |
| 2 | 197778099 | rs2712900 | C | T | 4 | 0.1318 | 0.5241 | 0.8623 | 0.8553 | 0.0033 | 78.15 |
| 12 | 87460779 | rs1492348 | A | G | 3 | 0.003257 | 0.5248 | 0.7368 | 0.8641 | 0.0426 | 68.31 |
| 18 | 20409134 | rs12960420 | C | T | 4 | 0.6867 | 0.5255 | 0.9851 | 1.0621 | 0.0017 | 80.24 |
| 3 | 56410482 | rs1546061 | C | G | 4 | 0.6184 | 0.5258 | 0.9824 | 1.0586 | 0.0019 | 79.91 |
| 13 | 89081759 | rs994066 | C | G | 4 | 0.5296 | 0.5261 | 1.0792 | 1.2041 | 0.0015 | 80.61 |
| 3 | 56414093 | rs6805882 | C | T | 4 | 0.6067 | 0.5267 | 0.9818 | 1.059 | 0.0016 | 80.29 |
| 6 | 136513400 | rs1471545 | C | T | 4 | 0.7607 | 0.5277 | 1.0108 | 1.0621 | 0.0006 | 82.65 |
| 2 | 51625919 | rs13001767 | G | T | 4 | 0.03305 | 0.5281 | 0.9277 | 0.9533 | 0.0123 | 72.45 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 5 | 104014181 | rs1120480 | C | T | 4 | 0.06883 | 0.5284 | 0.9173 | 0.9317 | 0.0034 | 78.01 |
| 4 | 72354222 | rs1840086 | A | G | 4 | 0.4404 | 0.5291 | 1.0396 | 1.0813 | 0.0024 | 79.13 |
| 15 | 58974308 | rs729978 | C | T | 4 | 0.06926 | 0.5291 | 0.9307 | 0.9315 | 0.0002 | 84.55 |
| 6 | 52599645 | rs9474262 | C | T | 3 | 0.0521 | 0.5296 | 1.2948 | 1.2618 | 0.0023 | 83.49 |
| 11 | 118009952 | rs633683 | C | T | 4 | 0.04916 | 0.5296 | 0.9313 | 0.9576 | 0.0357 | 64.95 |
| 6 | 136514132 | rs4896201 | A | G | 4 | 0.753 | 0.5297 | 1.0112 | 1.0596 | 0.0011 | 81.3 |
| 21 | 25543181 | rs17000817 | C | T | 4 | 0.1782 | 0.5299 | 1.1533 | 1.1775 | 0.0034 | 78.03 |
| 3 | 29736947 | rs6779932 | G | T | 4 | 0.6518 | 0.5301 | 0.9837 | 0.9493 | 0.0069 | 75.29 |
| 8 | 54357083 | rs2376418 | A | T | 4 | 0.02567 | 0.5305 | 1.1382 | 1.0857 | 0.007 | 75.26 |
| 21 | 32930403 | rs2833927 | C | T | 4 | 0.06114 | 0.5305 | 1.2009 | 1.1209 | 0.0409 | 63.68 |
| 21 | 40136828 | rs12627540 | A | C | 4 | 0.09168 | 0.5305 | 1.0662 | 1.0508 | 0.0174 | 70.43 |
| 6 | 136514189 | rs4896202 | G | T | 4 | 0.7422 | 0.5306 | 1.0117 | 1.0621 | 0.0005 | 82.9 |
| 10 | 110624642 | rs10884688 | A | G | 4 | 0.05251 | 0.5308 | 1.0922 | 1.0529 | 0.0516 | 61.26 |
| 4 | 15282435 | rs11723554 | C | G | 4 | 0.05504 | 0.531 | 0.8926 | 0.9178 | 0.0056 | 76.21 |
| 1 | 48006804 | rs12038866 | C | G | 4 | 0.1297 | 0.5312 | 1.0559 | 1.054 | 0.005 | 76.62 |
| 4 | 58784187 | rs2570071 | G | T | 4 | 0.01116 | 0.5312 | 1.1026 | 1.0573 | 0.0056 | 76.2 |
| 5 | 104007471 | rs11242529 | C | T | 4 | 0.1015 | 0.5313 | 1.0781 | 1.0724 | 0.0025 | 78.99 |
| 6 | 52600553 | rs9474264 | A | T | 3 | 0.06528 | 0.5314 | 1.2808 | 1.2518 | 0.0037 | 82.17 |
| 4 | 92541356 | rs12648320 | A | C | 4 | 0.7346 | 0.5315 | 1.0131 | 1.0591 | 0.0044 | 77.16 |
| 8 | 54411642 | rs7819906 | C | T | 4 | 0.02535 | 0.5316 | 1.1333 | 1.086 | 0.0046 | 76.93 |
| 7 | 48944124 | rs2215361 | A | G | 4 | 0.4917 | 0.5322 | 0.9728 | 0.9429 | 0.0046 | 76.98 |
| 2 | 51620902 | rs11680441 | A | G | 4 | 0.08158 | 0.5325 | 1.0665 | 1.0498 | 0.0142 | 71.64 |
| 8 | 14903851 | rs7005262 | A | G | 4 | 0.07418 | 0.5331 | 1.065 | 1.0422 | 0.0408 | 63.71 |
| 18 | 20409016 | rs12185417 | A | C | 4 | 0.6647 | 0.5334 | 1.0166 | 0.9406 | 0.0012 | 81.03 |
| 5 | 104101159 | rs161791 | G | T | 4 | 0.1015 | 0.5335 | 1.0793 | 1.0767 | 0.0013 | 80.85 |
| 7 | 124677258 | rs7776954 | A | G | 4 | 0.5748 | 0.5342 | 0.9767 | 0.9414 | 0.0051 | 76.52 |
| 8 | 97177903 | rs542253 | A | G | 4 | 0.9111 | 0.5344 | 1.0093 | 1.1521 | 0.0003 | 83.96 |
| 7 | 125578124 | rs635680 | C | G | 4 | 0.06836 | 0.5351 | 0.9078 | 0.9393 | 0.0348 | 65.19 |
| 15 | 58974360 | rs729977 | C | T | 4 | 0.07185 | 0.5352 | 1.0732 | 1.0716 | 0.0002 | 84.38 |
| 11 | 86016483 | rs12289252 | G | T | 4 | 0.6048 | 0.5356 | 0.9682 | 0.9193 | 0.0098 | 73.65 |
| 21 | 17230025 | rs11701807 | C | T | 4 | 0.006057 | 0.536 | 1.1178 | 1.0524 | 0.0225 | 68.69 |
| 4 | 13322444 | rs13147974 | C | G | 4 | 0.4047 | 0.5371 | 1.0307 | 1.0553 | 0.0037 | 77.76 |
| 13 | 39493139 | rs9603660 | C | T | 4 | 0.5818 | 0.5373 | 0.9807 | 0.9506 | 0.0053 | 76.43 |
| 8 | 135087435 | rs2896732 | A | C | 4 | 0.1078 | 0.5374 | 1.0579 | 1.0473 | 0.0134 | 71.97 |
| 4 | 15281298 | rs10516289 | C | T | 4 | 0.05966 | 0.538 | 0.8945 | 0.9188 | 0.0053 | 76.42 |
| 1 | 48870913 | rs7516699 | A | G | 4 | 0.85 | 0.5384 | 0.9883 | 0.9176 | 0.0071 | 75.15 |
| 5 | 104001831 | rs12514247 | C | T | 4 | 0.1122 | 0.5385 | 1.0752 | 1.0713 | 0.0023 | 79.29 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 7 | 125583266 | rs489655 | A | G | 4 | 0.07256 | 0.5385 | 1.1001 | 1.0636 | 0.0374 | 64.55 |
| 5 | 104004713 | rs17156764 | A | C | 4 | 0.1063 | 0.539 | 1.0769 | 1.0713 | 0.0024 | 79.17 |
| 11 | 115308412 | rs369845 | C | T | 4 | 0.04522 | 0.5392 | 1.0805 | 1.0526 | 0.0126 | 72.32 |
| 5 | 104100998 | rs161790 | C | T | 4 | 0.1061 | 0.5394 | 0.9275 | 0.9294 | 0.0012 | 81.03 |
| 5 | 40304970 | rs11950581 | A | G | 4 | 0.008013 | 0.5399 | 0.9035 | 0.9529 | 0.0191 | 69.82 |
| 5 | 104090005 | rs325571 | A | G | 4 | 0.09158 | 0.5407 | 1.0821 | 1.0773 | 0.0009 | 81.73 |
| 6 | 26816186 | rs12195114 | A | G | 4 | 0.8865 | 0.5409 | 0.9944 | 0.9453 | 0.0049 | 76.73 |
| 21 | 17229575 | rs2824149 | C | T | 4 | 0.01063 | 0.5413 | 0.9053 | 0.9538 | 0.0279 | 67.07 |
| 5 | 62568648 | rs346423 | G | A | 3 | 0.3978 | 0.5416 | 0.9405 | 0.8603 | 0.001 | 85.5 |
| 3 | 176309283 | rs11710345 | A | G | 4 | 0.66 | 0.5419 | 1.0155 | 1.0594 | 0.0006 | 82.75 |
| 7 | 125577694 | rs498875 | C | T | 4 | 0.06896 | 0.5419 | 0.908 | 0.9398 | 0.0327 | 65.74 |
| 8 | 4081661 | rs17069679 | A | G | 4 | 0.3611 | 0.5419 | 1.0835 | 1.1572 | 0.0003 | 83.82 |
| 6 | 26817570 | rs9467847 | C | T | 4 | 0.8887 | 0.5421 | 1.0055 | 1.0576 | 0.005 | 76.66 |
| 13 | 39454803 | rs7322623 | A | C | 4 | 0.7321 | 0.543 | 1.0126 | 1.0587 | 0.0012 | 81.09 |
| 6 | 51918458 | rs12194995 | C | T | 4 | 0.05488 | 0.5437 | 0.9195 | 0.9484 | 0.0233 | 68.42 |
| 12 | 87293154 | rs10777110 | A | G | 4 | 0.08702 | 0.5437 | 1.1173 | 1.0938 | 0.0062 | 75.77 |
| 6 | 136513493 | rs1471546 | C | T | 4 | 0.839 | 0.5438 | 1.0071 | 1.0598 | 0.0005 | 82.9 |
| 3 | 144997632 | rs6807571 | A | G | 4 | 0.001419 | 0.5439 | 1.1654 | 1.0651 | 0.0134 | 71.97 |
| 2 | 210413152 | rs10178431 | G | T | 4 | 0.001927 | 0.5442 | 0.8436 | 0.9284 | 0.0094 | 73.86 |
| 13 | 89090502 | rs9555925 | C | T | 4 | 0.5543 | 0.5444 | 1.0746 | 1.1974 | 0.0012 | 81.05 |
| 2 | 150391583 | rs9288698 | T | G | 3 | 0.4458 | 0.5446 | 1.0401 | 1.0997 | 0.0021 | 83.79 |
| 2 | 51622443 | rs2950945 | A | G | 4 | 0.08896 | 0.5451 | 1.0619 | 1.0442 | 0.0223 | 68.75 |
| 7 | 125579026 | rs650045 | A | G | 4 | 0.07174 | 0.5453 | 0.9089 | 0.9404 | 0.0332 | 65.6 |
| 5 | 73287077 | rs283616 | C | G | 4 | 0.02024 | 0.546 | 0.9202 | 0.9408 | 0.0003 | 83.84 |
| 7 | 49098405 | rs7796330 | C | T | 4 | 0.5921 | 0.546 | 0.9777 | 0.9404 | 0.0031 | 78.35 |
| 2 | 51617864 | rs17864534 | C | T | 4 | 0.09255 | 0.5463 | 1.0633 | 1.0469 | 0.0169 | 70.6 |
| 5 | 73286248 | rs283612 | C | T | 4 | 0.01848 | 0.5463 | 0.9191 | 0.9407 | 0.0003 | 83.92 |
| 7 | 49039292 | rs12718319 | C | T | 4 | 0.5573 | 0.5463 | 0.9759 | 0.9433 | 0.0047 | 76.85 |
| 18 | 20409841 | rs1945153 | A | G | 4 | 0.6138 | 0.5463 | 0.9813 | 1.06 | 0.0013 | 80.94 |
| 7 | 125580265 | rs475294 | C | T | 4 | 0.07398 | 0.5467 | 1.0995 | 1.0628 | 0.0344 | 65.31 |
| 7 | 125580852 | rs501483 | A | G | 4 | 0.07398 | 0.5467 | 1.0995 | 1.0628 | 0.0344 | 65.31 |
| 7 | 125581531 | rs507803 | C | T | 4 | 0.07499 | 0.5467 | 1.0991 | 1.0627 | 0.035 | 65.14 |
| 7 | 125581817 | rs613484 | A | G | 4 | 0.076 | 0.5467 | 1.0987 | 1.0625 | 0.0357 | 64.97 |
| 7 | 125584379 | rs520807 | C | T | 4 | 0.08018 | 0.5468 | 1.0973 | 1.0619 | 0.0384 | 64.29 |
| 7 | 125581262 | rs505793 | C | T | 4 | 0.0737 | 0.547 | 0.9095 | 0.9409 | 0.0341 | 65.37 |
| 3 | 176311011 | rs4505709 | A | G | 4 | 0.6562 | 0.5475 | 1.0158 | 1.0591 | 0.0005 | 82.96 |
| 9 | 123780890 | rs13299260 | C | T | 4 | 0.2995 | 0.5475 | 1.0372 | 1.0589 | 0.0006 | 82.73 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 2 | 38366026 | rs875653 | C | T | 4 | 0.7083 | 0.5479 | 0.9826 | 1.0761 | 0.0014 | 80.64 |
| 8 | 97181208 | rs546474 | A | G | 4 | 0.9086 | 0.5485 | 0.9906 | 0.8728 | 0.0003 | 84.04 |
| 7 | 125579381 | rs556478 | C | T | 4 | 0.07461 | 0.5487 | 0.9097 | 0.9411 | 0.0338 | 65.46 |
| 5 | 73286880 | rs283615 | A | T | 4 | 0.02044 | 0.549 | 0.9203 | 0.9411 | 0.0003 | 83.9 |
| 12 | 87291483 | rs10745479 | A | G | 4 | 0.09075 | 0.5497 | 0.8962 | 0.9152 | 0.006 | 75.89 |
| 15 | 58975113 | rs12592999 | A | G | 4 | 0.07648 | 0.5499 | 0.932 | 0.9348 | 0.0002 | 84.39 |
| 7 | 125579136 | rs553952 | C | T | 4 | 0.07417 | 0.55 | 1.0994 | 1.0626 | 0.0332 | 65.61 |
| 3 | 176306452 | rs17588879 | A | T | 4 | 0.6973 | 0.5501 | 1.0138 | 1.0605 | 0.0003 | 84.04 |
| 1 | 66953077 | rs1498354 | A | T | 4 | 0.08682 | 0.5502 | 1.0668 | 1.0441 | 0.0348 | 65.19 |
| 7 | 125584083 | rs518066 | C | T | 4 | 0.07931 | 0.5502 | 1.0976 | 1.0618 | 0.0364 | 64.78 |
| 1 | 107983470 | rs6693140 | C | T | 4 | 0.8015 | 0.5503 | 1.011 | 1.0705 | 0.001 | 81.65 |
| 15 | 86265806 | rs1836592 | A | T | 4 | 0.008642 | 0.5504 | 0.8895 | 0.9435 | 0.0094 | 73.87 |
| 7 | 125583763 | rs515267 | G | T | 4 | 0.07841 | 0.5505 | 0.9108 | 0.9417 | 0.0358 | 64.94 |
| 10 | 110614661 | rs11599840 | A | G | 4 | 0.05881 | 0.5506 | 0.9172 | 0.9516 | 0.0485 | 61.94 |
| 2 | 172434227 | rs12692978 | C | T | 4 | 0.328 | 0.5507 | 0.9619 | 0.9379 | 0.0006 | 82.79 |
| 3 | 176306392 | rs17588796 | A | G | 4 | 0.6986 | 0.5507 | 1.0137 | 1.0604 | 0.0003 | 84 |
| 3 | 176310488 | rs6782155 | A | G | 4 | 0.6712 | 0.5508 | 1.0149 | 1.0582 | 0.0005 | 82.92 |
| 6 | 26812951 | rs12202849 | A | G | 4 | 0.92 | 0.5509 | 1.0039 | 1.0564 | 0.0049 | 76.67 |
| 12 | 87297081 | rs4842604 | C | T | 4 | 0.1046 | 0.551 | 1.1126 | 1.0945 | 0.0051 | 76.57 |
| 10 | 110617893 | rs11194286 | C | T | 4 | 0.05938 | 0.5515 | 1.09 | 1.0507 | 0.0488 | 61.87 |
| 10 | 110618205 | rs10884687 | A | T | 4 | 0.05938 | 0.5515 | 1.09 | 1.0507 | 0.0488 | 61.87 |
| 2 | 197777124 | rs2579408 | A | G | 4 | 0.1663 | 0.5522 | 1.1457 | 1.1606 | 0.0025 | 79.07 |
| 4 | 72303517 | rs4521314 | A | C | 3 | 0.116 | 0.5522 | 1.1153 | 1.1773 | 0 | 90.16 |
| 13 | 75986324 | rs283982 | C | T | 4 | 0.04785 | 0.5523 | 1.0898 | 1.0508 | 0.0329 | 65.69 |
| 12 | 89248606 | rs825959 | C | T | 4 | 0.01012 | 0.5529 | 1.0985 | 1.0463 | 0.0163 | 70.81 |
| 3 | 176305423 | rs936474 | A | G | 4 | 0.7222 | 0.5531 | 0.9877 | 0.944 | 0.0003 | 83.78 |
| 6 | 73415061 | rs17749408 | A | G | 4 | 0.06763 | 0.5541 | 1.0847 | 1.0515 | 0.0354 | 65.04 |
| 5 | 73287272 | rs283618 | A | T | 4 | 0.02274 | 0.5543 | 0.9216 | 0.9418 | 0.0003 | 83.97 |
| 4 | 58828037 | rs13105776 | C | T | 4 | 0.02417 | 0.5549 | 1.1025 | 1.0556 | 0.0141 | 71.69 |
| 10 | 110615683 | rs12249791 | C | T | 4 | 0.06001 | 0.555 | 0.9176 | 0.952 | 0.0478 | 62.09 |
| 11 | 109527878 | rs1675981 | G | T | 3 | 0.6625 | 0.5551 | 1.0182 | 0.9234 | 0.0001 | 89.02 |
| 11 | 44189011 | rs4755234 | C | T | 4 | 0.958 | 0.5555 | 0.9981 | 0.9489 | 0.0024 | 79.22 |
| 1 | 66950593 | rs10889649 | A | G | 4 | 0.08885 | 0.5556 | 1.0663 | 1.0436 | 0.0339 | 65.43 |
| 2 | 51622416 | rs7592062 | A | G | 4 | 0.09364 | 0.5557 | 1.061 | 1.0434 | 0.0209 | 69.21 |
| 8 | 109516004 | rs10089406 | C | T | 4 | 0.1131 | 0.556 | 0.942 | 0.9527 | 0.0103 | 73.4 |
| 20 | 47357021 | rs11907908 | C | T | 4 | 0.01628 | 0.556 | 0.8412 | 0.9143 | 0.0156 | 71.09 |
| 2 | 38459723 | rs3806551 | C | G | 4 | 0.5022 | 0.5567 | 0.9761 | 0.9471 | 0.0015 | 80.56 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 12 | 87296649 | rs2111038 | C | T | 4 | 0.1088 | 0.5569 | 1.1112 | 1.0933 | 0.0049 | 76.7 |
| 11 | 44191829 | rs1532353 | C | T | 4 | 0.9617 | 0.557 | 1.0017 | 1.0537 | 0.0024 | 79.24 |
| 3 | 176309927 | rs6797428 | A | G | 4 | 0.6976 | 0.5575 | 1.0137 | 1.0571 | 0.0006 | 82.88 |
| 3 | 176309960 | rs6797510 | A | G | 4 | 0.6976 | 0.5575 | 1.0137 | 1.0571 | 0.0006 | 82.88 |
| 6 | 73415342 | rs17749420 | C | G | 4 | 0.07006 | 0.5581 | 1.084 | 1.051 | 0.0353 | 65.08 |
| 1 | 152592990 | rs6688376 | C | T | 4 | 0.8582 | 0.5585 | 0.993 | 0.9483 | 0.0065 | 75.58 |
| 4 | 58818055 | rs11133552 | A | G | 4 | 0.01377 | 0.5588 | 1.0993 | 1.0538 | 0.005 | 76.64 |
| 8 | 54427066 | rs11995645 | C | T | 4 | 0.02946 | 0.5588 | 1.1316 | 1.0816 | 0.0043 | 77.24 |
| 11 | 109528270 | rs667625 | G | T | 3 | 0.6515 | 0.5588 | 1.0189 | 0.9243 | 0.0001 | 88.97 |
| 2 | 107791059 | rs17021776 | C | T | 3 | 0.006494 | 0.5593 | 0.7643 | 0.8625 | 0.012 | 77.39 |
| 18 | 20402971 | rs9304466 | C | G | 4 | 0.5629 | 0.5596 | 0.9786 | 1.0584 | 0.0012 | 81.16 |
| 6 | 121495669 | rs9401370 | A | T | 4 | 0.01804 | 0.5605 | 0.8998 | 0.9499 | 0.0286 | 66.86 |
| 14 | 32679185 | rs7155495 | C | T | 4 | 0.08983 | 0.5606 | 0.9394 | 0.9595 | 0.0336 | 65.5 |
| 4 | 21478058 | rs2063657 | A | G | 4 | 0.8266 | 0.5607 | 0.9923 | 0.9462 | 0.0006 | 82.72 |
| 18 | 20407884 | rs4800186 | A | T | 4 | 0.5541 | 0.5608 | 0.9781 | 1.0585 | 0.0011 | 81.36 |
| 8 | 54427119 | rs11985025 | A | T | 4 | 0.03001 | 0.561 | 1.1311 | 1.0812 | 0.0042 | 77.3 |
| 6 | 29908080 | rs2517897 | A | C | 4 | 0.08385 | 0.5616 | 0.9154 | 0.9402 | 0.017 | 70.55 |
| 12 | 97086002 | rs1160327 | A | G | 4 | 0.5884 | 0.5616 | 1.0197 | 0.9506 | 0.0036 | 77.87 |
| 10 | 110625352 | rs12250102 | C | T | 4 | 0.05856 | 0.5622 | 1.0904 | 1.0497 | 0.0466 | 62.37 |
| 2 | 134735206 | rs3791266 | C | G | 4 | 0.02751 | 0.5628 | 0.8214 | 0.8876 | 0.0112 | 72.98 |
