## Materials and Methods

### RNA preparation

Total RNA was extracted from lymphoblastoid cell lines of the 210 unrelated individuals of the HapMap (*1*) (Coriell, Camden, New Jersey, United States). Two, one-quarter scale Message Amp II reactions (Ambion, Austin, Texas, United States) were performed for each RNA extraction using 200 ng of total RNA as previously described (*2*). 1.5 µg of the cRNA was hybridized to an array.

### Gene expression quantification

To assay transcript levels in the cell lines, we used Illumina's commercial whole genome expression array, Sentrix Human-6 Expression BeadChip (Illumina, San Diego, California, United States) (*3*). These arrays utilize a bead pool with ~48,000 unique bead types (one for each of 47,294 transcripts, plus controls), each with several hundred thousand gene-specific 50mer probes attached.

On a single BeadChip, six arrays were run in parallel. Each bead type (probe) is present on a single array on average 30 times. Each of the two IVT reactions from the 210 samples was hybridized to two arrays each, so that each cell line had four replicate hybridizations. cRNA was hybridized to arrays, and subsequently labelled with Cy3-streptavidin (Amersham Biosciences, Little Chalfont, United Kingdom) and scanned with a Bead Station (Illumina) as previously described (*2*). The full dataset is submitted to Gene Expression Omnibus under submission number series: GSE6536.

### Post-experimental raw data processing

### Normalization

With the Illumina bead technology, a single hybridization of RNA from one cell line to an array produces on average approximately 30 intensity values for each of 47,294 bead types. These background-corrected values for a single bead type are subsequently summarized by Illumina software and output to the user as a set of 47,294 intensity values for each individual hybridization (*4*). In our experiment, each cell line was hybridized to 4 arrays, thus resulting in 4 reported intensity values (as averages of the values from the 30 beads per probe) for each of the 47,294 bead types. To combine data from our multiple replicate hybridizations, raw data were read using the beadarray R package(*5*) and then normalized on a log scale using a quantile normalization method(*6*) across replicates of a single individual, followed by a median normalization method across individuals of a single population. These normalized values (for each probe, across replicates for each individual) are used in subsequent analyses.

## Association analyses

The association analysis employed: 1) Normalized quantitative gene expression measurements for the same samples using the Illumina Sentrix Human-6 Expression BeadChip, 2) SNP genotypes for the unrelated individuals of each HapMap population with minor allele frequency above 5% from the HapMap phase I map (rs numbers from HapMap version 16c.1, with genotypes extracted from HapMap version 20), and 3) $\log_2$ ratios from comparative genomic hybridization (CGH) of each HapMap individual against a common reference on an array comprising 26,564 large-insert clones (*7*). In addition, we filtered the CGH clone set on the basis of being called as being copy number variable in at least 2 HapMap individuals (*7*), thus representing a set of 1322 ‘CNV clones’ containing replicated CNVs.

Of the 47,294 probes for which we collected expression data, we selected the intersection of the top 18,000 most variable probes in each of the 4 populations.  This provided a set of 13,797 probes that are variable within all 4 populations.  We also selected an additional set of probes that have large differences in rank variability between populations.  To select this set, we ranked all transcripts by variability within each population and made all pairwise comparisons between populations to quantify difference in rank of each probe between each pair of populations.  We selected the top 1% (473) transcripts with largest absolute value rank difference from each population pair comparison, and took the union of the lists; this provided an additional 2,021 probes. After removing probes that mapped to chromosome X or Y, or to the mitochondrion genome, or that had no match to the human genome build 35, 14,925 probes remained for analysis.

For each of the selected probes interrogating expression and for each SNP, we fit a linear regression model as previously described (*2*). To test each probe- CGH-clone association, we fit the same model, the only difference being that the clone CGH-array data is continuous in nature ($\log_2$ ratios), as opposed to the discrete genotypic data. P-value distributions for each population are shown in Supplementary Figure 1. Note that it has previously been shown that SNPs in expression probes account for a negligible proportion of significant associations (*2*), and so will not perturb these distributions.

### Multiple-test correction

In order to assess significance of associations of expression variation to SNP genotype or copy number variation, we performed 10,000 permutations of each expression phenotype relative to the genotypes or CGH-$\log_2$ ratios. For associations to each type of data, we performed a *cis* analysis. For the SNP-expression association, we limited the analysis to those probes and SNPs where the distance from probe genomic midpoint to SNP genomic location was less than or equal to 1Mb. For the expression-CNV analysis, we conditioned on a distance of 2Mb from probe midpoint to CGH-clone midpoint. An association to a gene expression phenotype was considered significant if the p-value from the analysis of the observed data was lower than the threshold of the 0.001 tail of the distribution of the minimal p-values (among all comparisons for a given gene) from 10,000 permutations of the expression phenotypes (*8*, *9*).

### Accession Numbers

The expression data reported in this paper have been deposited in the Gene Expression Omnibus (GEO) (http://www.ncbi.nlm.nih.gov/geo) database (Series Accession Number pending).

1. IHMC, *Nature* **437**, 1299 (Oct 27, 2005).
2. B. E. Stranger *et al.*, *PLoS Genet* **1**, e78 (Dec, 2005).
3. K. Kuhn *et al.*, *Genome Res* **14**, 2347 (Nov, 2004).
4. M. J. Dunning, N. P. Thorne, I. Camilier, M. L. Smith, S. Tavare, *Revstat* **4**, 1 (2006).
5. M. J. Dunning, D. R. Smith, N. P. Thorne, S. Tavare, *R News* **Submitted** (2006).
6. B. M. Bolstad, R. A. Irizarry, M. Astrand, T. P. Speed, *Bioinformatics* **19**, 185 (Jan 22, 2003).
7. R. Redon *et al.*, *Nature* **in press** (2006).
8. G. A. Churchill, R. W. Doerge, *Genetics* **138**, 963 (Nov, 1994).
9. R. W. Doerge, G. A. Churchill, *Genetics* **142**, 285 (Jan, 1996).

## SUPPL. FIGURE AND TABLE LEGENDS

**Fig. S1**. Genomic location of significant *cis*- associations for (**A**) SNP-expression associations and (**B**) CNV clone-expression associations.

**Fig. S2.** Examples of SNP-expression and clone-expression associations in the four HapMap populations. (**A**) clone-expression association for *SMN2*; chr5. Significant associations between clones and expression are observed in CEU, CHB, and JPT, but not in YRI. (**B**) SNP-expression and clone-expression associations in the four HapMap populations. SNP-expression and clone-expression association for *GBP3*; chr1. Both SNPs and clones are significantly associated with expression of *GBP3* in CEU, CHB, and JPT, but not in YRI. In each plot, dotted lines show the 0.001 permutation significance threshold. For clone-expression associations, all clones in the window are shown, however the significance threshold was determined by permuting data only from those clones in CNVs where the CNV was present in at least two HapMap individuals. All coordinates shown are from Build 35 of the human genome. Inset panels show the relationship between mRNA levels and SNP genotypes or clone $\log_2$ ratios, for the most significant clone or SNP in that population, which may differ across populations.

**Fig. S3**. Distribution of p-values for all SNP-expression associations (SNP-probe distance < 1Mb) and all CGH-clone-expression associations (clone midpoint-probe distance < 2Mb) for each of the four HapMap populations. P-values from SNP associations are shown in red, CGH-clone associations are in black.

**Table S1** Number of genes and overlaps between permutation sets for SNPs and CNVs.

**Table S2.** Significant associations between SNPs and gene expression phenotypes with $p<0.001$, listing only the most significant association for each gene in each population.

**Table S3.** Significant associations between all CGH-clones and gene expression phenotypes with $p<0.001$, listing only the most significant association for each gene in each population.

**Table S4.** Significant associations between CNV clones and gene expression phenotypes with $p<0.001$, listing only the most significant association for each gene in each population.

**Table S5**. Significant associations at permutation corrected $p<0.001$ within 6 Mbs from genotypable CNVs in CEU and YRI.

## Permutation Stability

In theory when one attempts to estimate the threshold at p-value = 0.001 with 10,000 permutations, the estimate of the p-value is 0.001 +/- 0.00032 (mean +/- S.E.), based on the binomial distribution, so even with 10,000 permutations the estimate of the threshold is pretty good. We have empirically addressed this by performing another set of 10,000 permutations for each of the four populations and for both SNPs and CNV-clones. In table S1 we report the numbers of genes determined as significant in the original analysis, the new analysis and their overlap. It becomes apparent that the overlap is very high ranging from 90% to 98% between the two sets of analysis. In addition, for CEU we have performed an additional set of 50,000 permutations for both SNPs and CNV-clones. For 50,000 permutations the estimate of p-value is P = 0.001 +/- 0.00014. Again the numbers and proportions of overlap are very high at 96-100%. Both the theoretical and empirical approaches show that the estimates of thresholds in our manuscript are quite robust, given the number of permutations we have performed, and therefore the subsequent analyses are also robust and stable.

**Table S1**: Numbers of genes and overlaps between permutation sets for SNPs and CNVs

**SNP analysis: permutation threshold 0.001**

**#genes 10K permutations**

| | original | set2 | overlap of original with set2 | proportion overlap of original with set2 |
|---|---|---|---|---|
| **CEU** | 323 | 329 | 313 | 0.97 |
| **CHB** | 348 | 348 | 333 | 0.96 |
| **JPT** | 370 | 363 | 349 | 0.94 |
| **YRI** | 411 | 408 | 394 | 0.96 |

**CNV-clone analysis: permutation threshold 0.001**

**#genes 10K permutations**

| | original | set2 | overlap of original with set2 | proportion overlap of original with set2 |
|---|---|---|---|---|
| **CEU** | 40 | 40 | 39 | 0.98 |
| **CHB** | 32 | 33 | 31 | 0.97 |
| **JPT** | 40 | 38 | 37 | 0.93 |
| **YRI** | 42 | 40 | 38 | 0.90 |

**Comparison of thresholds with 10K vs. 50K permutations**

**#genes associated with SNPs**

| | 10K-set | 50K-set | overlap 10K-50K | proportion overlap 10K-50K |
|---|---|---|---|---|
| **CEU-original** | 323 | 324 | 312 | 0.98 |
| **CEU-set2** | 329 | 324 | 316 | 0.96 |

**#genes associated with CNV-clones**

| | 10K-set | 50K-set | overlap 10K-50K | proportion overlap 10K-50K |
|---|---|---|---|---|
| **CEU-original** | 40 | 42 | 40 | 1.00 |
| **CEU-set2** | 40 | 42 | 39 | 0.98 |

Table S2: Most siggnificant associations of SNPs with gene expression at 0.001

| Gene_label | Illumina_Gene_ID | SNP_rsID | chromosome | SNP_location B35 | Distance SNP-probe midpoint(bp) | -log10(p-value) | Adjusted_R^2 | permutation threshold_10-4 | permutation threshold_10-3 | permutation threshold_10-2 | permutation threshold_0.05 | population |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ABC1 | GI_38142463-S | rs8066241 | 17 | 55511931 | 36480 | 8.1969 | 0.434 | 6.7 | 5.21 | 4.02 | 3.22 | CEU |
| ABCD4 | GI_10947128-A | rs2075025 | 14 | 73266439 | 555646 | 5.4004 | 0.2973 | 6.61 | 5.14 | 4.15 | 3.49 | CEU |
| ABHD6 | GI_34147685-S | rs11130670 | 3 | 58633494 | 378180 | 6.2899 | 0.3438 | 6.16 | 5.43 | 4.38 | 3.63 | CEU |
| ACY1L2 | GI_37551403-S | rs9342178 | 6 | 89913169 | 15399 | 6.1804 | 0.3382 | 6.6 | 5.72 | 4.48 | 3.76 | CEU |
| AD-017 | GI_8923854-A | rs10865973 | 3 | 52693194 | 10629 | 6.7454 | 0.3877 | 7.17 | 5.21 | 4.22 | 3.48 | CEU |
| ADAT1 | GI_7382475-S | rs7500366 | 16 | 75175416 | 984446 | 5.6091 | 0.313 | 7.76 | 5.6 | 4.46 | 3.66 | CEU |
| ADSS | GI_34577062-S | rs4658574 | 1 | 239976757 | 921601 | 5.4984 | 0.3025 | 7.01 | 5.36 | 4.37 | 3.63 | CEU |
| ARHGEF12 | GI_7662087-S | rs7937444 | 11 | 120774936 | 909131 | 5.5512 | 0.3054 | 6.18 | 5.48 | 4.52 | 3.77 | CEU |
| ARNT | GI_30795239-A | rs1136774 | 1 | 147551270 | 44087 | 6.1902 | 0.3387 | 5.51 | 5.12 | 4.08 | 3.35 | CEU |
| ASAHL | GI_30794501-S | rs3796484 | 4 | 77231693 | 32603 | 7.5113 | 0.4084 | 5.92 | 5.32 | 4.39 | 3.64 | CEU |
| ATP13A | GI_9966896-S | rs2304130 | 19 | 19650528 | 33481 | 7.555 | 0.4105 | 6.91 | 5.82 | 4.29 | 3.47 | CEU |
| ATPIF1 | GI_30260191-I | rs1283621 | 1 | 28263137 | 14761 | 7.6681 | 0.4271 | 6.31 | 5.17 | 4.04 | 3.29 | CEU |
| AXIN1 | GI_31083143-A | rs393521 | 16 | 277679 | 20 | 11.4131 | 0.5598 | 6.26 | 5.61 | 4.38 | 3.64 | CEU |
| B7 | GI_42542401-A | rs1007923 | 12 | 6884368 | 9239 | 9.607 | 0.5052 | 6.64 | 5.67 | 4.59 | 3.8 | CEU |
| BBS2 | GI_22208996-S | rs13337155 | 16 | 55062225 | 13949 | 10.6247 | 0.5317 | 7.02 | 5.39 | 4.39 | 3.71 | CEU |
| BLK | GI_33469981-S | rs10100215 | 8 | 11399681 | 59607 | 5.4493 | 0.2999 | 6.49 | 5.43 | 4.53 | 3.73 | CEU |
| BTN3A2 | GI_34932495-S | rs9379851 | 6 | 26462759 | 21356 | 11.3811 | 0.5587 | 7.01 | 5.38 | 4.41 | 3.64 | CEU |
| C10orf88 | GI_13376420-S | rs4980169 | 10 | 124682576 | 1441 | 6.0889 | 0.3383 | 6.02 | 5.37 | 4.53 | 3.76 | CEU |
| C14orf130 | GI_28411949-A | rs1263389 | 14 | 92737473 | 18971 | 6.755 | 0.367 | 8.85 | 5.73 | 4.55 | 3.8 | CEU |
| C14orf52 | GI_21553312-S | rs4902332 | 14 | 64445731 | 25025 | 25.2026 | 0.8517 | 6.85 | 5.28 | 4.37 | 3.58 | CEU |
| C16orf5 | GI_7019336-S | rs3747600 | 16 | 4526223 | 25313 | 7.9686 | 0.4294 | 6.29 | 5.47 | 4.56 | 3.77 | CEU |
| C1orf16 | GI_42476073-A | rs2702178 | 1 | 180184202 | 70515 | 10.9569 | 0.55 | 5.83 | 5.5 | 4.3 | 3.51 | CEU |
| C20orf110 | GI_29745613-S | rs6087733 | 20 | 33762042 | 997468 | 5.5979 | 0.3124 | 8.14 | 5.58 | 4.29 | 3.4 | CEU |
| C20orf22 | GI_34147330-S | rs6107027 | 20 | 25236632 | 13023 | 7.3459 | 0.4006 | 6.1 | 5.23 | 4.2 | 3.45 | CEU |
| C21orf107 | GI_38026951-I | rs2836926 | 21 | 39458660 | 25667 | 15.9812 | 0.699 | 7.41 | 6.04 | 4.77 | 4 | CEU |
| C6orf18 | GI_40538792-S | rs7745906 | 6 | 31311987 | 93255 | 6.1479 | 0.3366 | 6.55 | 5.74 | 4.68 | 3.81 | CEU |
| C7orf13 | GI_14249145-S | rs4716648 | 7 | 155948932 | 17999 | 6.0552 | 0.3414 | 6.8 | 5.54 | 4.49 | 3.76 | CEU |
| C7orf29 | GI_19923960-S | rs10282458 | 7 | 149482950 | 15733 | 6.7864 | 0.3685 | 7.26 | 5.31 | 4.36 | 3.66 | CEU |
| C8orf13 | GI_32698772-S | rs2736340 | 8 | 11381382 | 64837 | 6.2147 | 0.34 | 6.05 | 5.56 | 4.52 | 3.74 | CEU |
| C8orf5 | GI_33300646-S | rs10089518 | 8 | 10877213 | 125818 | 5.6775 | 0.3166 | 6.81 | 5.57 | 4.55 | 3.81 | CEU |
| C9orf95 | GI_8923529-S | rs10869500 | 9 | 74937249 | 23717 | 7.5836 | 0.4063 | 6.25 | 5.32 | 4.51 | 3.81 | CEU |
| CAPZA1 | GI_5453596-S | rs7535636 | 1 | 112813841 | 112288 | 8.0851 | 0.4404 | 6.19 | 5.43 | 4.39 | 3.6 | CEU |
| CARD8 | GI_7662403-S | rs2009373 | 19 | 53411226 | 7838 | 11.8619 | 0.575 | 6.78 | 5.69 | 4.49 | 3.76 | CEU |
| CAT | GI_4557013-S | rs7112624 | 11 | 34382536 | 67061 | 9.17 | 0.4753 | 7.57 | 5.64 | 4.44 | 3.75 | CEU |
| CCNB1IP1 | GI_33519439-I | rs884368 | 14 | 19864349 | 8512 | 7.1573 | 0.3864 | 6.62 | 5.53 | 4.52 | 3.82 | CEU |
| CCNDBP1 | GI_16554567-I | rs16957244 | 15 | 40953321 | 312288 | 4.9555 | 0.277 | 6.38 | 4.87 | 3.85 | 3.07 | CEU |
| CD151 | GI_34328914-A | rs4075289 | 11 | 820670 | 8073 | 8.6953 | 0.4555 | 7.53 | 6.06 | 4.82 | 3.86 | CEU |
| CD79B | GI_11038675-A | rs3817182 | 17 | 59137640 | 222493 | 6.1632 | 0.3421 | 6.46 | 5.39 | 4.1 | 3.35 | CEU |
| CDK2AP1 | GI_17978492-S | rs655293 | 12 | 122053285 | 217307 | 5.5994 | 0.3171 | 7.15 | 5.17 | 4.19 | 3.41 | CEU |
| CDKN1A | GI_17978494-I | rs733590 | 6 | 36753181 | 1450 | 6.7874 | 0.3685 | 6.85 | 5.85 | 4.66 | 3.82 | CEU |
| CGI-111 | GI_7705613-S | rs3944133 | 5 | 128960037 | 482948 | 5.8363 | 0.3204 | 6.32 | 5.52 | 4.35 | 3.57 | CEU |
| CGI-62 | GI_7705774-S | rs1384804 | 8 | 79734777 | 55274 | 6.7894 | 0.3686 | 6.95 | 5.44 | 4.31 | 3.59 | CEU |
| CGI-96 | GI_25092724-S | rs4820470 | 22 | 41230802 | 2482 | 11.2888 | 0.5555 | 6.63 | 5.29 | 4.37 | 3.72 | CEU |
| CHCHD2 | GI_32307179-S | rs845552 | 7 | 55019716 | 923871 | 5.7968 | 0.3184 | 6.17 | 5.31 | 4.23 | 3.54 | CEU |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CHI3L2 | GI_11993934-S | rs942697 | 1 | 111503545 | 5615 | 6.81 | 0.3696 | 6.99 | 5.98 | 4.82 | 3.94 | CEU |
| CHRNE | GI_38327653-S | rs2302321 | 17 | 4728587 | 13594 | 10.4232 | 0.5243 | 9.2 | 7.05 | 5.42 | 4.3 | CEU |
| COPS7A | GI_7705329-S | rs714774 | 12 | 6489545 | 221475 | 5.4052 | 0.2975 | 6.37 | 5.35 | 4.5 | 3.74 | CEU |
| CP110 | GI_34222317-S | rs1475963 | 16 | 19412783 | 59263 | 6.262 | 0.3424 | 6.13 | 5.37 | 4.32 | 3.58 | CEU |
| CPEB4 | GI_32698754-S | rs10516107 | 5 | 173280762 | 36825 | 10.8238 | 0.539 | 5.97 | 5.68 | 4.58 | 3.82 | CEU |
| CPNE1 | GI_23397697-A | rs6060535 | 20 | 33698936 | 21264 | 12.4017 | 0.5927 | 7.23 | 5.63 | 4.29 | 3.36 | CEU |
| CRIPT | GI_41350204-S | rs1451156 | 2 | 46744253 | 19148 | 8.1268 | 0.4309 | 6.93 | 5.72 | 4.54 | 3.84 | CEU |
| CRNKL1 | GI_30795219-S | rs2073123 | 20 | 19978870 | 15505 | 5.7006 | 0.3133 | 7.28 | 5.53 | 4.5 | 3.73 | CEU |
| CSTB | GI_20357564-S | rs1041456 | 21 | 44030783 | 12403 | 8.2125 | 0.4403 | 6.75 | 5.76 | 4.68 | 3.87 | CEU |
| CSTF3 | GI_4557494-S | rs3758741 | 11 | 33063192 | 29 | 5.3589 | 0.295 | 5.85 | 5.3 | 4.38 | 3.58 | CEU |
| CTNS | GI_4826681-S | rs161370 | 17 | 3477002 | 34422 | 6.562 | 0.3574 | 6.7 | 5.44 | 4.54 | 3.81 | CEU |
| CTSH | GI_23110956-A | rs1036938 | 15 | 77024302 | 22891 | 8.4809 | 0.4464 | 6.3 | 5.45 | 4.56 | 3.74 | CEU |
| CTSK | GI_23110958-S | rs1136774 | 1 | 147551270 | 30875 | 7.2458 | 0.3906 | 6.89 | 5.43 | 4.24 | 3.45 | CEU |
| DCLRE1B | GI_24431998-S | rs878129 | 1 | 114171237 | 2889 | 8.7891 | 0.4595 | 7.2 | 5.63 | 4.44 | 3.67 | CEU |
| DCTD | GI_4503276-S | rs7277 | 4 | 184186662 | 176 | 8.596 | 0.4513 | 6.89 | 5.77 | 4.65 | 3.8 | CEU |
| DERP6 | GI_44662825-I | rs4562 | 17 | 7104463 | 8022 | 8.5043 | 0.4474 | 7.01 | 5.91 | 4.56 | 3.78 | CEU |
| dJ383J4.3 | GI_42655858-S | rs3791022 | 1 | 170466426 | 34050 | 11.5215 | 0.5635 | 8.67 | 6.5 | 4.7 | 3.67 | CEU |
| DKFZP434B172 | GI_27478061-S | rs33532 | 3 | 42390209 | 682769 | 6.3567 | 0.3472 | 7.52 | 6.13 | 4.83 | 3.83 | CEU |
| DKFZp434G0522 | GI_21314674-S | rs2290019 | 16 | 86299163 | 138 | 5.7834 | 0.3177 | 6.89 | 5.51 | 4.56 | 3.83 | CEU |
| DKFZp434N035 | GI_14149994-S | rs2930761 | 22 | 18753459 | 629915 | 6.8521 | 0.3717 | 7.47 | 5.99 | 4.7 | 3.81 | CEU |
| DKFZP566H073 | GI_14149701-S | rs400688 | 17 | 4780674 | 8503 | 7.9302 | 0.4277 | 6.36 | 5.28 | 4.52 | 3.76 | CEU |
| DKFZP566J2046 | GI_13654273-S | rs404772 | 16 | 1857175 | 38461 | 6.3343 | 0.3509 | 6.2 | 5.53 | 4.44 | 3.7 | CEU |
| DKFZP586D0919 | GI_24308058-S | rs10877011 | 12 | 56411259 | 51220 | 9.3901 | 0.4903 | 6.47 | 5.38 | 4.3 | 3.57 | CEU |
| DNAJD1 | GI_7019452-S | rs2281782 | 13 | 42496191 | 61733 | 6.4101 | 0.3548 | 7.43 | 5.55 | 4.49 | 3.7 | CEU |
| DPYSL4 | GI_11321616-S | rs12357377 | 10 | 133843968 | 25198 | 7.2903 | 0.3927 | 9.03 | 6.8 | 4.88 | 3.99 | CEU |
| DRIM | GI_7657040-S | rs10507131 | 12 | 100303365 | 20928 | 7.8037 | 0.4164 | 6.22 | 5.45 | 4.42 | 3.72 | CEU |
| DSCR5 | GI_24497598-A | rs1473807 | 21 | 37395043 | 33574 | 6.6351 | 0.361 | 7.74 | 5.81 | 4.64 | 3.84 | CEU |
| DTNB | GI_37577100-A | rs1369704 | 2 | 25535241 | 23436 | 6.2312 | 0.3408 | 6.28 | 5.38 | 4.31 | 3.56 | CEU |
| ECHDC3 | GI_31542717-S | rs3829154 | 10 | 11822759 | 23045 | 8.0864 | 0.4347 | 7.41 | 5.66 | 4.61 | 3.86 | CEU |
| EIF2S1 | GI_34147492-S | rs7141519 | 14 | 66594278 | 327255 | 5.9727 | 0.3322 | 6.51 | 5.4 | 4.19 | 3.39 | CEU |
| ENTPD1 | GI_45580699-S | rs1340837 | 10 | 97532025 | 84172 | 10.7256 | 0.5354 | 6.15 | 5.38 | 4.44 | 3.69 | CEU |
| ERMAP | GI_19923535-S | rs9960 | 1 | 42986886 | 7452 | 6.9788 | 0.3778 | 6.38 | 5.64 | 4.28 | 3.52 | CEU |
| FDX1 | GI_36054077-S | rs4576787 | 11 | 109822376 | 18049 | 6.6412 | 0.3614 | 7.06 | 5.58 | 4.32 | 3.58 | CEU |
| FLJ10252 | GI_8922312-S | rs2377567 | 1 | 213854419 | 138031 | 5.9504 | 0.3264 | 6.26 | 5.52 | 4.53 | 3.81 | CEU |
| FLJ12994 | GI_12383091-S | rs2249090 | 15 | 54345306 | 172986 | 7.01 | 0.3793 | 7.35 | 5.74 | 4.44 | 3.61 | CEU |
| FLJ12998 | GI_12232436-S | rs7206713 | 16 | 85155545 | 33431 | 6.8225 | 0.3702 | 8.07 | 6.18 | 4.81 | 4 | CEU |
| FLJ13576 | GI_21362101-S | rs259306 | 7 | 111334509 | 665397 | 5.8824 | 0.3228 | 7.07 | 5.21 | 4.25 | 3.56 | CEU |
| FLJ14753 | GI_14211858-S | rs7025878 | 9 | 94278347 | 24096 | 8.9292 | 0.4713 | 6.11 | 5.23 | 4.22 | 3.53 | CEU |
| FLJ20257 | GI_21361790-S | rs6945952 | 7 | 99626426 | 49833 | 8.1286 | 0.4366 | 6.3 | 5.26 | 4.16 | 3.45 | CEU |
| FLJ20444 | GI_44888815-S | rs2307055 | 9 | 64205260 | 1127 | 8.1207 | 0.4306 | 5.58 | 4.12 | 2.92 | 2.12 | CEU |
| FLJ20635 | GI_8923587-S | rs2205660 | 22 | 44052268 | 4823 | 11.061 | 0.5538 | 7.68 | 6.28 | 5.09 | 4.14 | CEU |
| FLJ20920 | GI_31542719-S | rs7627 | 17 | 45907153 | 3 | 11.5701 | 0.5652 | 6.61 | 5.61 | 4.45 | 3.76 | CEU |
| FLJ21347 | GI_31542722-S | rs8076632 | 17 | 45980927 | 7240 | 19.0726 | 0.7592 | 6.96 | 5.85 | 4.77 | 3.89 | CEU |
| FLJ21616 | GI_13375737-S | rs10088428 | 8 | 28965442 | 421 | 19.6959 | 0.7708 | 7.35 | 6.08 | 4.54 | 3.74 | CEU |
| FLJ22374 | GI_39752638-S | rs10282606 | 7 | 30608001 | 97126 | 7.2236 | 0.3895 | 7.36 | 6.01 | 4.64 | 3.8 | CEU |
| FLJ22573 | GI_13375912-S | rs2291067 | 19 | 40965374 | 43070 | 6.6199 | 0.3758 | 8.33 | 5.89 | 4.58 | 3.74 | CEU |
| FLJ22635 | GI_13376651-S | rs2242565 | 11 | 285343 | 40 | 6.5427 | 0.3565 | 6.2 | 5.2 | 4.27 | 3.49 | CEU |
| FLJ23235 | GI_13376422-S | rs2254075 | 4 | 38852749 | 61707 | 7.8981 | 0.4207 | 6.84 | 5.55 | 4.44 | 3.69 | CEU |
| FLJ34443 | GI_31341870-S | rs4130791 | 4 | 1404514 | 25127 | 7.813 | 0.4168 | 7.09 | 6.24 | 4.51 | 3.71 | CEU |
| FLJ36888 | GI_31341376-S | rs8100018 | 19 | 45443863 | 75033 | 7.0841 | 0.3829 | 8.87 | 5.67 | 4.41 | 3.66 | CEU |
| FLJ37970 | GI_40795670-S | rs612448 | 11 | 63881091 | 429 | 6.0096 | 0.3294 | 6.72 | 5.13 | 4.21 | 3.49 | CEU |
| FLJ40432 | GI_22749084-S | rs2248061 | 2 | 208320565 | 123860 | 6.8171 | 0.37 | 7.22 | 5.42 | 4.44 | 3.67 | CEU |
| FLJ46603 | GI_38348363-S | rs4789349 | 17 | 72217936 | 30427 | 18.8882 | 0.7557 | 8.15 | 6.93 | 5.1 | 4.14 | CEU |
| FLJ90036 | GI_31559781-S | rs10004179 | 4 | 121548 | 24320 | 6.7942 | 0.3689 | 6.25 | 5.18 | 4.07 | 3.27 | CEU |
| FTHFSDC1 | GI_40018634-S | rs6557112 | 6 | 151522071 | 7138 | 7.2626 | 0.3914 | 8.3 | 6.16 | 4.92 | 4.06 | CEU |
| FUT10 | GI_40805105-S | rs2304748 | 8 | 33489486 | 140780 | 5.4862 | 0.3019 | 7.62 | 5.45 | 4.22 | 3.47 | CEU |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GBP3 | GI_24308156-S | rs10922533 | 1 | 89168680 | 16511 | 13.2676 | 0.6195 | 7.53 | 5.48 | 4.41 | 3.59 | CEU |
| GSTM1 | GI_23065546-A | rs366631 | 1 | 109964514 | 20554 | 16.3427 | 0.7076 | 6.44 | 5.63 | 4.57 | 3.73 | CEU |
| GSTT1 | GI_4504184-S | rs407257 | 22 | 22671104 | 29852 | 20.0411 | 0.7769 | 7.05 | 5.89 | 4.83 | 3.87 | CEU |
| H17 | GI_21361764-S | rs574198 | 11 | 125575051 | 78062 | 6.3916 | 0.3489 | 7.02 | 5.78 | 4.55 | 3.84 | CEU |
| HABP4 | GI_24307946-S | rs10820626 | 9 | 96283735 | 48198 | 9.6967 | 0.4965 | 6.41 | 5.4 | 4.3 | 3.56 | CEU |
| HIBCH | GI_37594468-A | rs291427 | 2 | 191019565 | 124290 | 5.763 | 0.3166 | 6.64 | 4.96 | 4.16 | 3.5 | CEU |
| HLA-C | GI_19557676-S | rs6457374 | 6 | 31380240 | 35519 | 7.3274 | 0.3944 | 8.12 | 5.96 | 4.68 | 3.8 | CEU |
| HLA-DOB | GI_18641377-S | rs11244 | 6 | 32888702 | 17 | 11.3104 | 0.5562 | 7.42 | 5.52 | 4.54 | 3.74 | CEU |
| HLA-DQA1 | GI_18426974-S | rs9275141 | 6 | 32759095 | 40260 | 10.3708 | 0.5223 | 7.26 | 5.74 | 4.49 | 3.73 | CEU |
| HLA-DQA2 | GI_11095446-S | rs3793127 | 6 | 32479893 | 341140 | 14.1245 | 0.6443 | 8.24 | 5.45 | 4.37 | 3.65 | CEU |
| hmm1412 | hmm1412-S | rs2298746 | 11 | 74231482 | 1567 | 20.546 | 0.7857 | 7.35 | 5.54 | 4.45 | 3.65 | CEU |
| hmm23621 | hmm23621-S | rs4517848 | 17 | 20686412 | 151776 | 5.9719 | 0.3275 | 5.98 | 5.13 | 4.17 | 3.35 | CEU |
| hmm26268 | hmm26268-S | rs3010848 | 1 | 218333518 | 2744 | 13.7999 | 0.6351 | 6.69 | 5.47 | 4.42 | 3.59 | CEU |
| hmm31752 | hmm31752-S | rs2523871 | 6 | 31121988 | 10090 | 6.6239 | 0.3707 | 6.71 | 5.69 | 4.61 | 3.72 | CEU |
| hmm31999 | hmm31999-S | rs4840044 | 6 | 99994734 | 14330 | 7.3131 | 0.4046 | 6.96 | 5.39 | 4.5 | 3.79 | CEU |
| hmm5445 | hmm5445-S | rs883416 | 17 | 30594554 | 24000 | 10.1932 | 0.5156 | 7.17 | 5.68 | 4.59 | 3.73 | CEU |
| hmm665 | hmm665-S | rs12221075 | 10 | 126524845 | 97918 | 7.0233 | 0.38 | 8.1 | 5.81 | 4.62 | 3.77 | CEU |
| hmm8232 | hmm8232-S | rs1057533 | 1 | 46527856 | 11888 | 17.8541 | 0.7349 | 7.55 | 5.62 | 4.32 | 3.48 | CEU |
| Hs.124623 | Hs.124623-S | rs6518350 | 21 | 44446245 | 7633 | 11.8166 | 0.5799 | 10.4 | 6.29 | 5.08 | 4.11 | CEU |
| Hs.135624 | Hs.135624-S | rs7636818 | 3 | 180504817 | 66943 | 7.6584 | 0.4098 | 6.36 | 5.32 | 4.55 | 3.7 | CEU |
| Hs.153573 | Hs.153573-S | rs2032942 | 7 | 133771545 | 33462 | 6.59 | 0.3588 | 7.6 | 5.8 | 4.56 | 3.68 | CEU |
| Hs.155793 | Hs.155793-S | rs10814395 | 9 | 3650648 | 13225 | 6.5831 | 0.3585 | 8.46 | 6.17 | 4.81 | 4.07 | CEU |
| Hs.158943 | Hs.158943-S | rs9393790 | 6 | 27222031 | 616644 | 6.4414 | 0.3721 | 5.84 | 5.11 | 4.07 | 3.33 | CEU |
| Hs.164463 | Hs.164463-S | rs2246770 | 4 | 54397811 | 45576 | 10.7848 | 0.5376 | 9.39 | 6.76 | 5.27 | 4.15 | CEU |
| Hs.169006 | Hs.169006-S | rs11123170 | 2 | 113695171 | 19072 | 7.4636 | 0.4008 | 6.06 | 5.18 | 4.35 | 3.59 | CEU |
| Hs.171169 | Hs.171169-S | rs1009371 | 8 | 110567126 | 50295 | 6.2118 | 0.3398 | 8.22 | 5.97 | 4.47 | 3.6 | CEU |
| Hs.245997 | Hs.245997-S | rs401396 | 21 | 42871651 | 7105 | 8.5498 | 0.4671 | 6.08 | 5.32 | 4.67 | 3.96 | CEU |
| Hs.26039 | Hs.26039-S | rs7712435 | 5 | 10716402 | 6415 | 14.3226 | 0.6498 | 6.84 | 5.56 | 4.55 | 3.81 | CEU |
| Hs.264076 | Hs.264076-S | rs1408656 | 13 | 78784655 | 111714 | 5.9636 | 0.3271 | 6.39 | 5.32 | 4.3 | 3.6 | CEU |
| Hs.311977 | Hs.311977-S | rs11675957 | 2 | 241928782 | 175482 | 8.6489 | 0.4536 | 6.93 | 5.27 | 4.4 | 3.56 | CEU |
| Hs.333841 | Hs.333841-S | rs9289971 | 3 | 157872649 | 119 | 6.9067 | 0.3795 | 6.09 | 5.15 | 4.31 | 3.62 | CEU |
| Hs.379903 | Hs.379903-S | rs2286796 | 17 | 15824952 | 4262 | 9.669 | 0.5014 | 5.82 | 5.21 | 4.3 | 3.56 | CEU |
| Hs.396207 | Hs.396207-S | rs11211152 | 1 | 45783250 | 10256 | 27.6176 | 0.8775 | 6.16 | 5.47 | 4.21 | 3.39 | CEU |
| Hs.400876 | Hs.400876-S | rs1739652 | 20 | 36482373 | 412 | 8.7763 | 0.459 | 6.67 | 5.53 | 4.35 | 3.57 | CEU |
| Hs.40696 | Hs.40696-S | rs761906 | 22 | 45459178 | 19369 | 6.6898 | 0.3637 | 6.91 | 5.77 | 4.65 | 3.87 | CEU |
| Hs.42805 | Hs.42805-S | rs10751692 | 12 | 130910158 | 5 | 6.5112 | 0.3549 | 7.37 | 5.7 | 4.49 | 3.72 | CEU |
| Hs.431200 | Hs.431200-S | rs12469091 | 2 | 200950241 | 55730 | 6.1125 | 0.3347 | 6.59 | 5.52 | 4.47 | 3.58 | CEU |
| Hs.43687 | Hs.43687-S | rs7853349 | 9 | 97729814 | 13756 | 6.5305 | 0.3559 | 7.03 | 5.96 | 4.51 | 3.74 | CEU |
| Hs.453941 | Hs.453941-S | rs2460970 | 8 | 119698635 | 108759 | 14.8934 | 0.6652 | 6.36 | 5.69 | 4.74 | 3.94 | CEU |
| Hs.460359 | Hs.460359-S | rs3760106 | 16 | 23753297 | 58998 | 7.6169 | 0.4079 | 7.09 | 5.63 | 4.55 | 3.8 | CEU |
| Hs.465789 | Hs.465789-S | rs10411185 | 19 | 8009881 | 30281 | 6.1673 | 0.3375 | 6.88 | 5.66 | 4.6 | 3.83 | CEU |
| Hs.466924 | Hs.466924-S | rs10409138 | 19 | 50316143 | 5875 | 11.8788 | 0.5756 | 7.74 | 6.13 | 4.72 | 3.88 | CEU |
| Hs.473917 | Hs.473917-S | rs228070 | 21 | 42833590 | 14002 | 6.4151 | 0.355 | 7.21 | 5.99 | 4.99 | 4.15 | CEU |
| Hs.482037 | Hs.482037-S | rs6451694 | 5 | 43479504 | 71762 | 6.0046 | 0.3292 | 7.24 | 5.97 | 4.46 | 3.51 | CEU |
| Hs.485895 | Hs.485895-S | rs6921673 | 6 | 88061477 | 64787 | 9.7679 | 0.4993 | 6.52 | 5.19 | 4.43 | 3.67 | CEU |
| Hs.490095 | Hs.490095-S | rs7791880 | 7 | 130244703 | 435 | 8.4502 | 0.4508 | 9.34 | 7.37 | 5.67 | 4.51 | CEU |
| Hs.495422 | Hs.495422-S | rs886090 | 9 | 133229057 | 5583 | 8.6069 | 0.4518 | 6.93 | 5.59 | 4.56 | 3.84 | CEU |
| Hs.506072 | Hs.506072-S | rs6451535 | 5 | 40723788 | 138673 | 6.2348 | 0.341 | 6.25 | 5.15 | 4.24 | 3.56 | CEU |
| Hs.515955 | Hs.515955-S | rs6750539 | 2 | 42949323 | 20468 | 5.8028 | 0.3187 | 6.78 | 5.4 | 4.41 | 3.68 | CEU |
| Hs.517172 | Hs.517172-S | rs6010789 | 20 | 61031598 | 104 | 5.7759 | 0.3173 | 6.63 | 5.72 | 4.49 | 3.73 | CEU |
| Hs.519979 | Hs.519979-S | rs2517861 | 6 | 29929961 | 75385 | 8.8025 | 0.4601 | 6.56 | 5.46 | 4.31 | 3.53 | CEU |
| Hs.6637 | Hs.6637-S | rs1317149 | 11 | 47443461 | 140274 | 10.6293 | 0.5319 | 5.83 | 5.25 | 3.94 | 3.19 | CEU |
| HSRTSBETA | GI_42544116-I | rs7228136 | 18 | 722017 | 19625 | 9.076 | 0.4715 | 6.5 | 5.4 | 4.53 | 3.74 | CEU |
| IFIT5 | GI_6912629-S | rs10509571 | 10 | 91082538 | 87945 | 6.582 | 0.3584 | 6.73 | 5.83 | 4.51 | 3.76 | CEU |
| IL16 | GI_27262656-I | rs4778636 | 15 | 79378694 | 9201 | 7.0568 | 0.3816 | 7.51 | 5.43 | 4.44 | 3.73 | CEU |
| IMAGE3451454 | GI_26024192-S | rs10753434 | 1 | 223867335 | 408162 | 5.769 | 0.3169 | 6.37 | 5.26 | 4.21 | 3.47 | CEU |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| IMMT | GI_5803114-S | rs7588325 | 2 | 86327231 | 44082 | 6.5487 | 0.3618 | 5.6 | 5.11 | 4.3 | 3.57 | CEU |
| IPP | GI_5174472-S | rs3811436 | 1 | 45794973 | 38862 | 5.5884 | 0.3165 | 6.5 | 5.38 | 4.18 | 3.32 | CEU |
| IRAK1BP1 | GI_27498358-S | rs9359355 | 6 | 79659533 | 4990 | 5.2975 | 0.296 | 7.09 | 5.2 | 4.43 | 3.66 | CEU |
| IREB2 | GI_41352692-S | rs2036527 | 15 | 76638670 | 60396 | 5.9633 | 0.327 | 6.64 | 5.66 | 4.57 | 3.72 | CEU |
| IRF5 | GI_38683858-A | rs6969930 | 7 | 128224264 | 41122 | 19.0053 | 0.7579 | 6.87 | 5.65 | 4.53 | 3.71 | CEU |
| KIAA0251 | GI_37541419-S | rs4985124 | 16 | 15032942 | 4530 | 6.455 | 0.3521 | 5.8 | 5.16 | 4.22 | 3.44 | CEU |
| KIAA0265 | GI_44917618-S | rs4324873 | 7 | 129355034 | 12096 | 8.2234 | 0.4351 | 6.38 | 5.36 | 4.45 | 3.72 | CEU |
| KIAA0483 | GI_7662157-S | rs7524705 | 1 | 220645735 | 7708 | 6.8255 | 0.3704 | 6.57 | 5.31 | 4.19 | 3.45 | CEU |
| KIAA0643 | GI_13435144-S | rs8061528 | 16 | 3596483 | 69290 | 7.541 | 0.4044 | 8.83 | 5.92 | 4.59 | 3.76 | CEU |
| KIAA0748 | GI_7662281-S | rs2171497 | 12 | 53630400 | 1979 | 8.3146 | 0.4391 | 6.26 | 5.72 | 4.43 | 3.63 | CEU |
| KIAA1271 | GI_42734342-S | rs7262903 | 20 | 3791027 | 5791 | 5.4465 | 0.2998 | 6.73 | 5.36 | 4.39 | 3.76 | CEU |
| KIAA1463 | GI_39930390-S | rs2280503 | 12 | 49424954 | 39 | 28.9628 | 0.8899 | 6.98 | 5.53 | 4.41 | 3.55 | CEU |
| KIAA1627 | GI_34147341-S | rs3775836 | 4 | 120021334 | 32126 | 5.6359 | 0.3144 | 6.78 | 5.58 | 4.26 | 3.47 | CEU |
| LCMT1 | GI_15082255-I | rs7188975 | 16 | 25044950 | 71178 | 14.7967 | 0.6626 | 7.59 | 5.77 | 4.48 | 3.8 | CEU |
| LOC132001 | GI_34147617-S | rs404171 | 3 | 11862351 | 28552 | 9.6228 | 0.5536 | 8.14 | 5.53 | 4.48 | 3.7 | CEU |
| LOC132321 | GI_27735074-S | rs2162126 | 4 | 130136681 | 254530 | 6.476 | 0.3581 | 7.49 | 5.67 | 4.27 | 3.53 | CEU |
| LOC135043 | GI_17463264-S | rs2294335 | 6 | 166726541 | 465 | 12.4357 | 0.5937 | 7.11 | 5.59 | 4.6 | 3.87 | CEU |
| LOC147804 | GI_30154892-S | rs1984432 | 19 | 58650075 | 10454 | 7.9982 | 0.4252 | 7.6 | 5.89 | 4.62 | 3.89 | CEU |
| LOC151963 | GI_31341922-S | rs9869202 | 3 | 194107892 | 110325 | 8.857 | 0.4624 | 7.24 | 5.78 | 4.6 | 3.8 | CEU |
| LOC166867 | GI_27477322-S | rs4832971 | 4 | 37776393 | 14 | 11.72 | 0.5703 | 6.65 | 5.73 | 4.6 | 3.83 | CEU |
| LOC282956 | GI_27483210-S | rs2844529 | 6 | 31461572 | 8979 | 7.6218 | 0.4081 | 6.68 | 5.56 | 4.39 | 3.67 | CEU |
| LOC283710 | GI_27483466-S | rs1060493 | 15 | 29303762 | 1273 | 5.6661 | 0.3115 | 6.32 | 5.25 | 4.27 | 3.57 | CEU |
| LOC283970 | GI_40217627-S | rs9939092 | 16 | 68596778 | 28928 | 20.7681 | 0.7894 | 6.51 | 5.56 | 4.22 | 3.4 | CEU |
| LOC284184 | GI_27500527-S | rs2255166 | 17 | 76828157 | 146 | 19.2124 | 0.7678 | 6.76 | 5.58 | 4.48 | 3.71 | CEU |
| LOC284293 | GI_27485378-S | rs8090046 | 18 | 59773066 | 1480 | 15.6321 | 0.6841 | 9.19 | 6.84 | 5.04 | 4.02 | CEU |
| LOC285407 | GI_37550539-S | rs9758051 | 3 | 131297567 | 2507 | 6.2265 | 0.3406 | 6.7 | 5.37 | 4.15 | 3.41 | CEU |
| LOC286353 | GI_27478844-S | rs7871709 | 9 | 95640165 | 8105 | 8.2418 | 0.436 | 6.22 | 5.76 | 4.45 | 3.66 | CEU |
| LOC339231 | GI_29739147-S | rs7226091 | 17 | 77247772 | 11165 | 9.9599 | 0.5067 | 7.07 | 5.53 | 4.46 | 3.71 | CEU |
| LOC339803 | GI_42656315-S | rs2060824 | 2 | 61396207 | 115207 | 5.8816 | 0.3228 | 7.8 | 5.28 | 4.32 | 3.59 | CEU |
| LOC339804 | GI_37546921-S | rs1729660 | 2 | 61277463 | 24478 | 9.2264 | 0.4776 | 6.46 | 5.22 | 4.36 | 3.57 | CEU |
| LOC340435 | GI_29735811-S | rs1493198 | 8 | 72014511 | 232584 | 14.8383 | 0.6637 | 6.36 | 5.54 | 4.48 | 3.72 | CEU |
| LOC347981 | GI_30160064-S | rs2394180 | 6 | 29913178 | 49365 | 5.5372 | 0.3046 | 6.39 | 5.35 | 4.33 | 3.53 | CEU |
| LOC348094 | GI_38176293-S | rs4238397 | 15 | 62966217 | 71597 | 17.9295 | 0.7488 | 5.42 | 4.89 | 4.09 | 3.33 | CEU |
| LOC374758 | GI_37544593-S | rs4130140 | 17 | 257873 | 6297 | 15.3049 | 0.6758 | 7.14 | 6.15 | 4.84 | 3.92 | CEU |
| LOC375097 | GI_37555934-S | rs1739652 | 20 | 36482373 | 561 | 9.0894 | 0.472 | 7.55 | 5.46 | 4.39 | 3.6 | CEU |
| LOC375165 | GI_37563669-S | rs5755542 | 22 | 33767553 | 173150 | 7.0481 | 0.3812 | 10.6 | 6.76 | 5.37 | 4.27 | CEU |
| LOC375399 | GI_37540365-S | rs1048447 | 4 | 68312238 | 103237 | 6.0242 | 0.3302 | 6.26 | 5.21 | 4.22 | 3.46 | CEU |
| LOC378075 | GI_37538916-S | rs1113765 | 7 | 55663543 | 294391 | 14.2362 | 0.6474 | 6.04 | 5.37 | 4.33 | 3.57 | CEU |
| LOC399987 | GI_42660080-S | rs9300302 | 12 | 3737732 | 1669 | 8.3153 | 0.4392 | 7.78 | 6.6 | 4.86 | 4.03 | CEU |
| LOC400051 | GI_42659981-S | rs2051993 | 12 | 66699945 | 1068 | 8.3441 | 0.4404 | 8.49 | 7.62 | 5.57 | 4.39 | CEU |
| LOC400410 | GI_42660516-S | rs2303824 | 15 | 78002652 | 8639 | 8.7319 | 0.4571 | 7.32 | 5.67 | 4.59 | 3.81 | CEU |
| LOC400566 | GI_42661283-S | rs4130140 | 17 | 257873 | 6769 | 22.2377 | 0.8125 | 7.75 | 6.26 | 4.78 | 3.84 | CEU |
| LOC400642 | GI_42661344-S | rs12352 | 18 | 5233083 | 3268 | 16.883 | 0.7138 | 7.23 | 5.35 | 4.51 | 3.8 | CEU |