| 4 | 21478155 | rs2063656 | A | C | 4 | 0.8318 | 0.5629 | 1.0075 | 1.0567 | 0.0006 | 82.81 |
| 12 | 87295390 | rs2407649 | C | T | 4 | 0.103 | 0.5629 | 0.8993 | 0.9164 | 0.005 | 76.65 |
| 7 | 44212378 | rs917793 | A | T | 4 | 0.06223 | 0.563 | 0.9181 | 0.9522 | 0.0488 | 61.88 |
| 6 | 121498592 | rs9375002 | A | C | 4 | 0.01857 | 0.5631 | 1.1108 | 1.0524 | 0.0286 | 66.86 |
| 7 | 49076176 | rs11762613 | A | C | 4 | 0.6066 | 0.5634 | 1.0217 | 1.0604 | 0.0026 | 78.93 |
| 15 | 58977303 | rs17237465 | C | T | 4 | 0.08034 | 0.5634 | 0.9348 | 0.9387 | 0.0003 | 84.32 |
| 7 | 125571034 | rs648172 | A | T | 4 | 0.07506 | 0.5635 | 0.9099 | 0.942 | 0.0284 | 66.91 |
| 5 | 98306052 | rs327807 | A | G | 4 | 0.6526 | 0.5636 | 1.0169 | 1.0525 | 0.0041 | 77.35 |
| 18 | 20402119 | rs4800580 | A | G | 4 | 0.5455 | 0.5637 | 1.0228 | 0.9451 | 0.0011 | 81.4 |
| 11 | 44205402 | rs4755236 | C | G | 4 | 0.9494 | 0.5641 | 0.9977 | 0.9494 | 0.0017 | 80.12 |
| 1 | 202827613 | rs4951409 | A | T | 4 | 0.08928 | 0.5647 | 0.9387 | 0.9593 | 0.0334 | 65.55 |
| 2 | 38396077 | rs12712583 | C | T | 4 | 0.4644 | 0.565 | 0.9744 | 0.9492 | 0.0016 | 80.39 |
| 6 | 124526687 | rs811418 | A | C | 4 | 0.01381 | 0.5653 | 0.873 | 0.941 | 0.0282 | 66.98 |
| 13 | 39500347 | rs9603665 | C | T | 4 | 0.6784 | 0.5654 | 0.9853 | 0.9535 | 0.0052 | 76.5 |
| 7 | 49051370 | rs4129516 | C | T | 4 | 0.5771 | 0.5655 | 1.0236 | 1.062 | 0.0017 | 80.15 |
| 18 | 20403739 | rs9950310 | C | T | 4 | 0.5435 | 0.5658 | 1.023 | 0.9455 | 0.0011 | 81.31 |
| 18 | 20403162 | rs9304467 | A | G | 4 | 0.543 | 0.5663 | 1.023 | 0.9456 | 0.0011 | 81.3 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 66948145 | rs1547644 | A | G | 4 | 0.09539 | 0.5665 | 0.939 | 0.9592 | 0.0333 | 65.58 |
| 14 | 32677988 | rs8011345 | A | G | 4 | 0.086 | 0.5665 | 0.9387 | 0.9594 | 0.0293 | 66.65 |
| 2 | 38464515 | rs10182455 | A | G | 4 | 0.532 | 0.5668 | 0.9779 | 0.9482 | 0.0013 | 81 |
| 2 | 38374562 | rs3755025 | C | T | 4 | 0.4219 | 0.568 | 0.9717 | 0.9524 | 0.004 | 77.49 |
| 7 | 6384803 | rs2347338 | C | T | 4 | 0.9895 | 0.5682 | 1.0013 | 0.8639 | 0.0005 | 83.28 |
| 11 | 125258570 | rs540225 | C | T | 4 | 0.6935 | 0.5691 | 1.0149 | 1.0534 | 0.0031 | 78.4 |
| 20 | 14862709 | rs2423853 | A | T | 4 | 0.4278 | 0.5692 | 0.9724 | 0.9484 | 0.001 | 81.66 |
| 6 | 83338480 | rs9449500 | G | T | 4 | 0.8035 | 0.57 | 1.0263 | 1.158 | 0.0012 | 81.13 |
| 4 | 71149965 | rs6811318 | C | T | 4 | 0.1308 | 0.5701 | 1.0795 | 1.0675 | 0.0074 | 74.98 |
| 15 | 89929416 | rs12324460 | C | T | 4 | 0.8304 | 0.5704 | 1.0114 | 0.9321 | 0.0055 | 76.28 |
| 5 | 98947056 | rs17167077 | C | T | 4 | 0.07725 | 0.5712 | 0.8677 | 0.9164 | 0.0318 | 65.99 |
| 3 | 144993002 | rs16854336 | C | T | 4 | 0.001002 | 0.5715 | 0.854 | 0.9416 | 0.0106 | 73.28 |
| 4 | 71147532 | rs3775747 | C | T | 4 | 0.09973 | 0.5727 | 0.9158 | 0.9295 | 0.003 | 78.46 |
| 2 | 38374360 | rs4670861 | C | T | 4 | 0.4356 | 0.573 | 0.9725 | 0.953 | 0.004 | 77.49 |
| 15 | 58976901 | rs3803487 | A | G | 4 | 0.09012 | 0.5733 | 0.9367 | 0.9401 | 0.0002 | 84.38 |
| 20 | 47387176 | rs7261606 | C | T | 4 | 0.07729 | 0.5737 | 0.8895 | 0.9306 | 0.0353 | 65.07 |
| 5 | 62564201 | rs164105 | A | G | 4 | 0.6854 | 0.5742 | 0.9783 | 0.9262 | 0.0023 | 79.28 |
| 7 | 125574072 | rs585146 | C | T | 4 | 0.08045 | 0.5744 | 1.0972 | 1.06 | 0.0278 | 67.09 |
| 10 | 110512008 | rs7091393 | C | T | 4 | 0.04526 | 0.5747 | 1.1015 | 1.0527 | 0.0339 | 65.43 |
| 4 | 58821899 | rs2412885 | C | T | 4 | 0.01584 | 0.5748 | 0.9114 | 0.9506 | 0.0045 | 77.05 |
| 12 | 87265181 | rs10745477 | G | T | 4 | 0.1015 | 0.5749 | 0.8985 | 0.9214 | 0.0076 | 74.89 |
| 12 | 87296520 | rs2160432 | C | T | 4 | 0.1102 | 0.5753 | 0.9012 | 0.9181 | 0.0044 | 77.15 |
| 7 | 44202193 | rs4607517 | A | G | 4 | 0.06267 | 0.5762 | 1.0891 | 1.049 | 0.0454 | 62.65 |
| 12 | 9920781 | rs7313246 | A | T | 4 | 0.4903 | 0.5764 | 0.9735 | 1.0619 | 0.0004 | 83.38 |
| 3 | 176312988 | rs7646135 | A | T | 4 | 0.7031 | 0.5769 | 1.0135 | 1.0554 | 0.0005 | 83.26 |
| 1 | 202834775 | rs6594018 | A | G | 4 | 0.09614 | 0.577 | 1.064 | 1.0407 | 0.0353 | 65.07 |
| 16 | 7338030 | rs13330100 | C | T | 4 | 0.01691 | 0.5771 | 0.8791 | 0.9409 | 0.0255 | 67.75 |
| 3 | 117048396 | rs2972481 | A | G | 4 | 0.03193 | 0.5772 | 1.1577 | 1.0765 | 0.0346 | 65.24 |
| 12 | 32214624 | rs10506083 | A | G | 4 | 0.007623 | 0.5775 | 1.1017 | 1.0486 | 0.0042 | 77.28 |
| 5 | 62549494 | rs346405 | A | C | 4 | 0.6915 | 0.5779 | 1.0215 | 1.0788 | 0.0021 | 79.6 |
| 5 | 62564968 | rs346420 | G | T | 4 | 0.6705 | 0.5779 | 0.9771 | 0.926 | 0.0021 | 79.54 |
| 2 | 38397553 | rs1022076 | C | T | 4 | 0.4847 | 0.5784 | 1.025 | 1.0519 | 0.0015 | 80.61 |
| 8 | 109508139 | rs6469185 | A | T | 4 | 0.1726 | 0.579 | 1.0506 | 1.0485 | 0.0045 | 77.05 |
| 5 | 62565739 | rs346421 | G | T | 4 | 0.6682 | 0.5791 | 1.0238 | 1.0798 | 0.0022 | 79.45 |
| 13 | 39493988 | rs4943722 | A | G | 4 | 0.6855 | 0.5792 | 1.0146 | 1.0476 | 0.0044 | 77.12 |
| 8 | 2652265 | rs12542624 | A | G | 4 | 0.03435 | 0.5793 | 1.0903 | 1.0493 | 0.0151 | 71.29 |
| 8 | 135176557 | rs7830450 | C | T | 4 | 0.03233 | 0.5795 | 0.928 | 0.955 | 0.004 | 77.51 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 7 | 147248774 | rs7805492 | C | T | 4 | 0.3721 | 0.58 | 1.0359 | 1.0572 | 0.0016 | 80.38 |
| 10 | 110644569 | rs17778423 | C | G | 4 | 0.05227 | 0.5805 | 1.0922 | 1.048 | 0.0407 | 63.74 |
| 10 | 110644600 | rs17700240 | A | G | 4 | 0.05227 | 0.5805 | 1.0922 | 1.048 | 0.0407 | 63.74 |
| 7 | 147248819 | rs7805515 | C | T | 4 | 0.3727 | 0.5806 | 1.0358 | 1.057 | 0.0016 | 80.34 |
| 4 | 71150032 | rs6811366 | C | T | 4 | 0.1386 | 0.5808 | 1.0778 | 1.0661 | 0.0067 | 75.41 |
| 3 | 176306423 | rs9290531 | A | G | 4 | 0.9329 | 0.5813 | 0.9971 | 1.056 | 0.0002 | 84.4 |
| 11 | 13480447 | rs10832047 | A | T | 4 | 0.9228 | 0.5817 | 1.0036 | 0.9544 | 0.0061 | 75.83 |
| 20 | 47349857 | rs761498 | C | T | 4 | 0.01777 | 0.5821 | 0.8443 | 0.9183 | 0.0123 | 72.45 |
| 12 | 87270942 | rs10745478 | G | T | 4 | 0.1307 | 0.5823 | 0.9046 | 0.9181 | 0.004 | 77.48 |
| 7 | 44198411 | rs6975024 | C | T | 4 | 0.06432 | 0.5827 | 1.0885 | 1.0483 | 0.0443 | 62.9 |
| 3 | 176304842 | rs936475 | G | T | 4 | 0.7422 | 0.5828 | 0.9886 | 0.9474 | 0.0003 | 84.09 |
| 7 | 125570670 | rs473816 | A | G | 4 | 0.08057 | 0.5828 | 0.9114 | 0.9439 | 0.0249 | 67.94 |
| 21 | 36478878 | rs2252991 | A | G | 4 | 0.4578 | 0.5834 | 0.9722 | 0.9494 | 0.0023 | 79.32 |
| 21 | 29936192 | rs363529 | C | G | 4 | 0.6867 | 0.5837 | 0.9807 | 0.932 | 0.0007 | 82.33 |
| 7 | 147248660 | rs7805223 | C | T | 4 | 0.3839 | 0.5844 | 1.035 | 1.0565 | 0.0016 | 80.43 |
| 9 | 123781479 | rs7855045 | A | G | 4 | 0.4311 | 0.5844 | 1.0282 | 1.0515 | 0.0011 | 81.29 |
| 2 | 197769903 | rs2579409 | G | T | 4 | 0.1852 | 0.5849 | 0.8754 | 0.8678 | 0.0019 | 79.92 |
| 4 | 58824709 | rs2244536 | A | C | 4 | 0.01751 | 0.5849 | 1.0956 | 1.0508 | 0.0043 | 77.22 |
| 6 | 90707807 | rs3734662 | C | T | 3 | 0.4957 | 0.5855 | 0.9687 | 0.9253 | 0.0024 | 83.39 |
| 8 | 4081435 | rs17069674 | C | T | 4 | 0.4581 | 0.5858 | 1.0685 | 1.1388 | 0.0005 | 83.04 |
| 18 | 6396037 | rs11081233 | A | G | 4 | 0.08427 | 0.5862 | 0.9355 | 0.9581 | 0.0195 | 69.67 |
| 8 | 124803982 | rs3898733 | C | T | 4 | 0.9695 | 0.5863 | 0.9985 | 1.0582 | 0.001 | 81.65 |
| 14 | 34502938 | rs2273154 | C | T | 4 | 0.6274 | 0.5872 | 1.023 | 1.0649 | 0.0025 | 79.1 |
| 8 | 54353314 | rs9792306 | C | T | 4 | 0.03424 | 0.5874 | 0.8857 | 0.9331 | 0.0073 | 75.07 |
| 16 | 45096893 | rs9935841 | A | G | 4 | 0.8398 | 0.5882 | 0.99 | 1.0743 | 0.0005 | 83.02 |
| 20 | 47381910 | rs6012644 | C | G | 4 | 0.1101 | 0.5886 | 1.1192 | 1.0799 | 0.024 | 68.21 |
| 1 | 202833323 | rs11240761 | A | C | 4 | 0.09818 | 0.5888 | 0.9402 | 0.9616 | 0.0321 | 65.91 |
| 14 | 42258722 | rs1698517 | C | T | 4 | 0.2181 | 0.5891 | 1.0991 | 1.1176 | 0.0011 | 81.29 |
| 3 | 151306869 | rs9834782 | A | C | 4 | 0.7149 | 0.5896 | 1.0193 | 0.9335 | 0.0034 | 78.08 |
| 2 | 38371019 | rs11894455 | C | T | 4 | 0.4697 | 0.5897 | 1.0262 | 1.0476 | 0.0035 | 77.93 |
| 7 | 147249143 | rs7805990 | G | T | 4 | 0.3933 | 0.5904 | 1.0343 | 1.0557 | 0.0015 | 80.51 |
| 2 | 107969863 | rs2433718 | A | G | 4 | 0.1029 | 0.5907 | 0.9229 | 0.9431 | 0.0084 | 74.42 |
| 4 | 21465676 | rs1040036 | G | T | 4 | 0.9983 | 0.5908 | 0.9999 | 0.9504 | 0.0009 | 81.92 |
| 2 | 38403041 | rs7593981 | A | T | 4 | 0.5496 | 0.5909 | 0.979 | 0.9522 | 0.0015 | 80.58 |
| 2 | 38403917 | rs9808407 | A | C | 4 | 0.5496 | 0.5909 | 0.979 | 0.9522 | 0.0015 | 80.58 |
| 11 | 115297985 | rs374729 | A | G | 4 | 0.08279 | 0.5909 | 1.0693 | 1.0422 | 0.0264 | 67.48 |
| 7 | 147244691 | rs2538959 | G | T | 4 | 0.4119 | 0.591 | 1.0329 | 1.055 | 0.0018 | 80.06 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 5 | 159173066 | rs6862385 | A | C | 4 | 0.7965 | 0.5912 | 0.9621 | 0.8342 | 0.0039 | 77.54 |
| 10 | 110493441 | rs11597369 | A | C | 4 | 0.05063 | 0.5912 | 1.0948 | 1.0474 | 0.0405 | 63.78 |
| 4 | 171439939 | rs17055545 | G | T | 4 | 0.04891 | 0.5918 | 1.2343 | 1.1288 | 0.0237 | 68.3 |
| 3 | 24635868 | rs11129156 | A | G | 4 | 0.07606 | 0.592 | 1.0733 | 1.0485 | 0.0083 | 74.48 |
| 1 | 81202644 | rs7515605 | A | G | 4 | 0.07883 | 0.5924 | 0.9185 | 0.9477 | 0.0165 | 70.73 |
| 19 | 57268291 | rs8101936 | A | T | 4 | 0.8854 | 0.5927 | 0.9944 | 1.0499 | 0.0043 | 77.22 |
| 2 | 134740952 | rs3791273 | C | G | 4 | 0.0345 | 0.5937 | 1.1989 | 1.1053 | 0.0192 | 69.76 |
| 8 | 54378028 | rs11995818 | A | T | 4 | 0.03528 | 0.5938 | 1.1268 | 1.073 | 0.005 | 76.66 |
| 1 | 202831635 | rs2887429 | G | T | 4 | 0.1024 | 0.5942 | 1.0628 | 1.0395 | 0.031 | 66.19 |
| 5 | 159163705 | rs11957357 | A | C | 4 | 0.8034 | 0.5943 | 0.9635 | 0.835 | 0.0038 | 77.68 |
| 5 | 159164640 | rs1432711 | C | T | 4 | 0.8072 | 0.5943 | 0.9641 | 0.8353 | 0.0039 | 77.57 |
| 16 | 7343080 | rs17146172 | C | T | 4 | 0.01217 | 0.5947 | 1.1517 | 1.066 | 0.0156 | 71.08 |
| 1 | 202832806 | rs6682208 | C | T | 4 | 0.1019 | 0.5953 | 0.9409 | 0.962 | 0.0306 | 66.3 |
| 10 | 122586221 | rs12360470 | A | G | 4 | 0.395 | 0.5953 | 1.106 | 1.1893 | 0.0005 | 83.07 |
| 2 | 51330460 | rs2098441 | A | G | 4 | 0.5093 | 0.5956 | 0.976 | 0.9549 | 0.0041 | 77.34 |
| 15 | 51195489 | rs689991 | A | G | 4 | 0.02255 | 0.5957 | 0.9071 | 0.9516 | 0.01 | 73.55 |
| 19 | 57270159 | rs1560690 | A | G | 4 | 0.8723 | 0.5961 | 1.0062 | 0.9528 | 0.0042 | 77.33 |
| 1 | 46637098 | rs6429600 | A | G | 4 | 0.9552 | 0.5964 | 0.9977 | 0.9523 | 0.0061 | 75.85 |
| 15 | 31695395 | rs12593288 | C | T | 4 | 0.7121 | 0.5964 | 0.984 | 1.0599 | 0.0024 | 79.24 |
| 1 | 55446008 | rs6703366 | G | T | 4 | 0.02286 | 0.5967 | 1.1067 | 1.0468 | 0.0337 | 65.48 |
| 8 | 54386635 | rs7465082 | G | T | 4 | 0.03522 | 0.5975 | 1.1269 | 1.0727 | 0.0046 | 76.92 |
| 8 | 97172072 | rs16894295 | A | G | 4 | 0.8616 | 0.5977 | 0.9858 | 1.1274 | 0.0003 | 84.21 |
| 5 | 178252143 | rs6865216 | A | G | 4 | 0.5115 | 0.598 | 1.0388 | 1.0882 | 0.0003 | 83.95 |
| 7 | 147247057 | rs2538957 | C | T | 4 | 0.383 | 0.598 | 1.0351 | 1.055 | 0.0014 | 80.79 |
| 2 | 38391130 | rs2305245 | A | C | 4 | 0.5515 | 0.5983 | 1.0213 | 1.0492 | 0.0015 | 80.54 |
| 5 | 6573684 | rs931062 | C | T | 4 | 0.7895 | 0.5985 | 0.9879 | 1.0629 | 0.0014 | 80.67 |
| 5 | 178229512 | rs11950641 | C | T | 4 | 0.5436 | 0.5986 | 1.0345 | 1.0853 | 0.0003 | 84.11 |
| 14 | 32677389 | rs4982055 | G | T | 4 | 0.108 | 0.5987 | 0.942 | 0.9617 | 0.0255 | 67.77 |
| 6 | 136520887 | rs1038214 | A | G | 4 | 0.8433 | 0.599 | 0.993 | 0.9507 | 0.0006 | 82.73 |
| 13 | 39501308 | rs9549041 | C | T | 4 | 0.7419 | 0.5993 | 0.9883 | 0.957 | 0.0046 | 76.97 |
| 13 | 67631961 | rs17083147 | C | T | 3 | 0.1741 | 0.5996 | 0.8248 | 1.3173 | 0.0001 | 89.39 |
| 5 | 159168956 | rs6883903 | A | G | 4 | 0.8104 | 0.5998 | 1.0366 | 1.1932 | 0.0042 | 77.31 |
| 4 | 58828880 | rs1368608 | A | G | 4 | 0.02064 | 0.5999 | 0.9149 | 0.9533 | 0.0039 | 77.52 |
| 4 | 71136589 | rs1825033 | A | G | 4 | 0.1132 | 0.6001 | 0.923 | 0.938 | 0.0036 | 77.87 |
| 21 | 17225142 | rs2243683 | A | G | 4 | 0.04036 | 0.6002 | 1.0759 | 1.0383 | 0.0247 | 68.01 |
| 4 | 71146872 | rs17520678 | A | C | 4 | 0.1201 | 0.6006 | 1.0858 | 1.0676 | 0.0043 | 77.17 |
| 13 | 67606518 | rs11840273 | A | G | 3 | 0.1713 | 0.6008 | 0.8237 | 1.3166 | 0.0001 | 89.42 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 13 | 67611790 | rs2325107 | A | G | 3 | 0.1713 | 0.6008 | 0.8237 | 1.3166 | 0.0001 | 89.42 |
| 19 | 57264112 | rs11669439 | C | T | 4 | 0.8605 | 0.6009 | 1.0068 | 0.9534 | 0.0042 | 77.27 |
| 13 | 67598341 | rs17083120 | C | T | 3 | 0.1702 | 0.6013 | 1.2146 | 0.7596 | 0.0001 | 89.43 |
| 13 | 67599095 | rs17083124 | A | T | 3 | 0.1702 | 0.6013 | 1.2146 | 0.7596 | 0.0001 | 89.43 |
| 5 | 159168575 | rs6884390 | C | T | 4 | 0.8161 | 0.6022 | 0.9657 | 0.8391 | 0.0042 | 77.31 |
| 8 | 21342868 | rs7460673 | C | T | 4 | 0.516 | 0.6022 | 0.9719 | 0.9416 | 0.0008 | 82.17 |
| 3 | 134945497 | rs16840812 | C | T | 4 | 0.1488 | 0.6025 | 1.0708 | 1.0559 | 0.0085 | 74.34 |
| 7 | 44195593 | rs1799884 | C | T | 4 | 0.07248 | 0.6026 | 0.9211 | 0.9559 | 0.0402 | 63.86 |
| 11 | 125183381 | rs7929262 | A | T | 4 | 0.6952 | 0.6027 | 0.9854 | 0.9533 | 0.0029 | 78.63 |
| 4 | 92645841 | rs6849851 | A | G | 4 | 0.2521 | 0.6028 | 1.0429 | 1.0522 | 0.0009 | 81.69 |
| 5 | 6574202 | rs4702359 | A | G | 4 | 0.9908 | 0.6034 | 1.0005 | 0.942 | 0.0006 | 82.72 |
| 11 | 10881592 | rs11043009 | C | T | 4 | 0.06211 | 0.6035 | 1.1035 | 1.0582 | 0.0159 | 70.98 |
| 13 | 39500866 | rs366300 | C | T | 4 | 0.8263 | 0.6035 | 1.0078 | 1.0462 | 0.0027 | 78.76 |
| 2 | 51334759 | rs2098446 | A | G | 4 | 0.5256 | 0.6036 | 1.0236 | 1.0464 | 0.0039 | 77.59 |
| 2 | 38456015 | rs6760123 | C | T | 4 | 0.5918 | 0.6039 | 1.0194 | 1.0496 | 0.0012 | 81.09 |
| 12 | 87292097 | rs2407653 | A | C | 4 | 0.122 | 0.6043 | 0.9046 | 0.9228 | 0.0034 | 78.08 |
| 10 | 110531064 | rs945824 | C | T | 4 | 0.05854 | 0.6047 | 1.0902 | 1.0453 | 0.0386 | 64.24 |
| 2 | 51341929 | rs13420545 | C | T | 4 | 0.5553 | 0.6048 | 0.9785 | 0.9563 | 0.0048 | 76.78 |
| 3 | 176315311 | rs6774509 | A | T | 4 | 0.8825 | 0.6049 | 0.9949 | 0.9512 | 0.0004 | 83.51 |
| 9 | 24988099 | rs10966629 | A | G | 4 | 0.8825 | 0.605 | 0.9946 | 1.0469 | 0.0032 | 78.21 |
| 4 | 58850166 | rs17603347 | C | T | 4 | 0.03085 | 0.6055 | 1.095 | 1.0539 | 0.0029 | 78.59 |
| 3 | 176304233 | rs9869809 | A | T | 4 | 0.9993 | 0.6061 | 1 | 0.9478 | 0.0001 | 85.51 |
| 7 | 125572333 | rs674616 | C | T | 4 | 0.09202 | 0.607 | 0.9145 | 0.9468 | 0.0227 | 68.6 |
| 16 | 29901187 | rs9925915 | C | G | 4 | 0.7913 | 0.6074 | 0.9908 | 1.0466 | 0.0017 | 80.24 |
| 1 | 202835233 | rs6594019 | C | T | 4 | 0.1087 | 0.6075 | 0.942 | 0.9633 | 0.0307 | 66.27 |
| 8 | 21341257 | rs17607798 | A | C | 4 | 0.4755 | 0.6076 | 0.9705 | 0.9437 | 0.0006 | 82.8 |
| 6 | 124525535 | rs749212 | A | G | 4 | 0.01542 | 0.6077 | 1.1354 | 1.0547 | 0.0227 | 68.62 |
| 19 | 61166048 | rs12611033 | A | G | 4 | 0.8546 | 0.6083 | 1.009 | 0.9342 | 0.0007 | 82.33 |
| 16 | 29895850 | rs4283241 | A | G | 4 | 0.7835 | 0.6087 | 0.9905 | 1.0464 | 0.0016 | 80.27 |
| 1 | 46634494 | rs2145408 | A | G | 4 | 0.9935 | 0.6094 | 0.9997 | 1.0486 | 0.005 | 76.6 |
| 8 | 109494368 | rs13249775 | C | T | 4 | 0.1909 | 0.6094 | 0.954 | 0.9573 | 0.0044 | 77.11 |
| 20 | 47306203 | rs6012627 | A | G | 4 | 0.01644 | 0.6101 | 0.8416 | 0.9223 | 0.01 | 73.58 |
| 13 | 67594394 | rs17083114 | C | T | 3 | 0.1643 | 0.6104 | 1.2179 | 0.7666 | 0.0001 | 89.26 |
| 20 | 47147339 | rs2426130 | C | T | 4 | 0.04772 | 0.611 | 1.14 | 1.0687 | 0.0288 | 66.8 |
| 15 | 58089832 | rs9920841 | A | G | 3 | 0.6174 | 0.6111 | 1.0262 | 0.9233 | 0.0003 | 87.54 |
| 9 | 2663393 | rs1542358 | C | T | 4 | 0.6615 | 0.6116 | 0.9702 | 0.9126 | 0.0009 | 81.73 |
| 16 | 29894026 | rs11150577 | A | G | 4 | 0.7788 | 0.6119 | 0.9902 | 1.0456 | 0.0019 | 79.83 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 214179910 | rs772713 | A | C | 4 | 0.62 | 0.612 | 1.0233 | 0.932 | 0.0001 | 86.48 |
| 2 | 134735267 | rs3828175 | A | G | 4 | 0.03397 | 0.612 | 0.827 | 0.8993 | 0.0099 | 73.6 |
| 8 | 21342815 | rs734364 | C | T | 4 | 0.488 | 0.6121 | 1.0296 | 1.059 | 0.0006 | 82.86 |
| 9 | 2671397 | rs7870258 | G | T | 4 | 0.6343 | 0.6121 | 1.0281 | 1.0798 | 0.001 | 81.67 |
| 1 | 214178831 | rs492474 | G | T | 4 | 0.5962 | 0.6122 | 0.9759 | 1.0733 | 0 | 86.84 |
| 1 | 214171349 | rs647908 | A | C | 4 | 0.5865 | 0.6123 | 0.9751 | 1.0738 | 0 | 86.93 |
| 16 | 29892340 | rs4318227 | C | G | 4 | 0.7778 | 0.6124 | 1.0099 | 0.9565 | 0.0019 | 79.81 |
| 3 | 18165497 | rs13060927 | A | G | 4 | 0.8538 | 0.6125 | 0.9906 | 1.0648 | 0.0028 | 78.74 |
| 13 | 89090532 | rs9555926 | A | G | 4 | 0.7303 | 0.6127 | 1.0429 | 1.1698 | 0.0006 | 82.58 |
| 5 | 26174463 | rs11953897 | A | G | 3 | 0.146 | 0.6132 | 1.1359 | 1.1404 | 0.0022 | 83.61 |
| 1 | 160510650 | rs6427667 | C | G | 4 | 0.3317 | 0.6133 | 0.9558 | 0.9348 | 0.0003 | 84.25 |
| 7 | 6389325 | rs10234438 | A | G | 4 | 0.8087 | 0.6134 | 1.0232 | 0.876 | 0.0002 | 84.49 |
| 16 | 7339253 | rs17143484 | C | T | 4 | 0.01145 | 0.6135 | 1.1543 | 1.0629 | 0.0158 | 71.03 |
| 16 | 29903381 | rs4787489 | A | G | 4 | 0.7655 | 0.6138 | 0.9896 | 1.0459 | 0.0016 | 80.35 |
| 16 | 29891571 | rs11901 | C | G | 4 | 0.781 | 0.6145 | 1.0098 | 0.957 | 0.0021 | 79.51 |
| 1 | 95561952 | rs17113374 | C | T | 4 | 0.5236 | 0.6147 | 0.9646 | 0.9295 | 0.0014 | 80.7 |
| 16 | 29885063 | rs4787486 | A | T | 4 | 0.7815 | 0.6147 | 1.0097 | 0.957 | 0.0021 | 79.52 |
| 16 | 29881668 | rs6565173 | A | G | 4 | 0.7817 | 0.6154 | 0.9904 | 1.0447 | 0.0022 | 79.46 |
| 6 | 124523315 | rs802273 | G | T | 4 | 0.01756 | 0.6157 | 0.8824 | 0.9492 | 0.0229 | 68.55 |
| 9 | 117019231 | rs10817727 | A | G | 4 | 0.004988 | 0.6157 | 0.8499 | 0.9362 | 0.0098 | 73.68 |
| 20 | 47271275 | rs6019695 | A | G | 4 | 0.01907 | 0.616 | 1.1815 | 1.0841 | 0.0079 | 74.69 |
| 7 | 125567593 | rs492757 | A | T | 4 | 0.09412 | 0.6163 | 1.093 | 1.0552 | 0.0211 | 69.13 |
| 16 | 29902719 | rs4788204 | A | G | 4 | 0.7565 | 0.6163 | 0.9892 | 1.0456 | 0.0016 | 80.39 |
| 13 | 39470070 | rs276420 | G | T | 4 | 0.9085 | 0.6167 | 0.996 | 0.957 | 0.0016 | 80.34 |
| 3 | 176319542 | rs2862042 | C | T | 4 | 0.9003 | 0.6168 | 0.9956 | 0.9519 | 0.0004 | 83.72 |
| 6 | 124525158 | rs802274 | A | G | 4 | 0.01703 | 0.617 | 0.8824 | 0.9495 | 0.0229 | 68.56 |
| 8 | 54386673 | rs7462232 | A | G | 4 | 0.04731 | 0.6172 | 1.1196 | 1.0669 | 0.0065 | 75.53 |
| 4 | 71093585 | rs17148330 | A | G | 4 | 0.1197 | 0.6175 | 0.9243 | 0.9403 | 0.0031 | 78.4 |
| 4 | 71148222 | rs10518071 | C | T | 4 | 0.1697 | 0.6176 | 0.9329 | 0.9422 | 0.0048 | 76.81 |
| 4 | 71146110 | rs1849717 | C | T | 4 | 0.1411 | 0.6178 | 1.0773 | 1.0626 | 0.0037 | 77.75 |
| 10 | 110514731 | rs11591352 | G | T | 4 | 0.05581 | 0.6179 | 1.0926 | 1.0467 | 0.0255 | 67.77 |
| 3 | 176319087 | rs6774272 | C | T | 4 | 0.9131 | 0.618 | 1.0038 | 1.0498 | 0.0004 | 83.75 |
| 16 | 29910577 | rs9924686 | A | G | 4 | 0.7306 | 0.6186 | 0.9881 | 1.0459 | 0.0013 | 80.96 |
| 11 | 10869437 | rs16908503 | A | G | 4 | 0.0538 | 0.6188 | 1.102 | 1.0519 | 0.0202 | 69.43 |
| 4 | 71149649 | rs3775739 | A | G | 4 | 0.1621 | 0.6194 | 0.9323 | 0.9446 | 0.0056 | 76.2 |
| 10 | 122589381 | rs12355703 | C | G | 4 | 0.4443 | 0.6199 | 1.0968 | 1.1796 | 0.0005 | 83.14 |
| 3 | 176315077 | rs6796537 | C | T | 4 | 0.9009 | 0.62 | 0.9957 | 0.953 | 0.0004 | 83.69 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 3 | 176315114 | rs6809009 | G | T | 4 | 0.9069 | 0.6208 | 1.0041 | 1.0492 | 0.0004 | 83.72 |
| 3 | 176318751 | rs6773961 | A | T | 4 | 0.9069 | 0.6208 | 1.0041 | 1.0492 | 0.0004 | 83.72 |
| 6 | 124522342 | rs802270 | A | G | 4 | 0.01819 | 0.6212 | 1.1326 | 1.0526 | 0.0235 | 68.38 |
| 3 | 176299621 | rs1381130 | C | T | 4 | 0.6972 | 0.6215 | 1.0139 | 0.9545 | 0.0008 | 82.1 |
| 2 | 51625568 | rs12995836 | C | T | 4 | 0.1025 | 0.6216 | 0.9445 | 0.9634 | 0.0123 | 72.49 |
| 10 | 110659654 | rs11596191 | C | T | 4 | 0.06354 | 0.6217 | 0.9192 | 0.9586 | 0.0376 | 64.49 |
| 6 | 124512460 | rs2146252 | C | T | 4 | 0.02004 | 0.6218 | 1.1335 | 1.0537 | 0.0236 | 68.33 |
| 10 | 110511738 | rs17769672 | C | G | 4 | 0.05992 | 0.6219 | 1.0921 | 1.0444 | 0.0369 | 64.67 |
| 1 | 214169893 | rs517577 | A | G | 4 | 0.58 | 0.6221 | 0.9746 | 1.0709 | 0.0001 | 86.52 |
| 3 | 176318826 | rs6809556 | C | T | 4 | 0.9102 | 0.6221 | 0.9961 | 0.9533 | 0.0004 | 83.68 |
| 9 | 7518098 | rs10758880 | A | C | 4 | 0.1164 | 0.6224 | 1.0565 | 1.0366 | 0.0182 | 70.12 |
| 9 | 7518239 | rs10815626 | C | T | 4 | 0.1164 | 0.6224 | 1.0565 | 1.0366 | 0.0182 | 70.12 |
| 14 | 42262582 | rs10149887 | A | T | 3 | 0.4313 | 0.6225 | 1.0844 | 1.1643 | 0.0013 | 84.88 |
| 7 | 136935020 | rs706568 | A | T | 4 | 0.08333 | 0.6229 | 1.1407 | 1.1049 | 0.0007 | 82.25 |
| 1 | 21832177 | rs9426772 | C | T | 4 | 0.05397 | 0.623 | 0.9329 | 0.9656 | 0.0288 | 66.81 |
| 4 | 71136840 | rs1817460 | A | T | 4 | 0.1306 | 0.6232 | 0.9263 | 0.9407 | 0.0028 | 78.74 |
| 13 | 39479629 | rs276407 | A | G | 4 | 0.9557 | 0.6234 | 0.9981 | 0.958 | 0.0017 | 80.18 |
| 10 | 129848954 | rs6482659 | A | C | 3 | 0.775 | 0.6246 | 0.9851 | 1.0942 | 0.0002 | 88.47 |
| 1 | 214165817 | rs942837 | C | T | 4 | 0.5637 | 0.6254 | 1.0272 | 0.9343 | 0.0001 | 86.55 |
| 13 | 104283297 | rs7997861 | C | T | 4 | 0.9361 | 0.6257 | 0.9972 | 1.0469 | 0.0009 | 81.82 |
| 15 | 51195545 | rs584758 | A | G | 4 | 0.03198 | 0.6259 | 0.9125 | 0.955 | 0.0089 | 74.16 |
| 3 | 176311154 | rs4355289 | A | G | 4 | 0.9279 | 0.6261 | 1.0031 | 1.0485 | 0.0004 | 83.72 |
| 16 | 29896442 | rs4583255 | A | G | 4 | 0.7221 | 0.6261 | 1.0125 | 0.9574 | 0.0015 | 80.55 |
| 13 | 104282736 | rs1326452 | A | G | 4 | 0.9348 | 0.6265 | 0.9971 | 1.0467 | 0.0009 | 81.78 |
| 15 | 31694920 | rs4238566 | A | C | 4 | 0.7606 | 0.6269 | 1.0122 | 0.9531 | 0.0028 | 78.71 |
| 5 | 40303687 | rs2279170 | C | T | 4 | 0.009422 | 0.6271 | 1.1006 | 1.0392 | 0.0135 | 71.94 |
| 10 | 110503291 | rs12256452 | C | G | 4 | 0.04812 | 0.6271 | 1.0944 | 1.0439 | 0.03 | 66.47 |
| 3 | 176314128 | rs9877212 | C | T | 4 | 0.9309 | 0.6272 | 1.003 | 1.048 | 0.0004 | 83.71 |
| 3 | 176315642 | rs6763592 | G | T | 4 | 0.8306 | 0.6272 | 1.0077 | 1.0426 | 0.0033 | 78.11 |
| 1 | 214170400 | rs662355 | C | G | 4 | 0.5761 | 0.6273 | 1.0264 | 0.9348 | 0.0001 | 86.49 |
| 7 | 125571959 | rs654111 | C | T | 4 | 0.1017 | 0.6273 | 0.9168 | 0.949 | 0.0203 | 69.42 |
| 2 | 38403351 | rs7606701 | A | C | 4 | 0.6299 | 0.6274 | 1.0173 | 1.0459 | 0.0013 | 80.94 |
| 16 | 29902237 | rs3814884 | A | T | 4 | 0.7748 | 0.6275 | 0.9898 | 1.0436 | 0.0026 | 78.98 |
| 10 | 110517348 | rs17697405 | C | T | 4 | 0.05913 | 0.6276 | 0.917 | 0.9586 | 0.035 | 65.14 |
| 2 | 29148520 | rs10200693 | A | G | 4 | 0.1026 | 0.6277 | 0.9348 | 0.9597 | 0.0206 | 69.31 |
| 13 | 104284951 | rs1409470 | A | G | 4 | 0.9536 | 0.628 | 1.0021 | 0.9554 | 0.0011 | 81.34 |
| 13 | 104285669 | rs1853979 | A | G | 4 | 0.9392 | 0.6282 | 0.9972 | 1.0464 | 0.0013 | 80.99 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 66825324 | rs2166307 | C | T | 4 | 0.06538 | 0.6285 | 1.102 | 1.0524 | 0.029 | 66.73 |
| 6 | 124513424 | rs6569377 | C | T | 4 | 0.0203 | 0.6287 | 0.8831 | 0.9502 | 0.0235 | 68.36 |
| 13 | 104283684 | rs7139884 | A | C | 4 | 0.948 | 0.6287 | 0.9977 | 1.0465 | 0.001 | 81.61 |
| 5 | 26178629 | rs4701526 | C | G | 3 | 0.1347 | 0.6293 | 1.1399 | 1.1305 | 0.0029 | 82.85 |
| 6 | 124512495 | rs2146253 | A | G | 4 | 0.02172 | 0.6294 | 1.1316 | 1.0525 | 0.0238 | 68.26 |
| 8 | 4080287 | rs7819694 | C | T | 4 | 0.4919 | 0.6294 | 1.0648 | 1.1204 | 0.0011 | 81.44 |
| 4 | 71098553 | rs2306445 | A | G | 4 | 0.1304 | 0.6295 | 0.9263 | 0.9411 | 0.0023 | 79.24 |
| 13 | 104284523 | rs9519488 | A | T | 4 | 0.9271 | 0.6296 | 1.0033 | 0.9557 | 0.0011 | 81.42 |
| 2 | 232169359 | rs4973009 | A | G | 3 | 0.2019 | 0.6304 | 1.0857 | 1.1057 | 0.0001 | 88.95 |
| 6 | 124516437 | rs802253 | C | G | 4 | 0.02035 | 0.6304 | 0.8839 | 0.9509 | 0.024 | 68.21 |
| 3 | 176312381 | rs9847129 | C | T | 4 | 0.9472 | 0.6305 | 0.9977 | 0.9544 | 0.0004 | 83.69 |
| 6 | 124516266 | rs802251 | G | T | 4 | 0.02176 | 0.6309 | 0.8844 | 0.9508 | 0.0245 | 68.05 |
| 10 | 110512515 | rs6584895 | C | T | 4 | 0.06634 | 0.631 | 1.0888 | 1.0432 | 0.0347 | 65.22 |
| 4 | 71088800 | rs17148328 | C | T | 4 | 0.1234 | 0.6315 | 0.925 | 0.9425 | 0.003 | 78.48 |
| 7 | 125569040 | rs618766 | G | T | 4 | 0.1018 | 0.6317 | 0.9168 | 0.9493 | 0.019 | 69.84 |
| 1 | 214169419 | rs513746 | C | T | 4 | 0.5494 | 0.6318 | 1.0281 | 0.9361 | 0.0001 | 86.39 |
| 6 | 124516294 | rs802252 | C | T | 4 | 0.02227 | 0.6327 | 0.8849 | 0.9511 | 0.0245 | 68.06 |
| 9 | 86103553 | rs17427184 | A | G | 4 | 0.05171 | 0.6327 | 1.1343 | 1.09 | 0.0004 | 83.69 |
| 14 | 42261991 | rs1777075 | A | G | 3 | 0.4113 | 0.6327 | 1.0877 | 1.159 | 0.0012 | 85.19 |
| 6 | 124517096 | rs802255 | A | G | 4 | 0.02079 | 0.633 | 0.8843 | 0.9512 | 0.024 | 68.22 |
| 13 | 104287517 | rs9514325 | A | G | 4 | 0.9546 | 0.6331 | 0.9979 | 1.0461 | 0.0015 | 80.52 |
| 16 | 29875516 | rs7204797 | C | T | 4 | 0.7257 | 0.6332 | 1.0123 | 0.9591 | 0.002 | 79.69 |
| 16 | 22620480 | rs154537 | G | T | 4 | 0.06953 | 0.6333 | 1.0887 | 1.0433 | 0.0341 | 65.38 |
| 2 | 210413593 | rs10178675 | C | G | 4 | 0.003915 | 0.6334 | 0.8524 | 0.9439 | 0.0133 | 72.02 |
| 3 | 176299863 | rs9848123 | A | G | 4 | 0.6507 | 0.6337 | 1.0161 | 0.9558 | 0.0007 | 82.26 |
| 16 | 29908402 | rs3814881 | A | G | 4 | 0.6778 | 0.6337 | 0.9856 | 1.0442 | 0.0012 | 81.21 |
| 6 | 26794868 | rs7755721 | C | T | 4 | 0.9254 | 0.634 | 0.9963 | 1.0476 | 0.0028 | 78.66 |
| 6 | 124512907 | rs2008699 | C | T | 4 | 0.02055 | 0.6341 | 1.1321 | 1.0518 | 0.0228 | 68.58 |
| 6 | 124515810 | rs802249 | C | G | 4 | 0.02248 | 0.6345 | 1.13 | 1.0512 | 0.0245 | 68.07 |
| 7 | 136934899 | rs6949094 | C | T | 4 | 0.05343 | 0.6346 | 1.1693 | 1.1049 | 0.0013 | 80.94 |
| 4 | 58833846 | rs2553297 | C | T | 4 | 0.02315 | 0.6351 | 0.9164 | 0.9575 | 0.0039 | 77.59 |
| 12 | 87293574 | rs10858718 | C | G | 4 | 0.168 | 0.6351 | 1.0921 | 1.079 | 0.0018 | 79.99 |
| 10 | 122705142 | rs11199677 | A | C | 4 | 0.5899 | 0.6352 | 1.0704 | 1.1844 | 0.0004 | 83.49 |
| 3 | 144993820 | rs12233446 | C | T | 4 | 0.00129 | 0.6356 | 0.8588 | 0.9504 | 0.0084 | 74.43 |
| 6 | 124513036 | rs2008708 | A | G | 4 | 0.02127 | 0.6357 | 0.8839 | 0.9511 | 0.0232 | 68.46 |
| 7 | 44190467 | rs2908289 | A | G | 4 | 0.09102 | 0.6365 | 1.0815 | 1.0435 | 0.0322 | 65.87 |
| 10 | 110506325 | rs17769499 | A | C | 4 | 0.06427 | 0.6365 | 0.9179 | 0.9589 | 0.0327 | 65.74 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 11 | 10861334 | rs1589596 | G | T | 4 | 0.05687 | 0.6365 | 0.9075 | 0.951 | 0.0148 | 71.4 |
| 8 | 109423278 | rs4734174 | A | G | 4 | 0.1648 | 0.6368 | 1.0514 | 1.0384 | 0.0104 | 73.35 |
| 6 | 124513519 | rs6932946 | G | T | 4 | 0.02188 | 0.637 | 1.1306 | 1.0511 | 0.0233 | 68.42 |