| LOC400684 | GI_42661568-S | rs4805755 | 19 | 37546310 | 26656 | 6.0728 | 0.3327 | 7.06 | 5.42 | 4.34 | 3.63 | CEU |
| LOC400933 | GI_42662518-S | rs5770594 | 22 | 48339358 | 209894 | 14.6802 | 0.6595 | 7 | 5.89 | 4.82 | 4.02 | CEU |
| LOC400999 | GI_42656206-S | rs6747638 | 2 | 113138206 | 22507 | 11.2224 | 0.5595 | 7.56 | 5.77 | 4.49 | 3.64 | CEU |
| LOC401075 | GI_42656649-S | rs13093220 | 3 | 75853445 | 10487 | 5.5998 | 0.3424 | 5.83 | 5.12 | 4.2 | 3.49 | CEU |
| LOC401135 | GI_42657007-S | rs1048447 | 4 | 68312238 | 104593 | 5.9608 | 0.3269 | 6.11 | 5.17 | 4.24 | 3.46 | CEU |
| LOC401284 | GI_42657559-S | rs2294335 | 6 | 166726541 | 8502 | 10.007 | 0.5085 | 6.38 | 5.71 | 4.46 | 3.81 | CEU |
| LOC402476 | GI_42658265-S | rs4092051 | 7 | 32494319 | 80904 | 5.5341 | 0.3231 | 7.11 | 5.25 | 4.41 | 3.7 | CEU |
| LOC51240 | GI_31377759-S | rs893784 | 2 | 190361789 | 99203 | 24.5172 | 0.8435 | 6.09 | 5.31 | 4.23 | 3.48 | CEU |
| LOC90637 | GI_32698821-S | rs7809667 | 7 | 981681 | 15836 | 5.7244 | 0.3388 | 6.38 | 5.14 | 4.27 | 3.52 | CEU |
| LOC90693 | GI_40255028-S | rs11980035 | 7 | 23401773 | 54210 | 9.7067 | 0.5092 | 7.82 | 5.64 | 4.52 | 3.75 | CEU |
| LOC93349 | GI_20149710-S | rs725202 | 2 | 231079873 | 13936 | 11.5422 | 0.5642 | 6.58 | 5.54 | 4.44 | 3.73 | CEU |
| MAN1A2 | GI_40254840-S | rs1418452 | 1 | 117582420 | 195158 | 16.0068 | 0.6933 | 6.56 | 5.75 | 4.44 | 3.61 | CEU |
| MCMDC1 | GI_33469926-S | rs988098 | 6 | 119281925 | 8141 | 6.202 | 0.3393 | 6.65 | 5.23 | 4.33 | 3.57 | CEU |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MGC10120 | GI_28603839-S | rs12762869 | 10 | 101983702 | 40795 | 13.4081 | 0.6236 | 6.81 | 6.15 | 4.87 | 3.87 | CEU |
| MGC12458 | GI_14150107-S | rs616540 | 1 | 241522450 | 54630 | 15.0076 | 0.6682 | 6.86 | 5.66 | 4.62 | 3.88 | CEU |
| MGC19764 | GI_42661257-S | rs883416 | 17 | 30594554 | 24027 | 10.8539 | 0.5401 | 6.35 | 5.46 | 4.42 | 3.69 | CEU |
| MGC20481 | GI_33086946-S | rs1453183 | 15 | 38650222 | 17447 | 7.789 | 0.4157 | 6.83 | 5.44 | 4.28 | 3.54 | CEU |
| MGC20781 | GI_34147471-S | rs1128966 | 17 | 37237375 | 2224 | 6.6833 | 0.3634 | 6.27 | 5.11 | 4.18 | 3.48 | CEU |
| MGC22773 | GI_21687083-S | rs1412825 | 1 | 74375835 | 17816 | 6.5448 | 0.3566 | 5.96 | 5.14 | 4.24 | 3.48 | CEU |
| MGC22960 | GI_40316917-S | rs1057533 | 1 | 46527856 | 14625 | 7.3353 | 0.3948 | 6.83 | 5.38 | 4.31 | 3.44 | CEU |
| MGC24665 | GI_24308244-S | rs243323 | 16 | 11268703 | 84214 | 8.5539 | 0.4495 | 6.95 | 5.42 | 4.4 | 3.69 | CEU |
| MGC2752 | GI_33859747-S | rs4801614 | 19 | 63788762 | 3550 | 22.8227 | 0.821 | 6.15 | 5.15 | 4.1 | 3.35 | CEU |
| MGC3794 | GI_33239373-S | rs2235207 | 1 | 164890920 | 10296 | 7.4425 | 0.3998 | 7.21 | 5.42 | 4.45 | 3.74 | CEU |
| MGC4083 | GI_14210535-S | rs4796960 | 18 | 12308027 | 8169 | 5.5838 | 0.3162 | 7.25 | 5.55 | 4.48 | 3.71 | CEU |
| MGC45416 | GI_22748848-S | rs12504699 | 4 | 48775226 | 38261 | 5.2663 | 0.29 | 6.14 | 5.17 | 3.97 | 3.19 | CEU |
| MGC9084 | GI_15553096-S | rs12143161 | 1 | 166511322 | 17800 | 6.9254 | 0.3804 | 6.77 | 5.58 | 4.44 | 3.67 | CEU |
| MK-STYX | GI_32481212-S | rs8565 | 7 | 75274925 | 17 | 5.279 | 0.2907 | 6.4 | 5.12 | 4.1 | 3.44 | CEU |
| MMRP19 | GI_7705723-S | rs2956077 | 11 | 34919504 | 52976 | 6.0472 | 0.3361 | 6.45 | 5.23 | 4.4 | 3.74 | CEU |
| MOCOS | GI_8923660-S | rs617505 | 18 | 32051949 | 50616 | 6.1732 | 0.3427 | 8.1 | 5.81 | 4.65 | 3.74 | CEU |
| MRPL21 | GI_31652223-A | rs604524 | 11 | 68386505 | 28909 | 7.6359 | 0.4087 | 6.45 | 5.71 | 4.34 | 3.62 | CEU |
| MRPL43 | GI_28872737-I | rs735137 | 10 | 102725825 | 7970 | 18.1255 | 0.7405 | 7.3 | 5.61 | 4.46 | 3.64 | CEU |
| MRPL53 | GI_22035595-S | rs12621015 | 2 | 74864843 | 253449 | 5.6224 | 0.3092 | 6.64 | 5.27 | 4.33 | 3.62 | CEU |
| MTERF | GI_14790134-S | rs6972637 | 7 | 91251595 | 104412 | 9.7429 | 0.4983 | 6.43 | 5.59 | 4.31 | 3.59 | CEU |
| MYOM2 | GI_4505314-S | rs2280902 | 8 | 2064479 | 16074 | 7.3664 | 0.3962 | 7.56 | 5.95 | 4.77 | 4.03 | CEU |
| NDUFS5 | GI_4758789-S | rs10888650 | 1 | 39176254 | 15118 | 9.5608 | 0.4911 | 6.36 | 5.3 | 4.41 | 3.72 | CEU |
| NMNAT3 | GI_31342325-S | rs9822952 | 3 | 140867955 | 106092 | 11.5165 | 0.5633 | 7.38 | 6.03 | 4.58 | 3.75 | CEU |
| NUDT2 | GI_22265329-I | rs10814080 | 9 | 34216942 | 109312 | 8.6467 | 0.4535 | 6.99 | 5.56 | 4.33 | 3.57 | CEU |
| OAS1 | GI_8051622-I | rs2285934 | 12 | 111814240 | 4018 | 8.311 | 0.439 | 9.44 | 6.96 | 5.03 | 3.95 | CEU |
| PACSIN2 | GI_6005825-S | rs1546861 | 22 | 41679665 | 89192 | 5.88 | 0.3227 | 7.32 | 5.6 | 4.49 | 3.79 | CEU |
| PASK | GI_35038527-S | rs6437235 | 2 | 241742520 | 23448 | 6.3194 | 0.3604 | 7.55 | 5.54 | 4.47 | 3.66 | CEU |
| PBX4 | GI_15149471-S | rs10423674 | 19 | 18678903 | 854878 | 6.3257 | 0.3456 | 6.3 | 5.21 | 4.12 | 3.46 | CEU |
| PDLIM2 | GI_40288186-A | rs3735894 | 8 | 22510771 | 3117 | 5.6552 | 0.3154 | 6.93 | 5.65 | 4.51 | 3.77 | CEU |
| PEX5 | GI_37059745-S | rs3816424 | 12 | 7251496 | 3666 | 5.6886 | 0.3127 | 6.73 | 5.5 | 4.47 | 3.73 | CEU |
| PEX6 | GI_21361243-S | rs2296804 | 6 | 43039239 | 664 | 14.9901 | 0.6677 | 7.43 | 5.38 | 4.4 | 3.7 | CEU |
| PGS1 | GI_21314623-S | rs2376585 | 17 | 73929478 | 2532 | 8.1342 | 0.4312 | 7.36 | 5.9 | 4.7 | 3.95 | CEU |
| PHACS | GI_14211920-S | rs2074038 | 11 | 44044565 | 17304 | 15.5972 | 0.6832 | 9.37 | 6.73 | 5.03 | 4.03 | CEU |
| PHC2 | GI_37595529-A | rs1998624 | 1 | 33560242 | 101670 | 12.012 | 0.5929 | 6.73 | 5.53 | 4.43 | 3.63 | CEU |
| PHEMX | GI_37595532-A | rs937614 | 11 | 2283496 | 12377 | 5.9016 | 0.3238 | 6.52 | 5.72 | 4.52 | 3.79 | CEU |
| PIP5K1C | GI_31317308-S | rs1476591 | 19 | 3630607 | 49262 | 8.8446 | 0.4618 | 7.21 | 5.48 | 4.52 | 3.83 | CEU |
| PIP5K2A | GI_20302162-S | rs12768091 | 10 | 22488091 | 377874 | 6.248 | 0.3417 | 5.76 | 5.28 | 4.17 | 3.42 | CEU |
| PKHD1L1 | GI_31377831-S | rs1009371 | 8 | 110567126 | 41129 | 10.6428 | 0.5324 | 8.26 | 5.55 | 4.31 | 3.53 | CEU |
| POLR2E | GI_14589950-S | rs6843 | 19 | 1039285 | 9 | 16.6121 | 0.7076 | 6.36 | 5.37 | 4.54 | 3.87 | CEU |
| POLR2J | GI_21704275-S | rs4473948 | 7 | 101706117 | 1562 | 8.1919 | 0.4338 | 6.32 | 5.57 | 4.47 | 3.64 | CEU |
| PP3856 | GI_40255088-S | rs10282929 | 8 | 144752920 | 24787 | 9.9216 | 0.5052 | 6.39 | 5.63 | 4.59 | 3.71 | CEU |
| PP784 | GI_31559785-S | rs4493618 | 4 | 6819275 | 8484 | 7.3155 | 0.3939 | 7.42 | 6 | 4.63 | 3.92 | CEU |
| PPA2 | GI_31881619-A | rs11932428 | 4 | 106644740 | 3679 | 10.0827 | 0.5114 | 7.76 | 6.36 | 4.9 | 3.89 | CEU |
| PPFIA1 | GI_29171752-I | rs12295241 | 11 | 69872272 | 29712 | 6.4821 | 0.3584 | 6.8 | 5.54 | 4.62 | 3.81 | CEU |
| PPIL3 | GI_19557635-A | rs7606251 | 2 | 201562240 | 929 | 14.9112 | 0.6656 | 7.91 | 6.36 | 4.89 | 3.83 | CEU |
| PTER | GI_20070185-S | rs1055340 | 10 | 16595534 | 974 | 11.8775 | 0.5755 | 7.07 | 5.35 | 4.45 | 3.72 | CEU |
| QRSL1 | GI_19923522-S | rs1026619 | 6 | 107221054 | 740 | 15.4883 | 0.6805 | 6.67 | 5.66 | 4.57 | 3.84 | CEU |
| R29124_1 | GI_16117774-S | rs2302188 | 19 | 46777713 | 110 | 10.6592 | 0.533 | 7.19 | 5.18 | 4.22 | 3.5 | CEU |
| RAB40B | GI_5803162-S | rs2254862 | 17 | 78243554 | 34648 | 5.2707 | 0.2903 | 6.75 | 5.22 | 4.17 | 3.47 | CEU |
| RAPGEFL1 | GI_7705938-S | rs2715554 | 17 | 35742696 | 137361 | 8.1818 | 0.439 | 6.31 | 5.64 | 4.43 | 3.52 | CEU |
| RBMS2 | GI_4506448-S | rs3782235 | 12 | 55201814 | 67204 | 5.3883 | 0.2966 | 6.04 | 5.29 | 4.27 | 3.52 | CEU |
| RDH5 | GI_4506462-S | rs3138142 | 12 | 54401852 | 2824 | 6.7573 | 0.3722 | 5.78 | 5.24 | 4.2 | 3.49 | CEU |
| RPAP1 | GI_24430138-S | rs1867419 | 15 | 39593511 | 3379 | 6.1812 | 0.3383 | 6.27 | 5.25 | 4.22 | 3.49 | CEU |
| RPL36AL | GI_34335143-S | rs3007033 | 14 | 49173566 | 16491 | 7.0651 | 0.382 | 6.21 | 5.46 | 4.37 | 3.61 | CEU |
| RPL8 | GI_15431305-I | rs2955194 | 8 | 145959711 | 28773 | 7.8468 | 0.4184 | 6.82 | 5.52 | 4.37 | 3.66 | CEU |
| RPLP2 | GI_16905512-S | rs4131364 | 11 | 802188 | 1887 | 5.5964 | 0.3078 | 6.45 | 5.41 | 4.39 | 3.65 | CEU |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RPS6KB2 | GI_4506738-S | rs1476792 | 11 | 66952813 | 6532 | 8.7889 | 0.4653 | 6.47 | 5.28 | 4.09 | 3.37 | CEU |
| SARS2 | GI_20149644-S | rs10410544 | 19 | 44077372 | 20482 | 6.2798 | 0.3433 | 6.92 | 5.64 | 4.37 | 3.67 | CEU |
| SERPINB10 | GI_4826901-S | rs6567399 | 18 | 59695526 | 57666 | 11.4522 | 0.5611 | 6.33 | 5.63 | 4.43 | 3.72 | CEU |
| SF1 | GI_42544126-I | rs693235 | 11 | 64249338 | 50961 | 14.1409 | 0.6447 | 9.37 | 6.32 | 4.83 | 3.78 | CEU |
| SH3GLB2 | GI_24431995-S | rs10988156 | 9 | 128770063 | 80074 | 5.656 | 0.3109 | 6.37 | 5.37 | 4.48 | 3.75 | CEU |
| SHMT1 | GI_22547185-I | rs941451 | 17 | 18114705 | 64948 | 5.8053 | 0.3234 | 6.37 | 5.03 | 4.15 | 3.41 | CEU |
| SIVA | GI_11277467-I | rs3803304 | 14 | 104310191 | 17028 | 6.2521 | 0.3419 | 6.52 | 5.2 | 4.3 | 3.59 | CEU |
| SMAP-5 | GI_40255261-S | rs6875066 | 5 | 143535801 | 16027 | 5.6196 | 0.309 | 6.62 | 5.29 | 4.31 | 3.57 | CEU |
| SNAP29 | GI_18765736-S | rs853141 | 22 | 19343827 | 224644 | 5.5626 | 0.306 | 6.42 | 5.37 | 4.37 | 3.61 | CEU |
| SNX11 | GI_23111027-I | rs1452665 | 17 | 43652150 | 109054 | 7.5006 | 0.4079 | 7.54 | 5.32 | 4.36 | 3.55 | CEU |
| SPG7 | GI_40806172-I | rs8043788 | 16 | 88077063 | 54306 | 7.6816 | 0.4108 | 7.79 | 6.31 | 4.67 | 3.76 | CEU |
| SQSTM1 | GI_19923742-S | rs10277 | 5 | 179197337 | 249 | 8.5082 | 0.4475 | 6.78 | 5.67 | 4.48 | 3.78 | CEU |
| ST7L | GI_38201636-I | rs10857963 | 1 | 112803529 | 6980 | 9.744 | 0.4983 | 7.67 | 5.58 | 4.35 | 3.67 | CEU |
| STK25 | GI_34147665-S | rs2240482 | 2 | 242125011 | 29600 | 12.6598 | 0.6205 | 6.26 | 5.26 | 4.24 | 3.52 | CEU |
| SUPT3H | GI_4507308-A | rs1329715 | 6 | 45017493 | 11608 | 5.8126 | 0.3385 | 7.91 | 5.72 | 4.71 | 3.82 | CEU |
| SYMPK | GI_4759195-S | rs2014576 | 19 | 50960916 | 50714 | 5.6609 | 0.3112 | 6.3 | 5.5 | 4.54 | 3.83 | CEU |
| SYNGR1 | GI_39777618-I | rs909685 | 22 | 38072171 | 26570 | 9.2568 | 0.4789 | 7.12 | 5.97 | 4.66 | 3.79 | CEU |
| SYNGR3 | GI_22091456-S | rs1058474 | 16 | 1988797 | 4895 | 6.6957 | 0.364 | 6.79 | 6.1 | 4.44 | 3.7 | CEU |
| TAPBP-R | GI_34222333-S | rs2041385 | 12 | 6432554 | 9078 | 6.4355 | 0.3511 | 7.62 | 5.6 | 4.5 | 3.77 | CEU |
| TBC1D4 | GI_42660198-S | rs2297207 | 13 | 74771788 | 14413 | 7.8076 | 0.4278 | 7.43 | 5.57 | 4.57 | 3.76 | CEU |
| TEF | GI_34486096-S | rs5996091 | 22 | 40668766 | 549034 | 8.071 | 0.4284 | 6.52 | 5.37 | 4.07 | 3.31 | CEU |
| THAP5 | GI_32698887-S | rs40915 | 7 | 107776670 | 22024 | 10.8858 | 0.5412 | 6.51 | 5.69 | 4.4 | 3.66 | CEU |
| THAP6 | GI_37059751-S | rs6841171 | 4 | 76645835 | 165244 | 6.2267 | 0.3406 | 6.94 | 5.4 | 4.38 | 3.59 | CEU |
| THOC3 | GI_14150170-S | rs4958955 | 5 | 177192735 | 50976 | 8.503 | 0.4473 | 6.91 | 5.53 | 4.42 | 3.6 | CEU |
| TIMM10 | GI_6912707-S | rs2649662 | 11 | 57109138 | 56520 | 8.8099 | 0.4722 | 6.02 | 5.28 | 4.22 | 3.5 | CEU |
| TINP1 | GI_21359901-S | rs10515199 | 5 | 74135390 | 29871 | 7.5288 | 0.4038 | 6.7 | 5.7 | 4.41 | 3.67 | CEU |
| TMEM8 | GI_10864068-S | rs3830160 | 16 | 359093 | 3084 | 12.006 | 0.5798 | 7.1 | 5.51 | 4.33 | 3.63 | CEU |
| TMPIT | GI_13994299-S | rs7794040 | 7 | 75265292 | 4133 | 5.6368 | 0.3099 | 7.02 | 5.41 | 4.14 | 3.39 | CEU |
| TRAPPC4 | GI_7706666-S | rs7131534 | 11 | 118391866 | 7432 | 6.5448 | 0.3667 | 8.38 | 5.5 | 4.4 | 3.68 | CEU |
| TRIM4 | GI_15011940-A | rs2527919 | 7 | 99139164 | 5791 | 6.8293 | 0.3706 | 6.62 | 5.46 | 4.17 | 3.37 | CEU |
| TRPM7 | GI_29893551-S | rs8035534 | 15 | 48740323 | 99641 | 6.2657 | 0.3426 | 6.51 | 5.53 | 4.36 | 3.6 | CEU |
| TSGA10 | GI_41281983-I | rs4340581 | 2 | 99183543 | 32884 | 6.3801 | 0.3483 | 7.33 | 5.34 | 4.27 | 3.44 | CEU |
| TSGA2 | GI_18254455-S | rs2839533 | 21 | 42770095 | 4102 | 6.9227 | 0.3803 | 7.23 | 6.01 | 4.81 | 4.01 | CEU |
| TSSC1 | GI_4507702-S | rs17682 | 2 | 4731323 | 20 | 5.469 | 0.301 | 6.29 | 5.44 | 4.45 | 3.73 | CEU |
| TUBB | GI_4507728-S | rs4305774 | 6 | 3149678 | 50583 | 8.3603 | 0.4411 | 6.44 | 5.67 | 4.54 | 3.84 | CEU |
| UBA52 | GI_15451941-S | rs2283616 | 19 | 18543495 | 3485 | 28.0428 | 0.8816 | 7.21 | 5.92 | 4.48 | 3.69 | CEU |
| UBE2G1 | GI_33359696-A | rs7212158 | 17 | 3861900 | 259212 | 5.6446 | 0.3149 | 7.59 | 5.45 | 4.52 | 3.76 | CEU |
| UGT2B11 | GI_4507822-S | rs3100645 | 4 | 69671954 | 575169 | 13.7501 | 0.6336 | 7.16 | 5.89 | 4.37 | 3.52 | CEU |
| UGT2B17 | GI_4507820-S | rs3100645 | 4 | 69671954 | 440125 | 13.1178 | 0.6149 | 8.06 | 5.96 | 4.34 | 3.39 | CEU |
| UGT2B7 | GI_4507824-S | rs3100645 | 4 | 69671954 | 487102 | 12.9334 | 0.6093 | 7.48 | 5.93 | 4.27 | 3.44 | CEU |
| UROS | GI_4557872-S | rs7919631 | 10 | 127457290 | 9935 | 6.0083 | 0.3341 | 7 | 5.78 | 4.58 | 3.78 | CEU |
| USMG5 | GI_14249375-S | rs1163073 | 10 | 105012924 | 131111 | 23.4641 | 0.8298 | 6.16 | 5.16 | 4.27 | 3.52 | CEU |
| VPS11 | GI_17978476-S | rs1003081 | 11 | 118419203 | 38402 | 6.7946 | 0.3689 | 5.78 | 5.35 | 4.36 | 3.66 | CEU |
| WARS2 | GI_41352698-S | rs2765542 | 1 | 119272368 | 15368 | 8.0592 | 0.4279 | 7.68 | 5.56 | 4.4 | 3.61 | CEU |
| WBSCR27 | GI_30795189-S | rs8629 | 7 | 72690170 | 3632 | 14.2531 | 0.6478 | 6.75 | 5.45 | 4.16 | 3.38 | CEU |
| WWOX | GI_18860883-I | rs6564520 | 16 | 76863720 | 6316 | 7.7879 | 0.4212 | 7.51 | 5.9 | 4.8 | 4.01 | CEU |
| XRRA1 | GI_42659736-S | rs2298746 | 11 | 74231482 | 1489 | 16.0166 | 0.6935 | 6.62 | 5.46 | 4.36 | 3.61 | CEU |
| ZNF230 | GI_5454181-S | rs1060880 | 19 | 49207192 | 13 | 6.5585 | 0.3573 | 6.65 | 5.41 | 4.39 | 3.68 | CEU |
| ZNF266 | GI_37622342-A | rs6512121 | 19 | 9394805 | 10465 | 11.1428 | 0.5567 | 6.42 | 5.29 | 4.42 | 3.64 | CEU |
| ZNF384 | GI_36054193-S | rs10492096 | 12 | 6450843 | 195573 | 6.7528 | 0.3668 | 6.69 | 5.58 | 4.47 | 3.72 | CEU |
| ZNF493 | GI_40255231-S | rs1781873 | 19 | 21269271 | 131483 | 6.5573 | 0.3572 | 6.44 | 5.4 | 4.04 | 3.33 | CEU |
| ZNF587 | GI_14249531-S | rs7253130 | 19 | 63065942 | 5793 | 6.6247 | 0.3605 | 7.21 | 5.41 | 4.39 | 3.59 | CEU |
| ZNF79 | GI_24307936-S | rs2243898 | 9 | 127299544 | 12379 | 6.2668 | 0.3426 | 6.59 | 5.57 | 4.4 | 3.63 | CEU |
| ZNF85 | GI_4508038-S | rs10454111 | 19 | 20904788 | 20413 | 7.0152 | 0.3796 | 7.84 | 5.62 | 4.39 | 3.53 | CEU |
| ZRANB1 | GI_23943913-S | rs2114835 | 10 | 126620547 | 42948 | 6.449 | 0.3567 | 6.45 | 5.28 | 4.38 | 3.61 | CEU |
| 384D8-2 | GI_23097284-I | rs1008320 | 22 | 48289581 | 962243 | 6.1454 | 0.4258 | 6.82 | 5.07 | 4.18 | 3.49 | CHB |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ACN9 | GI_9910179-S | rs6973504 | 7 | 96392135 | 62985 | 7.3078 | 0.4916 | 6.47 | 5.78 | 4.4 | 3.6 | CHB |
| AD-017 | GI_8923854-A | rs3617 | 3 | 52808845 | 105022 | 8.6064 | 0.5564 | 6.44 | 5.34 | 4.24 | 3.49 | CHB |
| AMPD3 | GI_4502078-S | rs3741043 | 11 | 10456571 | 28166 | 5.4351 | 0.3818 | 7.95 | 5.4 | 4.31 | 3.64 | CHB |
| ANKRD27 | GI_14149802-S | rs2868145 | 19 | 37738954 | 40999 | 5.5241 | 0.3875 | 6.91 | 5.48 | 4.47 | 3.75 | CHB |
| AP3S2 | GI_39725670-S | rs2290351 | 15 | 88175785 | 2256 | 7.1143 | 0.4811 | 6.87 | 5.39 | 4.4 | 3.69 | CHB |
| APOBEC3B | GI_22907024-S | rs9611070 | 22 | 37720207 | 10176 | 7.6768 | 0.5109 | 7.39 | 5.95 | 4.64 | 3.82 | CHB |
| ARHGEF18 | GI_41327768-S | rs2967625 | 19 | 8204411 | 761251 | 5.5592 | 0.3897 | 6.49 | 5.55 | 4.48 | 3.77 | CHB |
| ARID1A | GI_21264568-A | rs4466675 | 1 | 26704154 | 88227 | 5.3857 | 0.3786 | 5.92 | 5.1 | 4.15 | 3.36 | CHB |
| AXIN1 | GI_31083143-A | rs393521 | 16 | 277679 | 20 | 7.096 | 0.4801 | 7.85 | 6.31 | 4.9 | 3.81 | CHB |
| B3GTL | GI_34996530-S | rs876540 | 13 | 30803449 | 106 | 7.695 | 0.5118 | 6.68 | 5.58 | 4.56 | 3.74 | CHB |
| B4GALT1 | GI_13929461-S | rs3780491 | 9 | 33119607 | 18689 | 9.8932 | 0.6128 | 6.5 | 5.22 | 4.42 | 3.67 | CHB |
| BARD1 | GI_4557348-S | rs280621 | 2 | 215416088 | 2901 | 5.5205 | 0.3873 | 6.41 | 5.31 | 4.33 | 3.56 | CHB |
| BTN3A2 | GI_34932495-S | rs9379851 | 6 | 26462759 | 21356 | 7.3691 | 0.4948 | 6.56 | 5.64 | 4.48 | 3.59 | CHB |
| C10orf68 | GI_13375961-S | rs2153875 | 10 | 33230573 | 18851 | 5.5891 | 0.3916 | 6.42 | 5.48 | 4.25 | 3.53 | CHB |
| C11orf21 | GI_7662662-S | rs2074022 | 11 | 2280617 | 6850 | 7.7403 | 0.5225 | 6.65 | 5.64 | 4.48 | 3.75 | CHB |
| C14orf130 | GI_28411949-A | rs2905 | 14 | 92763175 | 6731 | 8.9779 | 0.5735 | 7.64 | 5.37 | 4.38 | 3.7 | CHB |
| C14orf52 | GI_21553312-S | rs4902332 | 14 | 64445731 | 25025 | 23.1426 | 0.9055 | 7.8 | 6.22 | 4.73 | 3.81 | CHB |
| C1orf16 | GI_42476073-A | rs4047801 | 1 | 180146975 | 107742 | 6.0909 | 0.4226 | 6.79 | 5.12 | 4.21 | 3.48 | CHB |
| C21orf107 | GI_38026951-I | rs2836934 | 21 | 39486755 | 2428 | 15.4327 | 0.7849 | 7.92 | 6.46 | 5.21 | 4.22 | CHB |
| C6orf18 | GI_40538792-S | rs7745906 | 6 | 31311987 | 93255 | 6.5921 | 0.452 | 6.09 | 5.61 | 4.62 | 3.74 | CHB |
| C7orf13 | GI_14249145-S | rs6459698 | 7 | 155929790 | 1143 | 6.9816 | 0.4739 | 5.99 | 5.46 | 4.42 | 3.72 | CHB |
| C7orf32 | GI_42658665-S | rs7795944 | 7 | 149009114 | 6101 | 6.2549 | 0.4324 | 7.58 | 5.8 | 4.5 | 3.66 | CHB |
| C9orf88 | GI_24308286-S | rs7870985 | 9 | 127473353 | 126072 | 9.1454 | 0.581 | 10.2 | 7.09 | 5.26 | 4.05 | CHB |
| C9orf95 | GI_8923529-S | rs2273768 | 9 | 74927820 | 14288 | 7.3872 | 0.4958 | 6.07 | 5.5 | 4.37 | 3.76 | CHB |
| CAPN12 | GI_38707980-S | rs4802770 | 19 | 43915242 | 2083 | 6.5401 | 0.449 | 6.44 | 5.64 | 4.53 | 3.72 | CHB |
| CAPZA1 | GI_5453596-S | rs6682678 | 1 | 112918962 | 7167 | 7.6882 | 0.5115 | 6.24 | 5.36 | 4.28 | 3.51 | CHB |
| CARD8 | GI_7662403-S | rs2015209 | 19 | 53399477 | 3911 | 6.1993 | 0.4291 | 7.2 | 5.5 | 4.37 | 3.67 | CHB |
| CCNB1IP1 | GI_33519439-I | rs884368 | 14 | 19864349 | 8512 | 6.6332 | 0.4543 | 8.16 | 5.71 | 4.67 | 3.82 | CHB |
| CCNDBP1 | GI_16554567-I | rs540587 | 15 | 41265405 | 204 | 13.3917 | 0.7328 | 6.37 | 5.35 | 4.05 | 3.22 | CHB |
| CD151 | GI_34328914-A | rs3059 | 11 | 830319 | 1576 | 6.8408 | 0.4661 | 7.86 | 5.99 | 4.63 | 3.72 | CHB |
| CDK5RAP2 | GI_28872785-S | rs872423 | 9 | 120229045 | 1793 | 11.5552 | 0.6753 | 7.14 | 6.17 | 4.79 | 3.8 | CHB |
| CEP2 | GI_21735547-S | rs2248393 | 20 | 33389517 | 173483 | 4.7243 | 0.3479 | 5.72 | 4.62 | 3.85 | 3.2 | CHB |
| CGI-49 | GI_7705766-S | rs6689579 | 1 | 243217630 | 39314 | 6.3515 | 0.438 | 6.63 | 5.36 | 4.29 | 3.56 | CHB |
| CHCHD5 | GI_34147411-S | rs6760091 | 2 | 113093982 | 33897 | 5.8545 | 0.4082 | 6.47 | 5.21 | 4.22 | 3.51 | CHB |
| CHPT1 | GI_9910383-S | rs10860790 | 12 | 100700197 | 80766 | 7.0788 | 0.4873 | 6.35 | 5.64 | 4.48 | 3.7 | CHB |
| CKLF | GI_10092611-A | rs3743713 | 16 | 65140529 | 3527 | 6.3833 | 0.4399 | 7.13 | 5.53 | 4.19 | 3.44 | CHB |
| CKLFSF3 | GI_32130529-A | rs3743713 | 16 | 65140529 | 64378 | 7.2341 | 0.4876 | 6.28 | 5.34 | 4.28 | 3.48 | CHB |
| CN2 | GI_8922698-S | rs8084058 | 18 | 70328445 | 10530 | 5.8586 | 0.4084 | 7.62 | 5.71 | 4.69 | 3.93 | CHB |
| CORO2A | GI_34335234-A | rs2275708 | 9 | 98054873 | 88418 | 9.7024 | 0.6049 | 9.23 | 6.56 | 5.17 | 4.14 | CHB |
| CPEB4 | GI_32698754-S | rs7705502 | 5 | 173253421 | 64166 | 10.1955 | 0.625 | 10 | 6.42 | 4.86 | 3.95 | CHB |
| CPNE1 | GI_23397697-A | rs6060535 | 20 | 33698936 | 21264 | 6.4435 | 0.4593 | 6.91 | 5.25 | 4.14 | 3.31 | CHB |
| CRIPT | GI_41350204-S | rs1451156 | 2 | 46744253 | 19148 | 6.1087 | 0.4236 | 7.01 | 5.73 | 4.6 | 3.85 | CHB |
| CRYBB2 | GI_4503062-S | rs6519611 | 22 | 24170409 | 218080 | 37.9587 | 0.9806 | 8.09 | 6.77 | 5.24 | 4.11 | CHB |
| CSF2RB | GI_4559407-S | rs3817803 | 22 | 36224776 | 565673 | 6.5397 | 0.449 | 6.5 | 5.7 | 4.8 | 3.93 | CHB |
| CSTF3 | GI_4557494-S | rs3758741 | 11 | 33063192 | 29 | 6.7496 | 0.4609 | 6.87 | 5.32 | 4.23 | 3.51 | CHB |
| DCLRE1B | GI_24431998-S | rs10494163 | 1 | 114232754 | 64406 | 11.6873 | 0.6972 | 6.09 | 5.07 | 4.18 | 3.41 | CHB |
| DERP6 | GI_44662825-I | rs222843 | 17 | 7086705 | 9736 | 8.3669 | 0.5451 | 6.75 | 5.96 | 4.68 | 3.87 | CHB |
| DFNA5 | GI_4758153-S | rs754553 | 7 | 24532092 | 20763 | 7.9729 | 0.5259 | 7.74 | 5.35 | 4.5 | 3.73 | CHB |
| DHX38 | GI_41406095-S | rs7198572 | 16 | 70740721 | 36718 | 9.4701 | 0.6127 | 6.79 | 5.21 | 4.14 | 3.42 | CHB |
| dJ383J4.3 | GI_42655858-S | rs7539322 | 1 | 170347622 | 152854 | 14.494 | 0.7623 | 10.3 | 6.23 | 4.69 | 3.53 | CHB |
| DKFZP566H073 | GI_14149701-S | rs238230 | 17 | 4816290 | 27113 | 5.4888 | 0.3852 | 6.31 | 5.33 | 4.36 | 3.61 | CHB |
| DKFZP566J2046 | GI_13654273-S | rs2268670 | 16 | 1811330 | 7384 | 8.4667 | 0.5499 | 6.96 | 5.9 | 4.6 | 3.76 | CHB |
| DKFZP586D0919 | GI_24308058-S | rs2069502 | 12 | 56430932 | 31547 | 6.0583 | 0.4206 | 6.04 | 5.32 | 4.35 | 3.6 | CHB |
| DTNB | GI_37577100-A | rs6761076 | 2 | 25519409 | 7604 | 8.1355 | 0.5339 | 5.94 | 4.86 | 4.06 | 3.38 | CHB |
| EIF2S1 | GI_34147492-S | rs8004864 | 14 | 66942999 | 21466 | 7.6523 | 0.5096 | 6.52 | 5.28 | 4.18 | 3.36 | CHB |
| ELL3 | GI_13376767-S | rs689754 | 15 | 41563187 | 289222 | 6.6134 | 0.4611 | 6.9 | 4.96 | 3.81 | 3.16 | CHB |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ERAL1 | GI_24307898-S | rs9914988 | 17 | 24207230 | 4646 | 7.3416 | 0.4934 | 8.28 | 5.2 | 4 | 3.29 | CHB |
| ERCC1 | GI_42544170-A | rs2298881 | 19 | 50618756 | 8758 | 6.6394 | 0.4547 | 6.78 | 5.72 | 4.51 | 3.78 | CHB |
| EVER2 | GI_31377553-S | rs2871647 | 17 | 73649072 | 172 | 6.7109 | 0.4588 | 7.32 | 5.85 | 4.62 | 3.81 | CHB |
| F25965 | GI_28144915-S | rs3761090 | 19 | 40841290 | 95920 | 9.3736 | 0.5909 | 7.99 | 7.53 | 5.63 | 4.47 | CHB |
| FECH | GI_4557592-S | rs2272783 | 18 | 53389818 | 21579 | 6.4901 | 0.4461 | 6.39 | 5.59 | 4.57 | 3.81 | CHB |
| FGFR1OP | GI_36287109-A | rs3798308 | 6 | 167391205 | 32990 | 7.1128 | 0.4811 | 6.81 | 5.86 | 4.78 | 3.94 | CHB |
| FLJ10458 | GI_20070287-S | rs3744362 | 17 | 30483209 | 632 | 7.4091 | 0.4969 | 6.24 | 5.4 | 4.47 | 3.76 | CHB |
| FLJ10781 | GI_39780596-S | rs3745787 | 19 | 51663203 | 1435 | 24.5981 | 0.9191 | 8.44 | 7.07 | 5.42 | 4.19 | CHB |
| FLJ11273 | GI_40254892-S | rs1548882 | 7 | 12059465 | 13759 | 6.0277 | 0.4263 | 6.6 | 5.82 | 4.67 | 3.87 | CHB |
| FLJ11848 | GI_13376750-S | rs1670545 | 11 | 73263760 | 52450 | 7.2233 | 0.487 | 6.57 | 5.01 | 4.15 | 3.38 | CHB |
| FLJ12442 | GI_12597652-S | rs6445534 | 3 | 52718424 | 184746 | 10.1948 | 0.6612 | 6.31 | 5.3 | 4.1 | 3.34 | CHB |
| FLJ13220 | GI_11345459-S | rs2028321 | 4 | 44377928 | 163917 | 5.6672 | 0.4358 | 6.58 | 5.29 | 4.24 | 3.46 | CHB |
| FLJ14753 | GI_14211858-S | rs9299417 | 9 | 94098937 | 203506 | 13.9588 | 0.7484 | 9.7 | 7.33 | 5.63 | 4.28 | CHB |
| FLJ20635 | GI_8923587-S | rs104664 | 22 | 44032391 | 24700 | 13.4004 | 0.733 | 7.51 | 6.82 | 5.24 | 4.2 | CHB |
| FLJ20989 | GI_12751496-S | rs11782073 | 8 | 146271091 | 19432 | 5.2761 | 0.3715 | 6.05 | 4.81 | 3.81 | 3.06 | CHB |
| FLJ21347 | GI_31542722-S | rs1122634 | 17 | 45976364 | 11803 | 13.8454 | 0.7454 | 7.67 | 6.34 | 4.77 | 3.88 | CHB |
| FLJ22635 | GI_13376651-S | rs2242565 | 11 | 285343 | 40 | 6.1451 | 0.4258 | 6.03 | 4.79 | 3.97 | 3.28 | CHB |
| FLJ23235 | GI_13376422-S | rs2254075 | 4 | 38852749 | 61707 | 5.7592 | 0.4023 | 6.64 | 5.58 | 4.55 | 3.73 | CHB |
| FLJ32112 | GI_23308504-S | rs11206284 | 1 | 54290679 | 13575 | 7.9737 | 0.5259 | 6.6 | 5.64 | 4.57 | 3.77 | CHB |
| FLJ32191 | GI_34303923-S | rs8099987 | 19 | 42315312 | 3077 | 5.2252 | 0.3751 | 6.29 | 5.15 | 3.98 | 3.29 | CHB |
| FLJ32871 | GI_21389568-S | rs2541513 | 16 | 10668135 | 39119 | 7.048 | 0.4775 | 6.3 | 5.46 | 4.45 | 3.71 | CHB |
| FLJ46603 | GI_38348363-S | rs4789349 | 17 | 72217936 | 30427 | 22.9577 | 0.9089 | 8.12 | 6.54 | 5.15 | 4.05 | CHB |