| 7 | 125564351 | rs639166 | C | T | 4 | 0.1292 | 0.6374 | 1.0855 | 1.0523 | 0.0228 | 68.58 |
| 10 | 110506183 | rs17769443 | A | G | 4 | 0.06422 | 0.6376 | 1.0895 | 1.0427 | 0.0324 | 65.81 |
| 10 | 110537793 | rs7920198 | A | G | 4 | 0.06613 | 0.6379 | 1.088 | 1.0414 | 0.0372 | 64.6 |
| 1 | 95555047 | rs17113360 | C | T | 4 | 0.5251 | 0.6381 | 1.0364 | 1.0685 | 0.002 | 79.71 |
| 16 | 29925396 | rs3814880 | C | T | 4 | 0.7182 | 0.6383 | 0.9875 | 1.0439 | 0.0011 | 81.4 |
| 10 | 110501214 | rs11194258 | A | G | 4 | 0.05039 | 0.6387 | 1.0935 | 1.0427 | 0.0283 | 66.94 |
| 9 | 7517476 | rs10758876 | G | T | 4 | 0.1274 | 0.6393 | 0.948 | 0.966 | 0.0164 | 70.78 |
| 16 | 29941134 | rs12325539 | C | T | 4 | 0.6789 | 0.6395 | 0.9847 | 1.0485 | 0.0006 | 82.79 |
| 9 | 2682393 | rs11788193 | A | T | 4 | 0.5284 | 0.64 | 1.0496 | 1.09 | 0.0028 | 78.66 |
| 8 | 109448088 | rs11780184 | C | T | 4 | 0.1932 | 0.6402 | 1.0487 | 1.0397 | 0.0068 | 75.37 |
| 7 | 44190246 | rs730497 | A | G | 4 | 0.09094 | 0.6404 | 1.0816 | 1.0433 | 0.031 | 66.2 |
| 9 | 7517489 | rs10758877 | C | T | 4 | 0.1265 | 0.6407 | 1.055 | 1.0351 | 0.0161 | 70.92 |
| 11 | 10865614 | rs10840506 | C | T | 4 | 0.05277 | 0.641 | 0.9075 | 0.953 | 0.0173 | 70.44 |
| 16 | 29938200 | rs11150581 | C | T | 4 | 0.6856 | 0.641 | 0.985 | 1.0482 | 0.0006 | 82.81 |
| 3 | 176302128 | rs9859106 | A | T | 4 | 0.5598 | 0.6412 | 1.0208 | 0.9579 | 0.0012 | 81.2 |
| 5 | 125194811 | rs17560965 | A | G | 4 | 0.7045 | 0.6416 | 1.0331 | 1.1009 | 0.0031 | 78.36 |
| 16 | 7342542 | rs9933137 | G | T | 4 | 0.0148 | 0.6417 | 1.1486 | 1.0588 | 0.0134 | 71.98 |
| 20 | 3499637 | rs17709518 | A | G | 4 | 0.9069 | 0.6421 | 0.9913 | 0.9192 | 0.0029 | 78.57 |
| 10 | 110503533 | rs10509877 | A | G | 4 | 0.05234 | 0.6424 | 1.0926 | 1.0422 | 0.0286 | 66.86 |
| 1 | 202835999 | rs11240764 | C | T | 4 | 0.1238 | 0.6426 | 0.9443 | 0.9661 | 0.0263 | 67.53 |
| 8 | 109444070 | rs1597145 | G | T | 4 | 0.1965 | 0.6426 | 1.0484 | 1.0396 | 0.0065 | 75.55 |
| 2 | 210419671 | rs6752217 | G | T | 4 | 0.00485 | 0.6427 | 0.8548 | 0.945 | 0.0133 | 72.03 |
| 6 | 26866458 | rs4711122 | C | T | 4 | 0.8298 | 0.643 | 1.0086 | 0.956 | 0.0029 | 78.53 |
| 16 | 29937696 | rs11642612 | A | C | 4 | 0.6806 | 0.6431 | 1.0155 | 0.9543 | 0.0006 | 82.77 |
| 16 | 29920767 | rs4788209 | C | T | 4 | 0.7229 | 0.6433 | 1.0127 | 0.9592 | 0.0017 | 80.23 |
| 7 | 125564375 | rs639211 | A | C | 4 | 0.1219 | 0.6434 | 1.0867 | 1.0517 | 0.0208 | 69.25 |
| 7 | 125565143 | rs642710 | C | T | 4 | 0.1041 | 0.6434 | 1.0901 | 1.0515 | 0.0191 | 69.83 |
| 4 | 183400923 | rs6840036 | C | T | 4 | 0.1562 | 0.6435 | 1.0589 | 1.0483 | 0.0017 | 80.14 |
| 2 | 107976696 | rs333217 | A | G | 4 | 0.1367 | 0.6438 | 0.9311 | 0.9531 | 0.0099 | 73.62 |
| 20 | 3508191 | rs17782370 | C | T | 4 | 0.896 | 0.6439 | 0.9903 | 0.92 | 0.003 | 78.5 |
| 9 | 2684201 | rs748787 | A | G | 3 | 0.7561 | 0.644 | 1.0293 | 1.1466 | 0.0008 | 85.92 |
| 8 | 109497697 | rs10098022 | A | G | 4 | 0.2056 | 0.6441 | 1.0466 | 1.0401 | 0.0046 | 76.98 |
| 20 | 3504956 | rs17782347 | C | T | 4 | 0.9037 | 0.6443 | 1.0091 | 1.0869 | 0.003 | 78.45 |
| 16 | 29926001 | rs3935873 | C | T | 4 | 0.694 | 0.6447 | 1.0138 | 0.9586 | 0.001 | 81.51 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 2 | 210418651 | rs13028068 | G | T | 4 | 0.004367 | 0.6451 | 1.171 | 1.0577 | 0.0129 | 72.22 |
| 9 | 7517926 | rs10758879 | A | G | 4 | 0.1291 | 0.6452 | 1.0546 | 1.0347 | 0.0155 | 71.12 |
| 2 | 210418038 | rs12386218 | C | G | 4 | 0.004329 | 0.6456 | 0.8538 | 0.9455 | 0.0127 | 72.28 |
| 16 | 29902423 | rs3814883 | C | T | 4 | 0.6173 | 0.6457 | 1.0182 | 0.9561 | 0.0006 | 82.62 |
| 13 | 89120930 | rs6492439 | T | C | 3 | 0.08705 | 0.646 | 1.1951 | 1.1418 | 0.0025 | 83.29 |
| 8 | 109442301 | rs1448160 | C | T | 4 | 0.1989 | 0.6463 | 0.9541 | 0.9621 | 0.0061 | 75.8 |
| 13 | 39465395 | rs276422 | G | T | 4 | 0.9874 | 0.6466 | 1.0005 | 0.961 | 0.002 | 79.76 |
| 7 | 103388421 | rs10246267 | C | T | 4 | 0.3121 | 0.6468 | 1.078 | 1.0896 | 0.0029 | 78.63 |
| 2 | 210417278 | rs16843780 | C | G | 4 | 0.004639 | 0.6472 | 1.1698 | 1.0571 | 0.0133 | 72.03 |
| 4 | 21481084 | rs12504827 | A | G | 4 | 0.9266 | 0.6475 | 1.0032 | 1.0444 | 0.0006 | 82.84 |
| 11 | 62420235 | rs547248 | C | T | 4 | 0.8187 | 0.6477 | 0.9913 | 1.0412 | 0.005 | 76.59 |
| 9 | 81271470 | rs10867388 | A | G | 4 | 0.1104 | 0.6478 | 0.8441 | 0.9071 | 0.0245 | 68.07 |
| 20 | 47381122 | rs6019751 | C | T | 4 | 0.08942 | 0.6482 | 0.8925 | 0.9387 | 0.0195 | 69.68 |
| 13 | 39483845 | rs276402 | A | C | 4 | 0.9744 | 0.6486 | 0.9989 | 0.9608 | 0.0016 | 80.29 |
| 11 | 10857488 | rs11042998 | G | T | 4 | 0.06888 | 0.6487 | 0.9091 | 0.9497 | 0.0098 | 73.65 |
| 11 | 10858797 | rs2403431 | A | C | 4 | 0.06617 | 0.6487 | 0.9087 | 0.9501 | 0.0103 | 73.42 |
| 2 | 210415606 | rs10490024 | A | G | 4 | 0.004699 | 0.649 | 1.1694 | 1.0568 | 0.0131 | 72.11 |
| 11 | 10857160 | rs11042997 | A | C | 4 | 0.07084 | 0.6496 | 0.9093 | 0.9492 | 0.0089 | 74.12 |
| 1 | 160514456 | rs7525955 | A | G | 4 | 0.4608 | 0.6497 | 1.0345 | 1.0619 | 0.0003 | 84.34 |
| 9 | 2663801 | rs12347630 | A | G | 4 | 0.7667 | 0.6514 | 1.0204 | 1.0799 | 0.0019 | 79.89 |
| 1 | 95796000 | rs519693 | C | T | 4 | 0.9715 | 0.6516 | 1.0025 | 1.0761 | 0.0035 | 77.95 |
| 8 | 4101682 | rs12675002 | A | G | 4 | 0.351 | 0.6516 | 1.0676 | 1.0935 | 0.0002 | 84.53 |
| 9 | 2664864 | rs7874073 | A | G | 4 | 0.7338 | 0.6523 | 1.0231 | 1.0821 | 0.001 | 81.49 |
| 16 | 50225366 | rs2647971 | C | T | 4 | 0.6753 | 0.6527 | 0.9852 | 1.0428 | 0.001 | 81.63 |
| 2 | 172973708 | rs10497382 | C | T | 4 | 0.4909 | 0.6529 | 0.9693 | 0.9502 | 0.0021 | 79.55 |
| 2 | 210416012 | rs10188289 | A | G | 4 | 0.004899 | 0.6529 | 1.1685 | 1.0561 | 0.013 | 72.14 |
| 9 | 2664110 | rs7859818 | A | G | 4 | 0.7227 | 0.6534 | 0.9763 | 0.924 | 0.001 | 81.61 |
| 9 | 2673052 | rs7031441 | C | G | 4 | 0.7624 | 0.6538 | 1.0177 | 1.0708 | 0.0008 | 82.16 |
| 8 | 109495470 | rs1955032 | G | T | 4 | 0.203 | 0.654 | 0.9549 | 0.9623 | 0.0045 | 77.04 |
| 7 | 125565214 | rs653569 | A | G | 4 | 0.1098 | 0.6546 | 0.9186 | 0.9522 | 0.0177 | 70.3 |
| 3 | 144994842 | rs2121775 | A | G | 4 | 0.00157 | 0.6548 | 0.8603 | 0.9527 | 0.0078 | 74.73 |
| 3 | 176310661 | rs6782183 | C | T | 4 | 0.9288 | 0.6549 | 0.9968 | 0.9624 | 0.0031 | 78.34 |
| 2 | 38396294 | rs10202238 | C | T | 4 | 0.9251 | 0.6559 | 0.9964 | 0.9598 | 0.0031 | 78.36 |
| 8 | 109493977 | rs6998163 | C | T | 4 | 0.2191 | 0.6564 | 1.0452 | 1.039 | 0.004 | 77.5 |
| 10 | 122502220 | rs11199530 | A | G | 4 | 0.4248 | 0.6564 | 0.9091 | 0.8643 | 0.0007 | 82.24 |
| 9 | 2665728 | rs11793970 | C | G | 4 | 0.7433 | 0.657 | 1.0223 | 1.0807 | 0.0011 | 81.41 |
| 2 | 107931186 | rs7594860 | C | T | 3 | 0.009744 | 0.6572 | 0.8598 | 0.9389 | 0.0205 | 74.28 |

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|----|-----------|------------|---|---|---|-----------|--------|--------|--------|--------|-------|
| 9 | 2667429 | rs7029840 | A | C | 4 | 0.7498 | 0.6578 | 1.0217 | 1.0802 | 0.0011 | 81.28 |
| 6 | 94772045 | rs1488307 | C | T | 3 | 0.0007852 | 0.658 | 1.1782 | 1.0586 | 0.013 | 76.96 |
| 1 | 152458415 | rs9803857 | A | G | 4 | 0.4633 | 0.6584 | 1.0261 | 0.9554 | 0.0001 | 85.27 |
| 8 | 109492672 | rs4735063 | A | T | 4 | 0.2215 | 0.6586 | 0.9569 | 0.9627 | 0.004 | 77.46 |
| 1 | 160514063 | rs7525777 | C | T | 4 | 0.4414 | 0.6587 | 0.964 | 0.9416 | 0.0003 | 84.34 |
| 4 | 58848803 | rs17089214 | C | T | 4 | 0.03768 | 0.6587 | 0.9234 | 0.9608 | 0.0041 | 77.36 |
| 8 | 4097308 | rs2407941 | C | T | 4 | 0.4218 | 0.659 | 1.0577 | 1.0956 | 0.0001 | 85.89 |
| 8 | 109466087 | rs10108399 | C | T | 4 | 0.1996 | 0.6591 | 0.9549 | 0.9635 | 0.0052 | 76.5 |
| 20 | 47156669 | rs2426133 | C | T | 4 | 0.06467 | 0.6591 | 1.1548 | 1.0685 | 0.031 | 66.19 |
| 16 | 50225696 | rs2647972 | C | T | 4 | 0.6473 | 0.6592 | 0.9839 | 1.0421 | 0.0009 | 81.75 |
| 4 | 71114351 | rs17148361 | C | T | 4 | 0.1423 | 0.6593 | 1.077 | 1.0575 | 0.0021 | 79.64 |
| 5 | 6574824 | rs11742039 | G | T | 4 | 0.6641 | 0.6593 | 0.9803 | 1.0541 | 0.0009 | 81.68 |
| 4 | 21480772 | rs12512316 | A | G | 4 | 0.9346 | 0.6601 | 0.9971 | 0.9587 | 0.0005 | 83.21 |
| 7 | 125565195 | rs651763 | A | C | 4 | 0.116 | 0.6602 | 0.9203 | 0.9529 | 0.0167 | 70.66 |
| 2 | 172438261 | rs6725388 | C | G | 4 | 0.7179 | 0.6603 | 1.0137 | 1.0474 | 0.0003 | 83.91 |
| 8 | 109467321 | rs7812466 | A | G | 4 | 0.2035 | 0.6605 | 1.0469 | 1.0376 | 0.0054 | 76.36 |
| 5 | 51877283 | rs7730948 | C | T | 4 | 0.581 | 0.6608 | 1.062 | 1.1155 | 0.005 | 76.66 |
| 3 | 144995427 | rs6800578 | C | T | 4 | 0.001837 | 0.6612 | 0.862 | 0.9536 | 0.008 | 74.64 |
| 5 | 51883415 | rs10054300 | A | G | 4 | 0.5885 | 0.6624 | 1.0608 | 1.1151 | 0.0049 | 76.69 |
| 9 | 81234777 | rs17082380 | A | C | 4 | 0.1178 | 0.6625 | 0.8478 | 0.9116 | 0.0249 | 67.93 |
| 8 | 109492076 | rs4735062 | G | T | 4 | 0.2262 | 0.6626 | 0.9574 | 0.9631 | 0.0038 | 77.63 |
| 1 | 160514403 | rs7528328 | C | T | 4 | 0.49 | 0.663 | 0.9688 | 0.9436 | 0.0002 | 84.54 |
| 9 | 2667743 | rs7029311 | A | G | 4 | 0.7645 | 0.663 | 1.0204 | 1.0791 | 0.0011 | 81.41 |
| 2 | 38226868 | rs918804 | A | T | 4 | 0.0237 | 0.6634 | 0.8924 | 0.9487 | 0.0039 | 77.54 |
| 5 | 51871156 | rs16879891 | G | T | 4 | 0.6019 | 0.6645 | 0.945 | 0.8986 | 0.0054 | 76.35 |
| 8 | 109471830 | rs4363174 | C | T | 4 | 0.2078 | 0.6647 | 1.0464 | 1.0372 | 0.0051 | 76.53 |
| 3 | 178815700 | rs1466846 | A | G | 4 | 0.02615 | 0.665 | 0.9104 | 0.9488 | 0.0002 | 84.96 |
| 2 | 49146315 | rs4971622 | A | T | 4 | 0.9595 | 0.6651 | 0.9955 | 0.9155 | 0.0049 | 76.7 |
| 5 | 6575043 | rs11134164 | A | G | 4 | 0.6778 | 0.6654 | 1.0193 | 0.9495 | 0.001 | 81.65 |
| 5 | 73297869 | rs416286 | A | G | 4 | 0.01807 | 0.6659 | 1.0965 | 1.05 | 0.0002 | 84.72 |
| 5 | 73300336 | rs436777 | A | G | 4 | 0.01807 | 0.6659 | 1.0965 | 1.05 | 0.0002 | 84.72 |
| 13 | 104286376 | rs2031635 | A | G | 4 | 0.8754 | 0.6679 | 0.9941 | 1.0411 | 0.0022 | 79.49 |
| 16 | 29874935 | rs4788196 | A | G | 4 | 0.6848 | 0.6679 | 1.0143 | 0.9649 | 0.0042 | 77.26 |
| 8 | 109477725 | rs2156740 | C | G | 4 | 0.2125 | 0.6692 | 1.0459 | 1.0368 | 0.0049 | 76.73 |
| 1 | 152478140 | rs12062977 | C | T | 4 | 0.4803 | 0.6698 | 0.9756 | 1.0451 | 0.0001 | 85.34 |
| 1 | 152486342 | rs6427509 | C | T | 4 | 0.476 | 0.6715 | 0.9753 | 1.0449 | 0.0001 | 85.36 |
| 1 | 152484387 | rs10158820 | C | T | 4 | 0.4738 | 0.6718 | 0.9752 | 1.0448 | 0.0001 | 85.36 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 5 | 159144339 | rs6888211 | C | T | 4 | 0.8731 | 0.6725 | 0.9761 | 0.8663 | 0.0047 | 76.89 |
| 4 | 174752942 | rs10025532 | A | G | 4 | 0.2456 | 0.6729 | 0.9561 | 0.9594 | 0.0014 | 80.7 |
| 20 | 47380876 | rs6019750 | C | G | 4 | 0.0997 | 0.6732 | 0.8956 | 0.9422 | 0.0165 | 70.77 |
| 1 | 152491968 | rs2340473 | C | T | 4 | 0.4711 | 0.6735 | 1.0256 | 0.9573 | 0.0001 | 85.4 |
| 2 | 134738836 | rs3791270 | A | G | 4 | 0.04575 | 0.6737 | 0.8364 | 0.9167 | 0.0109 | 73.11 |
| 9 | 81234189 | rs11138206 | A | G | 4 | 0.1233 | 0.6738 | 1.1767 | 1.0941 | 0.0232 | 68.45 |
| 1 | 152470934 | rs2879788 | A | T | 4 | 0.4632 | 0.6743 | 0.9746 | 1.0445 | 0.0001 | 85.39 |
| 1 | 202857860 | rs884108 | A | G | 3 | 0.01364 | 0.6757 | 1.115 | 1.0456 | 0.0082 | 79.18 |
| 7 | 52131614 | rs2953422 | A | G | 4 | 0.1005 | 0.6758 | 0.9434 | 0.9646 | 0.0028 | 78.7 |
| 1 | 170633760 | rs4471302 | C | T | 4 | 0.6872 | 0.676 | 1.0201 | 0.9499 | 0.0032 | 78.24 |
| 2 | 210443331 | rs12328346 | A | G | 4 | 0.007564 | 0.6762 | 1.1593 | 1.0538 | 0.0098 | 73.65 |
| 9 | 2668077 | rs6475927 | A | G | 4 | 0.7912 | 0.6769 | 1.018 | 1.0763 | 0.001 | 81.66 |
| 13 | 67660291 | rs17083164 | C | T | 3 | 0.0656 | 0.6772 | 1.3088 | 0.8063 | 0.0008 | 86.08 |
| 9 | 81273412 | rs12339463 | A | G | 4 | 0.1243 | 0.6773 | 1.1772 | 1.0946 | 0.0211 | 69.14 |
| 8 | 109479131 | rs1893887 | C | G | 4 | 0.2216 | 0.6775 | 1.045 | 1.0361 | 0.0045 | 77.08 |
| 8 | 109479249 | rs1893886 | C | T | 4 | 0.223 | 0.6778 | 0.9571 | 0.9652 | 0.0045 | 77.02 |
| 3 | 176301721 | rs7627996 | C | T | 4 | 0.5434 | 0.6779 | 0.9787 | 1.0372 | 0.0023 | 79.29 |
| 13 | 67662316 | rs7984473 | A | G | 3 | 0.1201 | 0.678 | 1.2896 | 0.7941 | 0.0007 | 86.14 |
| 1 | 170633685 | rs10489284 | A | G | 4 | 0.681 | 0.6786 | 0.9799 | 1.0523 | 0.0032 | 78.21 |
| 1 | 152446303 | rs6719 | C | T | 4 | 0.4334 | 0.6787 | 1.0279 | 0.9579 | 0.0001 | 85.43 |
| 8 | 109479507 | rs2156739 | A | C | 4 | 0.2255 | 0.6787 | 1.0446 | 1.0358 | 0.0046 | 76.94 |
| 8 | 3078201 | rs2406453 | C | G | 4 | 0.9812 | 0.6788 | 1.002 | 1.0929 | 0.0013 | 80.95 |
| 13 | 104282823 | rs9514322 | C | T | 4 | 0.7478 | 0.6788 | 1.012 | 0.9606 | 0.001 | 81.67 |
| 10 | 122646633 | rs12355611 | A | C | 4 | 0.4672 | 0.6791 | 0.9131 | 0.8621 | 0.0005 | 82.91 |
| 9 | 81261735 | rs11138238 | C | T | 4 | 0.1265 | 0.6794 | 0.8503 | 0.915 | 0.0228 | 68.59 |
| 9 | 81266134 | rs11138240 | C | T | 4 | 0.125 | 0.6797 | 0.8497 | 0.9148 | 0.0223 | 68.76 |
| 9 | 2668427 | rs7847455 | A | T | 4 | 0.7988 | 0.68 | 0.9829 | 0.9297 | 0.0009 | 81.73 |
| 16 | 7437703 | rs9933246 | C | T | 4 | 0.5481 | 0.6811 | 1.0211 | 0.9637 | 0.0013 | 80.92 |
| 9 | 7517298 | rs4269591 | C | T | 4 | 0.1501 | 0.6812 | 0.9504 | 0.9695 | 0.0142 | 71.66 |
| 10 | 122678184 | rs12359177 | A | G | 4 | 0.526 | 0.6812 | 1.0828 | 1.1565 | 0.0007 | 82.32 |
| 9 | 2667787 | rs7046015 | A | G | 4 | 0.8038 | 0.6817 | 0.9834 | 0.93 | 0.0009 | 81.77 |