| FLJ90036 | GI_31559781-S | rs6599293 | 4 | 123027 | 22841 | 8.5776 | 0.5551 | 8.13 | 5.59 | 4.11 | 3.3 | CHB |
| FN3KRP | GI_20149679-S | rs2257084 | 17 | 78280764 | 1892 | 8.049 | 0.5296 | 5.86 | 4.92 | 4.05 | 3.36 | CHB |
| FN5 | GI_9910225-S | rs7123345 | 11 | 92951521 | 100045 | 6.3641 | 0.4388 | 5.98 | 5.16 | 4.33 | 3.58 | CHB |
| FREB | GI_42544162-S | rs1891020 | 1 | 158426112 | 10457 | 6.23 | 0.4309 | 6.87 | 5.57 | 4.46 | 3.68 | CHB |
| FTHFSDC1 | GI_40018634-S | rs6557112 | 6 | 151522071 | 7138 | 6.7922 | 0.4633 | 7.18 | 5.78 | 4.59 | 3.83 | CHB |
| GALM | GI_20270354-S | rs752987 | 2 | 38798367 | 74450 | 5.5039 | 0.3862 | 6.97 | 5.42 | 4.34 | 3.61 | CHB |
| GBP3 | GI_24308156-S | rs10922533 | 1 | 89168680 | 16511 | 5.8938 | 0.4106 | 6.94 | 5.19 | 4.16 | 3.44 | CHB |
| GNA12 | GI_42476110-S | rs757791 | 7 | 2640537 | 96351 | 8.1282 | 0.542 | 6.13 | 5.31 | 4.39 | 3.72 | CHB |
| GNMT | GI_24475636-S | rs2296804 | 6 | 43039239 | 150 | 5.5901 | 0.3917 | 6.55 | 5.21 | 4.32 | 3.62 | CHB |
| GSTM1 | GI_23065546-A | rs2071487 | 1 | 109945123 | 1163 | 21.5512 | 0.888 | 7.51 | 5.42 | 4.38 | 3.6 | CHB |
| GSTM2 | GI_23065549-S | rs366631 | 1 | 109964514 | 38296 | 10.3029 | 0.6292 | 6.54 | 5.4 | 4.3 | 3.58 | CHB |
| GSTT1 | GI_4504184-S | rs407257 | 22 | 22671104 | 29852 | 27.6624 | 0.9417 | 6.07 | 5.48 | 4.48 | 3.75 | CHB |
| HEBP2 | GI_41393567-S | rs9484143 | 6 | 138726192 | 42658 | 6.0279 | 0.4188 | 7.8 | 5.41 | 4.41 | 3.7 | CHB |
| hIAN6 | GI_28416955-S | rs1916931 | 7 | 149573406 | 40519 | 5.5984 | 0.3994 | 6.33 | 5.21 | 4.35 | 3.62 | CHB |
| HIST1H4K | GI_15718726-S | rs200501 | 6 | 27896921 | 10036 | 5.6744 | 0.397 | 5.82 | 5.27 | 4.07 | 3.3 | CHB |
| HLA-DOB | GI_18641377-S | rs11244 | 6 | 32888702 | 17 | 6.7427 | 0.4606 | 6.95 | 5.54 | 4.43 | 3.69 | CHB |
| HLA-DQA2 | GI_11095446-S | rs6457617 | 6 | 32771829 | 49204 | 5.9119 | 0.4117 | 7.05 | 5.73 | 4.51 | 3.74 | CHB |
| HLA-F | GI_9665231-S | rs2394660 | 6 | 29780665 | 19526 | 5.9469 | 0.4138 | 6.66 | 5.37 | 4.33 | 3.54 | CHB |
| hmm1412 | hmm1412-S | rs2298746 | 11 | 74231482 | 1567 | 14.6337 | 0.7658 | 6.41 | 5.43 | 4.4 | 3.52 | CHB |
| hmm14647 | hmm14647-S | rs3117035 | 6 | 33194227 | 29 | 6.1641 | 0.427 | 6.96 | 5.65 | 4.59 | 3.85 | CHB |
| hmm26268 | hmm26268-S | rs3003902 | 1 | 218336419 | 157 | 8.7324 | 0.5623 | 6.97 | 5.52 | 4.26 | 3.5 | CHB |
| hmm27769 | hmm27769-S | rs10177787 | 2 | 20698916 | 19898 | 8.4977 | 0.5513 | 8.55 | 7.36 | 5.32 | 4.14 | CHB |
| hmm3151 | hmm3151-S | rs712314 | 14 | 34478299 | 107136 | 5.824 | 0.4063 | 7.41 | 5.15 | 4.26 | 3.55 | CHB |
| hmm31585 | hmm31585-S | rs9379687 | 6 | 24829766 | 198296 | 5.605 | 0.3926 | 5.84 | 5.05 | 4.34 | 3.71 | CHB |
| hmm31752 | hmm31752-S | rs1265053 | 6 | 31187868 | 55790 | 9.521 | 0.5972 | 7.66 | 5.93 | 4.55 | 3.72 | CHB |
| hmm32897 | hmm32897-S | rs12532675 | 7 | 65150964 | 498640 | 8.341 | 0.5439 | 8.81 | 6.5 | 4.71 | 3.57 | CHB |
| hmm5445 | hmm5445-S | rs883416 | 17 | 30594554 | 24000 | 7.4156 | 0.4973 | 6.62 | 5.66 | 4.53 | 3.74 | CHB |
| hmm8932 | hmm8932-S | rs7556492 | 1 | 157842208 | 21575 | 5.5482 | 0.389 | 6.11 | 5.12 | 4.27 | 3.62 | CHB |
| HNLF | GI_33457307-S | rs740094 | 7 | 44442938 | 50758 | 6.8213 | 0.465 | 6.22 | 5.19 | 4.29 | 3.54 | CHB |
| HNRPL | GI_4557644-S | rs2278009 | 19 | 44019696 | 228 | 5.7676 | 0.4028 | 6.32 | 5.33 | 4.29 | 3.56 | CHB |
| HRI | GI_11125767-S | rs660547 | 7 | 5879972 | 43047 | 6.6538 | 0.4555 | 6.77 | 5.44 | 4.36 | 3.61 | CHB |
| Hs.11898 | Hs.11898-S | rs8036979 | 15 | 50735287 | 1343 | 11.6774 | 0.6794 | 6.69 | 5.83 | 4.63 | 3.81 | CHB |
| Hs.123474 | Hs.123474-S | rs1547710 | 13 | 50899986 | 26255 | 6.456 | 0.4441 | 6.02 | 5.11 | 4.25 | 3.54 | CHB |
| Hs.124623 | Hs.124623-S | rs7282137 | 21 | 44449095 | 4783 | 8.3609 | 0.5448 | 8.09 | 6.93 | 5.44 | 4.31 | CHB |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Hs.147006 | Hs.147006-S | rs16832394 | 2 | 136577042 | 92683 | 18.1832 | 0.8396 | 7.47 | 6.3 | 4.67 | 3.77 | CHB |
| Hs.164463 | Hs.164463-S | rs2246770 | 4 | 54397811 | 45576 | 8.4393 | 0.5486 | 8.17 | 6.07 | 4.77 | 3.85 | CHB |
| Hs.208685 | Hs.208685-S | rs9468153 | 6 | 27603100 | 123921 | 6.9516 | 0.4722 | 7.47 | 5.78 | 4.44 | 3.55 | CHB |
| Hs.211939 | Hs.211939-S | rs2480781 | 1 | 10527807 | 44697 | 6.1045 | 0.4234 | 7.17 | 5.37 | 4.37 | 3.6 | CHB |
| Hs.214235 | Hs.214235-S | rs5743595 | 4 | 38625210 | 13169 | 6.9478 | 0.472 | 6.27 | 5.51 | 4.52 | 3.75 | CHB |
| Hs.224849 | Hs.224849-S | rs3773491 | 3 | 14687046 | 9187 | 9.5291 | 0.5976 | 6.29 | 5.47 | 4.46 | 3.77 | CHB |
| Hs.245997 | Hs.245997-S | rs2839556 | 21 | 42863019 | 1527 | 9.2719 | 0.5865 | 9.65 | 7.41 | 5.38 | 4.31 | CHB |
| Hs.26039 | Hs.26039-S | rs7712435 | 5 | 10716402 | 6415 | 6.7608 | 0.4695 | 7.05 | 5.57 | 4.54 | 3.78 | CHB |
| Hs.264076 | Hs.264076-S | rs1408656 | 13 | 78784655 | 111714 | 7.5762 | 0.5057 | 7.67 | 5.21 | 4.33 | 3.59 | CHB |
| Hs.345389 | Hs.345389-S | rs6519611 | 22 | 24170409 | 1687 | 22.7203 | 0.9012 | 9.57 | 7.32 | 5.2 | 4.18 | CHB |
| Hs.379903 | Hs.379903-S | rs1045599 | 17 | 15820635 | 55 | 14.3722 | 0.7592 | 8.23 | 5.93 | 4.61 | 3.72 | CHB |
| Hs.396207 | Hs.396207-S | rs780954 | 1 | 45708170 | 64824 | 18.4989 | 0.8449 | 5.78 | 5.17 | 4.03 | 3.26 | CHB |
| Hs.400876 | Hs.400876-S | rs805531 | 20 | 36508140 | 25355 | 9.1555 | 0.5814 | 6.47 | 5.59 | 4.39 | 3.59 | CHB |
| Hs.40696 | Hs.40696-S | rs2295441 | 22 | 45478963 | 416 | 8.2537 | 0.5397 | 6.26 | 5.61 | 4.56 | 3.77 | CHB |
| Hs.421238 | Hs.421238-S | rs10924924 | 1 | 243609361 | 2050 | 6.8266 | 0.4653 | 6.98 | 5.34 | 4.2 | 3.53 | CHB |
| Hs.42805 | Hs.42805-S | rs10794424 | 12 | 130897087 | 13066 | 6.6956 | 0.4579 | 6.4 | 5.31 | 4.23 | 3.46 | CHB |
| Hs.43687 | Hs.43687-S | rs3758250 | 9 | 97693556 | 50014 | 7.4485 | 0.499 | 7.83 | 6.05 | 4.82 | 3.93 | CHB |
| Hs.440933 | Hs.440933-S | rs9525253 | 13 | 113871032 | 26232 | 6.0589 | 0.4206 | 8 | 5.91 | 4.6 | 3.63 | CHB |
| Hs.453941 | Hs.453941-S | rs2514592 | 8 | 119681861 | 125533 | 14.8618 | 0.7715 | 7.01 | 5.77 | 4.72 | 3.92 | CHB |
| Hs.465789 | Hs.465789-S | rs11670116 | 19 | 7981202 | 1602 | 10.1135 | 0.6217 | 6.42 | 5.64 | 4.52 | 3.74 | CHB |
| Hs.473917 | Hs.473917-S | rs228048 | 21 | 42825210 | 5622 | 7.5895 | 0.5147 | 7.54 | 6.55 | 5.15 | 4.24 | CHB |
| Hs.479894 | Hs.479894-S | rs4305590 | 4 | 70075491 | 20961 | 7.2508 | 0.4885 | 9.04 | 6.59 | 4.72 | 3.62 | CHB |
| Hs.480174 | Hs.480174-S | rs4693155 | 4 | 88277199 | 336 | 8.0139 | 0.5364 | 8.02 | 5.65 | 4.4 | 3.6 | CHB |
| Hs.485895 | Hs.485895-S | rs2983136 | 6 | 88084934 | 88244 | 8.6846 | 0.5687 | 6.04 | 5.36 | 4.27 | 3.55 | CHB |
| Hs.506072 | Hs.506072-S | rs6451535 | 5 | 40723788 | 138673 | 5.0459 | 0.3632 | 7.19 | 5.04 | 4.1 | 3.45 | CHB |
| Hs.517172 | Hs.517172-S | rs6010789 | 20 | 61031598 | 104 | 6.2914 | 0.4345 | 6.27 | 5.28 | 4.29 | 3.59 | CHB |
| Hs.54543 | Hs.54543-S | rs344027 | 3 | 157951095 | 3082 | 7.8036 | 0.5174 | 6.24 | 5.44 | 4.36 | 3.6 | CHB |
| Hs.6637 | Hs.6637-S | rs4752845 | 11 | 47496273 | 87462 | 14.4129 | 0.7603 | 5.41 | 4.97 | 3.91 | 3.1 | CHB |
| Hs.98028 | Hs.98028-S | rs646521 | 11 | 124183151 | 1184 | 6.2417 | 0.4316 | 7.61 | 5.83 | 4.64 | 3.77 | CHB |
| HSRTSBETA | GI_42544116-I | rs7235957 | 18 | 707229 | 4837 | 6.2654 | 0.433 | 6.62 | 5.27 | 4.3 | 3.55 | CHB |
| IAN4L1 | GI_28416948-S | rs4725927 | 7 | 149829653 | 48477 | 7.1069 | 0.4807 | 7.15 | 6.09 | 4.84 | 3.84 | CHB |
| IL10RA | GI_24430213-S | rs3802871 | 11 | 117281858 | 95157 | 5.5992 | 0.3922 | 6.25 | 5.54 | 4.44 | 3.7 | CHB |
| IL16 | GI_27262656-I | rs4778636 | 15 | 79378694 | 9201 | 9.5246 | 0.5974 | 6.76 | 5.53 | 4.49 | 3.73 | CHB |
| IRAK1BP1 | GI_27498358-S | rs6454082 | 6 | 79544001 | 120522 | 8.2759 | 0.5407 | 7.08 | 6.39 | 4.68 | 3.73 | CHB |
| IRF5 | GI_38683858-A | rs7807018 | 7 | 128234139 | 50997 | 12.0455 | 0.6917 | 7.16 | 5.5 | 4.33 | 3.46 | CHB |
| ITIH4 | GI_40288189-S | rs6445538 | 3 | 52849328 | 26852 | 6.2036 | 0.437 | 8.14 | 6.11 | 4.73 | 3.66 | CHB |
| IVD | GI_6031167-S | rs10518693 | 15 | 38487314 | 10730 | 6.4109 | 0.4415 | 6.42 | 5.33 | 4.32 | 3.57 | CHB |
| KIAA0265 | GI_44917618-S | rs12534379 | 7 | 129365068 | 2062 | 6.2532 | 0.4323 | 7.99 | 5.66 | 4.48 | 3.65 | CHB |
| KIAA1449 | GI_21314694-S | rs2056613 | 3 | 39100297 | 12379 | 5.3881 | 0.3788 | 5.81 | 5.37 | 4.39 | 3.63 | CHB |
| KIAA1463 | GI_39930390-S | rs11169520 | 12 | 49359790 | 65125 | 13.7844 | 0.7437 | 6.55 | 5.59 | 4.46 | 3.66 | CHB |
| KIAA1712 | GI_30794213-S | rs1553669 | 4 | 175612138 | 15920 | 7.8519 | 0.5198 | 6.9 | 5.92 | 4.58 | 3.74 | CHB |
| LCMT1 | GI_15082255-I | rs7188975 | 16 | 25044950 | 71178 | 18.6335 | 0.8471 | 7.29 | 5.74 | 4.42 | 3.7 | CHB |
| LGALS9 | GI_6806889-I | rs1984547 | 17 | 22987444 | 7275 | 5.8048 | 0.4202 | 6.71 | 5.32 | 4.14 | 3.38 | CHB |
| LIPT1 | GI_21729877-I | rs12105048 | 2 | 99039323 | 191174 | 5.3698 | 0.3776 | 6.36 | 5.15 | 4.18 | 3.4 | CHB |
| LOC130502 | GI_37539459-S | rs2304588 | 2 | 20023345 | 3942 | 5.5086 | 0.3865 | 6.08 | 5.5 | 4.47 | 3.67 | CHB |
| LOC132001 | GI_34147617-S | rs404171 | 3 | 11862351 | 28552 | 6.2282 | 0.4308 | 6.79 | 5.53 | 4.41 | 3.67 | CHB |
| LOC135043 | GI_17463264-S | rs4710042 | 6 | 166722088 | 4918 | 5.9187 | 0.4121 | 6.68 | 5.77 | 4.66 | 3.87 | CHB |
| LOC144097 | GI_37541019-S | rs8995 | 11 | 63351648 | 40 | 6.3148 | 0.4359 | 6.58 | 5.62 | 4.29 | 3.53 | CHB |
| LOC151963 | GI_31341922-S | rs2133864 | 3 | 194098959 | 101392 | 6.732 | 0.46 | 7.06 | 6.02 | 4.57 | 3.75 | CHB |
| LOC197322 | GI_28372536-S | rs3751688 | 16 | 88161940 | 412367 | 9.0701 | 0.5776 | 7.7 | 6.09 | 4.49 | 3.76 | CHB |
| LOC201175 | GI_42661174-S | rs1230106 | 17 | 40843751 | 18829 | 5.7036 | 0.3988 | 7.75 | 5.57 | 4.35 | 3.49 | CHB |
| LOC206962 | GI_22046332-S | rs3812561 | 9 | 136546713 | 13328 | 10.6601 | 0.6429 | 7.28 | 5.89 | 4.71 | 3.86 | CHB |
| LOC255812 | GI_37550242-S | rs2676860 | 3 | 196147605 | 743223 | 5.7121 | 0.3993 | 7.26 | 5.69 | 4.52 | 3.69 | CHB |
| LOC282956 | GI_27483210-S | rs2428486 | 6 | 31462083 | 8468 | 11.0004 | 0.6556 | 7.28 | 5.72 | 4.58 | 3.8 | CHB |
| LOC283970 | GI_40217627-S | rs3748386 | 16 | 68532160 | 35690 | 20.3254 | 0.8724 | 11 | 7.05 | 5.04 | 3.78 | CHB |
| LOC284184 | GI_27500527-S | rs1048775 | 17 | 76816924 | 11379 | 10.395 | 0.6328 | 6.08 | 5.66 | 4.34 | 3.56 | CHB |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC284293 | GI_27485378-S | rs9955410 | 18 | 59771017 | 569 | 16.3646 | 0.8052 | 8.21 | 7.23 | 5.26 | 4.16 | CHB |
| LOC284345 | GI_27485260-S | rs2682551 | 19 | 48695548 | 24309 | 5.2584 | 0.3704 | 6.58 | 5.23 | 4.14 | 3.44 | CHB |
| LOC285407 | GI_37550539-S | rs9758051 | 3 | 131297567 | 2507 | 7.835 | 0.5636 | 6.78 | 5.43 | 4.25 | 3.54 | CHB |
| LOC286353 | GI_27478844-S | rs12345187 | 9 | 95747925 | 99655 | 6.8187 | 0.4648 | 7.46 | 6.22 | 4.62 | 3.72 | CHB |
| LOC339053 | GI_29746836-S | rs7187976 | 16 | 19615697 | 9726 | 7.1933 | 0.4854 | 6.46 | 5.44 | 4.44 | 3.68 | CHB |
| LOC339229 | GI_41150782-S | rs3830068 | 17 | 77233304 | 9491 | 15.2537 | 0.7808 | 8.05 | 6.22 | 4.59 | 3.77 | CHB |
| LOC339230 | GI_29739145-S | rs3088016 | 17 | 77250454 | 2 | 5.7907 | 0.4042 | 7.68 | 5.58 | 4.4 | 3.63 | CHB |
| LOC339804 | GI_37546921-S | rs12473277 | 2 | 61270271 | 31670 | 9.133 | 0.5804 | 5.66 | 5.19 | 4.22 | 3.42 | CHB |
| LOC340435 | GI_29735811-S | rs2732091 | 8 | 72080977 | 299050 | 11.2972 | 0.6749 | 11.4 | 6.97 | 5.06 | 4.01 | CHB |
| LOC346171 | GI_37552164-S | rs3095267 | 6 | 29715025 | 33484 | 7.7597 | 0.5151 | 6.38 | 5.56 | 4.38 | 3.6 | CHB |
| LOC374758 | GI_37544593-S | rs8064453 | 17 | 265835 | 1665 | 10.8492 | 0.65 | 6.96 | 5.7 | 4.33 | 3.61 | CHB |
| LOC375097 | GI_37555934-S | rs805531 | 20 | 36508140 | 25206 | 8.6818 | 0.56 | 5.87 | 5.43 | 4.4 | 3.59 | CHB |
| LOC375399 | GI_37540365-S | rs7684656 | 4 | 68318415 | 97060 | 5.7788 | 0.4035 | 6.67 | 5.15 | 4.07 | 3.33 | CHB |
| LOC378075 | GI_37538916-S | rs10232851 | 7 | 55603043 | 354891 | 17.2515 | 0.8446 | 6.48 | 5.76 | 4.47 | 3.53 | CHB |
| LOC387647 | GI_42659552-S | rs4747659 | 10 | 29797497 | 44661 | 10.6878 | 0.644 | 6.39 | 5.56 | 4.52 | 3.77 | CHB |
| LOC387834 | GI_42660007-S | rs11050615 | 12 | 9427425 | 18927 | 7.1442 | 0.4828 | 6.82 | 5.59 | 4.6 | 3.75 | CHB |
| LOC387905 | GI_41202581-S | rs7336525 | 13 | 20816844 | 20 | 7.9796 | 0.5262 | 6.87 | 5.46 | 4.36 | 3.62 | CHB |
| LOC388519 | GI_41151129-S | rs11671929 | 19 | 20222848 | 124961 | 5.6156 | 0.4005 | 6.24 | 5.08 | 4.21 | 3.42 | CHB |
| LOC389362 | GI_41147302-S | rs9328157 | 6 | 3212709 | 403 | 13.2821 | 0.7296 | 6.7 | 5.67 | 4.53 | 3.79 | CHB |
| LOC392620 | GI_41147689-S | rs2644275 | 7 | 2627251 | 92353 | 12.5045 | 0.7236 | 6.89 | 5.77 | 4.69 | 3.84 | CHB |
| LOC399987 | GI_42660080-S | rs9300302 | 12 | 3737732 | 1669 | 11.8674 | 0.6858 | 7.5 | 5.53 | 4.51 | 3.8 | CHB |
| LOC400051 | GI_42659981-S | rs2051993 | 12 | 66699945 | 1068 | 7.5493 | 0.5043 | 6.6 | 5.79 | 4.67 | 3.89 | CHB |
| LOC400410 | GI_42660516-S | rs2115539 | 15 | 77977940 | 16073 | 9.5537 | 0.5986 | 6.2 | 5.54 | 4.48 | 3.74 | CHB |
| LOC400566 | GI_42661283-S | rs8064453 | 17 | 265835 | 1193 | 11.1985 | 0.6627 | 7.86 | 5.49 | 4.5 | 3.63 | CHB |
| LOC400571 | GI_42661084-S | rs8066665 | 17 | 7426576 | 198 | 7.7559 | 0.5233 | 6.74 | 5.79 | 4.57 | 3.88 | CHB |
| LOC400642 | GI_42661344-S | rs2135308 | 18 | 5212146 | 24205 | 9.9016 | 0.6131 | 9.84 | 7.49 | 5.3 | 4.18 | CHB |
| LOC400933 | GI_42662518-S | rs739243 | 22 | 48378072 | 248608 | 14.5217 | 0.763 | 6.93 | 5.82 | 4.74 | 3.94 | CHB |
| LOC401135 | GI_42657007-S | rs10518042 | 4 | 68431669 | 14838 | 8.435 | 0.5569 | 7.86 | 6.13 | 4.36 | 3.51 | CHB |
| LOC401245 | GI_42657607-S | rs261950 | 6 | 30377540 | 10059 | 6.7818 | 0.4628 | 6.19 | 5.4 | 4.51 | 3.69 | CHB |
| LOC401560 | GI_42659039-S | rs3812561 | 9 | 136546713 | 13381 | 11.3603 | 0.6685 | 6.97 | 6.28 | 4.89 | 3.96 | CHB |
| LOC402476 | GI_42658265-S | rs2290213 | 7 | 32371870 | 203353 | 5.8387 | 0.4146 | 7.1 | 5.49 | 4.43 | 3.65 | CHB |
| LOC51240 | GI_31377759-S | rs2289226 | 2 | 190351711 | 109281 | 18.1315 | 0.8387 | 6.17 | 5.47 | 4.3 | 3.49 | CHB |
| LOC87769 | GI_34147452-S | rs9557460 | 13 | 100039757 | 57780 | 13.6238 | 0.7476 | 6.37 | 5.71 | 4.56 | 3.74 | CHB |
| LSR7 | GI_33354278-S | rs9526021 | 13 | 44416641 | 83360 | 5.8707 | 0.4092 | 6.54 | 5.37 | 4.42 | 3.68 | CHB |
| LZIC | GI_40255081-S | rs11828 | 1 | 9921273 | 3269 | 7.7759 | 0.5159 | 6.26 | 5.55 | 4.43 | 3.68 | CHB |
| MASTL | GI_14249561-S | rs7896781 | 10 | 27295757 | 219693 | 7.176 | 0.4845 | 6.42 | 5.09 | 4.29 | 3.62 | CHB |
| MATR3 | GI_34335242-S | rs171951 | 5 | 139352333 | 658627 | 4.8719 | 0.3447 | 5.14 | 4.74 | 4 | 3.25 | CHB |
| MBIP | GI_7706610-S | rs2415330 | 14 | 35812371 | 25677 | 6.3513 | 0.438 | 7.83 | 5.67 | 4.47 | 3.69 | CHB |
| MCOLN2 | GI_37540072-S | rs507465 | 1 | 85131697 | 27447 | 5.5322 | 0.388 | 5.97 | 5.29 | 4.38 | 3.59 | CHB |
| MGC10744 | GI_34101277-A | rs2518023 | 17 | 7997331 | 20306 | 8.5367 | 0.5532 | 6.82 | 5.57 | 4.6 | 3.82 | CHB |
| MGC10946 | GI_13386481-S | rs3816655 | 12 | 21613281 | 40061 | 7.2455 | 0.4882 | 8.13 | 6.76 | 5.12 | 4.06 | CHB |
| MGC11324 | GI_40255053-S | rs4693092 | 4 | 84853523 | 30210 | 6.5366 | 0.4488 | 6.38 | 5.37 | 4.39 | 3.56 | CHB |
| MGC12458 | GI_14150107-S | rs1196366 | 1 | 241505229 | 71851 | 10.8071 | 0.6485 | 6.77 | 5.7 | 4.56 | 3.81 | CHB |
| MGC14801 | GI_32261296-S | rs1055565 | 1 | 207994092 | 25 | 5.6629 | 0.3963 | 7.28 | 5.47 | 4.38 | 3.66 | CHB |
| MGC16597 | GI_42661280-S | rs3088016 | 17 | 77250454 | 1 | 6.8038 | 0.464 | 6.53 | 5.42 | 4.39 | 3.59 | CHB |
| MGC19764 | GI_42661257-S | rs883416 | 17 | 30594554 | 24027 | 7.3907 | 0.496 | 6.36 | 5.71 | 4.66 | 3.83 | CHB |
| MGC20235 | GI_21450795-S | rs8176273 | 17 | 38465179 | 261653 | 5.2545 | 0.3771 | 7.09 | 5.07 | 4.01 | 3.29 | CHB |
| MGC20781 | GI_34147471-S | rs1128966 | 17 | 37237375 | 2224 | 6.3766 | 0.4395 | 5.83 | 4.99 | 4.06 | 3.37 | CHB |
| MGC22773 | GI_21687083-S | rs1412825 | 1 | 74375835 | 17816 | 8.3845 | 0.546 | 6.25 | 5.71 | 4.23 | 3.37 | CHB |
| MGC2752 | GI_33859747-S | rs4801614 | 19 | 63788762 | 3550 | 12.0997 | 0.6935 | 6.48 | 5.28 | 4.06 | 3.24 | CHB |
| MGC3036 | GI_13027615-S | rs7781827 | 7 | 149446506 | 26132 | 6.1638 | 0.4269 | 7.65 | 5.53 | 4.43 | 3.64 | CHB |
| MGC35033 | GI_34303924-S | rs7975269 | 12 | 47130923 | 45367 | 6.1981 | 0.429 | 6.48 | 5.52 | 4.34 | 3.59 | CHB |
| MGC35308 | GI_31341688-S | rs7759603 | 6 | 166675043 | 15350 | 8.3796 | 0.5457 | 5.9 | 5.5 | 4.45 | 3.74 | CHB |
| MGC3794 | GI_33239373-S | rs7517978 | 1 | 164869703 | 31513 | 7.1383 | 0.4824 | 6.4 | 5.45 | 4.38 | 3.67 | CHB |
| MGC4083 | GI_14210535-S | rs11663340 | 18 | 12323686 | 7490 | 7.8596 | 0.5202 | 6.11 | 5.52 | 4.33 | 3.58 | CHB |
| MGC45416 | GI_22748848-S | rs12504699 | 4 | 48775226 | 38261 | 7.8965 | 0.522 | 6.55 | 5.04 | 3.91 | 3.1 | CHB |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MMRP19 | GI_7705723-S | rs1011518 | 11 | 34967045 | 100517 | 6.9488 | 0.4885 | 7.03 | 5.5 | 4.44 | 3.7 | CHB |
| MPEG1 | GI_42659661-S | rs3847 | 11 | 58733287 | 540 | 5.1825 | 0.3654 | 6.34 | 5.18 | 4.18 | 3.44 | CHB |
| MRPL21 | GI_31652223-A | rs660614 | 11 | 68416064 | 650 | 6.6708 | 0.4644 | 6.14 | 5.48 | 4.35 | 3.6 | CHB |
| MRPL43 | GI_28872735-A | rs1056295 | 10 | 102705173 | 31436 | 16.9438 | 0.8169 | 6.44 | 5.31 | 4.27 | 3.53 | CHB |
| MTRR | GI_4505278-A | rs2613670 | 5 | 7974873 | 20883 | 5.9375 | 0.4133 | 6.06 | 5.78 | 4.45 | 3.67 | CHB |
| MUC20 | GI_23097330-S | rs2550240 | 3 | 196985463 | 35570 | 9.0512 | 0.5768 | 6.45 | 5.42 | 4.32 | 3.61 | CHB |
| MYBL2 | GI_31652260-S | rs4560183 | 20 | 41646027 | 132313 | 9.6085 | 0.601 | 6.35 | 5.13 | 4.4 | 3.66 | CHB |
| MYOM2 | GI_4505314-S | rs2280902 | 8 | 2064479 | 16074 | 12.1683 | 0.6957 | 7.1 | 6.03 | 4.59 | 3.88 | CHB |
| N2N | GI_44917616-S | rs10218795 | 1 | 142905100 | 134076 | 5.7478 | 0.4016 | 6.15 | 4.81 | 3.82 | 3.07 | CHB |
| NCKX6 | GI_39995085-S | rs3815890 | 12 | 112234656 | 34864 | 5.9475 | 0.4291 | 6.42 | 5.82 | 4.56 | 3.76 | CHB |
| NDUFA10 | GI_33519462-S | rs6732752 | 2 | 240676972 | 56521 | 5.9446 | 0.4723 | 6.32 | 5.57 | 4.51 | 3.76 | CHB |
| NDUFS5 | GI_4758789-S | rs11205622 | 1 | 39202494 | 41358 | 7.3004 | 0.4912 | 5.91 | 5.19 | 4.33 | 3.62 | CHB |
| NIPSNAP3B | GI_21361742-S | rs2162116 | 9 | 104608968 | 6853 | 8.5517 | 0.5539 | 5.99 | 5.14 | 4.35 | 3.63 | CHB |
| NOR1 | GI_45643130-I | rs3738836 | 1 | 36554101 | 9002 | 8.8976 | 0.5699 | 7.25 | 5.47 | 4.33 | 3.6 | CHB |
| NPL4 | GI_8923608-S | rs7222241 | 17 | 77185156 | 50514 | 10.4522 | 0.635 | 5.86 | 5.39 | 4.31 | 3.54 | CHB |
| NQO2 | GI_4505416-S | rs4149352 | 6 | 2947237 | 14912 | 6.7826 | 0.4628 | 7.22 | 6.26 | 4.86 | 3.93 | CHB |
| NR2F6 | GI_20070198-S | rs2288541 | 19 | 17198308 | 5579 | 7.6915 | 0.52 | 8.32 | 6.07 | 4.55 | 3.76 | CHB |
| NUDT13 | GI_34330151-S | rs3998306 | 10 | 74692076 | 131148 | 6.4928 | 0.4463 | 6.37 | 5.01 | 3.92 | 3.18 | CHB |
| NUDT2 | GI_22265329-I | rs10814098 | 9 | 34314168 | 12086 | 15.4539 | 0.7854 | 6.81 | 5.59 | 4.38 | 3.55 | CHB |
| NYREN18 | GI_32483375-S | rs7807594 | 7 | 150469155 | 43834 | 5.136 | 0.3623 | 6.01 | 5.09 | 4.33 | 3.68 | CHB |
| OAS1 | GI_8051622-I | rs2285934 | 12 | 111814240 | 4018 | 13.7884 | 0.7438 | 9.67 | 6.17 | 4.77 | 3.85 | CHB |
| PAX8 | GI_37577111-A | rs1110839 | 2 | 113710647 | 19204 | 7.0025 | 0.475 | 6.75 | 5.73 | 4.52 | 3.65 | CHB |
| PDCD4 | GI_34304340-A | rs942077 | 10 | 112585709 | 63897 | 7.4325 | 0.4982 | 6.63 | 5.66 | 4.57 | 3.71 | CHB |
| PDGFB | GI_15451785-A | rs968451 | 22 | 37995351 | 50851 | 6.9933 | 0.4745 | 7.78 | 6.03 | 4.62 | 3.77 | CHB |
| PECI | GI_45643118-A | rs9503936 | 6 | 4090533 | 27909 | 5.3176 | 0.3742 | 6.62 | 5.25 | 4.44 | 3.75 | CHB |
| PET112L | GI_4758893-S | rs2278304 | 4 | 152951014 | 1232 | 5.4722 | 0.3842 | 6.19 | 5.05 | 4.17 | 3.39 | CHB |
| PEX16 | GI_4758897-A | rs10838530 | 11 | 45899571 | 7593 | 6.8663 | 0.4675 | 6.14 | 5.32 | 4.25 | 3.49 | CHB |
| PEX6 | GI_21361243-S | rs2296804 | 6 | 43039239 | 664 | 16.0084 | 0.7977 | 7.41 | 6.15 | 4.65 | 3.78 | CHB |
| PHACS | GI_14211920-S | rs2074038 | 11 | 44044565 | 17304 | 19.2024 | 0.8561 | 6.17 | 5.45 | 4.37 | 3.68 | CHB |
| PHC2 | GI_37595529-A | rs10798939 | 1 | 33478530 | 19958 | 10.5943 | 0.6405 | 5.74 | 5.21 | 4.21 | 3.54 | CHB |
| PHEMX | GI_37595532-A | rs7941928 | 11 | 2271980 | 23893 | 7.1032 | 0.4805 | 6.5 | 5.51 | 4.4 | 3.73 | CHB |
| PITPNC1 | GI_32307139-A | rs2365403 | 17 | 63126561 | 6821 | 5.5381 | 0.3884 | 6.32 | 5.44 | 4.43 | 3.66 | CHB |
| PKHD1L1 | GI_31377831-S | rs2844257 | 8 | 110590653 | 17602 | 21.4107 | 0.8863 | 6.8 | 5.47 | 4.13 | 3.39 | CHB |
| PLA2G4C | GI_4505850-S | rs156633 | 19 | 53319074 | 76090 | 7.7746 | 0.5243 | 7.12 | 5.88 | 4.68 | 3.77 | CHB |
| PLD2 | GI_20070140-S | rs6502844 | 17 | 4960392 | 286914 | 6.0524 | 0.4202 | 6.3 | 5.54 | 4.4 | 3.67 | CHB |
| PNN | GI_33356173-S | rs10131369 | 14 | 38664129 | 56467 | 7.7 | 0.5121 | 8.54 | 5.73 | 4.35 | 3.56 | CHB |
| PNRC1 | GI_5802981-S | rs1590958 | 6 | 89865656 | 14274 | 8.4176 | 0.5475 | 7.33 | 6.18 | 5.07 | 3.97 | CHB |
| POLR1A | GI_7661685-S | rs2241434 | 2 | 86276011 | 109272 | 5.2122 | 0.3967 | 6.43 | 5.18 | 4.26 | 3.49 | CHB |
| POLR2E | GI_14589950-S | rs6843 | 19 | 1039285 | 9 | 17.643 | 0.8301 | 7.64 | 5.68 | 4.55 | 3.84 | CHB |
| POLR2J | GI_21704275-S | rs2270019 | 7 | 102650959 | 943280 | 6.1055 | 0.431 | 6.34 | 5.68 | 4.17 | 3.36 | CHB |
| PP | GI_29171760-S | rs10999176 | 10 | 71627118 | 8947 | 5.9525 | 0.4142 | 7.04 | 5.65 | 4.49 | 3.77 | CHB |
| PP3856 | GI_40255088-S | rs4874159 | 8 | 144742093 | 13960 | 12.9247 | 0.7192 | 7.16 | 5.66 | 4.43 | 3.65 | CHB |
| PPA2 | GI_31881619-A | rs924282 | 4 | 106639721 | 8698 | 13.6914 | 0.7412 | 7.01 | 5.62 | 4.32 | 3.47 | CHB |
| PPARG | GI_20336230-A | rs12629240 | 3 | 12326574 | 124104 | 6.2565 | 0.4829 | 8.29 | 6.18 | 4.74 | 3.83 | CHB |
| PRF1 | GI_40254807-S | rs4747061 | 10 | 72009074 | 18902 | 8.8526 | 0.5678 | 8.3 | 6.83 | 5.11 | 4.17 | CHB |
| PROL4 | GI_6005801-S | rs7316239 | 12 | 11055595 | 164644 | 5.6562 | 0.4266 | 6.55 | 5.56 | 4.47 | 3.72 | CHB |
| PTER | GI_20070185-S | rs1055340 | 10 | 16595534 | 974 | 17.9459 | 0.8355 | 6.66 | 5.72 | 4.53 | 3.73 | CHB |
| R29124_1 | GI_16117774-S | rs714106 | 19 | 46775689 | 1914 | 10.5869 | 0.6402 | 7 | 5.22 | 4.19 | 3.45 | CHB |
| RAB15 | GI_38371738-S | rs2296323 | 14 | 64540939 | 58465 | 6.573 | 0.4509 | 5.96 | 5.51 | 4.52 | 3.73 | CHB |
| RAB24 | GI_18640747-S | rs1546363 | 5 | 176533637 | 127526 | 6.9847 | 0.4821 | 6.03 | 5.12 | 4.22 | 3.45 | CHB |
| RABGEF1 | GI_7657495-S | rs4718398 | 7 | 65673785 | 46315 | 6.1993 | 0.4291 | 6.82 | 5.11 | 4.12 | 3.33 | CHB |
| RAD52B | GI_31563532-S | rs4795090 | 17 | 31147710 | 121566 | 6.3993 | 0.4408 | 6.15 | 5.32 | 4.41 | 3.61 | CHB |
| raptor | GI_22094986-S | rs1062935 | 17 | 76554452 | 37 | 6.3972 | 0.4407 | 6.32 | 5.44 | 4.34 | 3.62 | CHB |
| RBMS2 | GI_4506448-S | rs3782235 | 12 | 55201814 | 67204 | 8.0354 | 0.529 | 5.55 | 4.94 | 4.23 | 3.48 | CHB |
| RHOBTB2 | GI_14165285-S | rs7387692 | 8 | 23312979 | 379584 | 6.8488 | 0.4665 | 6.73 | 6.14 | 4.9 | 3.92 | CHB |
| RLN1 | GI_20143931-S | rs4740810 | 9 | 5312687 | 12616 | 6.378 | 0.4474 | 7.53 | 5.62 | 4.6 | 3.83 | CHB |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RNASEH2A | GI_38455390-S | rs1833619 | 19 | 13508830 | 723664 | 5.2776 | 0.3716 | 7 | 5.24 | 4.27 | 3.49 | CHB |
| RNGTT | GI_4506562-S | rs12173779 | 6 | 89717985 | 341168 | 6.3082 | 0.4355 | 5.87 | 5.47 | 4.25 | 3.56 | CHB |
| RPL12 | GI_15431291-S | rs2254622 | 9 | 127362393 | 69202 | 5.9009 | 0.411 | 6.54 | 5.27 | 4.29 | 3.62 | CHB |
| RPL37A | GI_16306561-S | rs3732019 | 2 | 217187892 | 1196 | 17.0486 | 0.8189 | 8.18 | 6.59 | 5.2 | 4.19 | CHB |
| RPL8 | GI_15431305-I | rs2958498 | 8 | 145981621 | 6863 | 5.8694 | 0.4091 | 6.7 | 5.56 | 4.31 | 3.62 | CHB |
| RPLP2 | GI_16905512-S | rs10902222 | 11 | 800882 | 581 | 5.6428 | 0.395 | 5.97 | 5.27 | 4.18 | 3.47 | CHB |
| RPS16 | GI_34335151-S | rs1865091 | 19 | 44623906 | 5494 | 7.1231 | 0.4816 | 6.58 | 5.64 | 4.39 | 3.63 | CHB |
| RPS6KB2 | GI_4506738-S | rs1638588 | 11 | 66956282 | 3063 | 11.0034 | 0.6557 | 7.04 | 5.88 | 4.32 | 3.45 | CHB |
| RWDD2 | GI_34222125-S | rs9444029 | 6 | 83844558 | 118256 | 6.015 | 0.418 | 7.54 | 5.29 | 4.33 | 3.51 | CHB |
| S100A13 | GI_41117409-S | rs2274739 | 1 | 150425206 | 13257 | 6.5009 | 0.4467 | 6.39 | 5.13 | 4.1 | 3.43 | CHB |
| SBZF3 | GI_31742527-S | rs2818886 | 1 | 243435449 | 408 | 5.6982 | 0.3985 | 7.37 | 5.49 | 4.29 | 3.53 | CHB |
| SCAND2 | GI_15991818-I | rs8182086 | 15 | 83142863 | 157380 | 6.6576 | 0.4557 | 6.31 | 4.95 | 4.19 | 3.46 | CHB |
| SERPINB10 | GI_4826901-S | rs12327162 | 18 | 59731189 | 22003 | 6.1483 | 0.426 | 6.98 | 5.79 | 4.6 | 3.79 | CHB |
| SF1 | GI_42544126-I | rs477549 | 11 | 64283656 | 16643 | 11.5859 | 0.685 | 6.14 | 5.25 | 4.25 | 3.48 | CHB |
| SFXN2 | GI_34222270-S | rs2902548 | 10 | 104477372 | 11419 | 11.819 | 0.6842 | 6.13 | 5.21 | 4.05 | 3.37 | CHB |
| SIRT3 | GI_13775603-S | rs2293168 | 11 | 201482 | 4784 | 8.8889 | 0.5781 | 6.85 | 5.4 | 4.02 | 3.26 | CHB |
| SLC12A7 | GI_5730042-S | rs4975593 | 5 | 1150281 | 46655 | 5.6519 | 0.3956 | 7.05 | 5.37 | 4.38 | 3.65 | CHB |
| SLC1A4 | GI_21314631-S | rs918060 | 2 | 65068109 | 94257 | 8.0381 | 0.5291 | 6.38 | 5.31 | 4.4 | 3.67 | CHB |
| SLC25A16 | GI_31652216-S | rs6480328 | 10 | 69794640 | 117938 | 6.5003 | 0.4467 | 6.54 | 5.41 | 4.18 | 3.4 | CHB |
| SLC26A2 | GI_4557538-S | rs1037714 | 5 | 148933587 | 408513 | 5.4006 | 0.3796 | 6.55 | 5.32 | 4.44 | 3.73 | CHB |
| SLC27A5 | GI_13325056-S | rs893186 | 19 | 63660991 | 40813 | 5.2438 | 0.3694 | 6.1 | 5.1 | 4.09 | 3.28 | CHB |
| SLC2A8 | GI_21361448-S | rs2247310 | 9 | 127292664 | 43273 | 6.9669 | 0.4731 | 7.02 | 5.3 | 4.43 | 3.66 | CHB |
| SLC7A7 | GI_21361562-S | rs4982676 | 14 | 22347843 | 35426 | 7.7977 | 0.5171 | 5.92 | 5.44 | 4.41 | 3.72 | CHB |
| SNCA | GI_6806897-A | rs1372523 | 4 | 91133101 | 128310 | 6.9808 | 0.4989 | 7.55 | 5.74 | 4.49 | 3.59 | CHB |
| SPG7 | GI_40806172-I | rs3922634 | 16 | 88104267 | 27102 | 6.7982 | 0.4637 | 5.88 | 5.32 | 4.25 | 3.53 | CHB |
| SPINK2 | GI_10863910-S | rs1708768 | 4 | 57531641 | 12801 | 6.7686 | 0.462 | 7.17 | 5.87 | 4.68 | 3.86 | CHB |
| SQSTM1 | GI_19923742-S | rs748197 | 5 | 179206426 | 8840 | 6.1968 | 0.4289 | 7.22 | 5.55 | 4.48 | 3.75 | CHB |
| ST7L | GI_38201636-I | rs7544663 | 1 | 112801048 | 4499 | 10.335 | 0.6304 | 6.63 | 5.45 | 4.29 | 3.55 | CHB |
| STAT6 | GI_23397677-S | rs841718 | 12 | 55779263 | 3670 | 8.001 | 0.5273 | 6.72 | 5.28 | 4.29 | 3.5 | CHB |
| STIM2 | GI_21070998-S | rs10022599 | 4 | 26570925 | 132029 | 6.2238 | 0.4305 | 6.52 | 5.46 | 4.38 | 3.66 | CHB |
| STK11IP | GI_24308375-S | rs4132708 | 2 | 220876801 | 570239 | 5.5104 | 0.3866 | 6.24 | 5.41 | 4.35 | 3.67 | CHB |
| STK25 | GI_34147665-S | rs2240482 | 2 | 242125011 | 29600 | 11.9041 | 0.687 | 5.75 | 5.09 | 4.21 | 3.46 | CHB |
| SURF1 | GI_19557683-S | rs886089 | 9 | 133229020 | 19854 | 6.5265 | 0.4561 | 7.94 | 5.91 | 4.65 | 3.81 | CHB |
| TCL6 | GI_21536345-A | rs3759537 | 14 | 95204869 | 2625 | 8.1209 | 0.5332 | 6.45 | 5.9 | 4.78 | 3.93 | CHB |
| TFAM | GI_4507400-I | rs10826176 | 10 | 59811543 | 14230 | 8.4023 | 0.5468 | 7.18 | 5.3 | 4.16 | 3.45 | CHB |
| TGM5 | GI_4759229-A | rs489509 | 15 | 41374199 | 61106 | 8.135 | 0.5339 | 6.39 | 4.96 | 3.94 | 3.19 | CHB |
| THAP6 | GI_37059751-S | rs7664140 | 4 | 76795815 | 15264 | 6.1827 | 0.4281 | 6.91 | 5.48 | 4.31 | 3.56 | CHB |
| TIMM10 | GI_6912707-S | rs2649662 | 11 | 57109138 | 56520 | 8.7141 | 0.5615 | 7.05 | 5.59 | 4.35 | 3.5 | CHB |
| TK2 | GI_33636700-S | rs3743713 | 16 | 65140529 | 38282 | 8.6324 | 0.5577 | 6.67 | 5.31 | 4.29 | 3.46 | CHB |
| TLR1 | GI_41350336-S | rs10776483 | 4 | 38597606 | 23083 | 6.4975 | 0.4466 | 6.41 | 5.7 | 4.59 | 3.79 | CHB |
| TLR10 | GI_13569929-S | rs3924112 | 4 | 38618376 | 20894 | 6.8164 | 0.4647 | 6.87 | 5.6 | 4.55 | 3.8 | CHB |
| TOMM34 | GI_40807467-S | rs10485453 | 20 | 43002140 | 2254 | 9.2351 | 0.5849 | 8.72 | 6.28 | 4.8 | 3.82 | CHB |
| TRIM4 | GI_15011940-A | rs474229 | 7 | 99111209 | 22164 | 6.1815 | 0.428 | 6.41 | 5.12 | 4.06 | 3.22 | CHB |
| TSGA10 | GI_41281983-I | rs13397765 | 2 | 99007672 | 208755 | 7.8911 | 0.5218 | 6.35 | 5.5 | 4.2 | 3.4 | CHB |
| TSGA2 | GI_18254455-S | rs2839533 | 21 | 42770095 | 4102 | 8.778 | 0.573 | 6.32 | 5.76 | 4.7 | 3.99 | CHB |
| UBA52 | GI_15451941-S | rs12609505 | 19 | 18535057 | 11923 | 23.7959 | 0.9119 | 6.67 | 5.5 | 4.36 | 3.61 | CHB |
| UGT2B10 | GI_27552756-S | rs13144491 | 4 | 69273573 | 603683 | 11.6815 | 0.6796 | 7.59 | 5.5 | 4.31 | 3.37 | CHB |
| UGT2B11 | GI_4507822-S | rs13144491 | 4 | 69273573 | 973550 | 26.528 | 0.9342 | 9.6 | 5.96 | 4.52 | 3.57 | CHB |
| UGT2B17 | GI_4507820-S | rs13144491 | 4 | 69273573 | 41744 | 32.4933 | 0.9652 | 6.91 | 6.17 | 4.46 | 3.47 | CHB |
| UGT2B7 | GI_4507824-S | rs13144491 | 4 | 69273573 | 885483 | 23.8972 | 0.9128 | 6.97 | 5.6 | 4.38 | 3.46 | CHB |
| UNQ2430 | GI_41190797-S | rs4264593 | 2 | 97472228 | 184269 | 5.1557 | 0.3636 | 5.68 | 5.02 | 3.86 | 3.17 | CHB |
| USMG5 | GI_14249375-S | rs11191686 | 10 | 105177736 | 33701 | 22.9002 | 0.903 | 6.51 | 5.38 | 4.2 | 3.47 | CHB |
| USP36 | GI_35250685-S | rs7207392 | 17 | 74233533 | 61740 | 7.9312 | 0.5238 | 6.79 | 5.59 | 4.55 | 3.75 | CHB |
| UTS2 | GI_12056480-I | rs161826 | 1 | 7914604 | 67277 | 10.2159 | 0.6345 | 7.7 | 6.04 | 4.65 | 3.68 | CHB |
| VAMP1 | GI_40549443-I | rs2532498 | 12 | 6433959 | 8201 | 5.5133 | 0.394 | 6.94 | 5.47 | 4.52 | 3.77 | CHB |
| VPS13A | GI_15619007-I | rs10491839 | 9 | 77270451 | 41099 | 7.0453 | 0.4774 | 7.03 | 5.7 | 4.69 | 3.85 | CHB |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| WBSCR27 | GI_30795189-S | rs6946037 | 7 | 72681366 | 12436 | 12.9675 | 0.7205 | 5.89 | 5.09 | 4.02 | 3.33 | CHB |
| WDR4 | GI_40217837-I | rs9980962 | 21 | 43101964 | 34453 | 5.821 | 0.4061 | 6.88 | 5.69 | 4.57 | 3.87 | CHB |
| XRRA1 | GI_42659736-S | rs2298746 | 11 | 74231482 | 1489 | 11.3774 | 0.6691 | 6.16 | 5.3 | 4.25 | 3.55 | CHB |
| ZNF213 | GI_32698677-S | rs170381 | 16 | 3144728 | 12225 | 6.1681 | 0.4272 | 6.91 | 5.22 | 4.34 | 3.63 | CHB |
| ZNF230 | GI_5454181-S | rs12753 | 19 | 49207354 | 175 | 6.2905 | 0.4422 | 7.38 | 5.63 | 4.39 | 3.61 | CHB |
| ZNF253 | GI_10567821-S | rs1019280 | 19 | 19908429 | 43815 | 5.915 | 0.4193 | 5.69 | 4.99 | 4.13 | 3.42 | CHB |
| ZNF257 | GI_15627000-S | rs4932932 | 19 | 21995054 | 69220 | 6.2917 | 0.4422 | 6.67 | 5.4 | 4.12 | 3.37 | CHB |
| ZNF266 | GI_37622342-A | rs6512130 | 19 | 9407351 | 23011 | 7.7446 | 0.5143 | 6.22 | 5.18 | 4.31 | 3.6 | CHB |
| ZNF281 | GI_40255235-S | rs1339575 | 1 | 197081822 | 25986 | 5.864 | 0.4088 | 6.5 | 5.66 | 4.35 | 3.65 | CHB |
| ZNF37A | GI_37551348-S | rs2505192 | 10 | 38435029 | 12496 | 5.2025 | 0.3667 | 7.4 | 4.72 | 3.81 | 2.99 | CHB |
| ZNF587 | GI_14249531-S | rs7245531 | 19 | 63080519 | 8784 | 6.8436 | 0.4742 | 6.87 | 5.27 | 4.26 | 3.53 | CHB |
| ABCD2 | GI_21536379-S | rs11172259 | 12 | 38156087 | 76842 | 6.3565 | 0.4541 | 6.26 | 5.44 | 4.43 | 3.65 | JPT |
| ABCF2 | GI_27881505-I | rs13240743 | 7 | 151004562 | 657064 | 6.0989 | 0.4306 | 7.38 | 5.4 | 4.5 | 3.67 | JPT |
| ACN9 | GI_9910179-S | rs6973504 | 7 | 96392135 | 62985 | 6.6934 | 0.4657 | 6.58 | 5.39 | 4.34 | 3.59 | JPT |
| ACY1L2 | GI_37551403-S | rs693932 | 6 | 89887093 | 41475 | 6.0229 | 0.426 | 7.61 | 5.13 | 4.4 | 3.58 | JPT |
| AK2 | GI_26665888-I | rs11581013 | 1 | 33122811 | 21556 | 5.5532 | 0.3965 | 8.08 | 5.5 | 4.37 | 3.63 | JPT |
| AKAP7 | GI_20336197-A | rs9372991 | 6 | 131493747 | 152338 | 6.0061 | 0.425 | 8 | 5.89 | 4.63 | 3.74 | JPT |
| ALDH8A1 | GI_25952151-A | rs3817776 | 6 | 135298449 | 17995 | 6.6954 | 0.4658 | 6.02 | 5.51 | 4.41 | 3.62 | JPT |
| ALS2CR4 | GI_22748830-S | rs2241135 | 2 | 202332738 | 16411 | 6.9005 | 0.4774 | 6.76 | 5.43 | 4.25 | 3.46 | JPT |
| ANXA2 | GI_4757755-S | rs4878501 | 9 | 32699876 | 915237 | 5.6992 | 0.4058 | 6.53 | 5.37 | 4.31 | 3.61 | JPT |
| APOBEC3B | GI_22907024-S | rs2142833 | 22 | 37716796 | 6765 | 7.0796 | 0.4874 | 8.16 | 6.67 | 4.91 | 3.88 | JPT |
| ASXL1 | GI_29570781-S | rs6088133 | 20 | 31238740 | 748120 | 5.067 | 0.3646 | 6.2 | 4.92 | 4.02 | 3.31 | JPT |
| ATP6V1C1 | GI_19913430-S | rs1018088 | 8 | 104162535 | 12355 | 6.2159 | 0.4377 | 7.01 | 5.52 | 4.4 | 3.6 | JPT |
| ATPIF1 | GI_30260191-I | rs2938867 | 1 | 28199434 | 48942 | 6.2433 | 0.4393 | 6.79 | 5.2 | 3.95 | 3.23 | JPT |
| B3GALT3 | GI_15451873-I | rs6772723 | 3 | 162377776 | 93267 | 7.0392 | 0.4851 | 6.71 | 5.43 | 4.28 | 3.44 | JPT |
| B3GTL | GI_34996530-S | rs912603 | 13 | 30803641 | 86 | 8.1259 | 0.5507 | 7.41 | 6.15 | 4.59 | 3.81 | JPT |
| B4GALT1 | GI_13929461-S | rs3780480 | 9 | 33153486 | 52568 | 7.8358 | 0.5274 | 6.07 | 5.45 | 4.37 | 3.66 | JPT |
| B7 | GI_42542401-A | rs2239163 | 12 | 6884337 | 9270 | 10.6999 | 0.6532 | 7.38 | 5.64 | 4.53 | 3.76 | JPT |
| BCAS1 | GI_4502372-S | rs290431 | 20 | 52109454 | 115356 | 6.0383 | 0.4429 | 5.96 | 5.34 | 4.37 | 3.65 | JPT |
| BM039 | GI_39725678-S | rs3743503 | 16 | 79613942 | 2583 | 6.9985 | 0.4829 | 7.79 | 5.64 | 4.57 | 3.8 | JPT |
| BTN3A2 | GI_34932495-S | rs9379851 | 6 | 26462759 | 21356 | 10.2297 | 0.6351 | 8.52 | 6.63 | 5.28 | 4.13 | JPT |
| C10orf32 | GI_21389380-S | rs10509758 | 10 | 104671700 | 67558 | 5.5059 | 0.4087 | 6.1 | 5.11 | 4.14 | 3.4 | JPT |
| C10orf68 | GI_13375961-S | rs2997515 | 10 | 32770832 | 440890 | 8.3141 | 0.5511 | 6.78 | 5.46 | 4.3 | 3.54 | JPT |
| C10orf88 | GI_13376420-S | rs2153669 | 10 | 124599273 | 81862 | 5.8536 | 0.4155 | 6.42 | 5.58 | 4.52 | 3.72 | JPT |
| C11orf21 | GI_7662662-S | rs2074021 | 11 | 2280104 | 6337 | 7.5144 | 0.5108 | 7.38 | 5.54 | 4.47 | 3.72 | JPT |
| C14orf124 | GI_9910257-S | rs1956921 | 14 | 24049256 | 70173 | 5.9715 | 0.4228 | 6.12 | 5.63 | 4.43 | 3.68 | JPT |
| C14orf130 | GI_28411949-A | rs2905 | 14 | 92763175 | 6731 | 6.854 | 0.4668 | 6.54 | 5.4 | 4.52 | 3.74 | JPT |
| C14orf52 | GI_21553312-S | rs4902345 | 14 | 64473657 | 2901 | 18.7363 | 0.8488 | 7.81 | 6.46 | 4.99 | 3.95 | JPT |
| C1QTNF3 | GI_13569918-I | rs6546 | 5 | 34055787 | 28 | 7.1033 | 0.4887 | 6.97 | 5.78 | 4.51 | 3.76 | JPT |
| C21orf107 | GI_38026951-I | rs8128118 | 21 | 39514099 | 29772 | 18.6786 | 0.8478 | 7.26 | 5.83 | 4.93 | 4.18 | JPT |
| C22orf2 | GI_21359898-S | rs138695 | 22 | 37444738 | 50631 | 9.6244 | 0.6103 | 6.48 | 5.45 | 4.35 | 3.61 | JPT |
| C6orf33 | GI_19115959-S | rs2268732 | 6 | 52504461 | 124100 | 7.4487 | 0.5073 | 7.91 | 6.55 | 4.89 | 3.85 | JPT |
| C9orf102 | GI_39930392-S | rs690495 | 9 | 95735348 | 120944 | 5.7353 | 0.4081 | 5.94 | 5.31 | 4.3 | 3.54 | JPT |
| CAPZA1 | GI_5453596-S | rs3790611 | 1 | 112779834 | 146295 | 9.052 | 0.5855 | 6.22 | 5.38 | 4.28 | 3.48 | JPT |
| CBS | GI_4557414-S | rs719038 | 21 | 43344013 | 2473 | 5.4949 | 0.3856 | 6.54 | 5.46 | 4.76 | 4.06 | JPT |
| CCNB1IP1 | GI_33519439-I | rs2318864 | 14 | 19837458 | 18379 | 7.3007 | 0.4994 | 6.95 | 5.65 | 4.51 | 3.72 | JPT |
| CCNDBP1 | GI_16554567-I | rs2899077 | 15 | 41297317 | 31708 | 8.2981 | 0.5591 | 7.03 | 5.36 | 3.92 | 3.15 | JPT |
| CD151 | GI_34328914-A | rs3059 | 11 | 830319 | 1576 | 6.0547 | 0.4279 | 7.53 | 5.88 | 4.39 | 3.61 | JPT |
| CDK5RAP2 | GI_28872785-S | rs872423 | 9 | 120229045 | 1793 | 10.779 | 0.6561 | 6.08 | 5.24 | 4.22 | 3.5 | JPT |
| CHKL | GI_23238259-I | rs2073604 | 22 | 49299069 | 8510 | 5.8441 | 0.4149 | 7.05 | 5.41 | 4.26 | 3.54 | JPT |
| CHPT1 | GI_9910383-S | rs2695281 | 12 | 100592467 | 26964 | 5.8978 | 0.4183 | 6.05 | 5.57 | 4.46 | 3.67 | JPT |
| CIAO1 | GI_38570089-S | rs3731930 | 2 | 96388535 | 29668 | 5.8746 | 0.4094 | 6.59 | 4.98 | 3.92 | 3.16 | JPT |
| CLECSF2 | GI_37577106-S | rs1597097 | 12 | 9911534 | 15079 | 7.8487 | 0.528 | 9.03 | 5.81 | 4.49 | 3.71 | JPT |
| COG4 | GI_21070955-A | rs8049475 | 16 | 69187810 | 115681 | 5.4733 | 0.3914 | 6.26 | 5.15 | 4.01 | 3.25 | JPT |
| CPA4 | GI_10047105-S | rs3807344 | 7 | 129528170 | 29489 | 5.9365 | 0.4365 | 6.69 | 5.88 | 4.5 | 3.67 | JPT |
| CPEB4 | GI_32698754-S | rs7705502 | 5 | 173253421 | 64166 | 7.378 | 0.5035 | 9.54 | 7.23 | 5.42 | 4.28 | JPT |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CPNE1 | GI_23397697-A | rs12481545 | 20 | 33871112 | 193440 | 7.9225 | 0.5233 | 7.04 | 5.56 | 4.23 | 3.33 | JPT |
| CRIPT | GI_41350204-S | rs1531133 | 2 | 46755282 | 8119 | 9.3713 | 0.6085 | 6.83 | 5.79 | 4.6 | 3.86 | JPT |
| CRYBB2 | GI_4503062-S | rs6519611 | 22 | 24170409 | 218080 | 34.7248 | 0.9749 | 11 | 7.93 | 5.59 | 4.37 | JPT |
| CSTF3 | GI_4557494-S | rs3758741 | 11 | 33063192 | 29 | 6.1667 | 0.4347 | 6.2 | 5.22 | 4.25 | 3.53 | JPT |
| CTNS | GI_4826681-S | rs4790530 | 17 | 3502173 | 9251 | 6.4605 | 0.4522 | 6.58 | 5.57 | 4.36 | 3.67 | JPT |
| CTSH | GI_23110956-A | rs10400902 | 15 | 77018671 | 17260 | 6.1294 | 0.4325 | 6.56 | 5.82 | 4.62 | 3.79 | JPT |
| CTSS | GI_23110961-S | rs12085336 | 1 | 147588853 | 72867 | 6.5389 | 0.4489 | 7.82 | 4.92 | 4.11 | 3.26 | JPT |
| DAPK3 | GI_4557510-S | rs2278438 | 19 | 3915106 | 5361 | 6.3831 | 0.4477 | 6.2 | 5.49 | 4.47 | 3.78 | JPT |
| DC6 | GI_34222364-S | rs10496660 | 2 | 127629274 | 911896 | 5.2 | 0.3735 | 6.25 | 5.15 | 4.25 | 3.51 | JPT |
| DCLRE1B | GI_24431998-S | rs10108 | 1 | 114228372 | 60024 | 7.0556 | 0.4861 | 6.59 | 5.43 | 4.13 | 3.4 | JPT |
| DDX17 | GI_38201709-I | rs138465 | 22 | 37232349 | 17146 | 8.248 | 0.5479 | 7.35 | 6.37 | 4.79 | 3.85 | JPT |
| DERP6 | GI_44662825-I | rs222843 | 17 | 7086705 | 9736 | 13.2917 | 0.7383 | 7.2 | 5.66 | 4.59 | 3.81 | JPT |
| DGCR6L | GI_15718677-S | rs752689 | 22 | 18683947 | 7569 | 6.0993 | 0.4307 | 6.84 | 5.8 | 4.51 | 3.83 | JPT |
| DHX30 | GI_20336291-A | rs11713693 | 3 | 47049910 | 816266 | 6.4862 | 0.4878 | 6.04 | 4.93 | 3.92 | 3.06 | JPT |
| dJ383J4.3 | GI_42655858-S | rs7539322 | 1 | 170347622 | 152854 | 9.0633 | 0.586 | 8.21 | 7.03 | 5.25 | 3.89 | JPT |
| DKFZp434H247 | GI_37552078-S | rs1057745 | 19 | 44580230 | 174 | 7.3286 | 0.5009 | 6.7 | 5.48 | 4.32 | 3.58 | JPT |
| DKFZP566H073 | GI_14149701-S | rs238245 | 17 | 4788188 | 989 | 9.6541 | 0.6116 | 6.85 | 5.78 | 4.47 | 3.71 | JPT |
| DKFZP586D0919 | GI_24308058-S | rs1021469 | 12 | 56494431 | 31952 | 7.0009 | 0.483 | 6.64 | 5.48 | 4.32 | 3.51 | JPT |
| DNASE1L3 | GI_4826697-S | rs9845458 | 3 | 58150400 | 8243 | 7.5072 | 0.5104 | 6.83 | 4.87 | 3.94 | 3.23 | JPT |
| DPYSL4 | GI_11321616-S | rs2637654 | 10 | 133828801 | 40365 | 6.4398 | 0.451 | 7.88 | 6.16 | 4.67 | 3.82 | JPT |
| DSCR5 | GI_24497594-I | rs2249828 | 21 | 37354491 | 11851 | 6.1003 | 0.4307 | 7.04 | 5.91 | 4.9 | 4.02 | JPT |
| DTNB | GI_37577100-A | rs6731296 | 2 | 25546478 | 34673 | 6.2469 | 0.4396 | 6.35 | 5.39 | 4.13 | 3.34 | JPT |
| EGFL5 | GI_42659252-S | rs7861226 | 9 | 120430675 | 12379 | 6.2798 | 0.4415 | 6.5 | 5.62 | 4.29 | 3.53 | JPT |
| EIF2S1 | GI_34147492-S | rs1045060 | 14 | 66875006 | 46527 | 10.6868 | 0.6616 | 6.31 | 4.87 | 3.92 | 3.26 | JPT |
| ENDOG | GI_4758269-S | rs2759009 | 9 | 128678562 | 14090 | 5.9502 | 0.4293 | 6.64 | 5.61 | 4.58 | 3.86 | JPT |
| ESRRBL1 | GI_19923513-S | rs162064 | 3 | 109306751 | 55652 | 6.2462 | 0.4395 | 6.25 | 5.4 | 4.15 | 3.42 | JPT |
| F25965 | GI_28144915-S | rs3787052 | 19 | 40893895 | 43315 | 13.6821 | 0.7492 | 7.3 | 6.17 | 4.79 | 3.88 | JPT |
| FECH | GI_4557592-S | rs317807 | 18 | 53401668 | 33429 | 6.2785 | 0.4415 | 6.76 | 5.75 | 4.6 | 3.79 | JPT |
| FGFR1OP | GI_36287109-A | rs3798308 | 6 | 167391205 | 32990 | 10.8915 | 0.6603 | 10.2 | 7.97 | 5.94 | 4.7 | JPT |
| FLJ10204 | GI_8922280-S | rs13272492 | 8 | 124505250 | 17874 | 5.7692 | 0.4103 | 6.41 | 5.56 | 4.45 | 3.76 | JPT |
| FLJ10458 | GI_20070287-S | rs3744362 | 17 | 30483209 | 632 | 11.9591 | 0.6975 | 7.03 | 5.67 | 4.56 | 3.82 | JPT |
| FLJ10781 | GI_39780596-S | rs12609521 | 19 | 51658767 | 3001 | 33.2418 | 0.9705 | 9.4 | 7.1 | 5.48 | 4.24 | JPT |
| FLJ11848 | GI_13376750-S | rs12366033 | 11 | 73056622 | 259588 | 6.2221 | 0.4381 | 6.34 | 5.39 | 4.18 | 3.41 | JPT |
| FLJ13615 | GI_13376688-S | rs3990713 | 12 | 87503410 | 495358 | 5.9346 | 0.4283 | 6.21 | 5.25 | 4.07 | 3.32 | JPT |
| FLJ14146 | GI_31542689-S | rs437078 | 1 | 217257022 | 3579 | 9.0958 | 0.5874 | 6.76 | 5.29 | 4.35 | 3.6 | JPT |
| FLJ14753 | GI_14211858-S | rs7859571 | 9 | 94211440 | 91003 | 7.9629 | 0.5338 | 7.16 | 5.91 | 4.48 | 3.62 | JPT |
| FLJ20580 | GI_8923540-S | rs7549319 | 1 | 53369588 | 22442 | 5.387 | 0.3858 | 5.77 | 5.2 | 4.18 | 3.5 | JPT |
| FLJ20605 | GI_31542712-S | rs437078 | 1 | 217257022 | 88648 | 6.158 | 0.4342 | 6.1 | 5.45 | 4.31 | 3.59 | JPT |
| FLJ20635 | GI_8923587-S | rs104664 | 22 | 44032391 | 24700 | 11.9373 | 0.6968 | 8.17 | 6.33 | 5.06 | 4.14 | JPT |
| FLJ21347 | GI_31542722-S | rs1122634 | 17 | 45976364 | 11803 | 7.0815 | 0.4875 | 6.91 | 5.63 | 4.39 | 3.67 | JPT |
| FLJ22175 | GI_19923616-S | rs3924327 | 17 | 77128811 | 11372 | 6.5945 | 0.46 | 6.78 | 5.63 | 4.4 | 3.59 | JPT |
| FLJ22635 | GI_13376651-S | rs2242565 | 11 | 285343 | 40 | 11.929 | 0.6965 | 7.06 | 5.13 | 4 | 3.25 | JPT |
| FLJ22729 | GI_13375953-S | rs999797 | 17 | 26183455 | 67079 | 5.9343 | 0.4283 | 5.87 | 5.1 | 4.05 | 3.3 | JPT |
| FLJ23235 | GI_13376422-S | rs2254075 | 4 | 38852749 | 61707 | 9.4225 | 0.6017 | 6.67 | 5.33 | 4.33 | 3.67 | JPT |
| FLJ23403 | GI_13384601-S | rs264200 | 18 | 10953991 | 293003 | 6.0443 | 0.4516 | 7.05 | 5.52 | 4.45 | 3.75 | JPT |
| FLJ31438 | GI_22748824-S | rs2576722 | 2 | 55373474 | 58929 | 6.266 | 0.4407 | 6.37 | 5.56 | 4.43 | 3.65 | JPT |
| FLJ32871 | GI_21389568-S | rs2719695 | 16 | 10671946 | 42930 | 5.3945 | 0.3863 | 6.19 | 5.31 | 4.44 | 3.68 | JPT |
| FLJ35036 | GI_37550554-S | rs4683404 | 3 | 142643069 | 4056 | 6.294 | 0.4424 | 6.27 | 5.26 | 4.28 | 3.54 | JPT |
| FLJ36175 | GI_22749102-S | rs714156 | 2 | 159966575 | 48444 | 7.5285 | 0.5115 | 7.28 | 5.38 | 4.46 | 3.59 | JPT |
| FLJ38984 | GI_22748804-S | rs2074676 | 1 | 35696804 | 152026 | 5.6782 | 0.4045 | 6.19 | 5.43 | 4.15 | 3.37 | JPT |
| FLJ40113 | GI_38016132-S | rs867370 | 15 | 80225317 | 290337 | 5.3086 | 0.3807 | 6.37 | 5 | 4.1 | 3.34 | JPT |
| FLJ46603 | GI_38348363-S | rs4789349 | 17 | 72217936 | 30427 | 25.9917 | 0.9389 | 7.98 | 6.29 | 4.95 | 3.99 | JPT |
| FLJ90036 | GI_31559781-S | rs2006748 | 4 | 77113 | 68755 | 6.5024 | 0.4547 | 5.65 | 4.9 | 3.9 | 3.23 | JPT |
| FN3KRP | GI_20149679-S | rs2243523 | 17 | 78273738 | 5134 | 6.4552 | 0.4519 | 6.24 | 5.13 | 4.15 | 3.35 | JPT |
| FTSJ3 | GI_17017990-S | rs716880 | 17 | 59256554 | 5722 | 5.7843 | 0.4038 | 6.93 | 4.9 | 3.88 | 3.22 | JPT |
| G0S2 | GI_20070269-S | rs2896936 | 1 | 205249867 | 988044 | 5.6982 | 0.4058 | 6.94 | 5.47 | 4.4 | 3.72 | JPT |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GALNT4 | GI_34452724-S | rs1492911 | 12 | 88331039 | 86945 | 5.4341 | 0.3889 | 6.39 | 5.27 | 4.2 | 3.52 | JPT |
| GBP3 | GI_24308156-S | rs10493821 | 1 | 89187156 | 1965 | 8.5583 | 0.5628 | 6.38 | 5.52 | 4.43 | 3.62 | JPT |
| GPNMB | GI_4505404-S | rs1468593 | 7 | 22953372 | 134214 | 6.2952 | 0.4587 | 6.56 | 5.38 | 4.42 | 3.64 | JPT |
| GSTM1 | GI_23065546-A | rs2014578 | 1 | 109953413 | 9453 | 29.4598 | 0.9553 | 6.8 | 5.5 | 4.36 | 3.62 | JPT |
| GSTM2 | GI_23065549-S | rs2071487 | 1 | 109945123 | 18905 | 7.8299 | 0.5271 | 7.16 | 5.44 | 4.39 | 3.62 | JPT |
| GSTM4 | GI_23065559-A | rs12745189 | 1 | 109898605 | 14939 | 5.5678 | 0.3975 | 6.53 | 5.37 | 4.48 | 3.64 | JPT |
| GSTP1 | GI_6552334-S | rs687316 | 11 | 67063408 | 46804 | 6.6899 | 0.4655 | 6.48 | 5.09 | 4.16 | 3.35 | JPT |
| GSTT1 | GI_4504184-S | rs5760147 | 22 | 22659502 | 41454 | 23.8865 | 0.9177 | 6.31 | 5.72 | 4.55 | 3.76 | JPT |
| GYPE | GI_38373678-A | rs2292362 | 4 | 144804124 | 351457 | 5.3685 | 0.3919 | 6.5 | 5.04 | 4.01 | 3.28 | JPT |
| HEBP2 | GI_41393567-S | rs2076273 | 6 | 138745333 | 23517 | 9.6363 | 0.6108 | 7.42 | 5.8 | 4.66 | 3.81 | JPT |
| HEMK | GI_7705408-S | rs9875961 | 3 | 50853126 | 255882 | 4.8575 | 0.4048 | 6.06 | 4.77 | 3.95 | 3.11 | JPT |
| HLA-DQA1 | GI_18426974-S | rs6457617 | 6 | 32771829 | 52994 | 6.7897 | 0.4794 | 9.09 | 6.65 | 5.05 | 3.89 | JPT |
| HLA-DQB1 | GI_24797068-S | rs465506 | 6 | 33466986 | 731136 | 5.7475 | 0.4089 | 6.35 | 5.45 | 4.41 | 3.63 | JPT |
| hmm1412 | hmm1412-S | rs2298746 | 11 | 74231482 | 1567 | 19.2657 | 0.8636 | 6.32 | 5.45 | 4.45 | 3.6 | JPT |
| hmm14470 | hmm14470-S | rs3812105 | 6 | 25212233 | 19510 | 6.3502 | 0.4457 | 9.11 | 5.83 | 4.55 | 3.78 | JPT |
| hmm26268 | hmm26268-S | rs3003902 | 1 | 218336419 | 157 | 9.3205 | 0.5973 | 9.04 | 6.2 | 4.8 | 3.75 | JPT |
| hmm2656 | hmm2656-S | rs1617132 | 12 | 125781577 | 25835 | 12.9466 | 0.7283 | 10.5 | 8.09 | 6.08 | 4.68 | JPT |
| hmm28069 | hmm28069-S | rs6733550 | 2 | 85739672 | 8101 | 7.7354 | 0.5223 | 6.43 | 5.14 | 4.23 | 3.46 | JPT |
| hmm30172 | hmm30172-S | rs6817520 | 4 | 119678315 | 36660 | 6.144 | 0.4334 | 6.55 | 5.39 | 4.37 | 3.61 | JPT |
| hmm31752 | hmm31752-S | rs2535310 | 6 | 31161236 | 29158 | 13.6009 | 0.7639 | 6.54 | 5.31 | 4.34 | 3.65 | JPT |
| hmm32897 | hmm32897-S | rs12537368 | 7 | 65343800 | 305804 | 7.7699 | 0.5156 | 6.72 | 5.29 | 4.11 | 3.27 | JPT |
| hmm5445 | hmm5445-S | rs883416 | 17 | 30594554 | 24000 | 8.8456 | 0.5761 | 6.51 | 5.28 | 4.51 | 3.69 | JPT |
| hmm8932 | hmm8932-S | rs1556259 | 1 | 157827722 | 7089 | 5.5555 | 0.3967 | 6.07 | 5.25 | 4.44 | 3.68 | JPT |
| HRI | GI_11125767-S | rs511969 | 7 | 5857551 | 20626 | 6.2486 | 0.4397 | 6.01 | 5.17 | 4.26 | 3.61 | JPT |
| Hs.11898 | Hs.11898-S | rs8036979 | 15 | 50735287 | 1343 | 8.9307 | 0.58 | 7.11 | 5.26 | 4.43 | 3.7 | JPT |
| Hs.128024 | Hs.128024-S | rs2160195 | 7 | 38178211 | 13021 | 6.1858 | 0.452 | 7.75 | 5.45 | 4.45 | 3.71 | JPT |
| Hs.147006 | Hs.147006-S | rs16832394 | 2 | 136577042 | 92683 | 14.6723 | 0.7748 | 8.92 | 7.05 | 5.13 | 3.94 | JPT |
| Hs.164463 | Hs.164463-S | rs2246770 | 4 | 54397811 | 45576 | 7.2623 | 0.5058 | 9.43 | 7.06 | 5.05 | 4.04 | JPT |
| Hs.214235 | Hs.214235-S | rs5743595 | 4 | 38625210 | 13169 | 6.5792 | 0.4591 | 6.13 | 5.38 | 4.48 | 3.72 | JPT |
| Hs.224849 | Hs.224849-S | rs2053017 | 3 | 14677276 | 18957 | 6.5442 | 0.4571 | 7.26 | 5.76 | 4.47 | 3.69 | JPT |
| Hs.245997 | Hs.245997-S | rs1788414 | 21 | 42878403 | 13857 | 9.2473 | 0.5854 | 8.89 | 7.29 | 5.83 | 4.76 | JPT |
| Hs.264076 | Hs.264076-S | rs1408656 | 13 | 78784655 | 111714 | 8.492 | 0.5596 | 7.01 | 5.27 | 4.36 | 3.59 | JPT |
| Hs.345389 | Hs.345389-S | rs6519611 | 22 | 24170409 | 1687 | 19.6164 | 0.8687 | 7.97 | 6.83 | 5.36 | 4.28 | JPT |
| Hs.36679 | Hs.36679-S | rs3848289 | 16 | 65564339 | 82143 | 5.4293 | 0.3885 | 6.02 | 5.22 | 4.09 | 3.33 | JPT |
| Hs.379903 | Hs.379903-S | rs1045599 | 17 | 15820635 | 55 | 13.85 | 0.7621 | 6.84 | 5.53 | 4.43 | 3.61 | JPT |
| Hs.396207 | Hs.396207-S | rs11211152 | 1 | 45783250 | 10256 | 22.6726 | 0.906 | 7.69 | 5.72 | 4.39 | 3.42 | JPT |
| Hs.397369 | Hs.397369-S | rs12912 | 7 | 100334220 | 1659 | 6.0891 | 0.43 | 6.2 | 5.34 | 4.15 | 3.47 | JPT |