| 9 | 81214260 | rs11138196 | A | T | 4 | 0.1257 | 0.6817 | 1.174 | 1.0935 | 0.0184 | 70.06 |
| 9 | 81239935 | rs12352718 | C | T | 4 | 0.1318 | 0.6817 | 0.8526 | 0.9157 | 0.0227 | 68.61 |
| 9 | 2668059 | rs6475926 | C | T | 4 | 0.8061 | 0.682 | 1.0167 | 1.0752 | 0.0009 | 81.79 |
| 10 | 122678943 | rs11199659 | A | T | 4 | 0.5151 | 0.682 | 1.0851 | 1.1562 | 0.0007 | 82.36 |
| 2 | 210447598 | rs1558474 | C | T | 4 | 0.008574 | 0.6822 | 0.864 | 0.95 | 0.0105 | 73.29 |
| 8 | 109481042 | rs1955025 | A | C | 4 | 0.2302 | 0.6828 | 1.0441 | 1.0355 | 0.0044 | 77.11 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 8 | 109483397 | rs2023107 | A | C | 4 | 0.2302 | 0.6828 | 1.0441 | 1.0355 | 0.0044 | 77.11 |
| 5 | 73293142 | rs1684851 | A | C | 4 | 0.02088 | 0.6836 | 1.0942 | 1.047 | 0.0002 | 84.65 |
| 7 | 136927210 | rs706562 | C | G | 4 | 0.06624 | 0.6839 | 1.173 | 1.086 | 0.0041 | 77.37 |
| 2 | 172832483 | rs7574225 | A | G | 4 | 0.01005 | 0.6843 | 0.9105 | 0.9587 | 0.0003 | 84.25 |
| 10 | 122645462 | rs11199632 | C | T | 4 | 0.4806 | 0.6847 | 0.9156 | 0.8638 | 0.0005 | 83.07 |
| 16 | 7435187 | rs2346943 | G | T | 4 | 0.5951 | 0.6853 | 1.0188 | 0.9636 | 0.0011 | 81.32 |
| 10 | 122679402 | rs11199660 | A | G | 4 | 0.5263 | 0.6854 | 1.0827 | 1.1546 | 0.0007 | 82.41 |
| 13 | 39454859 | rs276429 | A | G | 4 | 0.8664 | 0.6854 | 1.0059 | 0.9651 | 0.0021 | 79.59 |
| 10 | 122623411 | rs12355108 | C | T | 4 | 0.4829 | 0.6857 | 0.916 | 0.8639 | 0.0005 | 83.18 |
| 16 | 7340883 | rs17842417 | C | T | 4 | 0.01352 | 0.6868 | 1.1507 | 1.0521 | 0.0109 | 73.14 |
| 20 | 3489382 | rs17782078 | C | T | 4 | 0.9613 | 0.6868 | 0.9964 | 1.0783 | 0.002 | 79.74 |
| 4 | 71142292 | rs4460073 | C | T | 4 | 0.04589 | 0.687 | 0.8891 | 0.9422 | 0.002 | 79.78 |
| 10 | 122624977 | rs12355961 | A | G | 4 | 0.4867 | 0.6871 | 1.0909 | 1.1567 | 0.0005 | 83.17 |
| 10 | 122607331 | rs11199603 | A | G | 4 | 0.4855 | 0.6873 | 0.9165 | 0.8642 | 0.0005 | 83.27 |
| 2 | 210450278 | rs11682914 | A | G | 4 | 0.008441 | 0.6876 | 1.1577 | 1.0518 | 0.0102 | 73.48 |
| 8 | 109484593 | rs2023104 | A | G | 4 | 0.2382 | 0.6876 | 1.0434 | 1.0352 | 0.004 | 77.45 |
| 10 | 122622408 | rs11199613 | C | T | 4 | 0.4878 | 0.6877 | 1.0906 | 1.1565 | 0.0005 | 83.19 |
| 10 | 122680429 | rs12357022 | A | G | 4 | 0.5374 | 0.6895 | 0.9256 | 0.8678 | 0.0007 | 82.42 |
| 8 | 109476961 | rs13281088 | C | T | 4 | 0.2358 | 0.6897 | 1.0436 | 1.035 | 0.0039 | 77.59 |
| 2 | 134738884 | rs3791271 | C | T | 4 | 0.04806 | 0.69 | 1.1935 | 1.0861 | 0.0108 | 73.16 |
| 9 | 81242882 | rs1340123 | C | T | 4 | 0.1357 | 0.6906 | 1.1711 | 1.0898 | 0.0215 | 69.01 |
| 20 | 47379153 | rs1847326 | A | C | 4 | 0.1013 | 0.6909 | 1.117 | 1.0599 | 0.0123 | 72.47 |
| 2 | 210442080 | rs7593426 | A | G | 4 | 0.007233 | 0.6913 | 1.1592 | 1.0516 | 0.0086 | 74.32 |
| 10 | 122682094 | rs11199663 | A | G | 4 | 0.5428 | 0.6913 | 1.0793 | 1.1511 | 0.0007 | 82.38 |
| 10 | 122679558 | rs11199661 | A | G | 4 | 0.5418 | 0.6914 | 1.0795 | 1.1513 | 0.0007 | 82.43 |
| 2 | 172832429 | rs7574002 | C | T | 4 | 0.01116 | 0.6917 | 1.0968 | 1.042 | 0.0003 | 84.27 |
| 7 | 6389871 | rs10238136 | A | T | 4 | 0.6636 | 0.692 | 1.0421 | 0.899 | 0.0002 | 85.06 |
| 3 | 178795570 | rs4857716 | C | T | 4 | 0.05855 | 0.6929 | 0.9337 | 0.9609 | 0.0003 | 83.8 |
| 2 | 210423419 | rs10194322 | A | G | 4 | 0.009558 | 0.6932 | 1.1497 | 1.0513 | 0.0071 | 75.18 |
| 3 | 134947186 | rs8177184 | A | G | 4 | 0.1837 | 0.6935 | 0.9389 | 0.9595 | 0.0083 | 74.48 |
| 2 | 210441690 | rs10490026 | A | G | 4 | 0.01174 | 0.6937 | 1.1487 | 1.0492 | 0.0126 | 72.31 |
| 2 | 210444633 | rs12328884 | C | T | 4 | 0.008969 | 0.6937 | 1.1564 | 1.051 | 0.0096 | 73.76 |
| 2 | 134733887 | rs16830280 | A | T | 4 | 0.01903 | 0.694 | 0.8302 | 0.9231 | 0.0025 | 79.02 |
| 10 | 122621095 | rs11199612 | C | T | 4 | 0.5045 | 0.6947 | 0.9199 | 0.8675 | 0.0005 | 83.25 |
| 1 | 95634310 | rs17113478 | C | G | 4 | 0.8624 | 0.6953 | 0.9887 | 0.9361 | 0.0011 | 81.34 |
| 2 | 210447119 | rs17748692 | C | T | 4 | 0.00918 | 0.6955 | 1.1558 | 1.0506 | 0.0097 | 73.7 |
| 2 | 210443405 | rs10490028 | C | T | 4 | 0.008998 | 0.6957 | 0.8654 | 0.9519 | 0.0093 | 73.89 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 8 | 109488103 | rs13275153 | C | T | 4 | 0.2482 | 0.6957 | 1.0425 | 1.0344 | 0.0037 | 77.79 |
| 13 | 89117527 | rs2148775 | C | T | 4 | 0.582 | 0.6964 | 1.0423 | 1.0702 | 0.0042 | 77.28 |
| 10 | 122688268 | rs12355094 | C | T | 4 | 0.55 | 0.6968 | 0.9278 | 0.8717 | 0.0007 | 82.25 |
| 8 | 109459433 | rs2023100 | G | T | 4 | 0.2412 | 0.6969 | 1.0431 | 1.0347 | 0.0031 | 78.31 |
| 2 | 210444857 | rs12329303 | A | G | 4 | 0.009278 | 0.697 | 0.8653 | 0.952 | 0.0096 | 73.76 |
| 2 | 210446076 | rs7581628 | A | G | 4 | 0.009278 | 0.697 | 0.8653 | 0.952 | 0.0096 | 73.76 |
| 2 | 210446334 | rs7581974 | A | G | 4 | 0.009278 | 0.697 | 0.8653 | 0.952 | 0.0096 | 73.76 |
| 1 | 115209396 | rs12741053 | C | T | 4 | 0.8917 | 0.6976 | 1.0071 | 1.0493 | 0.0035 | 77.99 |
| 1 | 214171603 | rs498911 | A | C | 4 | 0.4916 | 0.698 | 0.9675 | 1.0545 | 0.0002 | 85.05 |
| 2 | 210447096 | rs17748674 | C | T | 4 | 0.009361 | 0.6982 | 1.1554 | 1.0502 | 0.0096 | 73.76 |
| 11 | 18884861 | rs6483549 | C | G | 4 | 0.03434 | 0.6983 | 0.8845 | 0.9485 | 0.0054 | 76.35 |
| 3 | 54723274 | rs604132 | A | T | 4 | 0.2026 | 0.6992 | 0.954 | 0.9649 | 0.0018 | 80.1 |
| 7 | 17412231 | rs10259316 | G | T | 4 | 0.802 | 0.6996 | 1.0095 | 0.9605 | 0.0004 | 83.48 |
| 1 | 95798397 | rs12125905 | C | G | 4 | 0.9837 | 0.6998 | 1.0014 | 0.9386 | 0.0044 | 77.14 |
| 4 | 1663729 | rs3958122 | C | T | 4 | 0.002199 | 0.7004 | 0.8923 | 0.9671 | 0.0051 | 76.59 |
| 3 | 18167244 | rs13071948 | A | G | 4 | 0.7056 | 0.7007 | 1.0198 | 0.9527 | 0.0025 | 79.1 |
| 2 | 107970060 | rs333238 | A | G | 4 | 0.1069 | 0.7022 | 0.9298 | 0.9599 | 0.0037 | 77.73 |
| 2 | 107970399 | rs333236 | A | G | 4 | 0.1074 | 0.7022 | 1.0753 | 1.0417 | 0.0038 | 77.69 |
| 1 | 55443484 | rs6671533 | C | G | 4 | 0.02706 | 0.7023 | 1.1044 | 1.0362 | 0.0194 | 69.71 |
| 2 | 210444413 | rs12328869 | A | T | 4 | 0.009084 | 0.7026 | 1.1575 | 1.0497 | 0.0096 | 73.74 |
| 1 | 21829826 | rs9426674 | C | G | 4 | 0.09071 | 0.7029 | 0.9401 | 0.9702 | 0.0108 | 73.19 |
| 10 | 122593274 | rs11199590 | C | T | 4 | 0.4701 | 0.7031 | 1.0939 | 1.152 | 0.0003 | 84.14 |
| 3 | 129060018 | rs7633928 | A | G | 4 | 0.01072 | 0.7032 | 0.8788 | 0.959 | 0.0125 | 72.39 |
| 18 | 6396648 | rs9947555 | C | T | 4 | 0.1237 | 0.7038 | 0.9418 | 0.9682 | 0.0097 | 73.7 |
| 4 | 58861907 | rs13148519 | A | G | 4 | 0.04479 | 0.7048 | 0.9259 | 0.9654 | 0.003 | 78.41 |
| 3 | 134946488 | rs8177181 | A | T | 4 | 0.1947 | 0.7049 | 1.0634 | 1.0407 | 0.008 | 74.64 |
| 8 | 135168960 | rs1457463 | A | G | 4 | 0.02911 | 0.7056 | 0.9267 | 0.9657 | 0.0008 | 81.95 |
| 6 | 26862629 | rs2504586 | C | G | 4 | 0.8989 | 0.7067 | 0.9945 | 1.0402 | 0.0028 | 78.66 |
| 2 | 210441645 | rs10490025 | A | T | 4 | 0.01335 | 0.7069 | 0.8727 | 0.9549 | 0.012 | 72.58 |
| 8 | 135163085 | rs7842645 | A | G | 4 | 0.0835 | 0.7071 | 1.0622 | 1.0311 | 0.005 | 76.62 |
| 3 | 178798779 | rs4241484 | A | C | 4 | 0.05414 | 0.7074 | 1.0717 | 1.0384 | 0.0003 | 83.9 |
| 2 | 210449837 | rs16843893 | C | T | 4 | 0.009934 | 0.7076 | 0.8665 | 0.9537 | 0.0095 | 73.83 |
| 10 | 110503646 | rs12258219 | G | T | 4 | 0.05519 | 0.7077 | 1.0966 | 1.0373 | 0.019 | 69.85 |
| 1 | 21828331 | rs9426770 | C | G | 4 | 0.0893 | 0.7081 | 0.9399 | 0.9705 | 0.01 | 73.54 |
| 4 | 1671115 | rs2247341 | A | G | 4 | 0.002113 | 0.7085 | 1.1202 | 1.033 | 0.0047 | 76.89 |
| 3 | 24666496 | rs4131483 | A | T | 4 | 0.07181 | 0.7088 | 1.0649 | 1.0285 | 0.0124 | 72.45 |
| 1 | 95798313 | rs12125877 | C | G | 4 | 0.9449 | 0.7089 | 1.0049 | 0.9404 | 0.0039 | 77.53 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 1 | 95633790 | rs11586346 | A | C | 4 | 0.9167 | 0.7093 | 0.9932 | 0.9388 | 0.001 | 81.49 |
| 11 | 18884296 | rs2896547 | A | G | 4 | 0.0382 | 0.7094 | 1.1277 | 1.0524 | 0.0051 | 76.56 |
| 4 | 58860984 | rs7690084 | A | G | 4 | 0.04704 | 0.7109 | 0.9266 | 0.9661 | 0.0029 | 78.54 |
| 12 | 128857653 | rs11060565 | C | T | 4 | 0.0955 | 0.7109 | 1.0801 | 1.0479 | 0.0005 | 83.04 |
| 3 | 102219726 | rs13085823 | G | T | 4 | 0.8238 | 0.7112 | 1.0083 | 0.9665 | 0.0024 | 79.17 |
| 1 | 95792027 | rs1355136 | C | T | 4 | 0.9349 | 0.7119 | 1.0056 | 0.9403 | 0.0025 | 79.06 |
| 4 | 58866253 | rs11945898 | C | T | 4 | 0.04723 | 0.7119 | 1.0791 | 1.035 | 0.0029 | 78.55 |
| 2 | 210440931 | rs13414802 | A | G | 4 | 0.01308 | 0.7122 | 0.8728 | 0.9558 | 0.0117 | 72.75 |
| 7 | 52130392 | rs2952763 | C | T | 4 | 0.1532 | 0.713 | 0.9518 | 0.97 | 0.0035 | 77.94 |
| 1 | 21831326 | rs9426771 | G | T | 4 | 0.05169 | 0.7136 | 1.073 | 1.0288 | 0.0133 | 72.03 |
| 12 | 9918211 | rs10219684 | C | T | 4 | 0.587 | 0.7138 | 1.0213 | 0.9634 | 0.001 | 81.44 |
| 11 | 80656128 | rs17141842 | C | T | 4 | 0.6446 | 0.714 | 0.9659 | 0.9216 | 0.0001 | 86.45 |
| 2 | 210443088 | rs12328328 | C | T | 4 | 0.01011 | 0.7143 | 0.8673 | 0.9544 | 0.0083 | 74.45 |
| 11 | 18886008 | rs1384648 | C | T | 4 | 0.03969 | 0.715 | 0.8875 | 0.9509 | 0.0047 | 76.9 |
| 2 | 29141970 | rs13012389 | C | T | 4 | 0.1663 | 0.7153 | 1.0583 | 1.0317 | 0.0172 | 70.49 |
| 2 | 29141985 | rs13031086 | C | T | 4 | 0.1494 | 0.7153 | 0.9431 | 0.9691 | 0.0156 | 71.08 |
| 1 | 206126982 | rs2556 | A | G | 4 | 0.08605 | 0.7155 | 0.8951 | 0.9477 | 0.0065 | 75.53 |
| 8 | 4109411 | rs9693235 | A | G | 4 | 0.6134 | 0.7157 | 1.0369 | 1.0717 | 0.0008 | 82.08 |
| 4 | 58866156 | rs11933359 | C | T | 4 | 0.04843 | 0.7159 | 0.9271 | 0.9666 | 0.0028 | 78.65 |
| 5 | 104120449 | rs12518236 | A | G | 4 | 0.1504 | 0.7165 | 1.0806 | 1.0517 | 0.0011 | 81.4 |
| 4 | 71084769 | rs17148325 | C | T | 3 | 0.2076 | 0.7166 | 1.0696 | 1.0528 | 0.0027 | 83.06 |
| 2 | 210781793 | rs1509571 | C | T | 4 | 0.01043 | 0.7169 | 1.1577 | 1.0491 | 0.0085 | 74.33 |
| 11 | 18898424 | rs2403354 | C | T | 4 | 0.04465 | 0.7169 | 1.1262 | 1.0517 | 0.0054 | 76.33 |
| 2 | 172835915 | rs7588418 | C | T | 4 | 0.0114 | 0.7184 | 1.0975 | 1.0392 | 0.0002 | 84.86 |
| 2 | 210443100 | rs12329111 | A | C | 4 | 0.01036 | 0.7186 | 0.8677 | 0.9551 | 0.0082 | 74.53 |
| 1 | 95798178 | rs12145270 | A | T | 4 | 0.8961 | 0.7189 | 0.991 | 1.0609 | 0.0038 | 77.69 |
| 9 | 2668958 | rs16909038 | C | G | 4 | 0.8409 | 0.7191 | 0.9865 | 0.9377 | 0.0008 | 82.18 |
| 11 | 18888602 | rs1973238 | C | G | 4 | 0.03958 | 0.7191 | 0.887 | 0.9514 | 0.0047 | 76.91 |
| 3 | 178804169 | rs11716881 | A | G | 4 | 0.06011 | 0.7194 | 1.0699 | 1.0369 | 0.0003 | 84.02 |
| 4 | 58862866 | rs2412887 | A | G | 4 | 0.04969 | 0.72 | 1.0782 | 1.0342 | 0.0027 | 78.84 |
| 4 | 183404530 | rs6552548 | A | C | 3 | 0.1483 | 0.7204 | 1.0585 | 1.0393 | 0.0023 | 83.58 |
| 21 | 16553299 | rs1389074 | C | T | 3 | 0.1435 | 0.7206 | 0.9474 | 0.9636 | 0.0013 | 84.87 |
| 4 | 58863520 | rs2140072 | A | G | 4 | 0.05078 | 0.721 | 1.0778 | 1.034 | 0.0028 | 78.74 |
| 1 | 115298685 | rs2008873 | A | T | 4 | 0.9161 | 0.7213 | 1.0055 | 1.046 | 0.0028 | 78.74 |
| 3 | 129059205 | rs6763775 | C | G | 4 | 0.01308 | 0.7216 | 0.8812 | 0.9611 | 0.0115 | 72.83 |
| 13 | 23529796 | rs9511023 | A | G | 4 | 0.16 | 0.7217 | 1.0585 | 1.0301 | 0.0195 | 69.69 |
| 1 | 21826881 | rs4654974 | C | T | 4 | 0.1025 | 0.7226 | 0.9422 | 0.9717 | 0.0086 | 74.32 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 1 | 98737106 | rs591545 | C | T | 4 | 0.2943 | 0.7232 | 0.9294 | 0.9421 | 0.0036 | 77.81 |
| 3 | 178805561 | rs6766914 | C | T | 4 | 0.05818 | 0.7232 | 1.0693 | 1.036 | 0.0003 | 84.1 |
| 8 | 4095458 | rs6998882 | A | C | 4 | 0.5968 | 0.7241 | 0.9611 | 0.922 | 0 | 86.91 |
| 2 | 197755262 | rs2697234 | C | T | 4 | 0.2176 | 0.7248 | 0.8861 | 0.9223 | 0.0033 | 78.19 |
| 2 | 197754509 | rs2697235 | A | G | 4 | 0.2172 | 0.725 | 1.1287 | 1.0844 | 0.0032 | 78.26 |
| 4 | 1689418 | rs743569 | G | T | 4 | 0.003078 | 0.7256 | 1.1165 | 1.0312 | 0.0046 | 76.98 |
| 2 | 197753891 | rs2697236 | C | G | 4 | 0.2188 | 0.7258 | 0.8864 | 0.9225 | 0.0032 | 78.22 |
| 2 | 210442197 | rs7566741 | A | G | 4 | 0.01027 | 0.7258 | 0.8676 | 0.956 | 0.0076 | 74.86 |
| 2 | 38221238 | rs2113389 | C | T | 4 | 0.03829 | 0.7275 | 0.9025 | 0.9574 | 0.0021 | 79.54 |
| 2 | 107974450 | rs2450280 | C | T | 4 | 0.1188 | 0.7281 | 1.0739 | 1.0384 | 0.0036 | 77.82 |
| 2 | 210450498 | rs2109970 | A | G | 4 | 0.01143 | 0.7281 | 0.8688 | 0.9567 | 0.0087 | 74.25 |
| 12 | 128850548 | rs1376797 | C | T | 4 | 0.1123 | 0.7285 | 1.0762 | 1.044 | 0.0007 | 82.35 |
| 4 | 52565714 | rs2319750 | C | T | 4 | 0.7257 | 0.7288 | 1.0175 | 0.9543 | 0.0007 | 82.34 |
| 8 | 4108928 | rs17069778 | A | T | 4 | 0.6357 | 0.7305 | 0.967 | 0.9383 | 0.001 | 81.44 |
| 2 | 210413138 | rs10178425 | G | T | 4 | 0.00656 | 0.7317 | 0.8591 | 0.9576 | 0.01 | 73.58 |
| 14 | 94392551 | rs10133971 | T | C | 3 | 0.1257 | 0.7317 | 1.1642 | 1.1206 | 0.0012 | 85.19 |
| 4 | 58871935 | rs1402960 | A | G | 4 | 0.05793 | 0.7321 | 0.9298 | 0.9685 | 0.0029 | 78.62 |
| 5 | 51859304 | rs16879856 | C | T | 4 | 0.7385 | 0.7322 | 0.9644 | 0.9159 | 0.0033 | 78.16 |
| 2 | 210442707 | rs10490027 | A | T | 4 | 0.01086 | 0.7326 | 1.1521 | 1.045 | 0.0076 | 74.87 |
| 13 | 45873366 | rs7333428 | C | T | 4 | 0.864 | 0.7328 | 0.9905 | 1.0479 | 0.003 | 78.47 |
| 3 | 45188375 | rs9850250 | A | T | 4 | 0.2075 | 0.7331 | 0.9561 | 0.9715 | 0.0039 | 77.61 |
| 1 | 154341469 | rs6661281 | C | T | 4 | 0.1631 | 0.7335 | 1.0521 | 1.0292 | 0.0058 | 76.01 |
| 2 | 210412445 | rs9288414 | A | C | 4 | 0.006078 | 0.7335 | 1.1674 | 1.0445 | 0.0092 | 73.96 |
| 8 | 4107562 | rs1394485 | C | T | 4 | 0.613 | 0.7347 | 0.9646 | 0.9384 | 0.0009 | 81.76 |
| 12 | 2205194 | rs7296039 | C | G | 4 | 0.4791 | 0.7349 | 1.076 | 0.9121 | 0.0017 | 80.27 |
| 2 | 107973532 | rs333235 | C | T | 4 | 0.1112 | 0.7358 | 0.9303 | 0.9639 | 0.0032 | 78.28 |
| 8 | 4095738 | rs971555 | A | G | 4 | 0.6415 | 0.736 | 0.9657 | 0.9249 | 0 | 87.1 |
| 4 | 58909359 | rs11133559 | A | C | 4 | 0.08996 | 0.7362 | 0.9359 | 0.9691 | 0.0037 | 77.73 |
| 12 | 93474128 | rs7955502 | A | C | 4 | 0.1773 | 0.7372 | 1.0776 | 1.042 | 0.0087 | 74.24 |
| 7 | 52985234 | rs4947759 | A | G | 4 | 0.5656 | 0.7386 | 0.9716 | 1.046 | 0.0008 | 81.96 |
| 4 | 58878691 | rs9312697 | A | G | 4 | 0.08658 | 0.7395 | 1.068 | 1.03 | 0.0054 | 76.33 |
| 4 | 58908862 | rs12511263 | A | G | 4 | 0.09352 | 0.7404 | 0.9366 | 0.9696 | 0.0036 | 77.82 |
| 4 | 58908498 | rs4865328 | C | T | 4 | 0.09455 | 0.7415 | 1.0674 | 1.0312 | 0.0037 | 77.78 |
| 2 | 210842791 | rs4558528 | A | T | 4 | 0.02039 | 0.7428 | 1.1434 | 1.0444 | 0.009 | 74.09 |
| 4 | 58908183 | rs10517438 | A | T | 4 | 0.09756 | 0.7431 | 1.0668 | 1.0311 | 0.0035 | 77.96 |
| 2 | 210437956 | rs7598071 | C | G | 4 | 0.0126 | 0.7435 | 1.1472 | 1.0427 | 0.0078 | 74.73 |
| 8 | 4089879 | rs7838274 | A | T | 4 | 0.653 | 0.7436 | 0.9618 | 0.9192 | 0.0001 | 86.06 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 3 | 58047511 | rs13315037 | G | T | 4 | 0.05256 | 0.7441 | 0.876 | 0.9503 | 0.0051 | 76.56 |
| 4 | 58906382 | rs2090901 | C | T | 4 | 0.0984 | 0.7446 | 1.0666 | 1.0304 | 0.0042 | 77.25 |
| 2 | 71088630 | rs10188275 | C | T | 4 | 0.5851 | 0.7449 | 0.9588 | 1.087 | 0 | 89.37 |
| 4 | 58903429 | rs11735710 | A | G | 4 | 0.09578 | 0.7451 | 0.9376 | 0.9711 | 0.0049 | 76.71 |
| 2 | 210844923 | rs1396831 | A | T | 4 | 0.02193 | 0.7454 | 1.1402 | 1.0438 | 0.0085 | 74.35 |
| 4 | 58904343 | rs17218140 | G | T | 4 | 0.09584 | 0.7454 | 1.0666 | 1.0297 | 0.0049 | 76.71 |
| 2 | 197749763 | rs2697239 | C | T | 4 | 0.2502 | 0.7455 | 0.8936 | 0.9242 | 0.0014 | 80.63 |
| 1 | 223940235 | rs2615060 | A | C | 4 | 0.08937 | 0.7459 | 1.0729 | 1.0305 | 0.0099 | 73.59 |
| 12 | 2203913 | rs11062164 | A | C | 4 | 0.4858 | 0.746 | 1.075 | 0.9152 | 0.0015 | 80.48 |
| 1 | 95774113 | rs1509178 | C | T | 4 | 0.9416 | 0.7462 | 0.9952 | 1.054 | 0.0021 | 79.62 |
| 4 | 1690348 | rs2854917 | C | T | 4 | 0.003885 | 0.7462 | 1.1135 | 1.0288 | 0.0044 | 77.09 |
| 4 | 58906337 | rs2090900 | A | C | 4 | 0.1003 | 0.7463 | 0.9379 | 0.9708 | 0.0044 | 77.16 |
| 12 | 9923537 | rs935537 | C | G | 4 | 0.3566 | 0.7471 | 0.9656 | 1.0324 | 0.0012 | 81.15 |
| 4 | 58880555 | rs11133555 | A | G | 4 | 0.09068 | 0.7472 | 1.0671 | 1.0292 | 0.0052 | 76.48 |
| 4 | 58905977 | rs12648092 | A | G | 4 | 0.09064 | 0.7474 | 0.9366 | 0.9709 | 0.0041 | 77.4 |
| 1 | 98737348 | rs3867319 | A | G | 4 | 0.2798 | 0.7475 | 0.9295 | 0.9513 | 0.0069 | 75.27 |
| 2 | 210423552 | rs10194333 | A | C | 4 | 0.01368 | 0.7479 | 1.1443 | 1.0427 | 0.006 | 75.9 |
| 16 | 7338996 | rs9924010 | A | G | 4 | 0.02998 | 0.7482 | 1.1293 | 1.0418 | 0.008 | 74.66 |
| 4 | 58903846 | rs11727794 | A | C | 4 | 0.09784 | 0.7483 | 0.938 | 0.9714 | 0.0048 | 76.78 |
| 4 | 58905626 | rs12647365 | A | G | 4 | 0.09553 | 0.7487 | 0.9375 | 0.9713 | 0.0045 | 77.01 |
| 4 | 58905886 | rs12648067 | A | G | 4 | 0.09327 | 0.749 | 0.9371 | 0.9712 | 0.0043 | 77.23 |
| 4 | 58905741 | rs12641535 | C | T | 4 | 0.09491 | 0.7495 | 1.0668 | 1.0295 | 0.0044 | 77.11 |
| 12 | 2204109 | rs11062165 | C | T | 4 | 0.4834 | 0.7501 | 1.0752 | 0.917 | 0.0016 | 80.35 |
| 4 | 3505974 | rs2073503 | C | G | 4 | 0.07667 | 0.7503 | 1.0697 | 1.0265 | 0.0119 | 72.64 |
| 11 | 103266219 | rs11601578 | C | T | 4 | 0.2944 | 0.7507 | 1.0409 | 1.0336 | 0.0005 | 82.91 |
| 1 | 166081092 | rs204262 | A | G | 4 | 0.08687 | 0.7519 | 1.074 | 1.0332 | 0.0024 | 79.23 |
| 1 | 152423714 | rs11265251 | C | T | 4 | 0.5438 | 0.7525 | 1.0223 | 0.9681 | 0.0003 | 84.27 |
| 8 | 4112508 | rs17069790 | A | G | 4 | 0.6707 | 0.7529 | 1.0315 | 1.0615 | 0.0011 | 81.33 |
| 2 | 172559748 | rs6752812 | A | C | 4 | 0.9034 | 0.7539 | 0.9955 | 1.0357 | 0.0001 | 86.15 |
| 2 | 134739376 | rs6735741 | A | G | 4 | 0.06675 | 0.7541 | 0.8496 | 0.9362 | 0.0085 | 74.33 |
| 2 | 210430270 | rs13010864 | A | G | 4 | 0.01084 | 0.7542 | 0.8678 | 0.9595 | 0.0058 | 76.01 |
| 4 | 1691146 | rs2854916 | A | G | 4 | 0.004227 | 0.7543 | 1.1125 | 1.0279 | 0.0045 | 77.07 |
| 4 | 151134607 | rs6823080 | A | C | 4 | 0.3259 | 0.7544 | 1.0467 | 0.9633 | 0.0018 | 80.07 |
| 7 | 107410778 | rs2701039 | A | G | 4 | 0.05956 | 0.7544 | 1.0691 | 1.0243 | 0.0132 | 72.08 |
| 9 | 91833463 | rs497510 | G | T | 4 | 0.03688 | 0.7546 | 1.0748 | 1.0247 | 0.0075 | 74.94 |
| 3 | 178817943 | rs9825151 | C | T | 4 | 0.0522 | 0.7556 | 1.0709 | 1.0328 | 0.0001 | 85.49 |
| 1 | 154345707 | rs915180 | C | T | 4 | 0.2069 | 0.756 | 0.9544 | 0.9729 | 0.0038 | 77.65 |

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|----|-----------|-------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 2 | 134741186 | rs3791276 | A | C | 4 | 0.06007 | 0.757 | 0.8456 | 0.9382 | 0.0104 | 73.34 |
| 3 | 24671288 | rs6793060 | A | G | 4 | 0.09516 | 0.7579 | 1.0595 | 1.0241 | 0.0086 | 74.31 |
| 15 | 51234395 | rs7181898 | A | G | 4 | 0.3311 | 0.7582 | 1.0405 | 0.9627 | 0.0001 | 86.09 |
| 19 | 17338318 | rs7248564 | C | T | 4 | 0.1615 | 0.7587 | 1.0521 | 1.029 | 0.0027 | 78.84 |
| 12 | 2204705 | rs7312354 | C | T | 4 | 0.4478 | 0.7593 | 1.0817 | 0.9209 | 0.0019 | 79.86 |
| 6 | 153438568 | rs9397585 | C | T | 4 | 0.2686 | 0.7597 | 1.0418 | 1.0297 | 0.0011 | 81.24 |
| 1 | 75093605 | rs12120668 | C | G | 4 | 0.7248 | 0.76 | 0.9872 | 1.0277 | 0.003 | 78.42 |
| 2 | 71089580 | rs10179209 | A | G | 4 | 0.5359 | 0.76 | 0.9522 | 1.0824 | 0 | 89.15 |
| 2 | 172475093 | rs6727017 | A | T | 4 | 0.9501 | 0.761 | 1.0024 | 1.0349 | 0.0001 | 85.71 |
| 4 | 58908044 | rs111133558 | A | G | 4 | 0.1068 | 0.7612 | 1.065 | 1.0285 | 0.0039 | 77.54 |
| 2 | 210433939 | rs9631001 | C | T | 4 | 0.01243 | 0.7613 | 0.8714 | 0.9613 | 0.0066 | 75.49 |
| 2 | 210437244 | rs9973787 | A | G | 4 | 0.01328 | 0.7614 | 0.8725 | 0.9616 | 0.0071 | 75.17 |
| 2 | 210844857 | rs1396830 | A | G | 4 | 0.02344 | 0.7619 | 0.8773 | 0.9605 | 0.0084 | 74.43 |
| 2 | 210478772 | rs11688226 | C | T | 4 | 0.01299 | 0.763 | 0.8709 | 0.9619 | 0.0079 | 74.71 |
| 7 | 107409524 | rs2237702 | A | G | 4 | 0.09304 | 0.764 | 0.9429 | 0.9766 | 0.0081 | 74.6 |
| 2 | 210480528 | rs11694132 | A | G | 4 | 0.01305 | 0.7645 | 0.871 | 0.9621 | 0.0078 | 74.74 |
| 7 | 107409386 | rs2237701 | A | G | 4 | 0.09373 | 0.7645 | 1.0605 | 1.0239 | 0.0081 | 74.56 |
| 1 | 95781532 | rs678378 | A | G | 4 | 0.9048 | 0.7653 | 0.992 | 1.0507 | 0.0019 | 79.86 |
| 4 | 1700924 | rs798761 | A | G | 4 | 0.003869 | 0.7658 | 1.1146 | 1.027 | 0.0039 | 77.58 |
| 5 | 159147091 | rs2116732 | A | G | 4 | 0.8475 | 0.7669 | 0.9718 | 1.108 | 0.0029 | 78.53 |
| 2 | 210454100 | rs17748818 | C | T | 4 | 0.01409 | 0.7679 | 0.8724 | 0.9625 | 0.0073 | 75.07 |
| 12 | 9937319 | rs576601 | A | C | 4 | 0.4146 | 0.7681 | 0.9691 | 1.03 | 0.0011 | 81.26 |
| 1 | 95771471 | rs12141480 | C | G | 4 | 0.8885 | 0.7682 | 0.9908 | 1.0497 | 0.0018 | 80.07 |
| 11 | 109527367 | rs12362273 | A | C | 4 | 0.5868 | 0.769 | 1.0226 | 0.9662 | 0.0002 | 84.82 |
| 7 | 136933752 | rs706567 | C | T | 4 | 0.155 | 0.7691 | 1.1227 | 1.0633 | 0.0015 | 80.6 |
| 2 | 71088542 | rs10196871 | A | G | 4 | 0.4477 | 0.7692 | 1.0614 | 0.9273 | 0 | 89.1 |
| 12 | 2206430 | rs2239031 | G | T | 4 | 0.4368 | 0.7696 | 0.9231 | 1.0812 | 0.0021 | 79.63 |
| 3 | 54693761 | rs515920 | C | T | 4 | 0.3207 | 0.7699 | 0.9656 | 1.0279 | 0.0007 | 82.33 |
| 9 | 86066135 | rs4877830 | G | T | 4 | 0.05632 | 0.7704 | 1.1243 | 1.0538 | 0.0002 | 84.97 |
| 2 | 210481545 | rs6739769 | C | T | 4 | 0.0135 | 0.7708 | 0.8715 | 0.963 | 0.0077 | 74.84 |
| 3 | 24627817 | rs17014951 | A | G | 4 | 0.187 | 0.7712 | 1.0552 | 1.0271 | 0.0064 | 75.64 |
| 4 | 58882568 | rs1522096 | A | G | 4 | 0.1086 | 0.7716 | 0.9403 | 0.9742 | 0.0046 | 76.92 |
| 10 | 61813354 | rs7895653 | C | T | 4 | 0.03916 | 0.7716 | 0.9132 | 1.0349 | 0.0011 | 81.24 |
| 4 | 1707300 | rs11248073 | C | T | 4 | 0.00475 | 0.7718 | 0.8965 | 0.9734 | 0.0033 | 78.16 |
| 3 | 54720595 | rs652424 | C | T | 4 | 0.2593 | 0.7756 | 1.0418 | 1.0258 | 0.0023 | 79.33 |
| 1 | 95769656 | rs12136757 | C | T | 4 | 0.8492 | 0.7757 | 0.9876 | 1.0478 | 0.0017 | 80.15 |
| 18 | 6392126 | rs9965853 | C | T | 4 | 0.08456 | 0.7757 | 1.0636 | 1.023 | 0.0078 | 74.76 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 3 | 54722284 | rs589281 | C | T | 4 | 0.2623 | 0.7758 | 1.0416 | 1.0258 | 0.0022 | 79.46 |
| 6 | 68836202 | rs12664094 | C | T | 3 | 0.1258 | 0.7761 | 1.2687 | 1.1131 | 0.0058 | 80.6 |
| 8 | 134282867 | rs2977527 | A | G | 4 | 0.3117 | 0.7765 | 0.9619 | 0.9738 | 0.0029 | 78.55 |
| 4 | 1712577 | rs1530588 | A | G | 4 | 0.00587 | 0.7772 | 1.1143 | 1.027 | 0.0032 | 78.25 |
| 2 | 210438805 | rs9973848 | A | G | 4 | 0.01604 | 0.7777 | 0.8759 | 0.9641 | 0.0067 | 75.43 |
| 2 | 134742338 | rs3791278 | A | G | 4 | 0.1038 | 0.7794 | 1.1638 | 1.0625 | 0.0091 | 74.01 |
| 2 | 210437762 | rs7595063 | A | C | 4 | 0.01621 | 0.7798 | 1.1415 | 1.037 | 0.0066 | 75.52 |
| 12 | 115328821 | rs17581242 | G | T | 4 | 0.1252 | 0.7801 | 1.0787 | 1.0361 | 0.0015 | 80.59 |
| 1 | 95757654 | rs881713 | A | G | 4 | 0.8826 | 0.7803 | 0.9904 | 1.0469 | 0.0015 | 80.49 |
| 2 | 210439257 | rs9973317 | C | T | 4 | 0.01635 | 0.7805 | 0.8762 | 0.9645 | 0.0066 | 75.49 |
| 20 | 39687101 | rs6124365 | A | C | 3 | 0.3244 | 0.7805 | 0.8295 | 0.8495 | 0.0023 | 83.56 |
| 15 | 51189302 | rs17545046 | A | G | 4 | 0.02282 | 0.7814 | 1.1171 | 1.0357 | 0.0011 | 81.4 |
| 11 | 109524916 | rs10891068 | A | G | 4 | 0.5284 | 0.7832 | 0.9743 | 1.0333 | 0.0001 | 85.23 |
| 18 | 6394347 | rs12961587 | A | G | 4 | 0.0484 | 0.7843 | 1.0732 | 1.023 | 0.005 | 76.66 |
| 1 | 154344873 | rs915179 | A | G | 4 | 0.2118 | 0.7844 | 0.9559 | 0.9765 | 0.0038 | 77.69 |
| 8 | 105323016 | rs2511586 | A | G | 4 | 0.2009 | 0.7852 | 0.9518 | 0.9766 | 0.0073 | 75.04 |
| 6 | 104916776 | rs156126 | C | T | 4 | 0.9608 | 0.7859 | 0.9978 | 0.969 | 0.001 | 81.45 |
| 3 | 24682368 | rs7644196 | C | G | 4 | 0.1319 | 0.7881 | 1.0545 | 1.0217 | 0.0071 | 75.19 |
| 2 | 210425175 | rs13013030 | C | G | 4 | 0.01613 | 0.7888 | 0.8763 | 0.9652 | 0.005 | 76.61 |
| 6 | 33106784 | rs9277029 | C | T | 4 | 0.1818 | 0.7889 | 1.0548 | 1.0237 | 0.0114 | 72.88 |
| 3 | 24656887 | rs9817530 | A | G | 4 | 0.0693 | 0.7902 | 0.9386 | 0.979 | 0.0064 | 75.59 |
| 3 | 24683878 | rs6767967 | A | G | 4 | 0.1439 | 0.7917 | 1.0524 | 1.0213 | 0.0064 | 75.6 |
| 11 | 109525001 | rs10891069 | C | T | 4 | 0.4984 | 0.7928 | 1.0279 | 0.9693 | 0.0001 | 85.49 |
| 20 | 5210168 | rs4580454 | C | G | 4 | 0.009679 | 0.793 | 0.9136 | 0.977 | 0.0018 | 80.1 |
| 6 | 153444523 | rs9478386 | A | G | 4 | 0.1621 | 0.7936 | 1.0507 | 1.0207 | 0.0089 | 74.11 |
| 15 | 51190404 | rs11858823 | A | G | 4 | 0.0138 | 0.7938 | 1.1141 | 1.0315 | 0.0007 | 82.35 |
| 2 | 210427142 | rs2159747 | C | T | 4 | 0.01736 | 0.7949 | 1.1402 | 1.035 | 0.0053 | 76.42 |
| 6 | 29937545 | rs2517830 | G | T | 2 | 0.007143 | 0.7952 | 1.3525 | 1.1004 | 0.0137 | 83.54 |
| 18 | 6392671 | rs12969887 | A | C | 4 | 0.07057 | 0.7952 | 1.0662 | 1.0214 | 0.0056 | 76.2 |
| 12 | 2212678 | rs7135319 | A | G | 4 | 0.4608 | 0.7953 | 0.9252 | 1.0733 | 0.0017 | 80.19 |
| 6 | 153444391 | rs9479502 | C | T | 4 | 0.1628 | 0.7954 | 1.0506 | 1.0205 | 0.0089 | 74.11 |
| 20 | 39646291 | rs6129876 | A | G | 3 | 0.3787 | 0.796 | 1.1757 | 1.1628 | 0.0019 | 84.02 |
| 2 | 210787411 | rs16844213 | C | T | 4 | 0.01841 | 0.7961 | 1.1444 | 1.0358 | 0.0062 | 75.79 |
| 20 | 39634949 | rs6093497 | A | G | 3 | 0.375 | 0.7966 | 0.8496 | 0.8603 | 0.0019 | 84.09 |
| 2 | 111309077 | rs13417566 | A | C | 4 | 0.1299 | 0.7968 | 0.9449 | 1.0255 | 0.001 | 81.58 |
| 3 | 24666213 | rs4452272 | C | T | 4 | 0.08965 | 0.797 | 0.942 | 0.9793 | 0.0055 | 76.29 |
| 6 | 153444170 | rs10872698 | A | G | 4 | 0.1662 | 0.7973 | 0.9522 | 0.9802 | 0.0092 | 73.95 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 8 | 134283373 | rs4382455 | A | C | 4 | 0.3472 | 0.7974 | 0.9645 | 0.9758 | 0.0022 | 79.44 |
| 12 | 97115342 | rs7980332 | A | C | 4 | 0.2631 | 0.7974 | 1.0627 | 0.9647 | 0.0009 | 81.86 |
| 6 | 104920459 | rs271880 | A | G | 4 | 0.9963 | 0.7978 | 0.9998 | 1.0303 | 0.001 | 81.6 |
| 4 | 8631852 | rs2270269 | C | T | 4 | 0.02629 | 0.7987 | 1.0824 | 1.0196 | 0.0131 | 72.13 |
| 8 | 4089356 | rs1504769 | C | T | 4 | 0.7563 | 0.7987 | 0.9731 | 0.9345 | 0.0001 | 86.55 |
| 20 | 55492405 | rs6099650 | C | T | 4 | 0.1498 | 0.7991 | 0.951 | 0.9792 | 0.0041 | 77.35 |
| 1 | 95758927 | rs11165434 | G | T | 4 | 0.8253 | 0.7996 | 1.0146 | 0.9588 | 0.0014 | 80.64 |
| 2 | 210788369 | rs13415601 | A | T | 4 | 0.01844 | 0.8003 | 1.145 | 1.0351 | 0.0062 | 75.78 |
| 3 | 117029070 | rs2918217 | C | T | 4 | 0.02676 | 0.8009 | 0.8934 | 0.9717 | 0.01 | 73.56 |
| 2 | 210429691 | rs7579121 | C | T | 4 | 0.01819 | 0.8017 | 1.1398 | 1.0338 | 0.0054 | 76.29 |
| 9 | 86111098 | rs10868141 | C | T | 4 | 0.1418 | 0.8018 | 0.9132 | 0.9573 | 0.0003 | 84.16 |
| 1 | 95765051 | rs12135050 | A | G | 4 | 0.7954 | 0.8025 | 0.9831 | 1.0425 | 0.0015 | 80.57 |
| 4 | 189573141 | rs178329 | A | G | 4 | 0.2595 | 0.8028 | 1.0516 | 1.0255 | 0.0085 | 74.35 |