| Hs.400876 | Hs.400876-S | rs805531 | 20 | 36508140 | 25355 | 7.6859 | 0.5197 | 6.22 | 5.38 | 4.32 | 3.51 | JPT |
| Hs.402723 | Hs.402723-S | rs4879852 | 9 | 35001305 | 59485 | 9.592 | 0.609 | 6.18 | 5.25 | 4.2 | 3.51 | JPT |
| Hs.453941 | Hs.453941-S | rs2514594 | 8 | 119694330 | 113064 | 10.6159 | 0.65 | 7.79 | 6.45 | 4.92 | 3.98 | JPT |
| Hs.465789 | Hs.465789-S | rs11670116 | 19 | 7981202 | 1602 | 6.2251 | 0.4383 | 6.07 | 5.51 | 4.38 | 3.68 | JPT |
| Hs.468081 | Hs.468081-S | rs1465975 | 2 | 31323016 | 794405 | 6.5532 | 0.4498 | 6.7 | 5.68 | 4.47 | 3.56 | JPT |
| Hs.470569 | Hs.470569-S | rs12072490 | 1 | 31257332 | 988961 | 6.2057 | 0.4371 | 7.57 | 5.15 | 4.11 | 3.41 | JPT |
| Hs.473917 | Hs.473917-S | rs228046 | 21 | 42825006 | 5418 | 7.8913 | 0.5218 | 9.76 | 7.45 | 5.74 | 4.66 | JPT |
| Hs.473973 | Hs.473973-S | rs2838456 | 21 | 44221396 | 14199 | 6.17 | 0.4349 | 6.5 | 5.8 | 4.84 | 4.05 | JPT |
| Hs.48344 | Hs.48344-S | rs6781014 | 3 | 114239776 | 23089 | 5.3122 | 0.3809 | 6.05 | 5.3 | 4.32 | 3.62 | JPT |
| Hs.485895 | Hs.485895-S | rs9450619 | 6 | 87884546 | 112144 | 10.8366 | 0.6583 | 6.59 | 5.46 | 4.33 | 3.59 | JPT |
| Hs.517172 | Hs.517172-S | rs1883848 | 20 | 60998751 | 32951 | 9.3971 | 0.6006 | 6.1 | 5.57 | 4.33 | 3.6 | JPT |
| Hs.54543 | Hs.54543-S | rs1430410 | 3 | 158008264 | 60251 | 8.7762 | 0.5729 | 6.34 | 5.41 | 4.42 | 3.59 | JPT |
| Hs.6637 | Hs.6637-S | rs4752999 | 11 | 47385141 | 198594 | 14.4002 | 0.768 | 6.19 | 4.9 | 3.86 | 3.03 | JPT |
| Hs.98028 | Hs.98028-S | rs580213 | 11 | 124183179 | 1156 | 6.5349 | 0.4566 | 7.37 | 5.51 | 4.48 | 3.7 | JPT |
| HSPC157 | GI_7661813-S | rs1063117 | 1 | 22102194 | 605 | 6.609 | 0.4609 | 6.49 | 5.52 | 4.48 | 3.72 | JPT |
| HSRTSBETA | GI_42544116-I | rs2847325 | 18 | 693442 | 8950 | 14.8609 | 0.7794 | 7.06 | 5.53 | 4.24 | 3.53 | JPT |
| IL16 | GI_27262656-I | rs3898677 | 15 | 79383617 | 4278 | 7.0652 | 0.4866 | 7.86 | 6.14 | 4.62 | 3.75 | JPT |
| IPP | GI_5174472-S | rs2253862 | 1 | 45751053 | 82782 | 7.7224 | 0.5216 | 6.41 | 5.41 | 4.21 | 3.32 | JPT |
| IRF5 | GI_38683858-A | rs8043 | 7 | 128201335 | 18193 | 13.441 | 0.7425 | 5.88 | 5.23 | 4.27 | 3.51 | JPT |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ITIH4 | GI_40288189-S | rs2535627 | 3 | 52820145 | 2331 | 6.9638 | 0.481 | 5.83 | 5.24 | 4.25 | 3.47 | JPT |
| IVD | GI_6031167-S | rs2075624 | 15 | 38498015 | 29 | 7.0608 | 0.4947 | 7.12 | 5.26 | 4.31 | 3.55 | JPT |
| KIAA0265 | GI_44917618-S | rs12534379 | 7 | 129365068 | 2062 | 8.5428 | 0.5709 | 6.1 | 5.56 | 4.42 | 3.54 | JPT |
| KIAA1074 | GI_7662473-S | rs1557167 | 10 | 27512116 | 170157 | 5.8296 | 0.414 | 7.21 | 5.44 | 4.37 | 3.62 | JPT |
| KIAA1449 | GI_21314694-S | rs1053530 | 3 | 39113086 | 410 | 9.2671 | 0.5863 | 6.9 | 5.25 | 4.36 | 3.58 | JPT |
| KIAA1463 | GI_39930390-S | rs11169520 | 12 | 49359790 | 65125 | 9.8523 | 0.6198 | 8.41 | 5.95 | 4.75 | 3.76 | JPT |
| KIAA1712 | GI_30794213-S | rs1553669 | 4 | 175612138 | 15920 | 7.1201 | 0.5067 | 6.4 | 5.33 | 4.42 | 3.65 | JPT |
| KIAA1913 | GI_40538800-S | rs12214250 | 6 | 130643473 | 162161 | 16.3597 | 0.8051 | 7.59 | 5.56 | 4.48 | 3.73 | JPT |
| KIAA1972 | GI_45387948-S | rs2305695 | 16 | 55725936 | 104382 | 6.6322 | 0.4622 | 7.67 | 5.89 | 4.67 | 3.9 | JPT |
| KUB3 | GI_32698766-S | rs10747788 | 12 | 56601605 | 35151 | 8.3311 | 0.5519 | 6.76 | 5.53 | 4.31 | 3.59 | JPT |
| LAMC1 | GI_9845497-S | rs4652769 | 1 | 179740853 | 105440 | 6.8845 | 0.4765 | 5.69 | 5.11 | 4.29 | 3.58 | JPT |
| LCMT1 | GI_15082255-I | rs11074678 | 16 | 25057227 | 83455 | 12.8946 | 0.7267 | 7.86 | 5.75 | 4.54 | 3.73 | JPT |
| LGALS8 | GI_42544184-A | rs1041939 | 1 | 233037659 | 788 | 6.5585 | 0.5112 | 8.46 | 6.41 | 5.06 | 4.01 | JPT |
| LILRB3 | GI_5803059-S | rs11672654 | 19 | 59425145 | 12513 | 8.8032 | 0.5656 | 9.69 | 6.48 | 5.19 | 4.22 | JPT |
| LOC126208 | GI_27485046-S | rs516022 | 19 | 61301183 | 10299 | 6.1 | 0.4467 | 6.26 | 5.58 | 4.49 | 3.75 | JPT |
| LOC130502 | GI_37539459-S | rs2293671 | 2 | 20059492 | 40089 | 8.5217 | 0.561 | 8.56 | 5.39 | 4.4 | 3.68 | JPT |
| LOC132241 | GI_42656828-S | rs7622524 | 3 | 130601620 | 8703 | 6.7327 | 0.4679 | 6.27 | 5.43 | 4.21 | 3.44 | JPT |
| LOC135043 | GI_17463264-S | rs10946158 | 6 | 166701700 | 25306 | 13.7487 | 0.751 | 7.2 | 5.41 | 4.54 | 3.81 | JPT |
| LOC144097 | GI_37541019-S | rs643634 | 11 | 63342380 | 9308 | 6.6457 | 0.463 | 7.39 | 5.6 | 4.25 | 3.48 | JPT |
| LOC147804 | GI_30154892-S | rs7248917 | 19 | 58631479 | 8142 | 6.315 | 0.4436 | 7 | 5.77 | 4.5 | 3.79 | JPT |
| LOC151963 | GI_31341922-S | rs2133864 | 3 | 194098959 | 101392 | 6.4868 | 0.4538 | 7.18 | 6.09 | 4.84 | 3.85 | JPT |
| LOC197322 | GI_28372536-S | rs3785414 | 16 | 87777900 | 28327 | 14.4858 | 0.7784 | 6.73 | 5.5 | 4.38 | 3.63 | JPT |
| LOC206962 | GI_22046332-S | rs3812561 | 9 | 136546713 | 13328 | 8.09 | 0.5401 | 7.26 | 6.34 | 4.79 | 3.89 | JPT |
| LOC222701 | GI_27498465-S | rs9283884 | 6 | 28243639 | 1563 | 5.6585 | 0.4108 | 6.88 | 5.08 | 4.12 | 3.3 | JPT |
| LOC282956 | GI_27483210-S | rs2428486 | 6 | 31462083 | 8468 | 12.9379 | 0.7196 | 7.17 | 5.39 | 4.37 | 3.68 | JPT |
| LOC283377 | GI_37542981-S | rs7302925 | 12 | 55147725 | 1805 | 8.6502 | 0.5671 | 7.48 | 6.47 | 4.9 | 3.77 | JPT |
| LOC283970 | GI_40217627-S | rs9939092 | 16 | 68596778 | 28928 | 20.3245 | 0.8785 | 7.03 | 5.27 | 4.18 | 3.31 | JPT |
| LOC284184 | GI_27500527-S | rs1048775 | 17 | 76816924 | 11379 | 6.2943 | 0.4424 | 5.99 | 5.29 | 4.25 | 3.56 | JPT |
| LOC284293 | GI_27485378-S | rs9955410 | 18 | 59771017 | 569 | 13.8846 | 0.7546 | 7.47 | 6.63 | 4.79 | 3.87 | JPT |
| LOC285407 | GI_37550539-S | rs9758051 | 3 | 131297567 | 2507 | 5.8824 | 0.4499 | 6.63 | 5.34 | 4.25 | 3.48 | JPT |
| LOC286353 | GI_27478844-S | rs1836404 | 9 | 95629819 | 18451 | 6.4388 | 0.4509 | 7.25 | 5.27 | 4.25 | 3.5 | JPT |
| LOC339053 | GI_29746836-S | rs7191155 | 16 | 19707714 | 82291 | 6.9125 | 0.4864 | 7.26 | 5.57 | 4.45 | 3.64 | JPT |
| LOC339229 | GI_41150782-S | rs7502869 | 17 | 77241821 | 974 | 5.9392 | 0.4286 | 6.1 | 5.42 | 4.31 | 3.55 | JPT |
| LOC339803 | GI_42656315-S | rs1729662 | 2 | 61302956 | 21956 | 9.2257 | 0.5845 | 6.62 | 5.13 | 4.18 | 3.4 | JPT |
| LOC339804 | GI_37546921-S | rs11498 | 2 | 61282470 | 19471 | 15.0649 | 0.7842 | 6.15 | 5.25 | 4.13 | 3.38 | JPT |
| LOC340435 | GI_29735811-S | rs6988053 | 8 | 71709517 | 72410 | 14.981 | 0.7823 | 7.16 | 5.75 | 4.53 | 3.71 | JPT |
| LOC345462 | GI_37550406-S | rs2047354 | 5 | 178387853 | 5273 | 6.3945 | 0.4483 | 7.02 | 5.85 | 4.54 | 3.74 | JPT |
| LOC347981 | GI_30160064-S | rs4078116 | 6 | 29960516 | 2027 | 12.7477 | 0.7223 | 6.06 | 5.4 | 4.35 | 3.55 | JPT |
| LOC374747 | GI_37541845-S | rs4567733 | 16 | 76302851 | 30261 | 6.6312 | 0.4621 | 7.34 | 6.09 | 4.79 | 4.01 | JPT |
| LOC374758 | GI_37544593-S | rs8064453 | 17 | 265835 | 1665 | 6.2115 | 0.4374 | 7.42 | 5.46 | 4.48 | 3.66 | JPT |
| LOC375097 | GI_37555934-S | rs805531 | 20 | 36508140 | 25206 | 7.9565 | 0.5335 | 7.52 | 5.36 | 4.27 | 3.52 | JPT |
| LOC375249 | GI_37547210-S | rs2290127 | 2 | 97777553 | 547289 | 7.7121 | 0.5127 | 7.83 | 6.16 | 4.59 | 3.5 | JPT |
| LOC375671 | GI_37556019-S | rs2546220 | 8 | 74331172 | 621 | 5.9987 | 0.4245 | 6.38 | 5.43 | 4.39 | 3.65 | JPT |
| LOC377696 | GI_37555914-S | rs2514594 | 8 | 119694330 | 32156 | 9.4459 | 0.6027 | 7.1 | 6.04 | 4.91 | 3.97 | JPT |
| LOC378075 | GI_37538916-S | rs10232851 | 7 | 55603043 | 354891 | 14.1986 | 0.7795 | 7 | 5.76 | 4.49 | 3.56 | JPT |
| LOC387895 | GI_41149833-S | rs1617132 | 12 | 125781577 | 24174 | 15.5943 | 0.7963 | 13 | 8.74 | 6.08 | 4.66 | JPT |
| LOC387905 | GI_41202581-S | rs7336525 | 13 | 20816844 | 20 | 6.8622 | 0.4753 | 6.68 | 5.57 | 4.4 | 3.64 | JPT |
| LOC388274 | GI_41150288-S | rs1420871 | 16 | 49372933 | 44899 | 5.6605 | 0.4034 | 5.96 | 5.24 | 4.33 | 3.62 | JPT |
| LOC388299 | GI_41150379-S | rs4567733 | 16 | 76302851 | 30231 | 6.8545 | 0.4748 | 6.5 | 5.81 | 4.64 | 3.86 | JPT |
| LOC389362 | GI_41147302-S | rs4602754 | 6 | 3207500 | 5612 | 7.8602 | 0.5286 | 7.25 | 5.63 | 4.49 | 3.76 | JPT |
| LOC389456 | GI_41147544-S | rs12535516 | 7 | 887681 | 3080 | 5.6952 | 0.4132 | 8 | 5.63 | 4.5 | 3.59 | JPT |
| LOC389562 | GI_41147546-S | rs2270164 | 7 | 138935139 | 15196 | 6.7566 | 0.4693 | 6.96 | 5.76 | 4.6 | 3.74 | JPT |
| LOC392620 | GI_41147689-S | rs798497 | 7 | 2569198 | 34300 | 6.0592 | 0.4442 | 6.4 | 5.36 | 4.39 | 3.66 | JPT |
| LOC399987 | GI_42660080-S | rs9300302 | 12 | 3737732 | 1669 | 11.7124 | 0.6893 | 6.54 | 5.5 | 4.52 | 3.86 | JPT |
| LOC400051 | GI_42659981-S | rs2051993 | 12 | 66699945 | 1068 | 11.1965 | 0.6714 | 6.32 | 5.75 | 4.5 | 3.79 | JPT |
| LOC400410 | GI_42660516-S | rs2586183 | 15 | 77967161 | 26852 | 11.2554 | 0.6735 | 7.36 | 5.51 | 4.42 | 3.74 | JPT |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC400566 | GI_42661283-S | rs8064453 | 17 | 265835 | 1193 | 10.6679 | 0.652 | 6.69 | 5.47 | 4.39 | 3.57 | JPT |
| LOC400571 | GI_42661084-S | rs10438740 | 17 | 7413608 | 12770 | 8.0096 | 0.5361 | 6.66 | 5.16 | 4.43 | 3.67 | JPT |
| LOC400642 | GI_42661344-S | rs2135308 | 18 | 5212146 | 24205 | 13.7484 | 0.751 | 8.54 | 7.1 | 5.01 | 3.99 | JPT |
| LOC400933 | GI_42662518-S | rs135878 | 22 | 48335230 | 205766 | 12.5819 | 0.7348 | 6.98 | 5.85 | 4.6 | 3.92 | JPT |
| LOC401135 | GI_42657007-S | rs10518042 | 4 | 68431669 | 14838 | 7.0868 | 0.4878 | 6.62 | 5.53 | 4.19 | 3.42 | JPT |
| LOC401245 | GI_42657607-S | rs9380167 | 6 | 30382440 | 14959 | 7.0005 | 0.4749 | 6.78 | 5.57 | 4.38 | 3.65 | JPT |
| LOC401560 | GI_42659039-S | rs3812561 | 9 | 136546713 | 13381 | 8.8639 | 0.577 | 8.38 | 6.8 | 5.33 | 4.14 | JPT |
| LOC51240 | GI_31377759-S | rs1055091 | 2 | 190460649 | 343 | 19.2345 | 0.8631 | 6.25 | 5.21 | 4.28 | 3.42 | JPT |
| LOC87769 | GI_34147452-S | rs9554707 | 13 | 100037593 | 55616 | 11.9597 | 0.6975 | 6.92 | 5.97 | 4.74 | 3.85 | JPT |
| LOC91120 | GI_15150800-S | rs7248612 | 19 | 19824086 | 154231 | 5.6003 | 0.3996 | 6.05 | 5.16 | 4.12 | 3.4 | JPT |
| LTBR | GI_4505038-S | rs10774430 | 12 | 6375034 | 4306 | 6.7917 | 0.506 | 9.84 | 6.07 | 4.78 | 3.96 | JPT |
| LZIC | GI_40255081-S | rs3003376 | 1 | 10005567 | 81025 | 10.3061 | 0.6381 | 6.96 | 5.39 | 4.51 | 3.72 | JPT |
| MAP1B | GI_14165455-A | rs1217816 | 5 | 71424094 | 113859 | 7.5253 | 0.5113 | 7.51 | 5.53 | 4.34 | 3.48 | JPT |
| MASTL | GI_14249561-S | rs11015588 | 10 | 27508768 | 6682 | 6.762 | 0.4696 | 6.41 | 5.49 | 4.43 | 3.66 | JPT |
| MGC10120 | GI_28603839-S | rs12762869 | 10 | 101983702 | 40795 | 11.4576 | 0.6806 | 6.13 | 5.67 | 4.53 | 3.63 | JPT |
| MGC10854 | GI_40254984-S | rs925368 | 12 | 108853699 | 36366 | 5.6929 | 0.4054 | 6.14 | 5.15 | 4.35 | 3.46 | JPT |
| MGC12458 | GI_14150107-S | rs586013 | 1 | 241517934 | 59146 | 13.8528 | 0.7538 | 6.62 | 5.57 | 4.63 | 3.84 | JPT |
| MGC15763 | GI_19923906-S | rs567541 | 3 | 16339621 | 21379 | 6.9208 | 0.4786 | 6.63 | 5.44 | 4.57 | 3.69 | JPT |
| MGC19764 | GI_42661257-S | rs883416 | 17 | 30594554 | 24027 | 10.1381 | 0.6314 | 6.53 | 5.56 | 4.46 | 3.7 | JPT |
| MGC20781 | GI_34147471-S | rs2074162 | 17 | 37468202 | 233051 | 9.1482 | 0.5987 | 6.79 | 5.2 | 3.99 | 3.29 | JPT |
| MGC21518 | GI_21687219-S | rs2189387 | 17 | 36293632 | 48847 | 4.9818 | 0.3588 | 5.41 | 4.92 | 4.09 | 3.4 | JPT |
| MGC21644 | GI_45505153-A | rs340033 | 5 | 145170174 | 50052 | 5.7928 | 0.4117 | 8.7 | 5.47 | 4.37 | 3.48 | JPT |
| MGC22773 | GI_21687083-S | rs1412825 | 1 | 74375835 | 17816 | 14.9484 | 0.7815 | 6.95 | 5.48 | 4.04 | 3.34 | JPT |
| MGC22960 | GI_40316917-S | rs4660963 | 1 | 47045856 | 503375 | 5.4949 | 0.3928 | 5.93 | 5.05 | 4.13 | 3.37 | JPT |
| MGC24665 | GI_24308244-S | rs12445900 | 16 | 11312331 | 40586 | 7.1467 | 0.4829 | 6.61 | 5.37 | 4.4 | 3.71 | JPT |
| MGC2752 | GI_33859747-S | rs3794965 | 19 | 63761165 | 24047 | 16.0593 | 0.8064 | 6.36 | 5.37 | 4.05 | 3.28 | JPT |
| MGC3248 | GI_34147426-S | rs26764 | 16 | 23619426 | 31036 | 6.8979 | 0.4773 | 6.22 | 5.15 | 4.42 | 3.62 | JPT |
| MGC35033 | GI_34303924-S | rs2468939 | 12 | 47134509 | 41781 | 7.7774 | 0.533 | 8.98 | 6.44 | 4.89 | 3.83 | JPT |
| MGC35308 | GI_31341688-S | rs7759603 | 6 | 166675043 | 15350 | 5.4877 | 0.3923 | 7.17 | 5.41 | 4.56 | 3.81 | JPT |
| MGC3794 | GI_33239373-S | rs4657739 | 1 | 164874147 | 27069 | 10.9046 | 0.6608 | 6.7 | 5.36 | 4.31 | 3.63 | JPT |
| MGC39633 | GI_22749136-S | rs1005056 | 5 | 114608641 | 23880 | 5.9755 | 0.4231 | 7 | 5.78 | 4.66 | 3.72 | JPT |
| MGC40397 | GI_22748696-S | rs10861310 | 12 | 103930868 | 42882 | 5.6991 | 0.4213 | 6.92 | 5.52 | 4.39 | 3.72 | JPT |
| MGC4083 | GI_14210535-S | rs11663340 | 18 | 12323686 | 7490 | 5.3644 | 0.3916 | 6.8 | 5.2 | 4.3 | 3.57 | JPT |
| MGC5391 | GI_29126184-S | rs10496660 | 2 | 127629274 | 548037 | 5.5028 | 0.3933 | 7.05 | 5.33 | 4.28 | 3.48 | JPT |
| MK-STYX | GI_32481212-S | rs8565 | 7 | 75274925 | 17 | 5.8416 | 0.4148 | 5.66 | 4.99 | 4.07 | 3.36 | JPT |
| MMRP19 | GI_7705723-S | rs2288667 | 11 | 34860975 | 5553 | 6.7278 | 0.4677 | 6.59 | 5.46 | 4.46 | 3.75 | JPT |
| MPHOSPH1 | GI_7705347-S | rs727427 | 10 | 91390364 | 134203 | 6.3832 | 0.4477 | 6.8 | 5.49 | 4.58 | 3.69 | JPT |
| MRPL21 | GI_31652223-A | rs483626 | 11 | 68441431 | 26017 | 12.8057 | 0.7156 | 6.93 | 5.75 | 4.56 | 3.71 | JPT |
| MRPL43 | GI_28872735-A | rs927302 | 10 | 102712906 | 23703 | 15.1202 | 0.7855 | 8.21 | 5.41 | 4.24 | 3.44 | JPT |
| MRPL53 | GI_22035595-S | rs3771744 | 2 | 74490191 | 121203 | 7.6359 | 0.5171 | 6.51 | 5.18 | 4.24 | 3.49 | JPT |
| MRVLDC2 | GI_21687269-S | rs26685 | 5 | 68068766 | 706741 | 5.9798 | 0.4311 | 6.94 | 5.05 | 3.97 | 3.18 | JPT |
| MTRR | GI_4505278-A | rs6555501 | 5 | 7932983 | 21007 | 6.9928 | 0.4826 | 6.53 | 5.59 | 4.4 | 3.68 | JPT |
| MYBL2 | GI_31652260-S | rs439115 | 20 | 41704335 | 74005 | 5.7506 | 0.4091 | 7.24 | 5.4 | 4.35 | 3.66 | JPT |
| MYOM2 | GI_4505314-S | rs6990007 | 8 | 2054882 | 25671 | 6.0555 | 0.4204 | 7.68 | 5.36 | 4.56 | 3.88 | JPT |
| N2N | GI_44917616-S | rs2143909 | 1 | 143594029 | 823005 | 4.6845 | 0.3383 | 5.46 | 4.48 | 3.73 | 3.03 | JPT |
| NBEA | GI_21536251-S | rs7334333 | 13 | 34411594 | 732792 | 6.8638 | 0.4754 | 7.71 | 6.6 | 5.21 | 4.08 | JPT |
| NDUFS5 | GI_4758789-S | rs12032116 | 1 | 39189402 | 28266 | 11.4224 | 0.6793 | 6.2 | 5.27 | 4.4 | 3.62 | JPT |
| NDUFV3 | GI_21361323-S | rs2839603 | 21 | 43197575 | 4490 | 8.9241 | 0.5711 | 8.52 | 7.55 | 5.47 | 4.42 | JPT |
| NIPSNAP3B | GI_21361742-S | rs2162116 | 9 | 104608968 | 6853 | 5.742 | 0.4085 | 7.03 | 5.71 | 4.43 | 3.66 | JPT |
| NMNAT3 | GI_31342325-S | rs10935342 | 3 | 140888040 | 126177 | 11.9406 | 0.6969 | 7.12 | 6.18 | 4.79 | 3.85 | JPT |
| NOR1 | GI_45643130-I | rs3738836 | 1 | 36554101 | 9002 | 11.9818 | 0.6982 | 6.97 | 5.81 | 4.61 | 3.67 | JPT |
| NPEPL1 | GI_20070332-S | rs2426778 | 20 | 56726884 | 2673 | 7.0134 | 0.4756 | 6.42 | 5.45 | 4.43 | 3.69 | JPT |
| NQO2 | GI_4505416-S | rs1143684 | 6 | 2955389 | 6760 | 8.6322 | 0.5663 | 7.24 | 5.57 | 4.6 | 3.79 | JPT |
| NR2F2 | GI_31377723-S | rs981923 | 15 | 94384637 | 298009 | 7.6788 | 0.5193 | 7.61 | 6.64 | 5.08 | 4.05 | JPT |
| NUDT2 | GI_22265329-I | rs4310287 | 9 | 34364979 | 38725 | 20.4581 | 0.8803 | 7.16 | 5.67 | 4.32 | 3.54 | JPT |
| OAS1 | GI_8051622-I | rs4767027 | 12 | 111821877 | 3619 | 10.3692 | 0.6318 | 7.49 | 5.84 | 4.56 | 3.74 | JPT |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PAQR6 | GI_24432010-S | rs1543294 | 1 | 153022930 | 3518 | 5.6046 | 0.3998 | 5.61 | 4.92 | 4.03 | 3.36 | JPT |
| PBP | GI_38016928-S | rs428073 | 12 | 117145471 | 99535 | 5.4583 | 0.3904 | 6.3 | 5.43 | 4.51 | 3.8 | JPT |
| PEX6 | GI_21361243-S | rs2395943 | 6 | 43048651 | 8748 | 10.5537 | 0.6389 | 7.11 | 5.35 | 4.42 | 3.64 | JPT |
| PFAAP5 | GI_7656970-S | rs718444 | 13 | 32045052 | 55774 | 6.2677 | 0.4331 | 6.88 | 5.24 | 4.39 | 3.65 | JPT |
| PHACS | GI_14211920-S | rs2074038 | 11 | 44044565 | 17304 | 21.2355 | 0.89 | 7.05 | 6.19 | 4.52 | 3.79 | JPT |
| PIGN | GI_34328903-A | rs565610 | 18 | 57848576 | 14414 | 8.2654 | 0.5488 | 6.3 | 5.55 | 4.45 | 3.66 | JPT |
| PKHD1L1 | GI_31377831-S | rs1563580 | 8 | 110575280 | 32975 | 19.3952 | 0.8655 | 6.09 | 5.35 | 4.21 | 3.4 | JPT |
| PLA2G4C | GI_4505850-S | rs2307279 | 19 | 53300410 | 57426 | 5.9278 | 0.4201 | 6.53 | 5.48 | 4.48 | 3.7 | JPT |
| PNN | GI_33356173-S | rs8018720 | 14 | 38625936 | 94660 | 12.5052 | 0.7149 | 6.2 | 5.43 | 4.24 | 3.54 | JPT |
| POLE4 | GI_38455393-S | rs12617404 | 2 | 75102296 | 6017 | 6.7843 | 0.4709 | 5.92 | 5.22 | 4.44 | 3.64 | JPT |
| POLR1A | GI_7661685-S | rs1978842 | 2 | 86138197 | 28542 | 11.7421 | 0.6903 | 7.14 | 6 | 4.66 | 3.67 | JPT |
| POLR2E | GI_14589950-S | rs6843 | 19 | 1039285 | 9 | 14.2939 | 0.7653 | 6.52 | 5.9 | 4.69 | 3.88 | JPT |
| POLR3F | GI_33598951-S | rs2295557 | 20 | 18471864 | 58792 | 6.3234 | 0.4364 | 6.31 | 5.29 | 4.39 | 3.62 | JPT |
| PP3856 | GI_40255088-S | rs4874159 | 8 | 144742093 | 13960 | 8.3762 | 0.5541 | 6.53 | 5.71 | 4.52 | 3.69 | JPT |
| PPA2 | GI_31881619-A | rs11932428 | 4 | 106644740 | 3679 | 15.1682 | 0.7946 | 6.79 | 5.26 | 4.18 | 3.36 | JPT |
| PPIH | GI_45439322-S | rs3738516 | 1 | 43109294 | 307122 | 5.182 | 0.3795 | 6.2 | 5.07 | 4.19 | 3.45 | JPT |
| PRIC285 | GI_34335259-S | rs1291206 | 20 | 61799613 | 139576 | 5.9804 | 0.4234 | 6.45 | 5.69 | 4.31 | 3.58 | JPT |
| PRKCM | GI_4506074-S | rs4441176 | 14 | 29388428 | 272228 | 6.7374 | 0.4603 | 6.3 | 5.25 | 4.22 | 3.54 | JPT |
| PRO0149 | GI_38016918-S | rs9926522 | 16 | 9124449 | 3613 | 6.7895 | 0.4712 | 6.43 | 5.61 | 4.49 | 3.73 | JPT |
| PROL4 | GI_6005801-S | rs1376251 | 12 | 11030119 | 139168 | 6.3519 | 0.4458 | 7.76 | 6.2 | 4.98 | 4.05 | JPT |
| PTER | GI_20070185-S | rs1055340 | 10 | 16595534 | 974 | 12.9569 | 0.7286 | 8.78 | 6.79 | 5.1 | 4.03 | JPT |
| R29124_1 | GI_16117774-S | rs714106 | 19 | 46775689 | 1914 | 8.4588 | 0.5581 | 6.91 | 5.4 | 4.19 | 3.45 | JPT |
| RAB6C | GI_14149798-S | rs17049711 | 2 | 130240265 | 216002 | 5.2835 | 0.379 | 7.15 | 5.26 | 4.14 | 3.45 | JPT |
| RABGEF1 | GI_7657495-S | rs3735141 | 7 | 64864490 | 855610 | 9.4932 | 0.6048 | 7.43 | 5.62 | 4.31 | 3.41 | JPT |
| RAD18 | GI_14550404-S | rs250405 | 3 | 8900041 | 2983 | 8.2233 | 0.5645 | 6.81 | 5.39 | 4.37 | 3.71 | JPT |
| RAD51C | GI_17402895-I | rs714959 | 17 | 53983600 | 145568 | 7.074 | 0.4871 | 7.26 | 5.4 | 4.06 | 3.31 | JPT |
| RAMP1 | GI_5032018-S | rs6741923 | 2 | 238581206 | 21449 | 8.8099 | 0.5834 | 6.2 | 5.39 | 4.46 | 3.68 | JPT |
| raptor | GI_22094986-S | rs1062935 | 17 | 76554452 | 37 | 7.6361 | 0.5171 | 6.72 | 5.33 | 4.34 | 3.64 | JPT |
| RASSF6 | GI_41393612-A | rs1247583 | 4 | 74854306 | 38232 | 5.2547 | 0.3771 | 6.27 | 4.94 | 4.12 | 3.44 | JPT |
| RBMS2 | GI_4506448-S | rs3782235 | 12 | 55201814 | 67204 | 6.1181 | 0.4318 | 6.47 | 5.6 | 4.4 | 3.57 | JPT |
| RPH3AL | GI_31543557-S | rs4890194 | 17 | 81136 | 18755 | 8.5707 | 0.5634 | 7.89 | 6.01 | 4.49 | 3.66 | JPT |
| RPL37A | GI_16306561-S | rs3732019 | 2 | 217187892 | 1196 | 18.8386 | 0.8571 | 9.24 | 6.99 | 5.65 | 4.42 | JPT |
| RPS6KB2 | GI_4506738-S | rs1476792 | 11 | 66952813 | 6532 | 7.8184 | 0.5265 | 6.71 | 5.63 | 4.48 | 3.52 | JPT |
| S100A13 | GI_41117409-S | rs2274739 | 1 | 150425206 | 13257 | 9.5507 | 0.6072 | 6.12 | 5.16 | 4.14 | 3.44 | JPT |
| SCLY | GI_39725671-S | rs2252416 | 2 | 238768386 | 21424 | 5.6235 | 0.401 | 6.83 | 5.57 | 4.54 | 3.74 | JPT |
| SERPINB10 | GI_4826901-S | rs10513932 | 18 | 59719294 | 33898 | 8.9785 | 0.6192 | 7.82 | 5.68 | 4.57 | 3.8 | JPT |
| SF1 | GI_42544126-I | rs523200 | 11 | 64289155 | 11144 | 16.4601 | 0.8147 | 8.44 | 5.51 | 4.24 | 3.46 | JPT |
| SFRS10 | GI_4759097-S | rs2251407 | 3 | 187137626 | 20262 | 7.5527 | 0.5128 | 7.45 | 5.55 | 4.51 | 3.72 | JPT |
| SFXN2 | GI_34222270-S | rs2902548 | 10 | 104477372 | 11419 | 10.8874 | 0.6602 | 6.34 | 5.1 | 4.16 | 3.36 | JPT |
| SHMT1 | GI_22547185-I | rs854773 | 17 | 17995593 | 184060 | 6.0747 | 0.4451 | 6.04 | 5.51 | 4.23 | 3.43 | JPT |
| SIVA | GI_11277467-I | rs4983543 | 14 | 104283444 | 9719 | 7.4374 | 0.5067 | 6.28 | 5.23 | 4.24 | 3.5 | JPT |
| SLC2A8 | GI_21361448-S | rs2298182 | 9 | 127286223 | 36832 | 5.8304 | 0.4141 | 7.71 | 5.34 | 4.4 | 3.65 | JPT |
| SLC37A2 | GI_38093648-S | rs2155355 | 11 | 125369536 | 905261 | 5.542 | 0.3958 | 8.21 | 5.35 | 4.37 | 3.63 | JPT |
| SLC7A7 | GI_21361562-S | rs2281678 | 14 | 22354008 | 41591 | 9.166 | 0.5905 | 6.01 | 5.57 | 4.53 | 3.68 | JPT |
| SNX16 | GI_23238247-A | rs4272332 | 8 | 82870584 | 3975 | 10.1425 | 0.6316 | 6.45 | 5.58 | 4.34 | 3.55 | JPT |
| SNX7 | GI_23111054-A | rs9285629 | 1 | 98849718 | 87955 | 13.4225 | 0.742 | 14.7 | 8.67 | 5.6 | 4.2 | JPT |
| SOS1 | GI_15529995-S | rs921433 | 2 | 38934562 | 190188 | 7.5301 | 0.5033 | 7.19 | 5.81 | 4.64 | 3.76 | JPT |
| SPA17 | GI_15718773-S | rs11825168 | 11 | 124043411 | 26063 | 8.6845 | 0.5601 | 6.37 | 5.56 | 4.35 | 3.68 | JPT |
| SPG7 | GI_40806172-I | rs3803676 | 16 | 88123607 | 7762 | 6.9402 | 0.4797 | 6.16 | 5.28 | 4.33 | 3.58 | JPT |
| SPINT2 | GI_10863908-S | rs3786870 | 19 | 43447704 | 26914 | 7.4068 | 0.5051 | 6.84 | 5.6 | 4.31 | 3.55 | JPT |
| SQSTM1 | GI_19923742-S | rs10277 | 5 | 179197337 | 249 | 5.5261 | 0.3948 | 6.45 | 5.43 | 4.46 | 3.71 | JPT |
| ST7L | GI_38201636-A | rs3748656 | 1 | 112948723 | 152024 | 6.0581 | 0.4206 | 6.41 | 5.42 | 4.27 | 3.53 | JPT |
| STAT6 | GI_23397677-S | rs324019 | 12 | 55772914 | 2679 | 7.9797 | 0.5615 | 6.75 | 5.58 | 4.28 | 3.5 | JPT |
| STEAP | GI_22027487-S | rs13224065 | 7 | 89447014 | 8383 | 7.104 | 0.524 | 7.38 | 5.34 | 4.38 | 3.59 | JPT |
| STK25 | GI_34147665-S | rs7568 | 2 | 242011733 | 142878 | 11.7962 | 0.6921 | 6.52 | 5.2 | 4.24 | 3.49 | JPT |
| SUPT3H | GI_4507308-A | rs1284988 | 6 | 45172750 | 143649 | 10.1632 | 0.6505 | 7.19 | 5.65 | 4.38 | 3.59 | JPT |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SURF1 | GI_19557683-S | rs12335 | 9 | 133227388 | 21486 | 6.9472 | 0.48 | 6.58 | 5.57 | 4.49 | 3.72 | JPT |
| TAF4B | GI_37545625-S | rs7228427 | 18 | 22572837 | 347689 | 6.1161 | 0.4317 | 7.11 | 5.54 | 4.47 | 3.76 | JPT |
| TAP2 | GI_9961247-I | rs3916765 | 6 | 32793528 | 104346 | 10.9574 | 0.6716 | 7.13 | 6.1 | 4.86 | 3.88 | JPT |
| TAPBP-R | GI_34222333-S | rs2532496 | 12 | 6434709 | 6923 | 6.7247 | 0.4757 | 6.94 | 5.44 | 4.46 | 3.77 | JPT |
| TBC1D4 | GI_42660198-S | rs529638 | 13 | 74762518 | 5143 | 5.9678 | 0.4226 | 7.09 | 5.35 | 4.38 | 3.61 | JPT |
| TCL6 | GI_21536345-A | rs3759537 | 14 | 95204869 | 2625 | 12.6294 | 0.7102 | 8.46 | 6.52 | 5.13 | 4.08 | JPT |
| TEAD4 | GI_4507426-S | rs10774085 | 12 | 2930485 | 89581 | 5.9937 | 0.4242 | 6.52 | 5.66 | 4.53 | 3.84 | JPT |
| TFAM | GI_4507400-I | rs10826176 | 10 | 59811543 | 14230 | 12.4922 | 0.7145 | 6.51 | 5.41 | 4.22 | 3.49 | JPT |
| THAP5 | GI_32698887-S | rs40915 | 7 | 107776670 | 22024 | 8.5268 | 0.5613 | 6.83 | 5.57 | 4.57 | 3.69 | JPT |
| THAP6 | GI_37059751-S | rs1478174 | 4 | 76750368 | 60711 | 5.6164 | 0.4006 | 6.03 | 5.54 | 4.22 | 3.47 | JPT |
| TIMM10 | GI_6912707-S | rs2649662 | 11 | 57109138 | 56520 | 8.6968 | 0.5693 | 7.25 | 6.31 | 4.86 | 3.64 | JPT |
| TK2 | GI_33636700-S | rs725131 | 16 | 65143211 | 40964 | 5.8861 | 0.4176 | 6.63 | 5.28 | 4.16 | 3.36 | JPT |
| TLR1 | GI_41350336-S | rs3924112 | 4 | 38618376 | 2313 | 5.5848 | 0.3986 | 6.4 | 5.52 | 4.46 | 3.75 | JPT |
| TLR10 | GI_13569929-S | rs5743595 | 4 | 38625210 | 27728 | 7.0009 | 0.483 | 6.73 | 5.45 | 4.46 | 3.78 | JPT |
| TLR6 | GI_20143970-S | rs5743595 | 4 | 38625210 | 25910 | 5.8139 | 0.4131 | 7.03 | 5.48 | 4.51 | 3.79 | JPT |