| 2 | 210816047 | rs263666 | A | G | 4 | 0.01775 | 0.8039 | 0.8685 | 0.9662 | 0.0074 | 74.99 |
| 3 | 24661552 | rs9843745 | A | G | 4 | 0.09123 | 0.8041 | 0.9423 | 0.9803 | 0.0064 | 75.6 |
| 4 | 8631775 | rs2270270 | C | G | 4 | 0.02718 | 0.8054 | 1.0819 | 1.0189 | 0.0128 | 72.24 |
| 3 | 60013318 | rs212041 | G | T | 4 | 0.6456 | 0.8055 | 1.0281 | 0.9617 | 0.0008 | 82.19 |
| 2 | 210781582 | rs1509572 | A | T | 4 | 0.01886 | 0.806 | 1.1445 | 1.0341 | 0.0063 | 75.72 |
| 6 | 104917442 | rs13219556 | C | T | 4 | 0.9795 | 0.806 | 1.0011 | 0.9721 | 0.0011 | 81.41 |
| 3 | 60013621 | rs212039 | C | T | 4 | 0.6471 | 0.8064 | 1.0281 | 0.9617 | 0.0008 | 82.17 |
| 2 | 210775646 | rs263680 | A | G | 4 | 0.017 | 0.8072 | 1.1478 | 1.0338 | 0.0067 | 75.44 |
| 20 | 39586586 | rs16985881 | A | G | 3 | 0.3996 | 0.8072 | 0.8566 | 0.8663 | 0.0017 | 84.33 |
| 20 | 39585961 | rs16985879 | C | T | 3 | 0.4021 | 0.808 | 1.1664 | 1.1535 | 0.0017 | 84.31 |
| 20 | 39591123 | rs6102451 | A | G | 3 | 0.4021 | 0.808 | 1.1664 | 1.1535 | 0.0017 | 84.31 |
| 2 | 210771597 | rs263681 | C | G | 4 | 0.01738 | 0.8083 | 1.1466 | 1.0336 | 0.0066 | 75.52 |
| 6 | 33114200 | rs9277053 | A | G | 4 | 0.199 | 0.8083 | 0.9499 | 0.9787 | 0.0095 | 73.83 |
| 2 | 107922950 | rs6734993 | C | T | 4 | 0.1748 | 0.8084 | 0.9406 | 0.9745 | 0.0039 | 77.53 |
| 1 | 202838673 | rs10900601 | A | G | 4 | 0.09013 | 0.8087 | 1.068 | 1.0197 | 0.0186 | 69.97 |
| 2 | 210427017 | rs2191909 | C | G | 4 | 0.01826 | 0.8087 | 0.878 | 0.9681 | 0.0046 | 76.95 |
| 2 | 210777256 | rs1509568 | C | T | 4 | 0.0191 | 0.8089 | 0.8745 | 0.9676 | 0.006 | 75.9 |
| 6 | 33106216 | rs9277027 | A | G | 4 | 0.1966 | 0.809 | 1.053 | 1.0216 | 0.01 | 73.55 |
| 8 | 134284294 | rs2977530 | A | G | 4 | 0.3974 | 0.809 | 0.9682 | 0.977 | 0.0018 | 80.01 |
| 10 | 124083263 | rs10887132 | C | T | 4 | 0.06599 | 0.809 | 0.9236 | 0.9727 | 0.0007 | 82.27 |
| 3 | 11452387 | rs7623889 | C | T | 4 | 0.153 | 0.8093 | 1.127 | 1.0427 | 0.0134 | 71.98 |
| 11 | 109531136 | rs584008 | C | T | 4 | 0.595 | 0.8093 | 1.0222 | 0.9721 | 0.0002 | 84.54 |
| 1 | 55471611 | rs10788998 | A | G | 4 | 0.1337 | 0.8094 | 0.9409 | 0.9799 | 0.0196 | 69.65 |
| 1 | 202873597 | rs4951084 | C | G | 4 | 0.02202 | 0.8103 | 1.1024 | 1.0234 | 0.0069 | 75.27 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 21 | 19396021 | rs8129059 | C | T | 3 | 0.3133 | 0.8104 | 0.9595 | 1.0324 | 0.0002 | 88.45 |
| 2 | 111314462 | rs1533295 | A | G | 4 | 0.07786 | 0.8113 | 0.936 | 0.9804 | 0.0099 | 73.62 |
| 3 | 24678903 | rs11928551 | G | T | 4 | 0.108 | 0.8115 | 1.0578 | 1.0196 | 0.0053 | 76.43 |
| 2 | 111308878 | rs2175824 | G | T | 4 | 0.1152 | 0.8117 | 1.0607 | 0.977 | 0.001 | 81.51 |
| 4 | 189571191 | rs12504780 | C | T | 4 | 0.3018 | 0.8121 | 0.9555 | 0.9758 | 0.006 | 75.9 |
| 2 | 210425771 | rs7584039 | C | T | 4 | 0.01867 | 0.8124 | 1.1385 | 1.0323 | 0.0045 | 77.02 |
| 10 | 124083189 | rs10887131 | C | G | 4 | 0.06732 | 0.8126 | 0.924 | 0.9732 | 0.0007 | 82.35 |
| 6 | 104918438 | rs156123 | A | G | 4 | 0.9556 | 0.8128 | 1.0024 | 0.9731 | 0.0011 | 81.31 |
| 3 | 178817999 | rs9880740 | A | G | 4 | 0.06407 | 0.8131 | 1.0674 | 1.0247 | 0.0001 | 85.37 |
| 1 | 152525899 | rs1760802 | C | G | 4 | 0.4319 | 0.8135 | 1.0284 | 0.9789 | 0.0017 | 80.13 |
| 1 | 152512136 | rs1194593 | A | G | 4 | 0.4361 | 0.8143 | 1.0281 | 0.9791 | 0.0018 | 79.96 |
| 12 | 2196442 | rs10848641 | C | T | 4 | 0.3548 | 0.8148 | 1.1005 | 0.9399 | 0.0024 | 79.19 |
| 2 | 210762844 | rs1155845 | C | T | 4 | 0.01715 | 0.8156 | 1.1476 | 1.0323 | 0.0068 | 75.39 |
| 12 | 2212897 | rs7305301 | C | G | 4 | 0.5435 | 0.8159 | 0.94 | 1.064 | 0.0016 | 80.28 |
| 12 | 2201258 | rs12228890 | A | C | 4 | 0.3652 | 0.8164 | 1.0979 | 0.9406 | 0.0025 | 79.1 |
| 1 | 152509739 | rs1044013 | C | T | 4 | 0.4211 | 0.8168 | 1.0288 | 0.9795 | 0.0018 | 80.03 |
| 2 | 210826582 | rs6716836 | A | G | 4 | 0.009598 | 0.8181 | 1.1846 | 1.0346 | 0.0119 | 72.65 |
| 6 | 154734212 | rs9397710 | A | C | 4 | 0.2312 | 0.8182 | 0.9089 | 0.9575 | 0.0044 | 77.15 |
| 7 | 5295742 | rs6959643 | A | T | 4 | 0.1594 | 0.8182 | 1.0519 | 0.9796 | 0.0022 | 79.48 |
| 7 | 26507861 | rs7811868 | A | G | 4 | 0.1835 | 0.8186 | 1.0498 | 0.9799 | 0.0032 | 78.27 |
| 12 | 2196430 | rs10848640 | C | G | 4 | 0.3484 | 0.8187 | 0.9075 | 1.0623 | 0.0025 | 79.02 |
| 3 | 113068623 | rs17424938 | A | G | 4 | 0.6522 | 0.819 | 1.0228 | 0.9727 | 0.0028 | 78.7 |
| 3 | 24690109 | rs1984874 | C | T | 4 | 0.05767 | 0.8194 | 1.0685 | 1.0206 | 0.0015 | 80.61 |
| 11 | 109524141 | rs653992 | C | T | 4 | 0.5113 | 0.8198 | 1.0265 | 0.9747 | 0.0003 | 84.31 |
| 2 | 111312209 | rs12463526 | A | G | 4 | 0.1028 | 0.8205 | 1.0621 | 0.9789 | 0.0016 | 80.32 |
| 14 | 94394040 | rs11160216 | A | G | 3 | 0.2561 | 0.8205 | 1.1185 | 1.0776 | 0.0009 | 85.75 |
| 12 | 2196239 | rs11062158 | C | T | 4 | 0.342 | 0.8213 | 1.1033 | 0.9422 | 0.0026 | 78.99 |
| 2 | 29141613 | rs12620307 | A | G | 4 | 0.2099 | 0.8215 | 0.95 | 0.9804 | 0.0137 | 71.88 |
| 2 | 29141728 | rs12714260 | C | G | 4 | 0.2076 | 0.8217 | 1.0529 | 1.0199 | 0.0139 | 71.8 |
| 3 | 24686017 | rs6770162 | A | G | 4 | 0.15 | 0.8218 | 0.9506 | 0.9815 | 0.0045 | 77.03 |
| 2 | 29141212 | rs10182566 | C | T | 4 | 0.1703 | 0.822 | 0.945 | 0.98 | 0.0118 | 72.69 |
| 3 | 24683078 | rs17787397 | C | T | 4 | 0.1396 | 0.8225 | 1.0535 | 1.0183 | 0.0063 | 75.66 |
| 6 | 154734269 | rs9371793 | C | T | 4 | 0.2423 | 0.8251 | 1.0978 | 1.0427 | 0.0041 | 77.35 |
| 6 | 154739604 | rs7744573 | C | T | 4 | 0.2373 | 0.8257 | 0.9115 | 0.9601 | 0.0046 | 76.93 |
| 11 | 109524562 | rs694974 | C | T | 4 | 0.4755 | 0.826 | 1.0289 | 0.9755 | 0.0002 | 84.47 |
| 6 | 154732717 | rs9397709 | C | T | 4 | 0.2433 | 0.8266 | 1.098 | 1.0425 | 0.0042 | 77.33 |
| 2 | 210826755 | rs6760874 | C | T | 4 | 0.02543 | 0.827 | 0.8793 | 0.9703 | 0.0056 | 76.18 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 2 | 71089555 | rs10189222 | C | T | 3 | 0.1246 | 0.8271 | 0.8497 | 1.0953 | 0 | 92.05 |
| 1 | 202846320 | rs898386 | A | G | 4 | 0.08388 | 0.8294 | 1.0682 | 1.0182 | 0.0106 | 73.25 |
| 3 | 178825162 | rs1875102 | C | T | 4 | 0.07828 | 0.8302 | 1.064 | 1.0224 | 0.0001 | 85.42 |
| 3 | 24675281 | rs2362754 | C | G | 4 | 0.09812 | 0.8313 | 0.9443 | 0.9824 | 0.0034 | 78.01 |
| 6 | 154735267 | rs9383704 | A | G | 4 | 0.2472 | 0.8313 | 1.0961 | 1.0412 | 0.0039 | 77.59 |
| 6 | 154735871 | rs9384206 | C | T | 4 | 0.2453 | 0.8314 | 1.0968 | 1.0409 | 0.0042 | 77.27 |
| 11 | 109525740 | rs602189 | A | G | 4 | 0.508 | 0.8315 | 0.972 | 1.0257 | 0.0003 | 84.06 |
| 21 | 19398897 | rs1475897 | A | G | 3 | 0.3314 | 0.8317 | 1.0403 | 0.9725 | 0.0002 | 88.26 |
| 6 | 154735852 | rs9371795 | C | T | 4 | 0.2513 | 0.8328 | 1.0952 | 1.0407 | 0.004 | 77.45 |
| 6 | 153441972 | rs9479499 | A | T | 4 | 0.1964 | 0.833 | 0.9553 | 0.9833 | 0.0071 | 75.18 |
| 6 | 153442739 | rs10872697 | G | T | 4 | 0.1964 | 0.833 | 0.9553 | 0.9833 | 0.0071 | 75.18 |
| 6 | 154734121 | rs9384205 | C | T | 4 | 0.2547 | 0.8364 | 0.9131 | 0.9613 | 0.0037 | 77.73 |
| 11 | 109526143 | rs683593 | A | C | 4 | 0.4623 | 0.8364 | 1.0298 | 0.9769 | 0.0002 | 84.58 |
| 2 | 210810084 | rs13009758 | C | T | 4 | 0.02463 | 0.8365 | 1.1372 | 1.029 | 0.0051 | 76.58 |
| 15 | 51214304 | rs17545312 | A | G | 4 | 0.04732 | 0.8383 | 0.9137 | 0.9742 | 0.0003 | 84.13 |
| 5 | 40665104 | rs11739531 | C | T | 4 | 0.02608 | 0.8384 | 0.922 | 0.9831 | 0.006 | 75.88 |
| 15 | 51322236 | rs17628504 | A | G | 4 | 0.1939 | 0.8386 | 0.9387 | 1.0287 | 0.0003 | 84.12 |
| 1 | 55481326 | rs12063029 | A | G | 4 | 0.1453 | 0.8388 | 1.0625 | 1.0178 | 0.0188 | 69.93 |
| 2 | 111318413 | rs10180446 | C | G | 4 | 0.09094 | 0.839 | 1.0649 | 1.0171 | 0.0088 | 74.16 |
| 11 | 109527592 | rs581464 | G | T | 4 | 0.4531 | 0.8411 | 1.0304 | 0.9776 | 0.0002 | 84.54 |
| 6 | 154740453 | rs6557347 | C | T | 4 | 0.2416 | 0.8414 | 0.9126 | 0.964 | 0.0051 | 76.57 |
| 4 | 183403974 | rs7656126 | G | T | 3 | 0.1844 | 0.842 | 1.0554 | 1.0225 | 0.0022 | 83.71 |
| 3 | 24680225 | rs9812637 | A | G | 4 | 0.1152 | 0.8425 | 0.9465 | 0.9838 | 0.0046 | 76.98 |
| 11 | 109527801 | rs2846615 | C | T | 4 | 0.447 | 0.8425 | 1.0308 | 0.9777 | 0.0002 | 84.58 |
| 3 | 24690139 | rs1984870 | G | T | 4 | 0.06693 | 0.8429 | 1.0661 | 1.0181 | 0.0012 | 81.13 |
| 3 | 176290623 | rs1463524 | C | T | 4 | 0.3026 | 0.8442 | 0.9642 | 1.0173 | 0.0025 | 79.1 |
| 7 | 52977371 | rs1689299 | A | T | 4 | 0.3638 | 0.8458 | 0.9557 | 1.0261 | 0.001 | 81.53 |
| 6 | 104920190 | rs17458588 | C | T | 4 | 0.9588 | 0.846 | 0.9977 | 1.0231 | 0.0008 | 82.17 |
| 11 | 109526092 | rs600421 | G | T | 4 | 0.4145 | 0.847 | 0.9682 | 1.0221 | 0.0002 | 84.78 |
| 11 | 109528374 | rs622822 | G | T | 4 | 0.4381 | 0.8477 | 0.9695 | 1.0219 | 0.0002 | 84.46 |
| 2 | 210745449 | rs263675 | A | G | 4 | 0.02216 | 0.8479 | 0.8754 | 0.974 | 0.0067 | 75.43 |
| 4 | 109392362 | rs931771 | C | T | 4 | 0.07874 | 0.8482 | 1.073 | 1.0171 | 0.0095 | 73.81 |
| 1 | 152505007 | rs1194596 | A | G | 4 | 0.3581 | 0.8493 | 1.0327 | 0.9833 | 0.0018 | 80.02 |
| 11 | 115317381 | rs1145180 | A | G | 4 | 0.2206 | 0.8494 | 0.9566 | 0.9842 | 0.0058 | 76.05 |
| 21 | 29929217 | rs2245338 | C | T | 4 | 0.5248 | 0.8535 | 1.0343 | 0.9699 | 0 | 87.2 |
| 2 | 111320584 | rs1554006 | A | G | 4 | 0.07623 | 0.8543 | 1.0716 | 1.0163 | 0.0072 | 75.11 |
| 11 | 109528838 | rs665013 | C | T | 4 | 0.4176 | 0.8553 | 0.9682 | 1.0208 | 0.0002 | 84.52 |

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|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 2 | 111321113 | rs13019266 | C | T | 4 | 0.1067 | 0.8558 | 0.9412 | 0.985 | 0.0094 | 73.84 |
| 8 | 135108870 | rs16905053 | A | T | 4 | 0.2066 | 0.8569 | 0.9389 | 0.9782 | 0.0025 | 79.06 |
| 15 | 51195790 | rs12442241 | A | T | 4 | 0.06282 | 0.8596 | 0.9127 | 0.9775 | 0.0008 | 82.14 |
| 6 | 30040979 | rs3873283 | A | G | 4 | 0.2007 | 0.8603 | 1.0681 | 1.02 | 0.0082 | 74.52 |
| 1 | 202845996 | rs898387 | A | G | 4 | 0.09986 | 0.8609 | 0.9391 | 0.9852 | 0.009 | 74.1 |
| 3 | 54683416 | rs517729 | A | G | 4 | 0.1922 | 0.8614 | 0.9554 | 1.0161 | 0.001 | 81.6 |
| 2 | 210508108 | rs10200921 | A | G | 4 | 0.1408 | 0.8615 | 1.0818 | 0.9772 | 0.0037 | 77.79 |
| 11 | 109529896 | rs633410 | C | T | 4 | 0.4375 | 0.8617 | 0.9695 | 1.0198 | 0.0003 | 84.29 |
| 1 | 214171639 | rs646576 | A | G | 3 | 0.2974 | 0.8622 | 0.9507 | 1.029 | 0 | 90.04 |
| 15 | 51214080 | rs17627721 | G | T | 4 | 0.04767 | 0.8624 | 0.9137 | 0.9778 | 0.0002 | 84.41 |
| 3 | 59364649 | rs4679546 | A | C | 4 | 0.06769 | 0.8626 | 1.0814 | 1.0161 | 0.0143 | 71.61 |
| 6 | 104923637 | rs1417665 | C | T | 4 | 0.8954 | 0.8634 | 0.9943 | 1.0206 | 0.0007 | 82.36 |
| 6 | 104924468 | rs17459015 | C | T | 4 | 0.8907 | 0.8634 | 0.994 | 1.0205 | 0.0007 | 82.22 |
| 2 | 181898803 | rs17198619 | G | T | 4 | 0.1114 | 0.8673 | 0.903 | 0.9706 | 0.0006 | 82.67 |
| 2 | 111323872 | rs7576541 | C | T | 4 | 0.1142 | 0.8679 | 1.0611 | 1.0141 | 0.0085 | 74.35 |
| 2 | 151933334 | rs10432476 | C | T | 4 | 0.08342 | 0.8679 | 1.0642 | 1.013 | 0.0118 | 72.67 |
| 6 | 154741048 | rs7746647 | A | T | 4 | 0.2842 | 0.8682 | 1.0843 | 1.0303 | 0.0047 | 76.89 |
| 8 | 4075094 | rs17069640 | G | T | 4 | 0.8613 | 0.8688 | 1.0162 | 1.0395 | 0.0014 | 80.78 |
| 2 | 151932585 | rs3771895 | A | G | 4 | 0.08528 | 0.8696 | 1.0638 | 1.0128 | 0.0121 | 72.54 |
| 2 | 111311960 | rs12463442 | A | G | 4 | 0.09849 | 0.8712 | 1.0634 | 0.985 | 0.0021 | 79.62 |
| 11 | 109529837 | rs649847 | C | G | 4 | 0.4063 | 0.872 | 0.9674 | 1.0184 | 0.0002 | 84.54 |
| 6 | 30040645 | rs9260734 | A | G | 4 | 0.2212 | 0.8729 | 0.9393 | 0.9821 | 0.0073 | 75.03 |
| 20 | 10167799 | rs363012 | A | G | 4 | 0.4392 | 0.8735 | 0.9715 | 1.0168 | 0.0005 | 83.11 |
| 2 | 111323062 | rs9917154 | C | G | 4 | 0.1184 | 0.8749 | 0.9431 | 0.9868 | 0.0084 | 74.43 |
| 11 | 109530847 | rs585334 | A | G | 4 | 0.4035 | 0.8752 | 0.9672 | 1.0179 | 0.0002 | 84.44 |
| 6 | 104904271 | rs17517558 | A | C | 4 | 0.8324 | 0.8771 | 1.0093 | 0.9817 | 0.0006 | 82.78 |
| 6 | 104904758 | rs156153 | A | G | 4 | 0.8324 | 0.8771 | 1.0093 | 0.9817 | 0.0006 | 82.78 |
| 6 | 104905700 | rs156151 | C | G | 4 | 0.8356 | 0.8772 | 0.9909 | 1.0186 | 0.0006 | 82.71 |
| 6 | 104912555 | rs155510 | G | T | 4 | 0.8202 | 0.8805 | 0.9901 | 1.0181 | 0.0006 | 82.68 |
| 2 | 111315753 | rs10210955 | C | G | 4 | 0.02706 | 0.8809 | 0.9258 | 0.9875 | 0.0033 | 78.11 |
| 5 | 40682317 | rs7716982 | G | T | 4 | 0.0291 | 0.881 | 0.9234 | 0.9873 | 0.0048 | 76.76 |
| 8 | 134285128 | rs753722 | C | G | 4 | 0.4431 | 0.8814 | 0.9712 | 0.9854 | 0.0012 | 81.03 |
| 11 | 109531670 | rs679264 | A | G | 4 | 0.3886 | 0.8825 | 1.035 | 0.9835 | 0.0002 | 84.39 |
| 11 | 109531787 | rs678835 | C | T | 4 | 0.3875 | 0.8835 | 0.9661 | 1.0166 | 0.0003 | 84.36 |
| 8 | 135109347 | rs16905054 | A | G | 4 | 0.2427 | 0.8836 | 1.0601 | 1.0184 | 0.0019 | 79.82 |
| 11 | 109532396 | rs17110877 | A | G | 4 | 0.3804 | 0.8873 | 1.0356 | 0.9842 | 0.0003 | 84.36 |
| 6 | 104891512 | rs270678 | C | T | 4 | 0.7612 | 0.8887 | 0.9868 | 1.0168 | 0.0006 | 82.61 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 4 | 189571301 | rs12504808 | C | T | 4 | 0.3784 | 0.8888 | 0.9617 | 0.9851 | 0.0037 | 77.71 |
| 3 | 172708739 | rs7651813 | A | G | 4 | 0.3599 | 0.89 | 1.0387 | 1.0142 | 0.0023 | 79.31 |
| 15 | 51194001 | rs690535 | G | T | 4 | 0.04594 | 0.8902 | 1.095 | 1.0177 | 0.0003 | 83.83 |
| 5 | 40683520 | rs6882769 | C | T | 4 | 0.06214 | 0.8916 | 0.933 | 0.989 | 0.0109 | 73.12 |
| 20 | 10827336 | rs4346455 | C | T | 4 | 0.2483 | 0.8935 | 0.9602 | 0.9889 | 0.0043 | 77.23 |
| 13 | 100537995 | rs4265682 | G | T | 4 | 0.3424 | 0.8953 | 1.0355 | 1.012 | 0.0023 | 79.29 |
| 15 | 51238288 | rs11070957 | G | T | 4 | 0.06851 | 0.8989 | 0.9204 | 0.9833 | 0.0002 | 85.17 |
| 3 | 24682097 | rs7643926 | C | T | 4 | 0.07209 | 0.8993 | 1.0665 | 1.0103 | 0.0071 | 75.2 |
| 5 | 40693709 | rs7730020 | C | T | 4 | 0.03208 | 0.8995 | 1.0814 | 1.0109 | 0.0044 | 77.11 |
| 6 | 68815788 | rs9445968 | G | T | 3 | 0.286 | 0.9001 | 1.1777 | 1.0532 | 0.0018 | 84.14 |
| 8 | 14915797 | rs7817295 | A | T | 4 | 0.04377 | 0.9007 | 0.9312 | 0.989 | 0.002 | 79.75 |
| 11 | 109540511 | rs1026607 | A | G | 4 | 0.4101 | 0.9007 | 1.0334 | 0.9859 | 0.0002 | 84.65 |
| 11 | 109540472 | rs1026608 | A | G | 4 | 0.4115 | 0.9013 | 1.0333 | 0.986 | 0.0002 | 84.61 |
| 3 | 30365684 | rs977305 | A | G | 4 | 0.3905 | 0.9016 | 1.0323 | 0.9886 | 0.0018 | 79.97 |
| 11 | 109538856 | rs621672 | C | T | 4 | 0.3799 | 0.9025 | 1.0357 | 0.9863 | 0.0002 | 84.38 |
| 3 | 30362570 | rs12634878 | A | G | 4 | 0.386 | 0.9026 | 1.0324 | 0.9888 | 0.002 | 79.75 |
| 15 | 51240801 | rs10518706 | C | T | 4 | 0.06925 | 0.9042 | 0.9206 | 0.9841 | 0.0001 | 85.24 |
| 2 | 232078303 | rs4449121 | A | C | 4 | 0.3988 | 0.9044 | 0.9447 | 0.9778 | 0.0003 | 84.25 |
| 3 | 24691768 | rs2362756 | G | T | 4 | 0.09052 | 0.9066 | 1.0615 | 1.0108 | 0.0011 | 81.25 |
| 11 | 109533247 | rs3017769 | A | G | 4 | 0.3679 | 0.9066 | 0.9647 | 1.0133 | 0.0002 | 84.43 |
| 4 | 109416443 | rs11725852 | C | T | 4 | 0.04638 | 0.908 | 1.0815 | 1.0105 | 0.0058 | 76.02 |
| 7 | 52974032 | rs11769082 | C | T | 4 | 0.2264 | 0.9082 | 1.0634 | 0.9855 | 0.0027 | 78.81 |
| 11 | 109538447 | rs622192 | A | T | 4 | 0.361 | 0.9097 | 0.9642 | 1.0129 | 0.0002 | 84.39 |
| 1 | 4503964 | rs241215 | A | T | 4 | 0.2212 | 0.9109 | 1.0451 | 0.9899 | 0.0016 | 80.37 |
| 15 | 51245627 | rs10518710 | C | G | 4 | 0.09016 | 0.9115 | 1.0777 | 1.0132 | 0.0008 | 82.11 |
| 13 | 46486944 | rs754325 | C | T | 4 | 0.155 | 0.9141 | 0.9461 | 0.9909 | 0.0101 | 73.5 |
| 13 | 44583847 | rs2025418 | C | T | 4 | 0.135 | 0.9164 | 1.0737 | 0.988 | 0.0039 | 77.6 |
| 3 | 146903072 | rs3844271 | A | G | 4 | 0.004665 | 0.9231 | 0.9007 | 0.9908 | 0.0012 | 81.19 |
| 2 | 210710058 | rs2160020 | C | T | 4 | 0.04616 | 0.9261 | 1.1247 | 1.0127 | 0.0089 | 74.15 |
| 6 | 33124706 | rs375912 | C | T | 4 | 0.1455 | 0.9264 | 0.9463 | 0.9924 | 0.0111 | 73.01 |
| 4 | 109399892 | rs3913354 | A | T | 4 | 0.04552 | 0.927 | 1.0813 | 1.0083 | 0.0056 | 76.16 |
| 3 | 30361864 | rs17623772 | C | T | 4 | 0.3665 | 0.9277 | 1.0338 | 0.9917 | 0.0021 | 79.56 |
| 2 | 232142905 | rs10460338 | C | T | 4 | 0.582 | 0.9281 | 1.035 | 0.9823 | 0 | 87.33 |
| 5 | 172714540 | rs4867706 | A | G | 4 | 0.3287 | 0.9294 | 1.0404 | 1.0083 | 0.0063 | 75.66 |
| 15 | 51225655 | rs16965587 | G | T | 4 | 0.09787 | 0.9295 | 0.9245 | 0.9879 | 0.0002 | 85.17 |
| 2 | 232144608 | rs6727830 | A | G | 4 | 0.4819 | 0.9299 | 0.9567 | 1.0174 | 0 | 86.97 |
| 3 | 30335858 | rs9876727 | A | C | 4 | 0.1404 | 0.9304 | 0.9489 | 0.9927 | 0.0047 | 76.88 |

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|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 3 | 11219825 | rs12493961 | A | G | 4 | 0.3063 | 0.9344 | 1.1081 | 0.9794 | 0.0012 | 81.01 |
| 6 | 104874894 | rs17516082 | A | G | 4 | 0.6452 | 0.9352 | 1.0203 | 0.9903 | 0.0005 | 83.07 |
| 3 | 30335640 | rs9876671 | A | G | 4 | 0.1458 | 0.9356 | 0.9496 | 0.9933 | 0.0045 | 77.03 |
| 2 | 111316177 | rs4849121 | A | G | 4 | 0.0336 | 0.936 | 0.9296 | 0.9933 | 0.0033 | 78.13 |
| 3 | 30328416 | rs6809482 | A | G | 4 | 0.1468 | 0.9382 | 0.9497 | 0.9936 | 0.0049 | 76.74 |
| 3 | 30330791 | rs6781057 | G | T | 4 | 0.1468 | 0.9382 | 0.9497 | 0.9936 | 0.0049 | 76.74 |
| 6 | 104878861 | rs4945639 | C | T | 4 | 0.5975 | 0.9386 | 1.0233 | 0.991 | 0.0007 | 82.42 |
| 2 | 67716071 | rs6726828 | G | T | 4 | 0.4616 | 0.9404 | 1.0274 | 1.0069 | 0.0017 | 80.15 |
| 1 | 55462173 | rs4926672 | A | G | 4 | 0.2084 | 0.9409 | 1.0525 | 1.0067 | 0.0106 | 73.26 |
| 6 | 104872515 | rs17456339 | C | T | 4 | 0.625 | 0.941 | 1.0215 | 0.9911 | 0.0005 | 83.1 |
| 1 | 4508910 | rs241221 | C | T | 4 | 0.2141 | 0.9412 | 1.0458 | 0.9938 | 0.0047 | 76.9 |
| 2 | 67713993 | rs6760893 | A | G | 4 | 0.4291 | 0.9426 | 1.0292 | 1.0067 | 0.0015 | 80.53 |
| 1 | 55460604 | rs11206524 | C | T | 4 | 0.2165 | 0.9427 | 1.0515 | 1.0065 | 0.0102 | 73.47 |
| 3 | 30323764 | rs6549981 | C | T | 4 | 0.1495 | 0.9427 | 1.0526 | 1.006 | 0.0049 | 76.74 |
| 3 | 30361546 | rs7629687 | A | T | 4 | 0.2208 | 0.9435 | 0.9566 | 1.0064 | 0.0021 | 79.58 |
| 3 | 134947308 | rs8177185 | A | G | 3 | 0.002635 | 0.9439 | 1.3816 | 0.9707 | 0.008 | 79.26 |
| 2 | 67713787 | rs17033996 | A | G | 4 | 0.4348 | 0.9454 | 0.972 | 0.9936 | 0.0014 | 80.68 |
| 2 | 67714314 | rs6732490 | A | C | 4 | 0.4348 | 0.9454 | 0.972 | 0.9936 | 0.0014 | 80.68 |
| 3 | 134947891 | rs8177186 | G | T | 3 | 0.002491 | 0.9472 | 0.7225 | 1.0283 | 0.0081 | 79.24 |
| 2 | 43704094 | rs11886047 | C | T | 4 | 0.2825 | 0.9508 | 0.9539 | 0.9938 | 0.005 | 76.61 |
| 1 | 62513884 | rs17123324 | A | G | 4 | 0.2039 | 0.9522 | 1.2156 | 1.0231 | 0.0029 | 78.62 |
| 3 | 30330534 | rs6780847 | C | T | 4 | 0.1593 | 0.9526 | 0.9512 | 0.995 | 0.0044 | 77.12 |
| 6 | 104880442 | rs13197557 | A | G | 4 | 0.6012 | 0.953 | 1.023 | 0.993 | 0.0006 | 82.69 |
| 3 | 30329364 | rs11129397 | C | T | 4 | 0.1605 | 0.9531 | 1.0512 | 1.005 | 0.0043 | 77.23 |
| 2 | 232140542 | rs4340504 | A | C | 4 | 0.5325 | 0.9536 | 1.04 | 0.9888 | 0.0001 | 86.49 |
| 3 | 134949575 | rs4532136 | A | G | 3 | 0.002645 | 0.9536 | 1.3845 | 0.9758 | 0.0082 | 79.19 |
| 8 | 14907805 | rs1125265 | C | T | 4 | 0.1336 | 0.9544 | 0.9485 | 0.9953 | 0.0049 | 76.72 |
| 2 | 232145603 | rs10498258 | A | G | 4 | 0.5273 | 0.9552 | 1.0396 | 0.9893 | 0 | 86.77 |
| 18 | 21695157 | rs8098773 | C | T | 4 | 0.4259 | 0.9566 | 1.029 | 1.0048 | 0.0022 | 79.48 |
| 8 | 4064166 | rs12674947 | A | G | 4 | 0.7109 | 0.9568 | 0.9665 | 0.9866 | 0.0008 | 82.16 |
| 8 | 135162883 | rs1870126 | C | T | 4 | 0.2888 | 0.9574 | 0.9637 | 0.9956 | 0.0038 | 77.68 |
| 3 | 134917507 | rs11715340 | A | T | 3 | 0.008424 | 0.9605 | 1.3321 | 0.9788 | 0.0085 | 79.03 |
| 1 | 4503184 | rs694935 | A | T | 4 | 0.1693 | 0.9612 | 1.0508 | 0.9957 | 0.0024 | 79.23 |
| 2 | 21281690 | rs312052 | A | G | 4 | 0.2708 | 0.9631 | 0.9554 | 1.0045 | 0.0065 | 75.54 |
| 3 | 30319780 | rs1390298 | C | T | 4 | 0.1659 | 0.9637 | 1.0505 | 1.0038 | 0.0049 | 76.7 |
| 8 | 134275461 | rs16893344 | C | T | 4 | 0.6407 | 0.9653 | 1.0171 | 0.9955 | 0.0002 | 84.66 |
| 7 | 52979122 | rs1689304 | A | C | 4 | 0.07523 | 0.9655 | 1.0794 | 1.0047 | 0.0018 | 80.04 |

| | | | | | | | | | | | |
|----|-----------|------------|---|---|---|----------|--------|--------|--------|--------|-------|
| 2 | 232149419 | rs13025854 | A | C | 4 | 0.4514 | 0.9669 | 0.954 | 0.9922 | 0.0001 | 86 |
| 18 | 21693248 | rs1626332 | A | T | 4 | 0.4634 | 0.9709 | 0.9741 | 0.9967 | 0.0018 | 80.01 |
| 7 | 52979766 | rs1689306 | A | G | 4 | 0.07729 | 0.9713 | 1.0788 | 1.0039 | 0.0018 | 80.03 |
| 7 | 53069533 | rs1689330 | C | G | 4 | 0.09915 | 0.9722 | 1.074 | 1.0035 | 0.0064 | 75.59 |
| 1 | 4499103 | rs592726 | C | T | 4 | 0.126 | 0.9777 | 0.9459 | 0.9976 | 0.0038 | 77.65 |
| 3 | 30322459 | rs1495578 | A | G | 4 | 0.1598 | 0.9799 | 0.9508 | 1.0022 | 0.0038 | 77.62 |
| 13 | 44574009 | rs4483759 | C | G | 4 | 0.08765 | 0.9802 | 0.9221 | 0.9972 | 0.0056 | 76.17 |
| 4 | 58886180 | rs7435172 | C | T | 3 | 0.1433 | 0.9804 | 1.0598 | 1.0027 | 0.0017 | 84.34 |
| 3 | 30322358 | rs1495579 | G | T | 4 | 0.1844 | 0.981 | 1.0483 | 1.002 | 0.0039 | 77.58 |
| 1 | 55456607 | rs12409699 | A | G | 4 | 0.3107 | 0.9821 | 0.9584 | 1.0022 | 0.0064 | 75.62 |
| 1 | 55459204 | rs17111725 | A | G | 4 | 0.2051 | 0.9832 | 0.9497 | 0.998 | 0.0054 | 76.32 |
| 12 | 87284400 | rs10777108 | A | C | 4 | 0.0892 | 0.9858 | 1.2084 | 1.0053 | 0.0019 | 79.91 |
| 3 | 30343934 | rs7653488 | C | T | 4 | 0.2956 | 0.9861 | 0.9626 | 1.0015 | 0.0035 | 77.98 |
| 1 | 4497861 | rs608492 | C | G | 4 | 0.1412 | 0.9867 | 1.055 | 1.0014 | 0.0036 | 77.81 |
| 2 | 232148981 | rs10182727 | A | T | 4 | 0.4446 | 0.9869 | 1.0489 | 1.0031 | 0.0001 | 85.72 |
| 3 | 134933123 | rs16840751 | A | G | 3 | 0.008903 | 0.9872 | 1.3262 | 0.9936 | 0.0106 | 78 |
| 8 | 14906737 | rs10888094 | A | G | 4 | 0.1909 | 0.9873 | 1.0472 | 0.9987 | 0.0037 | 77.76 |
| 8 | 14906785 | rs10888095 | A | C | 4 | 0.138 | 0.9874 | 1.0532 | 1.0013 | 0.0034 | 78.07 |
| 3 | 134936517 | rs10935083 | C | T | 3 | 0.00896 | 0.9875 | 1.3317 | 1.0064 | 0.0109 | 77.86 |
| 15 | 51288845 | rs17545973 | C | T | 4 | 0.1089 | 0.9877 | 0.9263 | 1.002 | 0.0006 | 82.61 |
| 7 | 53069854 | rs4947777 | G | T | 4 | 0.1006 | 0.9881 | 1.0737 | 1.0015 | 0.0058 | 76.03 |
| 2 | 232133520 | rs6733018 | A | G | 4 | 0.5246 | 0.9885 | 1.0411 | 0.9973 | 0.0001 | 85.6 |
| 8 | 14907628 | rs2012994 | A | G | 4 | 0.1925 | 0.9885 | 1.047 | 1.0011 | 0.0081 | 74.57 |
| 3 | 134920716 | rs4582061 | A | G | 3 | 0.009927 | 0.9888 | 1.3127 | 0.9945 | 0.012 | 77.39 |
| 3 | 134920291 | rs16840699 | C | T | 3 | 0.01004 | 0.989 | 0.7621 | 1.0055 | 0.0122 | 77.32 |
| 1 | 55456395 | rs6668777 | A | C | 4 | 0.3092 | 0.9891 | 0.9591 | 1.0013 | 0.0045 | 77.05 |
| 2 | 232134007 | rs12993888 | A | G | 4 | 0.5001 | 0.9893 | 1.0434 | 0.9975 | 0.0001 | 85.92 |
| 3 | 134920954 | rs11717407 | A | G | 3 | 0.009699 | 0.9902 | 0.7612 | 1.0048 | 0.012 | 77.4 |
| 3 | 134921034 | rs9847885 | C | T | 3 | 0.009699 | 0.9902 | 0.7612 | 1.0048 | 0.012 | 77.4 |
| 1 | 202851008 | rs2045624 | C | G | 4 | 0.258 | 0.9904 | 0.9584 | 1.001 | 0.0056 | 76.15 |
| 8 | 82122134 | rs2127938 | C | T | 4 | 0.01483 | 0.9909 | 0.8297 | 0.9978 | 0.0036 | 77.88 |
| 1 | 55457932 | rs7529366 | A | G | 4 | 0.2588 | 0.9912 | 1.0474 | 1.0011 | 0.0051 | 76.53 |
| 3 | 24691672 | rs2362755 | G | T | 4 | 0.1617 | 0.9921 | 1.0505 | 0.9992 | 0.0046 | 76.98 |
| 7 | 52978744 | rs1919945 | C | T | 4 | 0.08493 | 0.9928 | 0.9197 | 0.9989 | 0.0031 | 78.41 |
| 8 | 82124010 | rs11986666 | A | C | 4 | 0.01805 | 0.9928 | 1.1965 | 0.9983 | 0.0036 | 77.85 |
| 1 | 4508064 | rs241220 | A | G | 4 | 0.1431 | 0.993 | 1.0538 | 1.0007 | 0.0039 | 77.59 |
| 8 | 82125199 | rs4585701 | C | T | 4 | 0.01881 | 0.994 | 1.1913 | 0.9986 | 0.0035 | 77.99 |

| | | | | | | | | | | | |
|----|-----------|------------|---|---|---|---------|--------|--------|--------|--------|-------|
| 15 | 51305758 | rs7168646 | A | G | 4 | 0.08202 | 0.9941 | 0.9241 | 1.001 | 0.0003 | 84.19 |
| 2 | 232130501 | rs1797392 | C | T | 4 | 0.5173 | 0.9948 | 0.9598 | 1.0012 | 0.0001 | 85.58 |
| 8 | 134268958 | rs16904845 | C | T | 4 | 0.5211 | 0.995 | 0.9753 | 1.0006 | 0.0008 | 82.05 |
| 6 | 95082112 | rs1235830 | C | T | 4 | 0.1997 | 0.9957 | 1.0648 | 0.9994 | 0.0043 | 77.24 |
| 1 | 4500481 | rs542688 | C | G | 4 | 0.1442 | 0.9964 | 0.9483 | 1.0004 | 0.0032 | 78.24 |
| 7 | 26498670 | rs757393 | C | T | 4 | 0.1213 | 0.9982 | 0.9441 | 0.9998 | 0.0074 | 74.99 |
| 3 | 30348345 | rs9841664 | C | T | 4 | 0.2584 | 0.9988 | 1.0421 | 1.0001 | 0.0048 | 76.75 |
| 3 | 134952715 | rs8177203 | A | G | 4 | 0.0551 | 0.9988 | 0.8514 | 1.0004 | 0.0015 | 80.52 |
| 2 | 232122582 | rs1797386 | C | T | 4 | 0.242 | 0.9994 | 0.9243 | 1.0001 | 0.0007 | 82.4 |

Supplemental Table 4. SNPs with strongest evidence of association in 'candidate' suicide genes

| | BD | | | | MDD | | | |
|--------------------------|------------|----|------------|------|------------|----|------------|------|
| | Best SNP | A1 | min_p | OR | Best SNP | A1 | min_p | OR |
| <i>ACE</i> | rs6517653 | A | 0.002333 | 0.80 | rs763211 | A | 0.001852 | 1.95 |
| <i>ADRA2A</i> | rs17128356 | C | 0.2814 | 1.14 | rs11195418 | A | 0.06722 | 1.97 |
| <i>AKT1</i> | rs1130214 | A | 0.2021 | 1.08 | rs1130214 | A | 0.4135 | 1.11 |
| <i>COMT</i> | rs887199 | A | 0.004835 | 0.79 | rs933271 | C | 0.1746 | 0.83 |
| <i>CRHBP</i> | rs2055627 | A | 0.012 | 0.81 | rs3792738 | A | 0.08426 | 1.46 |
| <i>CRHR1</i> | rs4074461 | G | 0.047 | 1.16 | rs4074461 | G | 0.06317 | 1.25 |
| <i>CRHR2</i> | rs4722999 | C | 0.1377 | 0.92 | rs255121 | C | 0.02146 | 0.65 |
| <i>DRD2</i> | rs4245147 | C | 0.2325 | 0.94 | rs4421776 | A | 0.05143 | 0.78 |
| <i>FKBP5</i> | rs9296158 | A | 0.01261 | 1.15 | rs1413896 | C | 0.0144 | 0.71 |
| <i>HTR1A</i> | rs12653018 | A | 0.06849 | 1.10 | rs13361335 | G | 0.2481 | 1.24 |
| <i>HTR2A</i> | rs10507546 | A | 0.007531 | 0.85 | rs17288723 | C | 0.03458 | 1.41 |
| <i>LSAMP</i> | rs2918217 | C | 0.0001916* | 0.76 | rs17647013 | C | 0.02548 | 0.66 |
| <i>NGFR</i> [^] | rs600120 | A | 0.008181 | 0.87 | rs11466124 | C | 0.1773 | 2.23 |
| <i>NOS1</i> | rs12307921 | A | 0.004323 | 0.73 | rs7528328 | C | 0.0004705~ | 0.52 |
| <i>NTRK2</i> | rs10780688 | A | 0.003991 | 0.86 | rs17087824 | G | 0.003523 | 1.75 |
| <i>SLC6A4</i> | rs7214991 | A | 0.00946 | 1.16 | rs2054847 | A | 0.02365 | 1.30 |
| <i>TAAR6</i> | rs7764564 | C | 0.2019 | 1.18 | rs9493390 | G | 0.1094 | 0.82 |
| <i>TPH1</i> | rs10766452 | C | 0.105 | 0.92 | rs17794760 | A | 0.1763 | 1.23 |
| <i>TPH2</i> | rs11179015 | C | 0.1916 | 0.77 | rs7955501 | A | 0.1702 | 0.85 |

~ in NESDA replication cohort, p=0.014, OR=1.47 for 'C' allele

* in GAIN replication cohort, p=0.73

A1, reference allele; OR, odds ratio

[^] Nerve Growth Factor Receptor (NGFR; referred to as p75(NTR) in original publication