| TMPIT | GI_13994299-S | rs3801472 | 7 | 75274429 | 13270 | 6.195 | 0.4444 | 7.76 | 5.4 | 4.31 | 3.51 | JPT |
| TNFRSF18 | GI_23238193-A | rs6603793 | 1 | 1590522 | 411687 | 5.1053 | 0.3743 | 5.54 | 4.95 | 3.89 | 3.18 | JPT |
| TNFRSF6 | GI_23510430-A | rs7915235 | 10 | 90769077 | 3897 | 5.7876 | 0.4114 | 6.17 | 5.23 | 4.28 | 3.67 | JPT |
| TOMM34 | GI_40807467-S | rs10485453 | 20 | 43002140 | 2254 | 7.6717 | 0.519 | 6.49 | 5.4 | 4.4 | 3.58 | JPT |
| TRIM4 | GI_15011940-A | rs1048705 | 7 | 99133591 | 218 | 6.7181 | 0.4671 | 6.14 | 5.05 | 3.95 | 3.26 | JPT |
| TSGA10 | GI_41281983-I | rs7606635 | 2 | 99103300 | 113127 | 6.1282 | 0.4248 | 6.82 | 5.31 | 4.16 | 3.39 | JPT |
| UBA52 | GI_15451941-S | rs12609505 | 19 | 18535057 | 11923 | 23.8507 | 0.9174 | 8.36 | 5.17 | 4.25 | 3.54 | JPT |
| UBE2L3 | GI_38157977-A | rs5754295 | 22 | 20276294 | 26473 | 5.8252 | 0.4138 | 6.29 | 5.55 | 4.48 | 3.73 | JPT |
| UGT2B10 | GI_27552756-S | rs3100645 | 4 | 69671954 | 205302 | 14.7923 | 0.7777 | 8.16 | 6.05 | 4.43 | 3.48 | JPT |
| UGT2B11 | GI_4507822-S | rs13144491 | 4 | 69273573 | 973550 | 29.7187 | 0.9565 | 9.85 | 6.15 | 4.57 | 3.64 | JPT |
| UGT2B17 | GI_4507820-S | rs13144491 | 4 | 69273573 | 41744 | 29.6363 | 0.9561 | 8.05 | 5.74 | 4.36 | 3.48 | JPT |
| UGT2B7 | GI_4507824-S | rs13144491 | 4 | 69273573 | 885483 | 26.9553 | 0.9412 | 7.78 | 6.14 | 4.68 | 3.65 | JPT |
| UMP-CMPK | GI_7706496-S | rs4492666 | 1 | 47512865 | 43160 | 5.6699 | 0.4194 | 6.19 | 5.23 | 4.28 | 3.56 | JPT |
| UMPS | GI_4507834-S | rs333312 | 3 | 125822164 | 123725 | 6.7851 | 0.4709 | 6.39 | 5.54 | 4.41 | 3.62 | JPT |
| UNQ2430 | GI_41190797-S | rs2276645 | 2 | 97788570 | 500611 | 5.7637 | 0.4099 | 6.55 | 5.21 | 4.35 | 3.46 | JPT |
| USMG5 | GI_14249375-S | rs7831 | 10 | 105195292 | 51257 | 20.1499 | 0.8762 | 6.25 | 5.3 | 4.27 | 3.5 | JPT |
| UTS2 | GI_12056478-I | rs161803 | 1 | 7910055 | 62324 | 7.5268 | 0.5114 | 8.01 | 6.09 | 4.7 | 3.79 | JPT |
| VPS13A | GI_15619007-I | rs10491839 | 9 | 77270451 | 41099 | 15.2591 | 0.7888 | 6.7 | 5.61 | 4.49 | 3.74 | JPT |
| WBSCR27 | GI_30795189-S | rs6946037 | 7 | 72681366 | 12436 | 8.0216 | 0.5367 | 5.95 | 5 | 4.06 | 3.33 | JPT |
| WDFY1 | GI_30795191-I | rs633956 | 2 | 224564462 | 43716 | 6.1144 | 0.4316 | 7.56 | 5.4 | 4.48 | 3.69 | JPT |
| WDR33 | GI_19923528-S | rs10496660 | 2 | 127629274 | 550773 | 5.1351 | 0.3691 | 6.6 | 5.09 | 4.27 | 3.53 | JPT |
| XRRA1 | GI_42659736-S | rs2298746 | 11 | 74231482 | 1489 | 16.2085 | 0.8095 | 6.74 | 5.5 | 4.29 | 3.54 | JPT |
| ZCCHC4 | GI_42657116-S | rs3796779 | 4 | 25020616 | 27553 | 8.0556 | 0.5472 | 7.33 | 5.85 | 4.77 | 3.88 | JPT |
| ZMYND12 | GI_34222153-S | rs3748846 | 1 | 42608114 | 42711 | 6.9091 | 0.4779 | 6.12 | 5.53 | 4.29 | 3.51 | JPT |
| ZNF175 | GI_37594438-S | rs1379284 | 19 | 56763379 | 21351 | 5.9197 | 0.4122 | 6.97 | 5.59 | 4.51 | 3.79 | JPT |
| ZNF230 | GI_5454181-S | rs12753 | 19 | 49207354 | 175 | 6.9839 | 0.4821 | 7.11 | 5.46 | 4.45 | 3.67 | JPT |
| ZNF587 | GI_14249531-S | rs1047405 | 19 | 63072690 | 955 | 5.0918 | 0.3662 | 6.63 | 5.05 | 4.18 | 3.49 | JPT |
| ZNF79 | GI_24307936-S | rs10739692 | 9 | 127272319 | 14846 | 6.3596 | 0.4463 | 6.92 | 5.48 | 4.49 | 3.61 | JPT |
| ZNFN1A1 | GI_31657112-S | rs7792486 | 7 | 50260518 | 16155 | 8.9187 | 0.5795 | 8.29 | 5.31 | 4.31 | 3.6 | JPT |
| ZNRD1 | GI_25777706-I | rs11755984 | 6 | 30061014 | 76191 | 6.454 | 0.444 | 7.55 | 5.73 | 4.6 | 3.71 | JPT |
| ABC1 | GI_38142463-S | rs10515177 | 17 | 55522267 | 46816 | 13.7608 | 0.6404 | 6.19 | 5.54 | 4.32 | 4.32 | YRI |
| ACN9 | GI_9910179-S | rs6973504 | 7 | 96392135 | 62985 | 6.0153 | 0.3297 | 7.33 | 5.72 | 4.69 | 4.69 | YRI |
| ACY1L2 | GI_37551403-S | rs4053639 | 6 | 89921398 | 7170 | 6.2041 | 0.3822 | 6.71 | 5.75 | 4.62 | 4.62 | YRI |
| AK2 | GI_26665889-I | rs11811191 | 1 | 33206037 | 58188 | 8.1005 | 0.4297 | 6.94 | 5.57 | 4.52 | 4.52 | YRI |
| ALDH1A3 | GI_4502040-S | rs11852748 | 15 | 99191558 | 82041 | 9.9951 | 0.5081 | 12.2 | 9.18 | 6.32 | 6.32 | YRI |
| AP4M1 | GI_14917110-S | rs3807479 | 7 | 99361552 | 12404 | 8.0167 | 0.4316 | 7.44 | 5.62 | 4.36 | 4.36 | YRI |
| APOA1BP | GI_21426826-S | rs4661189 | 1 | 153373634 | 3431 | 6.9241 | 0.3752 | 6.7 | 5.47 | 4.59 | 4.59 | YRI |
| ARHGAP12 | GI_26986533-S | rs12269395 | 10 | 32165259 | 29923 | 5.7975 | 0.323 | 6.45 | 5.48 | 4.43 | 4.43 | YRI |
| ARL6IP4 | GI_8923906-A | rs752164 | 12 | 122032694 | 40409 | 6.1126 | 0.3347 | 6.63 | 5.27 | 4.31 | 4.31 | YRI |
| ARNT | GI_30795239-A | rs3754210 | 1 | 147767334 | 171977 | 6.0623 | 0.3322 | 7.27 | 5.56 | 4.31 | 4.31 | YRI |
| ARPC3 | GI_23397667-S | rs2338754 | 12 | 108954453 | 381233 | 9.2891 | 0.4862 | 9.29 | 7.17 | 5.25 | 5.25 | YRI |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ARTS-1 | GI_20149636-S | rs7063 | 5 | 96135967 | 7329 | 7.7118 | 0.4122 | 6.48 | 5.62 | 4.55 | 4.55 | YRI |
| ASAHL | GI_30794501-S | rs13138223 | 4 | 77216794 | 17704 | 7.8376 | 0.4179 | 6.13 | 5.81 | 4.68 | 4.68 | YRI |
| ASRGL1 | GI_23308566-S | rs1881535 | 11 | 61878199 | 38117 | 6.4002 | 0.3493 | 6.58 | 5.72 | 4.52 | 4.52 | YRI |
| ATPAF2 | GI_22538424-S | rs8067146 | 17 | 17865681 | 3232 | 12.6738 | 0.6013 | 9.53 | 6.93 | 5.19 | 5.19 | YRI |
| ATPIF1 | GI_30260191-I | rs8559 | 1 | 28248394 | 18 | 10.0533 | 0.5103 | 7.7 | 5.3 | 4.36 | 4.36 | YRI |
| AXIN1 | GI_31083143-A | rs393521 | 16 | 277679 | 20 | 19.5993 | 0.769 | 7.36 | 5.6 | 4.47 | 4.47 | YRI |
| B3GTL | GI_34996530-S | rs912603 | 13 | 30803641 | 86 | 6.4779 | 0.3532 | 7.19 | 6.33 | 4.93 | 4.93 | YRI |
| BBP | GI_17738309-S | rs1390450 | 1 | 61852409 | 26242 | 8.0271 | 0.4265 | 8 | 5.55 | 4.59 | 4.59 | YRI |
| BFSP2 | GI_21536442-S | rs2737717 | 3 | 134668532 | 8193 | 12.6396 | 0.6002 | 6.48 | 5.35 | 4.49 | 4.49 | YRI |
| BIK | GI_21536418-S | rs4988394 | 22 | 41840631 | 9407 | 6.4821 | 0.3534 | 7.48 | 5.77 | 4.86 | 4.86 | YRI |
| C10orf26 | GI_41152103-S | rs619824 | 10 | 104571278 | 6897 | 6.035 | 0.3308 | 6.59 | 5.1 | 4.22 | 4.22 | YRI |
| C10orf88 | GI_13376420-S | rs4980169 | 10 | 124682576 | 1441 | 6.4851 | 0.3536 | 6.4 | 5.56 | 4.48 | 4.48 | YRI |
| C11orf17 | GI_21361869-A | rs3751068 | 11 | 8903526 | 5796 | 8.5674 | 0.4501 | 6.74 | 5.96 | 4.69 | 4.69 | YRI |
| C11orf21 | GI_7662662-S | rs2074021 | 11 | 2280104 | 6337 | 9.8504 | 0.5086 | 7.51 | 5.4 | 4.56 | 4.56 | YRI |
| C14orf118 | GI_40018643-A | rs10498533 | 14 | 75719885 | 18542 | 6.9681 | 0.3773 | 6.97 | 6.25 | 4.87 | 4.87 | YRI |
| C14orf122 | GI_34222327-S | rs8010715 | 14 | 23678987 | 865 | 9.2963 | 0.4805 | 6.92 | 5.85 | 4.62 | 4.62 | YRI |
| C14orf52 | GI_21553312-S | rs4902332 | 14 | 64445731 | 25025 | 29.4466 | 0.8941 | 7.51 | 5.55 | 4.48 | 4.48 | YRI |
| C1QTNF3 | GI_13569918-I | rs6546 | 5 | 34055787 | 28 | 5.4116 | 0.2979 | 6.52 | 5.41 | 4.48 | 4.48 | YRI |
| C20orf22 | GI_34147330-S | rs2500405 | 20 | 25308826 | 85217 | 7.1709 | 0.387 | 7.34 | 5.67 | 4.49 | 4.49 | YRI |
| C21orf56 | GI_23346426-S | rs8133082 | 21 | 46424341 | 18815 | 11.2751 | 0.555 | 9.88 | 7.09 | 5.25 | 5.25 | YRI |
| C22orf2 | GI_21359898-S | rs6519132 | 22 | 37395422 | 1315 | 8.9167 | 0.4648 | 6.6 | 5.75 | 4.66 | 4.66 | YRI |
| C2orf3 | GI_44890064-S | rs7573143 | 2 | 75916040 | 112738 | 6.1797 | 0.3382 | 8.15 | 5.71 | 4.62 | 4.62 | YRI |
| C6orf18 | GI_40538792-S | rs1265115 | 6 | 31225054 | 6322 | 8.1259 | 0.4308 | 6.41 | 5.46 | 4.55 | 4.55 | YRI |
| C7orf13 | GI_14249145-S | rs4716437 | 7 | 155941511 | 10578 | 7.8064 | 0.4221 | 7.28 | 6.08 | 4.76 | 4.76 | YRI |
| C8orf5 | GI_33300646-S | rs13266785 | 8 | 11026931 | 23900 | 9.181 | 0.4758 | 7.21 | 5.95 | 4.62 | 4.62 | YRI |
| CAPZA1 | GI_5453596-S | rs1238 | 1 | 112926139 | 10 | 13.1743 | 0.6167 | 6.44 | 5.44 | 4.5 | 4.5 | YRI |
| CATSPER2 | GI_26051226-A | rs8033995 | 15 | 41800801 | 81600 | 5.5627 | 0.306 | 7.53 | 5.38 | 4.4 | 4.4 | YRI |
| CBR1 | GI_4502598-S | rs735142 | 21 | 36382034 | 15101 | 7.0623 | 0.3818 | 8.34 | 6.38 | 5.13 | 5.13 | YRI |
| CCNDBP1 | GI_16554567-I | rs540587 | 15 | 41265405 | 204 | 17.8037 | 0.7338 | 7.95 | 5.64 | 4.31 | 4.31 | YRI |
| CD151 | GI_34328914-A | rs7924806 | 11 | 823668 | 5075 | 8.3962 | 0.4484 | 6.76 | 5.63 | 4.57 | 4.57 | YRI |
| CDK5RAP2 | GI_28872785-S | rs7037806 | 9 | 120230679 | 159 | 15.3291 | 0.6893 | 12.3 | 6.13 | 4.91 | 4.91 | YRI |
| CGI-49 | GI_7705766-S | rs12409066 | 1 | 243273590 | 16646 | 7.9931 | 0.4249 | 7.89 | 5.72 | 4.62 | 4.62 | YRI |
| CGI-62 | GI_7705774-S | rs1384804 | 8 | 79734777 | 55274 | 14.0392 | 0.6419 | 6.61 | 5.57 | 4.57 | 4.57 | YRI |
| CHKL | GI_23238259-I | rs2269383 | 22 | 49302919 | 4660 | 11.2416 | 0.5538 | 7.55 | 5.5 | 4.33 | 4.33 | YRI |
| CHPT1 | GI_9910383-S | rs2695281 | 12 | 100592467 | 26964 | 7.4853 | 0.4018 | 6.99 | 5.82 | 4.73 | 4.73 | YRI |
| CLECSF2 | GI_37577106-S | rs33871 | 12 | 9899164 | 2709 | 5.8728 | 0.3223 | 7.03 | 5.8 | 4.84 | 4.84 | YRI |
| CML66 | GI_31377641-S | rs6469251 | 8 | 110374265 | 51746 | 6.3531 | 0.347 | 6.49 | 5.37 | 4.48 | 4.48 | YRI |
| COPG2 | GI_6912319-S | rs7803211 | 7 | 129748552 | 8004 | 6.5118 | 0.3599 | 7.31 | 5.53 | 4.63 | 4.63 | YRI |
| CORO2A | GI_34335234-A | rs10985382 | 9 | 98039087 | 72632 | 7.6742 | 0.4105 | 6.84 | 5.95 | 4.78 | 4.78 | YRI |
| CP110 | GI_34222317-S | rs2256152 | 16 | 19417101 | 54945 | 5.6542 | 0.3108 | 6.72 | 5.61 | 4.56 | 4.56 | YRI |
| CPNE1 | GI_23397697-A | rs6060535 | 20 | 33698936 | 21264 | 6.7617 | 0.3673 | 8 | 6.12 | 4.83 | 4.83 | YRI |
| CRYBB2 | GI_4503062-S | rs760554 | 22 | 24197146 | 244817 | 14.9274 | 0.6661 | 8.16 | 6.73 | 5.45 | 5.45 | YRI |
| CSNK1D | GI_20544143-A | rs7215409 | 17 | 77788066 | 7554 | 8.74 | 0.4633 | 6.88 | 5.55 | 4.5 | 4.5 | YRI |
| CWF19L2 | GI_22748918-S | rs17106965 | 11 | 106829010 | 126524 | 6.1727 | 0.3378 | 6.67 | 5.75 | 4.64 | 4.64 | YRI |
| DAPK3 | GI_4557510-S | rs2278438 | 19 | 3915106 | 5361 | 7.5391 | 0.4043 | 6.26 | 5.69 | 4.57 | 4.57 | YRI |
| DDB2 | GI_4557514-S | rs7129661 | 11 | 47225120 | 7999 | 5.9239 | 0.3297 | 6.37 | 5.31 | 4.23 | 4.23 | YRI |
| DDHD1 | GI_37545942-S | rs8003676 | 14 | 52567792 | 15549 | 7.9176 | 0.4215 | 6.36 | 5.78 | 4.68 | 4.68 | YRI |
| DDX17 | GI_38201709-I | rs6001137 | 22 | 37199993 | 15210 | 6.4061 | 0.3496 | 7.25 | 5.99 | 4.8 | 4.8 | YRI |
| DERP6 | GI_44662825-I | rs222843 | 17 | 7086705 | 9736 | 13.4402 | 0.6246 | 7.83 | 6.02 | 4.87 | 4.87 | YRI |
| DGUOK | GI_18426964-I | rs6737156 | 2 | 74071389 | 45 | 5.6413 | 0.3102 | 6.65 | 5.63 | 4.56 | 4.56 | YRI |
| DHX34 | GI_38158021-A | rs2694561 | 19 | 52552328 | 25290 | 9.4543 | 0.4868 | 6.84 | 5.62 | 4.52 | 4.52 | YRI |
| DIABLO | GI_42544196-A | rs3809116 | 12 | 121240415 | 23199 | 6.4417 | 0.3514 | 7.22 | 5.93 | 4.68 | 4.68 | YRI |
| DKFZP434F0318 | GI_13540611-S | rs10845611 | 12 | 12743649 | 91824 | 8.9171 | 0.4958 | 7.1 | 6 | 4.79 | 4.79 | YRI |
| DKFZp434H247 | GI_37552078-S | rs1057745 | 19 | 44580230 | 174 | 6.1158 | 0.3349 | 7.23 | 5.53 | 4.54 | 4.54 | YRI |
| DKFZp761A078 | GI_35038600-S | rs6660019 | 1 | 100262466 | 933 | 8.1766 | 0.4331 | 6.44 | 5.78 | 4.56 | 4.56 | YRI |
| DMXL1 | GI_21536473-S | rs3943550 | 5 | 118364004 | 248432 | 8.4472 | 0.4565 | 7.47 | 5.78 | 4.56 | 4.56 | YRI |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DNA2L | GI_37551214-S | rs10823224 | 10 | 69960835 | 116726 | 6.2692 | 0.3427 | 6.11 | 5.61 | 4.47 | 4.47 | YRI |
| DPYSL4 | GI_11321616-S | rs10781563 | 10 | 133858802 | 10364 | 7.5548 | 0.405 | 6.95 | 5.62 | 4.62 | 4.62 | YRI |
| DTNB | GI_37577100-A | rs7571570 | 2 | 25533181 | 21376 | 6.5759 | 0.3581 | 6.43 | 5.66 | 4.46 | 4.46 | YRI |
| EBRP | GI_14211872-S | rs3809325 | 13 | 49164110 | 30844 | 5.6843 | 0.3124 | 6.64 | 5.36 | 4.46 | 4.46 | YRI |
| EIF2S1 | GI_34147492-S | rs8009318 | 14 | 66762525 | 159008 | 16.1416 | 0.6965 | 6.04 | 5.16 | 4.35 | 4.35 | YRI |
| ETAA16 | GI_37059813-S | rs923184 | 2 | 67541609 | 2435 | 18.0932 | 0.7398 | 10.4 | 7.25 | 5.62 | 5.62 | YRI |
| FANCA | GI_4503654-S | rs2159113 | 16 | 88359584 | 27924 | 7.4698 | 0.4011 | 5.87 | 5.5 | 4.5 | 4.5 | YRI |
| FKBP1A | GI_17149835-I | rs6041749 | 20 | 1298672 | 1831 | 11.4884 | 0.5624 | 8.36 | 6.1 | 4.94 | 4.94 | YRI |
| FKBP9 | GI_33469984-S | rs6976843 | 7 | 32876543 | 57278 | 5.8483 | 0.3257 | 6.5 | 5.58 | 4.56 | 4.56 | YRI |
| FLJ10300 | GI_21361686-S | rs2657381 | 7 | 158150563 | 87408 | 7.1709 | 0.387 | 7.06 | 5.61 | 4.48 | 4.48 | YRI |
| FLJ10305 | GI_39780551-S | rs8058702 | 16 | 69359737 | 80738 | 6.0308 | 0.3305 | 6.54 | 5.65 | 4.38 | 4.38 | YRI |
| FLJ10375 | GI_27545335-S | rs2036617 | 3 | 43364243 | 18807 | 7.1665 | 0.3921 | 7.1 | 6.05 | 4.6 | 4.6 | YRI |
| FLJ10525 | GI_8922490-S | rs1983138 | 4 | 41742296 | 56347 | 7.2325 | 0.3899 | 6.63 | 5.81 | 4.62 | 4.62 | YRI |
| FLJ10891 | GI_8922743-S | rs544769 | 19 | 57776173 | 3121 | 8.7523 | 0.4579 | 7.48 | 5.78 | 4.64 | 4.64 | YRI |
| FLJ10986 | GI_21361729-S | rs7528596 | 1 | 59523609 | 328172 | 6.634 | 0.3766 | 7.37 | 5.76 | 4.77 | 4.77 | YRI |
| FLJ11730 | GI_40255019-S | rs4653296 | 1 | 37647866 | 19389 | 5.8292 | 0.3201 | 7.17 | 5.35 | 4.57 | 4.57 | YRI |
| FLJ11838 | GI_13375918-S | rs10493111 | 1 | 42536366 | 58450 | 7.9949 | 0.425 | 11.2 | 7.35 | 5.62 | 5.62 | YRI |
| FLJ12785 | GI_31542679-S | rs2245231 | 20 | 36829534 | 4543 | 6.1923 | 0.3388 | 7.82 | 5.46 | 4.53 | 4.53 | YRI |
| FLJ13491 | GI_13375845-S | rs752164 | 12 | 122032694 | 43354 | 10.1615 | 0.5144 | 6.27 | 5.5 | 4.36 | 4.36 | YRI |
| FLJ14753 | GI_14211858-S | rs7046779 | 9 | 94290447 | 11996 | 22.0397 | 0.8095 | 7.94 | 6.53 | 5.1 | 5.1 | YRI |
| FLJ20291 | GI_34147582-S | rs7214654 | 17 | 34225779 | 14625 | 8.707 | 0.456 | 6.37 | 5.25 | 4.31 | 4.31 | YRI |
| FLJ20542 | GI_39725639-I | rs307347 | 1 | 1300683 | 13598 | 5.8651 | 0.3363 | 6.52 | 5.14 | 4.01 | 4.01 | YRI |
| FLJ20635 | GI_8923587-S | rs1473953 | 22 | 44038578 | 18513 | 20.1125 | 0.7782 | 11.1 | 8.6 | 6.63 | 6.63 | YRI |
| FLJ20699 | GI_8923627-S | rs6008553 | 22 | 45008840 | 1414 | 16.4232 | 0.7032 | 6.92 | 5.85 | 4.88 | 4.88 | YRI |
| FLJ20920 | GI_31542719-S | rs7627 | 17 | 45907153 | 3 | 13.9029 | 0.638 | 8 | 5.65 | 4.56 | 4.56 | YRI |
| FLJ21347 | GI_31542722-S | rs1122634 | 17 | 45976364 | 11803 | 11.5116 | 0.5695 | 7.23 | 6.11 | 4.76 | 4.76 | YRI |
| FLJ21613 | GI_39725954-S | rs2297002 | 9 | 85880924 | 14471 | 6.3742 | 0.348 | 6.73 | 5.71 | 4.75 | 4.75 | YRI |
| FLJ21616 | GI_13375737-S | rs10088428 | 8 | 28965442 | 421 | 20.0691 | 0.7774 | 5.98 | 5.41 | 4.6 | 4.6 | YRI |
| FLJ21945 | GI_13376797-S | rs1115856 | 2 | 24288282 | 124177 | 6.0549 | 0.3318 | 6.58 | 5.73 | 4.46 | 4.46 | YRI |
| FLJ22374 | GI_39752638-S | rs11768076 | 7 | 30602279 | 102848 | 5.8931 | 0.3281 | 7.15 | 5.73 | 4.66 | 4.66 | YRI |
| FLJ22494 | GI_40254968-S | rs7836362 | 8 | 22026371 | 5905 | 6.6754 | 0.363 | 7.45 | 5.51 | 4.6 | 4.6 | YRI |
| FLJ22875 | GI_34147465-S | rs3887731 | 15 | 62185229 | 33047 | 5.6855 | 0.3125 | 7.07 | 5.47 | 4.43 | 4.43 | YRI |
| FLJ23235 | GI_13376422-S | rs2711981 | 4 | 38861824 | 70782 | 9.6239 | 0.4936 | 7.27 | 5.83 | 4.57 | 4.57 | YRI |
| FLJ30435 | GI_31340828-S | rs6606188 | 9 | 65018691 | 51597 | 5.0882 | 0.2803 | 4.62 | 3.49 | 2.59 | 2.59 | YRI |
| FLJ32112 | GI_23308504-S | rs11206284 | 1 | 54290679 | 13575 | 14.4056 | 0.652 | 6.52 | 6.05 | 4.71 | 4.71 | YRI |
| FLJ32871 | GI_21389568-S | rs2541513 | 16 | 10668135 | 39119 | 8.2706 | 0.4372 | 8.93 | 7 | 5.37 | 5.37 | YRI |
| FLJ34443 | GI_31341870-S | rs7656122 | 4 | 1362872 | 16515 | 6.0474 | 0.3314 | 7.22 | 5.3 | 4.43 | 4.43 | YRI |
| FLJ34790 | GI_27734741-S | rs7210250 | 17 | 8067534 | 2540 | 5.5232 | 0.3039 | 6.65 | 5.45 | 4.5 | 4.5 | YRI |
| FLJ35867 | GI_31542776-S | rs2242069 | 15 | 41500926 | 60332 | 6.6388 | 0.3612 | 5.92 | 5.21 | 4.21 | 4.21 | YRI |
| FLJ39616 | GI_34594658-S | rs2285727 | 12 | 110555798 | 184736 | 5.6326 | 0.3097 | 6.81 | 5.55 | 4.4 | 4.4 | YRI |
| FLJ46603 | GI_38348363-S | rs237059 | 17 | 72242438 | 54929 | 8.0762 | 0.4286 | 6.34 | 5.7 | 4.47 | 4.47 | YRI |
| FLJ90036 | GI_31559781-S | rs6599293 | 4 | 123027 | 22841 | 15.9641 | 0.6923 | 8.54 | 5.97 | 4.45 | 4.45 | YRI |
| FTHFSDC1 | GI_40018634-S | rs2295733 | 6 | 151514814 | 119 | 11.8974 | 0.5826 | 6.37 | 5.64 | 4.6 | 4.6 | YRI |
| GOT2 | GI_4504068-S | rs8060056 | 16 | 57308344 | 9602 | 5.9865 | 0.3282 | 6.48 | 5.35 | 4.51 | 4.51 | YRI |
| GPR63 | GI_13540556-S | rs2143392 | 6 | 97280526 | 72571 | 5.7743 | 0.3172 | 6.72 | 5.71 | 4.54 | 4.54 | YRI |
| GSG2 | GI_13994373-S | rs2976230 | 17 | 3577990 | 1525 | 5.618 | 0.3134 | 6.3 | 5.52 | 4.57 | 4.57 | YRI |
| GSTM1 | GI_23065546-A | rs366732 | 1 | 109935049 | 8911 | 24.6872 | 0.8455 | 7.06 | 6.35 | 4.91 | 4.91 | YRI |
| GSTM2 | GI_23065549-S | rs366732 | 1 | 109935049 | 8831 | 8.7697 | 0.4587 | 6.04 | 5.44 | 4.56 | 4.56 | YRI |
| GSTO1 | GI_4758483-S | rs12244332 | 10 | 106010130 | 6998 | 6.8934 | 0.3737 | 6.56 | 5.91 | 4.85 | 4.85 | YRI |
| GSTT1 | GI_4504184-S | rs407257 | 22 | 22671104 | 29852 | 6.2196 | 0.3402 | 7.03 | 6.08 | 4.83 | 4.83 | YRI |
| GTF2H3 | GI_28376643-S | rs6488889 | 12 | 122669673 | 317 | 6.2135 | 0.3399 | 6.47 | 5.56 | 4.46 | 4.46 | YRI |
| HABP4 | GI_24307946-S | rs10820666 | 9 | 96314552 | 17381 | 8.9645 | 0.4668 | 6.92 | 5.51 | 4.58 | 4.58 | YRI |
| HAPLN3 | GI_32455240-S | rs2280467 | 15 | 87218242 | 3448 | 6.4666 | 0.3576 | 7.21 | 5.81 | 4.69 | 4.69 | YRI |
| HEBP2 | GI_41393567-S | rs6570232 | 6 | 138771357 | 2507 | 17.1071 | 0.7188 | 8.81 | 6.45 | 4.96 | 4.96 | YRI |
| HEMK | GI_7705408-S | rs2239752 | 3 | 50620417 | 23173 | 10.6541 | 0.5328 | 6.93 | 5.39 | 4.14 | 4.14 | YRI |
| HERC2 | GI_5729867-S | rs4778244 | 15 | 26029944 | 2 | 19.6852 | 0.7765 | 6.73 | 5.51 | 4.38 | 4.38 | YRI |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| HHLA3 | GI_5901965-S | rs2151540 | 1 | 70620478 | 87756 | 14.6643 | 0.6591 | 9.45 | 7.45 | 5.48 | 5.48 | YRI |
| HIBADH | GI_41393565-S | rs1014373 | 7 | 27344333 | 5242 | 7.8698 | 0.4194 | 6.88 | 5.91 | 4.86 | 4.86 | YRI |
| HLA-DQA1 | GI_18426974-S | rs9275141 | 6 | 32759095 | 40260 | 7.9847 | 0.4302 | 7.81 | 5.72 | 4.57 | 4.57 | YRI |
| HLA-DQB1 | GI_24797068-S | rs6457663 | 6 | 32847290 | 111440 | 6.1708 | 0.3377 | 6.85 | 5.56 | 4.37 | 4.37 | YRI |
| HLA-DRB5 | GI_26665892-S | rs9268614 | 6 | 32510756 | 82469 | 6.2242 | 0.3404 | 7.46 | 5.43 | 4.43 | 4.43 | YRI |
| hmm13275 | hmm13275-S | rs7663568 | 4 | 89765780 | 45194 | 5.7034 | 0.3135 | 6.16 | 5.54 | 4.57 | 4.57 | YRI |
| hmm1412 | hmm1412-S | rs4944950 | 11 | 74159279 | 70636 | 19.2112 | 0.7618 | 9.89 | 6.33 | 4.95 | 4.95 | YRI |
| hmm19532 | hmm19532-S | rs3120272 | 10 | 43511620 | 6616 | 6.4354 | 0.3511 | 6.99 | 5.63 | 4.58 | 4.58 | YRI |
| hmm25128 | hmm25128-S | rs8100253 | 19 | 63779291 | 10162 | 6.955 | 0.3767 | 6.43 | 5.4 | 4.24 | 4.24 | YRI |
| hmm28369 | hmm28369-S | rs10803576 | 2 | 132090707 | 6383 | 7.5165 | 0.4032 | 8.57 | 6.19 | 4.82 | 4.82 | YRI |
| hmm31752 | hmm31752-S | rs2844665 | 6 | 31114834 | 17244 | 9.2485 | 0.4785 | 7.22 | 5.97 | 4.76 | 4.76 | YRI |
| hmm31999 | hmm31999-S | rs6570064 | 6 | 99989858 | 9454 | 10.252 | 0.5179 | 8.42 | 5.69 | 4.62 | 4.62 | YRI |
| hmm35174 | hmm35174-S | rs3942977 | 8 | 142614039 | 193461 | 5.8359 | 0.3204 | 6.71 | 5.78 | 4.73 | 4.73 | YRI |
| hmm5445 | hmm5445-S | rs883416 | 17 | 30594554 | 24000 | 10.2431 | 0.5175 | 6.96 | 6.28 | 5.02 | 5.02 | YRI |
| hmm8232 | hmm8232-S | rs1057535 | 1 | 46527918 | 11826 | 16.3241 | 0.7009 | 9.24 | 6.82 | 4.8 | 4.8 | YRI |
| hmm9596 | hmm9596-S | rs4142416 | 20 | 7940324 | 29949 | 7.0063 | 0.3791 | 6.77 | 5.97 | 4.76 | 4.76 | YRI |
| Hs.118609 | Hs.118609-S | rs12083302 | 1 | 53515660 | 1116 | 6.2258 | 0.3405 | 6.76 | 5.88 | 4.67 | 4.67 | YRI |
| Hs.11898 | Hs.11898-S | rs8036979 | 15 | 50735287 | 1343 | 5.9735 | 0.3276 | 7.52 | 5.72 | 4.6 | 4.6 | YRI |
| Hs.146747 | Hs.146747-S | rs3218619 | 10 | 90752781 | 13687 | 7.9124 | 0.4213 | 7.37 | 6.17 | 4.89 | 4.89 | YRI |
| Hs.150050 | Hs.150050-S | rs760554 | 22 | 24197146 | 44163 | 15.405 | 0.6784 | 7.06 | 6.1 | 4.94 | 4.94 | YRI |
| Hs.158943 | Hs.158943-S | rs7740062 | 6 | 27813577 | 25098 | 27.2925 | 0.8743 | 7.02 | 5.76 | 4.57 | 4.57 | YRI |
| Hs.208685 | Hs.208685-S | rs980962 | 6 | 27468987 | 10192 | 7.5477 | 0.4047 | 7.05 | 5.27 | 4.29 | 4.29 | YRI |
| Hs.211939 | Hs.211939-S | rs6663688 | 1 | 10558581 | 13923 | 7.2539 | 0.3909 | 6.97 | 5.36 | 4.51 | 4.51 | YRI |
| Hs.212658 | Hs.212658-S | rs4699634 | 4 | 99721799 | 127 | 7.8687 | 0.4193 | 8.26 | 5.92 | 4.64 | 4.64 | YRI |
| Hs.224849 | Hs.224849-S | rs1901 | 3 | 14687477 | 8756 | 10.9891 | 0.5449 | 7.73 | 5.74 | 4.69 | 4.69 | YRI |
| Hs.26039 | Hs.26039-S | rs3733758 | 5 | 10708842 | 1145 | 10.9852 | 0.5448 | 6.35 | 5.41 | 4.65 | 4.65 | YRI |
| Hs.28465 | Hs.28465-S | rs9285280 | 13 | 72204160 | 23252 | 8.6045 | 0.4887 | 6.5 | 5.56 | 4.68 | 4.68 | YRI |
| Hs.304334 | Hs.304334-S | rs4899260 | 14 | 68347957 | 4012 | 13.9597 | 0.6396 | 7.17 | 5.75 | 4.68 | 4.68 | YRI |
| Hs.311038 | Hs.311038-S | rs16944716 | 15 | 89006612 | 2197 | 7.4724 | 0.4066 | 8.82 | 6.33 | 5.13 | 5.13 | YRI |
| Hs.333492 | Hs.333492-S | rs11155589 | 6 | 149069059 | 270269 | 5.6595 | 0.3111 | 6.95 | 5.53 | 4.71 | 4.71 | YRI |
| Hs.345389 | Hs.345389-S | rs760554 | 22 | 24197146 | 28424 | 12.7581 | 0.6039 | 9.97 | 7.08 | 5.39 | 5.39 | YRI |
| Hs.379903 | Hs.379903-S | rs1045599 | 17 | 15820635 | 55 | 13.8534 | 0.6366 | 6.83 | 5.85 | 4.63 | 4.63 | YRI |
| Hs.39429 | Hs.39429-S | rs2948 | 12 | 16078899 | 111 | 9.9517 | 0.5064 | 7.59 | 5.73 | 4.57 | 4.57 | YRI |
| Hs.396207 | Hs.396207-S | rs1084086 | 1 | 45710193 | 62801 | 15.3663 | 0.6774 | 7.97 | 6.35 | 4.62 | 4.62 | YRI |
| Hs.400876 | Hs.400876-S | rs752774 | 20 | 36488429 | 5644 | 19.8194 | 0.773 | 6.9 | 5.55 | 4.5 | 4.5 | YRI |
| Hs.402723 | Hs.402723-S | rs2073576 | 9 | 35058948 | 1842 | 9.8584 | 0.5028 | 7.18 | 5.81 | 4.56 | 4.56 | YRI |
| Hs.406038 | Hs.406038-S | rs12116935 | 1 | 36458639 | 5110 | 6.1381 | 0.3361 | 6.86 | 5.88 | 4.68 | 4.68 | YRI |
| Hs.421238 | Hs.421238-S | rs4925715 | 1 | 243614510 | 3099 | 11.5789 | 0.5655 | 7.1 | 5.97 | 4.77 | 4.77 | YRI |
| Hs.42217 | Hs.42217-S | rs9328707 | 16 | 45716367 | 257579 | 8.6114 | 0.4824 | 8.66 | 5.36 | 4.29 | 4.29 | YRI |
| Hs.42805 | Hs.42805-S | rs3741526 | 12 | 130906571 | 3582 | 7.6392 | 0.4089 | 9.03 | 6.67 | 5.11 | 5.11 | YRI |
| Hs.43687 | Hs.43687-S | rs6586 | 9 | 97746486 | 2916 | 12.7435 | 0.6034 | 6.65 | 5.77 | 4.73 | 4.73 | YRI |
| Hs.453941 | Hs.453941-S | rs880033 | 8 | 119702375 | 105019 | 15.4351 | 0.6855 | 9.22 | 7.82 | 6 | 6 | YRI |
| Hs.460359 | Hs.460359-S | rs6497694 | 16 | 23802234 | 10061 | 6.5707 | 0.3629 | 7.18 | 6.35 | 5 | 5 | YRI |
| Hs.473309 | Hs.473309-S | rs2427554 | 20 | 62020009 | 3031 | 5.7424 | 0.3155 | 6.57 | 5.67 | 4.35 | 4.35 | YRI |
| Hs.482037 | Hs.482037-S | rs7716564 | 5 | 43537149 | 14117 | 11.1495 | 0.5506 | 7.45 | 6.06 | 4.54 | 4.54 | YRI |
| Hs.483613 | Hs.483613-S | rs10036567 | 5 | 141288017 | 4486 | 8.0035 | 0.4254 | 6.62 | 5.84 | 4.52 | 4.52 | YRI |
| Hs.510003 | Hs.510003-S | rs3741600 | 12 | 67440272 | 8299 | 12.9498 | 0.6098 | 6.41 | 5.59 | 4.71 | 4.71 | YRI |
| Hs.519704 | Hs.519704-S | rs4262087 | 5 | 156995295 | 34858 | 8.2843 | 0.4435 | 7.51 | 6.56 | 5.25 | 5.25 | YRI |
| Hs.519979 | Hs.519979-S | rs2523971 | 6 | 30046237 | 40891 | 15.0537 | 0.6694 | 7.11 | 6.17 | 4.68 | 4.68 | YRI |
| Hs.98028 | Hs.98028-S | rs646521 | 11 | 124183151 | 1184 | 6.8451 | 0.3713 | 6.15 | 5.58 | 4.57 | 4.57 | YRI |
| HSCARG | GI_24476001-S | rs7191458 | 16 | 4451753 | 128 | 10.1827 | 0.5152 | 6.63 | 5.78 | 4.61 | 4.61 | YRI |
| HSD17B12 | GI_7705854-S | rs7131110 | 11 | 43803426 | 31055 | 10.2791 | 0.5189 | 6.07 | 5.41 | 4.66 | 4.66 | YRI |
| HSF2BP | GI_5901979-S | rs1836856 | 21 | 43789066 | 15271 | 8.5058 | 0.4474 | 7.31 | 6.24 | 4.82 | 4.82 | YRI |
| HSPC157 | GI_7661813-S | rs1883421 | 1 | 22101946 | 853 | 6.8397 | 0.3711 | 7.17 | 6 | 4.69 | 4.69 | YRI |
| INADL | GI_29029547-I | rs10889286 | 1 | 62298119 | 5635 | 5.7868 | 0.3224 | 6.76 | 5.44 | 4.6 | 4.6 | YRI |
| IPP | GI_5174472-S | rs780954 | 1 | 45708170 | 125665 | 6.8718 | 0.3778 | 6.79 | 5.3 | 4.32 | 4.32 | YRI |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| IRF5 | GI_38683858-A | rs10239340 | 7 | 128262461 | 79319 | 20.6223 | 0.787 | 6.5 | 5.45 | 4.49 | 4.49 | YRI |
| JFC1 | GI_14249613-S | rs10751722 | 1 | 27227665 | 136738 | 5.21 | 0.287 | 6.72 | 5.17 | 4.33 | 4.33 | YRI |
| KIAA0089 | GI_34222096-S | rs748607 | 3 | 32123720 | 61182 | 5.8892 | 0.3479 | 6.35 | 5.72 | 4.58 | 4.58 | YRI |
| KIAA0415 | GI_37538331-S | rs7810433 | 7 | 4590701 | 16508 | 6.957 | 0.3768 | 6.83 | 5.45 | 4.55 | 4.55 | YRI |
| KIAA0748 | GI_7662281-S | rs11171192 | 12 | 53634959 | 6538 | 6.9816 | 0.378 | 8.51 | 6.58 | 5.06 | 5.06 | YRI |
| KIAA0972 | GI_7662423-S | rs12115682 | 9 | 96516889 | 80951 | 7.9844 | 0.4245 | 7.63 | 6.12 | 4.7 | 4.7 | YRI |
| KIAA1274 | GI_22050996-S | rs1871595 | 10 | 71910576 | 87462 | 11.8543 | 0.5748 | 6.37 | 6 | 4.7 | 4.7 | YRI |
| KIAA1463 | GI_39930390-S | rs11169520 | 12 | 49359790 | 65125 | 27.7457 | 0.9008 | 11.9 | 8.3 | 5.47 | 5.47 | YRI |
| KIAA1712 | GI_30794213-S | rs7658307 | 4 | 175581254 | 46804 | 15.0871 | 0.6702 | 7.51 | 5.87 | 4.81 | 4.81 | YRI |
| KIAA1913 | GI_40538800-S | rs11154535 | 6 | 130605876 | 199758 | 6.1215 | 0.3352 | 6.38 | 6.06 | 4.96 | 4.96 | YRI |
| LCMT1 | GI_15082255-I | rs277886 | 16 | 25070005 | 96233 | 13.0016 | 0.6114 | 7.49 | 6.04 | 4.87 | 4.87 | YRI |
| LNK | GI_4885454-S | rs11831659 | 12 | 110318398 | 33409 | 8.7888 | 0.4713 | 6.43 | 5.24 | 4.38 | 4.38 | YRI |
| LOC114984 | GI_34147539-S | rs8055206 | 16 | 2872763 | 16451 | 6.1725 | 0.3378 | 6.66 | 5.52 | 4.54 | 4.54 | YRI |
| LOC119710 | GI_42476215-S | rs4151030 | 11 | 36552336 | 73862 | 9.5514 | 0.4907 | 7.11 | 5.72 | 4.57 | 4.57 | YRI |
| LOC120376 | GI_37540715-S | rs7126039 | 11 | 110716002 | 31452 | 6.0555 | 0.3318 | 6.81 | 5.56 | 4.59 | 4.59 | YRI |
| LOC126208 | GI_27485046-S | rs11673628 | 19 | 61314878 | 23994 | 9.1514 | 0.4746 | 7.69 | 6.53 | 5.13 | 5.13 | YRI |
| LOC133957 | GI_34222184-S | rs13474 | 5 | 258077 | 179 | 5.4333 | 0.2991 | 5.72 | 5.08 | 4.27 | 4.27 | YRI |
| LOC144404 | GI_37543220-S | rs3893308 | 12 | 120671212 | 7029 | 5.9414 | 0.3259 | 6.62 | 5.27 | 4.36 | 4.36 | YRI |
| LOC151963 | GI_31341922-S | rs2133864 | 3 | 194098959 | 101392 | 6.1281 | 0.3355 | 6.5 | 5.93 | 4.68 | 4.68 | YRI |
| LOC166867 | GI_27477322-S | rs2380953 | 4 | 37773414 | 2993 | 10.7596 | 0.5367 | 7.2 | 5.91 | 4.83 | 4.83 | YRI |
| LOC199777 | GI_21699081-S | rs8100147 | 19 | 20613255 | 6823 | 7.0682 | 0.3821 | 5.82 | 5.45 | 4.32 | 4.32 | YRI |
| LOC200933 | GI_37550262-S | rs9825103 | 3 | 197802521 | 9614 | 5.6874 | 0.3126 | 6.64 | 5.55 | 4.46 | 4.46 | YRI |
| LOC205251 | GI_28372544-S | rs10171646 | 2 | 110334732 | 7360 | 11.798 | 0.5729 | 6.17 | 5.09 | 4.03 | 4.03 | YRI |
| LOC221362 | GI_27498596-S | rs1000809 | 6 | 52643233 | 1873 | 7.3047 | 0.4276 | 7.14 | 5.67 | 4.76 | 4.76 | YRI |
| LOC222701 | GI_27498465-S | rs868987 | 6 | 28218127 | 27075 | 11.0949 | 0.5487 | 6.18 | 5.61 | 4.41 | 4.41 | YRI |
| LOC282956 | GI_27483210-S | rs2523467 | 6 | 31470909 | 358 | 12.4663 | 0.5947 | 6.37 | 5.47 | 4.47 | 4.47 | YRI |
| LOC283726 | GI_37540927-S | rs1267658 | 15 | 81011209 | 647257 | 12.0077 | 0.5799 | 6.75 | 5.87 | 4.7 | 4.7 | YRI |
| LOC284293 | GI_27485378-S | rs8090046 | 18 | 59773066 | 1480 | 25.975 | 0.8748 | 7.06 | 5.81 | 4.77 | 4.77 | YRI |
| LOC285256 | GI_27481220-S | rs6775459 | 3 | 130025163 | 1857 | 7.2725 | 0.3918 | 6.56 | 5.67 | 4.55 | 4.55 | YRI |
| LOC285407 | GI_37550539-S | rs10934906 | 3 | 131295760 | 4314 | 10.1043 | 0.5123 | 6.61 | 5.78 | 4.7 | 4.7 | YRI |
| LOC286356 | GI_27478865-S | rs1046795 | 9 | 96734913 | 1163 | 17.0277 | 0.717 | 6.45 | 5.76 | 4.57 | 4.57 | YRI |
| LOC339229 | GI_41150782-S | rs7502869 | 17 | 77241821 | 974 | 8.2597 | 0.4424 | 8.16 | 5.79 | 4.58 | 4.58 | YRI |
| LOC339231 | GI_29739147-S | rs6565620 | 17 | 77268505 | 9568 | 7.1162 | 0.3844 | 7.25 | 5.66 | 4.57 | 4.57 | YRI |
| LOC339804 | GI_37546921-S | rs1729660 | 2 | 61277463 | 24478 | 15.4757 | 0.6802 | 6.95 | 5.7 | 4.48 | 4.48 | YRI |
| LOC340435 | GI_29735811-S | rs13252719 | 8 | 71897123 | 115196 | 15.8559 | 0.6896 | 7.16 | 6.04 | 4.91 | 4.91 | YRI |
| LOC346171 | GI_37552164-S | rs2535241 | 6 | 29748764 | 255 | 6.5169 | 0.3552 | 7.04 | 5.79 | 4.56 | 4.56 | YRI |
| LOC347981 | GI_30160064-S | rs1611527 | 6 | 29980936 | 18393 | 8.1017 | 0.4298 | 7.14 | 5.66 | 4.43 | 4.43 | YRI |
| LOC348094 | GI_38176293-S | rs871447 | 15 | 62957490 | 80324 | 13.706 | 0.6324 | 7.4 | 6.06 | 4.92 | 4.92 | YRI |
| LOC374421 | GI_37541454-S | rs1011993 | 11 | 93079070 | 23689 | 10.0331 | 0.5157 | 6.03 | 5.48 | 4.5 | 4.5 | YRI |
| LOC375097 | GI_37555934-S | rs752774 | 20 | 36488429 | 5495 | 18.7639 | 0.7533 | 7.08 | 5.69 | 4.53 | 4.53 | YRI |
| LOC375399 | GI_37540365-S | rs12640455 | 4 | 68387605 | 27870 | 7.652 | 0.4095 | 6.97 | 5.73 | 4.5 | 4.5 | YRI |
| LOC377696 | GI_37555914-S | rs2460970 | 8 | 119698635 | 36461 | 9.4405 | 0.4863 | 6.92 | 6.21 | 5.15 | 5.15 | YRI |
| LOC387647 | GI_42659552-S | rs4749424 | 10 | 29759251 | 6415 | 11.7515 | 0.5713 | 7.74 | 5.82 | 4.74 | 4.74 | YRI |
| LOC387905 | GI_41202581-S | rs7336525 | 13 | 20816844 | 20 | 6.7522 | 0.3668 | 7.64 | 5.96 | 4.78 | 4.78 | YRI |
| LOC388327 | GI_42661079-S | rs930526 | 17 | 6414077 | 82951 | 5.8439 | 0.3208 | 6.34 | 5.67 | 4.69 | 4.69 | YRI |
| LOC388673 | GI_41115452-S | rs10494258 | 1 | 146525817 | 136389 | 5.4268 | 0.2987 | 6.83 | 5.25 | 4.06 | 4.06 | YRI |
| LOC388918 | GI_42662524-S | rs131777 | 22 | 49281177 | 1293 | 6.183 | 0.3383 | 7.37 | 5.67 | 4.45 | 4.45 | YRI |
| LOC389338 | GI_41146997-S | rs10062143 | 5 | 151127235 | 2710 | 6.5797 | 0.3583 | 7.29 | 6.09 | 4.78 | 4.78 | YRI |
| LOC389362 | GI_41147302-S | rs1127477 | 6 | 3215509 | 2397 | 6.7462 | 0.3716 | 6.86 | 5.7 | 4.66 | 4.66 | YRI |
| LOC389366 | GI_42657574-S | rs12661484 | 6 | 10805426 | 25719 | 14.9709 | 0.6801 | 8.18 | 5.86 | 4.63 | 4.63 | YRI |
| LOC392620 | GI_41147689-S | rs1636264 | 7 | 2637827 | 102929 | 9.3645 | 0.4832 | 7.66 | 5.84 | 4.76 | 4.76 | YRI |
| LOC399818 | GI_42659420-S | rs7898003 | 10 | 126441375 | 4789 | 13.2517 | 0.619 | 6.46 | 5.96 | 4.69 | 4.69 | YRI |
| LOC399987 | GI_42660080-S | rs9300302 | 12 | 3737732 | 1669 | 10.253 | 0.5179 | 7.27 | 5.6 | 4.67 | 4.67 | YRI |
| LOC400051 | GI_42659981-S | rs2051993 | 12 | 66699945 | 1068 | 7.2433 | 0.3904 | 8.24 | 6.52 | 5.23 | 5.23 | YRI |
| LOC400571 | GI_42661084-S | rs8066665 | 17 | 7426576 | 198 | 8.0372 | 0.4269 | 6.52 | 5.57 | 4.7 | 4.7 | YRI |
| LOC400642 | GI_42661344-S | rs8576 | 18 | 5236398 | 47 | 7.5979 | 0.407 | 6.85 | 5.68 | 4.64 | 4.64 | YRI |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC400843 | GI_42662295-S | rs2275274 | 20 | 33320958 | 6878 | 9.7335 | 0.4979 | 6.23 | 5.4 | 4.35 | 4.35 | YRI |
| LOC401135 | GI_42657007-S | rs1048447 | 4 | 68312238 | 104593 | 9.1546 | 0.4747 | 7.57 | 5.97 | 4.74 | 4.74 | YRI |
| LOC401245 | GI_42657607-S | rs6900042 | 6 | 30397250 | 29769 | 7.8266 | 0.4174 | 6.52 | 5.9 | 4.62 | 4.62 | YRI |
| LOC402476 | GI_42658265-S | rs4723187 | 7 | 32476141 | 99082 | 11.3537 | 0.5641 | 7.64 | 6.04 | 4.85 | 4.85 | YRI |
| LOC402573 | GI_42658526-S | rs11761784 | 7 | 99684621 | 14384 | 6.0476 | 0.3361 | 7.03 | 5.51 | 4.3 | 4.3 | YRI |
| LOC51240 | GI_31377759-S | rs10210345 | 2 | 190444992 | 16000 | 8.2221 | 0.4351 | 6.95 | 5.33 | 4.54 | 4.54 | YRI |
| LOC51693 | GI_7706428-S | rs3784879 | 16 | 87441447 | 13502 | 7.3548 | 0.3957 | 7.7 | 5.58 | 4.62 | 4.62 | YRI |
| LOC87769 | GI_34147452-S | rs2760307 | 13 | 99988330 | 6353 | 7.7258 | 0.4129 | 6.99 | 6.07 | 4.9 | 4.9 | YRI |
| LOC90693 | GI_40255028-S | rs12700451 | 7 | 23421954 | 34029 | 6.4554 | 0.3521 | 8.25 | 5.8 | 4.78 | 4.78 | YRI |
| LOC93349 | GI_20149710-S | rs7559665 | 2 | 231082317 | 11492 | 10.0957 | 0.5181 | 8.09 | 6.43 | 5.02 | 5.02 | YRI |
| MALT1 | GI_27886565-A | rs7227586 | 18 | 54516958 | 51162 | 6.4047 | 0.3496 | 7.48 | 5.65 | 4.81 | 4.81 | YRI |
| MAML1 | GI_41350321-S | rs7566 | 5 | 179089055 | 47486 | 6.7185 | 0.3652 | 6.77 | 5.52 | 4.55 | 4.55 | YRI |
| MAN1A2 | GI_40254840-S | rs4460623 | 1 | 117659287 | 118291 | 9.4495 | 0.4867 | 7.67 | 6.01 | 4.79 | 4.79 | YRI |
| MAP2K2 | GI_21614527-S | rs350818 | 19 | 4037807 | 3566 | 5.9418 | 0.3259 | 8.15 | 5.83 | 4.74 | 4.74 | YRI |
| MAP3K2 | GI_21735555-S | rs1011019 | 2 | 127753790 | 26391 | 8.0145 | 0.4259 | 7.05 | 5.64 | 4.54 | 4.54 | YRI |
| MAP3K8 | GI_22035597-S | rs7475513 | 10 | 30112200 | 678153 | 6.8185 | 0.3701 | 6.86 | 5.55 | 4.67 | 4.67 | YRI |
| MAP3K9 | GI_37545956-S | rs2158531 | 14 | 70316721 | 51614 | 10.7012 | 0.5345 | 6.86 | 5.61 | 4.52 | 4.52 | YRI |
| MAP4K3 | GI_15451901-S | rs2043188 | 2 | 38840632 | 548854 | 6.3554 | 0.3471 | 8.27 | 5.89 | 4.85 | 4.85 | YRI |
| MASTL | GI_14249561-S | rs7068375 | 10 | 27494117 | 21333 | 11.6329 | 0.5673 | 6.76 | 5.53 | 4.64 | 4.64 | YRI |
| MED8 | GI_42490745-A | rs11172 | 1 | 43519566 | 828 | 5.9237 | 0.325 | 7.69 | 5.49 | 4.48 | 4.48 | YRI |
| MGC:13379 | GI_19923799-S | rs10897159 | 11 | 60948930 | 26177 | 5.5846 | 0.3072 | 6.86 | 5.53 | 4.54 | 4.54 | YRI |
| MGC10120 | GI_28603839-S | rs12762869 | 10 | 101983702 | 40795 | 21.0317 | 0.7937 | 13 | 9.95 | 7.13 | 7.13 | YRI |
| MGC10744 | GI_34101277-A | rs9900848 | 17 | 8040096 | 22459 | 9.3216 | 0.4815 | 8.03 | 6.81 | 5.03 | 5.03 | YRI |
| MGC12458 | GI_14150107-S | rs576872 | 1 | 241549105 | 27975 | 8.3587 | 0.4411 | 6.93 | 5.91 | 4.71 | 4.71 | YRI |
| MGC15763 | GI_19923906-S | rs478483 | 3 | 16337133 | 18891 | 6.4483 | 0.3618 | 7.05 | 6.06 | 4.86 | 4.86 | YRI |
| MGC16597 | GI_42661280-S | rs7209877 | 17 | 77248042 | 2413 | 5.932 | 0.3254 | 6.58 | 5.62 | 4.54 | 4.54 | YRI |
| MGC19764 | GI_42661257-S | rs883416 | 17 | 30594554 | 24027 | 10.5625 | 0.5294 | 7.91 | 5.94 | 4.88 | 4.88 | YRI |
| MGC20235 | GI_21450795-S | rs915945 | 17 | 38433390 | 293442 | 6.2413 | 0.3413 | 7.89 | 5.55 | 4.42 | 4.42 | YRI |
| MGC20781 | GI_34147471-S | rs4796715 | 17 | 37247297 | 12146 | 8.5382 | 0.4488 | 6.61 | 5.36 | 4.45 | 4.45 | YRI |
| MGC21675 | GI_16418362-S | rs3811733 | 4 | 1249480 | 13914 | 6.1021 | 0.3342 | 6.86 | 5.86 | 4.56 | 4.56 | YRI |
| MGC2198 | GI_20270388-S | rs1065212 | 5 | 175743739 | 5325 | 7.4151 | 0.3985 | 6.38 | 5.77 | 4.64 | 4.64 | YRI |
| MGC22773 | GI_21687083-S | rs2069302 | 1 | 74377628 | 19609 | 10.131 | 0.5194 | 6.87 | 5.74 | 4.55 | 4.55 | YRI |
| MGC22960 | GI_40316917-S | rs1057535 | 1 | 46527918 | 14563 | 7.2155 | 0.3891 | 6.4 | 5.31 | 4.38 | 4.38 | YRI |
| MGC2744 | GI_34147388-S | rs8064783 | 17 | 38375814 | 18400 | 5.219 | 0.2874 | 6.51 | 5.2 | 4.41 | 4.41 | YRI |
| MGC2747 | GI_34147357-S | rs16981374 | 19 | 16630216 | 12059 | 6.2871 | 0.3535 | 6.27 | 5.42 | 4.45 | 4.45 | YRI |
| MGC3248 | GI_34147426-S | rs7588 | 16 | 23588666 | 276 | 6.8927 | 0.3737 | 6.51 | 5.77 | 4.58 | 4.58 | YRI |
| MGC3265 | GI_31543180-S | rs352346 | 5 | 148706014 | 23038 | 6.4922 | 0.354 | 6.75 | 5.52 | 4.59 | 4.59 | YRI |
| MGC33948 | GI_40255122-S | rs17107980 | 11 | 107732685 | 36509 | 10.3079 | 0.52 | 7.31 | 6.06 | 4.7 | 4.7 | YRI |
| MGC5242 | GI_13162284-S | rs2718151 | 7 | 134131445 | 176579 | 6.7675 | 0.3779 | 6.85 | 5.61 | 4.57 | 4.57 | YRI |
| MK-STYX | GI_32481212-S | rs8565 | 7 | 75274925 | 17 | 6.9804 | 0.3779 | 6.52 | 5.4 | 4.33 | 4.33 | YRI |
| MMRP19 | GI_7705723-S | rs1571133 | 11 | 34866502 | 26 | 11.7126 | 0.57 | 7.37 | 5.74 | 4.73 | 4.73 | YRI |
| MPST | GI_23510449-S | rs5756489 | 22 | 35741697 | 8369 | 7.1411 | 0.3909 | 7.83 | 5.84 | 4.81 | 4.81 | YRI |
| MR1 | GI_4504416-S | rs10797666 | 1 | 177750456 | 3963 | 7.2227 | 0.3895 | 6.2 | 5.53 | 4.6 | 4.6 | YRI |
| MRPL21 | GI_31652223-A | rs685320 | 11 | 68448717 | 33303 | 6.0125 | 0.3296 | 6.29 | 5.53 | 4.59 | 4.59 | YRI |
| MRPL35 | GI_22035593-A | rs11127018 | 2 | 86366572 | 15127 | 7.0549 | 0.3815 | 8.26 | 5.68 | 4.51 | 4.51 | YRI |
| MRPL43 | GI_28872735-A | rs2863095 | 10 | 102736493 | 116 | 22.8283 | 0.8211 | 7.42 | 5.61 | 4.47 | 4.47 | YRI |
| MRPL53 | GI_22035595-S | rs1047911 | 2 | 74611433 | 39 | 7.3453 | 0.3953 | 7.03 | 5.97 | 4.61 | 4.61 | YRI |
| MRPL54 | GI_27436907-S | rs13960 | 19 | 3713698 | 2608 | 7.5503 | 0.4048 | 6.47 | 5.6 | 4.56 | 4.56 | YRI |
| MRPS12 | GI_11056055-I | rs2070250 | 19 | 44113768 | 55 | 11.6486 | 0.5678 | 7.05 | 5.58 | 4.64 | 4.64 | YRI |
| MRPS9 | GI_33188462-S | rs11897155 | 2 | 105142765 | 31930 | 6.2164 | 0.3401 | 6.66 | 5.98 | 4.83 | 4.83 | YRI |
| MTRR | GI_4505278-A | rs162036 | 5 | 7938959 | 15031 | 9.5389 | 0.4902 | 8.05 | 5.35 | 4.49 | 4.49 | YRI |
| NARF | GI_14165459-A | rs4789773 | 17 | 77984973 | 54139 | 6.0059 | 0.3292 | 6.85 | 5.64 | 4.47 | 4.47 | YRI |
| NDP52 | GI_33519473-S | rs8078984 | 17 | 44267550 | 29473 | 10.366 | 0.5222 | 6.33 | 5.42 | 4.5 | 4.5 | YRI |
| NDUFS5 | GI_4758789-S | rs10888650 | 1 | 39176254 | 15118 | 6.1625 | 0.3373 | 6.88 | 5.81 | 4.8 | 4.8 | YRI |
| NOL6 | GI_39777589-A | rs476059 | 9 | 33448577 | 2846 | 6.481 | 0.3534 | 6.85 | 6.07 | 4.69 | 4.69 | YRI |
| NR4A3 | GI_27894358-A | rs7863319 | 9 | 99340111 | 335030 | 6.3003 | 0.3443 | 7.86 | 5.88 | 4.71 | 4.71 | YRI |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NUCB2 | GI_4826869-S | rs10741725 | 11 | 17277373 | 31032 | 5.8737 | 0.3224 | 7.3 | 5.58 | 4.47 | 4.47 | YRI |
| NUDT13 | GI_34330151-S | rs7894359 | 10 | 74534394 | 26534 | 7.6568 | 0.4097 | 7.3 | 5.42 | 4.34 | 4.34 | YRI |
| NUDT2 | GI_22219466-A | rs7867248 | 9 | 34310264 | 23239 | 15.2667 | 0.6749 | 6.75 | 5.75 | 4.48 | 4.48 | YRI |
| NUDT8 | GI_32469514-S | rs7938563 | 11 | 67060707 | 91487 | 5.4279 | 0.2988 | 6.15 | 5.35 | 4.42 | 4.42 | YRI |
| NUDT9 | GI_37594456-A | rs6811514 | 4 | 89205195 | 468831 | 6.7686 | 0.3676 | 6.57 | 5.56 | 4.61 | 4.61 | YRI |
| NUP50 | GI_24497446-A | rs132863 | 22 | 43884964 | 15941 | 7.8174 | 0.417 | 6.49 | 5.79 | 4.81 | 4.81 | YRI |
| ORMDL3 | GI_27544926-S | rs8067378 | 17 | 35304874 | 26224 | 7.7676 | 0.4203 | 6.37 | 5.35 | 4.31 | 4.31 | YRI |
| P66beta | GI_21218437-S | rs6695083 | 1 | 150723573 | 130907 | 8.644 | 0.4534 | 6.53 | 5.52 | 4.43 | 4.43 | YRI |
| PHEMX | GI_37595532-A | rs2074021 | 11 | 2280104 | 15769 | 12.4207 | 0.5997 | 6.44 | 5.54 | 4.6 | 4.6 | YRI |
| PHYH | GI_17999532-S | rs661457 | 10 | 13350742 | 12339 | 7.2217 | 0.3894 | 7.44 | 6.18 | 5.02 | 5.02 | YRI |
| PIAS3 | GI_31543399-S | rs2799118 | 1 | 143205766 | 130338 | 6.4556 | 0.3521 | 6.73 | 5.2 | 4.16 | 4.16 | YRI |
| PIGF | GI_27894289-A | rs10167561 | 2 | 46879702 | 148397 | 6.9912 | 0.3784 | 6.84 | 5.68 | 4.65 | 4.65 | YRI |
| PKHD1L1 | GI_31377831-S | rs2844257 | 8 | 110590653 | 17602 | 17.0162 | 0.7168 | 6.08 | 5.23 | 4.52 | 4.52 | YRI |
| PNRC1 | GI_5802981-S | rs2274819 | 6 | 89871775 | 20393 | 9.8836 | 0.5038 | 7.43 | 5.97 | 4.67 | 4.67 | YRI |
| POLR1A | GI_7661685-S | rs12124 | 2 | 86165166 | 1573 | 11.6359 | 0.5674 | 6.35 | 5.73 | 4.56 | 4.56 | YRI |
| POLR2E | GI_14589950-S | rs6843 | 19 | 1039285 | 9 | 14.575 | 0.6567 | 6.78 | 5.73 | 4.76 | 4.76 | YRI |
| POLR3F | GI_33598951-S | rs6075351 | 20 | 18438913 | 25841 | 7.76 | 0.4144 | 7.62 | 5.61 | 4.51 | 4.51 | YRI |
| PP3856 | GI_40255088-S | rs2242089 | 8 | 144760289 | 32156 | 10.4984 | 0.5271 | 10.2 | 7.46 | 5.44 | 5.44 | YRI |
| PPA2 | GI_31881619-A | rs2726526 | 4 | 106649725 | 1306 | 7.9782 | 0.4299 | 6.87 | 5.47 | 4.56 | 4.56 | YRI |
| PPIL3 | GI_19557635-A | rs11892372 | 2 | 201644989 | 83678 | 21.9454 | 0.8081 | 6.93 | 5.7 | 4.5 | 4.5 | YRI |
| PPP1R12A | GI_4505316-S | rs2430863 | 12 | 78663339 | 7611 | 5.8864 | 0.323 | 6.4 | 5.66 | 4.52 | 4.52 | YRI |
| PRKCL1 | GI_42476156-S | rs2241357 | 19 | 14451919 | 9297 | 7.2313 | 0.3899 | 6.05 | 5.48 | 4.48 | 4.48 | YRI |
| PRRG2 | GI_4506136-S | rs11878999 | 19 | 54809873 | 23894 | 7.2221 | 0.3894 | 7.38 | 5.71 | 4.54 | 4.54 | YRI |
| PSMF1 | GI_30581144-A | rs1217 | 20 | 1110615 | 14780 | 8.0693 | 0.4283 | 7.73 | 6.05 | 5 | 5 | YRI |
| PTCH | GI_25121959-S | rs10761333 | 9 | 94392139 | 894106 | 6.009 | 0.3294 | 7.55 | 5.87 | 4.5 | 4.5 | YRI |
| PTER | GI_20070185-S | rs1055340 | 10 | 16595534 | 974 | 20.0607 | 0.7773 | 7.85 | 5.74 | 4.64 | 4.64 | YRI |
| PTGS1 | GI_18104968-A | rs2282169 | 9 | 122220250 | 17191 | 8.512 | 0.4477 | 8.53 | 5.95 | 4.76 | 4.76 | YRI |
| QRSL1 | GI_19923522-S | rs1026619 | 6 | 107221054 | 740 | 6.3731 | 0.3529 | 7 | 5.76 | 4.6 | 4.6 | YRI |
| RAB18 | GI_34222129-S | rs12261672 | 10 | 27803085 | 64300 | 7.9791 | 0.4243 | 7.44 | 5.58 | 4.72 | 4.72 | YRI |
| RAB31 | GI_33589860-S | rs1893126 | 18 | 9702098 | 150233 | 8.5404 | 0.4489 | 6.88 | 5.93 | 4.75 | 4.75 | YRI |
| RAB40B | GI_5803162-S | rs4796860 | 17 | 77536764 | 672142 | 6.6048 | 0.3595 | 7.84 | 6.37 | 4.95 | 4.95 | YRI |
| RABIF | GI_31543539-S | rs7523420 | 1 | 199597361 | 17100 | 9.5065 | 0.4889 | 7.08 | 5.88 | 4.73 | 4.73 | YRI |
| RAD51 | GI_19924134-A | rs2304582 | 15 | 38818157 | 6860 | 8.7562 | 0.4639 | 6.75 | 5.69 | 4.62 | 4.62 | YRI |
| RAMP1 | GI_5032018-S | rs6741923 | 2 | 238581206 | 21449 | 6.1397 | 0.3361 | 7.03 | 6.06 | 4.81 | 4.81 | YRI |
| RAPGEFL1 | GI_7705938-S | rs8065665 | 17 | 35735789 | 130454 | 8.0636 | 0.4281 | 7.26 | 5.37 | 4.39 | 4.39 | YRI |
| raptor | GI_22094986-S | rs1062935 | 17 | 76554452 | 37 | 6.5294 | 0.3558 | 7.27 | 5.36 | 4.51 | 4.51 | YRI |
| RLN1 | GI_20143931-S | rs2273782 | 9 | 5325470 | 167 | 5.6898 | 0.3127 | 6.66 | 5.62 | 4.74 | 4.74 | YRI |
| RPL13 | GI_15431296-A | rs462464 | 16 | 88140538 | 16489 | 5.9037 | 0.3239 | 7.5 | 5.64 | 4.55 | 4.55 | YRI |
| RPL28 | GI_34486095-S | rs10408088 | 19 | 60596405 | 1348 | 10.5671 | 0.5296 | 6.44 | 5.66 | 4.68 | 4.68 | YRI |
| RPL36AL | GI_34335143-S | rs2985696 | 14 | 49164663 | 7588 | 11.44 | 0.5607 | 6.51 | 5.18 | 4.48 | 4.48 | YRI |
| RPL37A | GI_16306561-S | rs3732019 | 2 | 217187892 | 1196 | 10.2312 | 0.5171 | 7.15 | 6.31 | 5.06 | 5.06 | YRI |
| RPS15A | GI_34335150-S | rs735173 | 16 | 18747289 | 38195 | 7.3704 | 0.3964 | 6.1 | 5.23 | 4.39 | 4.39 | YRI |
| RPS6KB2 | GI_4506738-S | rs2302264 | 11 | 66964002 | 4657 | 10.8339 | 0.5393 | 5.8 | 5.1 | 4.35 | 4.35 | YRI |
| RWDD3 | GI_21361481-S | rs915502 | 1 | 95308132 | 113917 | 8.2011 | 0.4398 | 7.3 | 5.93 | 4.87 | 4.87 | YRI |
| SACM1L | GI_41281578-S | rs2373047 | 3 | 45722501 | 39276 | 6.0129 | 0.3296 | 7.12 | 5.71 | 4.64 | 4.64 | YRI |
| SBP1 | GI_30017464-S | rs13346092 | 19 | 47579296 | 4623 | 8.1751 | 0.433 | 6.7 | 5.53 | 4.4 | 4.4 | YRI |
| SCAMP5 | GI_42544128-S | rs11633539 | 15 | 72853349 | 247217 | 11.7299 | 0.5706 | 8.2 | 5.9 | 4.7 | 4.7 | YRI |
| SEC10L1 | GI_38202212-S | rs4608256 | 14 | 56787043 | 46496 | 12.1029 | 0.583 | 9.16 | 7.18 | 5.42 | 5.42 | YRI |
| SELS | GI_45439348-I | rs9874 | 15 | 99628927 | 129 | 7.644 | 0.4091 | 6.62 | 5.75 | 4.57 | 4.57 | YRI |
| SERPINB10 | GI_4826901-S | rs12327162 | 18 | 59731189 | 22003 | 7.5991 | 0.407 | 6.46 | 5.67 | 4.83 | 4.83 | YRI |
| SESTD1 | GI_31342410-S | rs2289993 | 2 | 179805436 | 5365 | 6.62 | 0.3603 | 6.28 | 5.24 | 4.44 | 4.44 | YRI |
| SF1 | GI_42544126-I | rs550930 | 11 | 64263891 | 36408 | 8.2441 | 0.4361 | 7.08 | 5.45 | 4.41 | 4.41 | YRI |
| SFRS10 | GI_4759097-S | rs2251407 | 3 | 187137626 | 20262 | 7.1982 | 0.3883 | 7.28 | 6.16 | 4.88 | 4.88 | YRI |
| SFXN2 | GI_34222270-S | rs11191393 | 10 | 104517420 | 28629 | 7.7717 | 0.4149 | 6.99 | 5.45 | 4.29 | 4.29 | YRI |
| SIAT8E | GI_28373100-S | rs3809958 | 18 | 42591684 | 78394 | 10.1978 | 0.5158 | 7.32 | 6.25 | 4.83 | 4.83 | YRI |
| SLB | GI_37546863-S | rs813592 | 2 | 27633622 | 54659 | 6.1761 | 0.338 | 6.4 | 5.67 | 4.58 | 4.58 | YRI |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SLC11A2 | GI_10835168-S | rs150909 | 12 | 49667344 | 1208 | 6.6443 | 0.3615 | 6.68 | 5.4 | 4.43 | 4.43 | YRI |
| SLC25A16 | GI_31652216-S | rs10998210 | 10 | 69907166 | 5412 | 12.7309 | 0.6031 | 6.36 | 5.54 | 4.52 | 4.52 | YRI |
| SLC35A5 | GI_31543636-S | rs2705517 | 3 | 113802373 | 16909 | 6.266 | 0.3426 | 8.07 | 5.44 | 4.43 | 4.43 | YRI |
| SLC35B3 | GI_21361502-S | rs10484748 | 6 | 8376192 | 17575 | 6.453 | 0.362 | 7.11 | 5.56 | 4.59 | 4.59 | YRI |
| SNX11 | GI_23111027-I | rs6504025 | 17 | 43521072 | 22024 | 7.6625 | 0.41 | 7.67 | 5.52 | 4.51 | 4.51 | YRI |
| SNX17 | GI_23238249-S | rs780092 | 2 | 27654805 | 143504 | 5.9496 | 0.3263 | 6.51 | 5.62 | 4.47 | 4.47 | YRI |
| SORD | GI_34147623-S | rs269868 | 15 | 43179367 | 25086 | 6.5595 | 0.3573 | 8.79 | 5.56 | 4.46 | 4.46 | YRI |
| SOS1 | GI_15529995-S | rs1037495 | 2 | 39121077 | 3673 | 12.4949 | 0.5956 | 6.71 | 5.71 | 4.61 | 4.61 | YRI |
| SPA17 | GI_15718773-S | rs7927406 | 11 | 124049013 | 20461 | 8.5893 | 0.451 | 6.68 | 5.42 | 4.49 | 4.49 | YRI |
| SPG7 | GI_40806172-I | rs382745 | 16 | 88131087 | 282 | 6.6608 | 0.3623 | 7.47 | 5.56 | 4.42 | 4.42 | YRI |
| SPTLC1 | GI_30474870-I | rs7871997 | 9 | 91861919 | 59451 | 21.0815 | 0.7946 | 7.52 | 5.65 | 4.46 | 4.46 | YRI |
| SQSTM1 | GI_19923742-S | rs10277 | 5 | 179197337 | 249 | 7.0706 | 0.3822 | 6.63 | 5.41 | 4.62 | 4.62 | YRI |
| SSR2 | GI_6552341-S | rs1750305 | 1 | 153267457 | 475328 | 5.6519 | 0.3107 | 6.38 | 5.32 | 4.5 | 4.5 | YRI |
| ST7L | GI_38201636-A | rs7415820 | 1 | 112881491 | 84792 | 14.2519 | 0.6478 | 7.09 | 5.78 | 4.67 | 4.67 | YRI |
| STK25 | GI_34147665-S | rs2240482 | 2 | 242125011 | 29600 | 14.8714 | 0.6646 | 6.95 | 6.03 | 4.82 | 4.82 | YRI |
| SURF6 | GI_39812452-S | rs12335 | 9 | 133227388 | 225 | 10.8934 | 0.5415 | 8.22 | 5.85 | 4.72 | 4.72 | YRI |
| SVH | GI_31377662-S | rs6950177 | 7 | 102334634 | 1255 | 7.0346 | 0.3805 | 6.29 | 5.69 | 4.5 | 4.5 | YRI |
| SYNGR1 | GI_22035699-A | rs909685 | 22 | 38072171 | 24459 | 16.0636 | 0.6947 | 7.94 | 5.7 | 4.63 | 4.63 | YRI |
| TAP2 | GI_9961245-I | rs2071543 | 6 | 32919607 | 16414 | 8.6901 | 0.4553 | 11.5 | 6.99 | 5.13 | 5.13 | YRI |
| TAPBP | GI_27436892-I | rs1801823 | 6 | 33367560 | 7932 | 8.2583 | 0.4367 | 6.82 | 5.58 | 4.6 | 4.6 | YRI |
| THAP1 | GI_40068498-S | rs7461288 | 8 | 42805356 | 6086 | 5.5144 | 0.3034 | 7.09 | 5.24 | 4.3 | 4.3 | YRI |
| THAP5 | GI_32698887-S | rs40947 | 7 | 107800604 | 1910 | 11.9573 | 0.5846 | 7.54 | 6.19 | 4.9 | 4.9 | YRI |
| THAP6 | GI_37059751-S | rs7673610 | 4 | 76817715 | 6636 | 5.7365 | 0.3152 | 6.41 | 5.65 | 4.5 | 4.5 | YRI |
| TINP1 | GI_21359901-S | rs6877188 | 5 | 74067281 | 38238 | 19.3492 | 0.7644 | 7.78 | 5.92 | 4.67 | 4.67 | YRI |
| TJP2 | GI_42518069-S | rs2486452 | 9 | 69050460 | 48585 | 6.1154 | 0.3397 | 7.8 | 5.87 | 4.68 | 4.68 | YRI |
| TOMM34 | GI_40807467-S | rs10485453 | 20 | 43002140 | 2254 | 8.364 | 0.4413 | 6.64 | 5.56 | 4.47 | 4.47 | YRI |
| TOP1MT | GI_16418460-S | rs901773 | 8 | 144489976 | 20399 | 7.8242 | 0.4173 | 6.35 | 5.61 | 4.54 | 4.54 | YRI |
| TOP2B | GI_19913407-S | rs6799331 | 3 | 25678644 | 63749 | 6.7476 | 0.3666 | 6.08 | 5.44 | 4.62 | 4.62 | YRI |
| TP53AP1 | GI_6005909-S | rs10499902 | 7 | 86609620 | 10225 | 6.7693 | 0.3676 | 6.46 | 5.41 | 4.39 | 4.39 | YRI |
| TRIM4 | GI_15011940-A | rs1048705 | 7 | 99133591 | 218 | 7.6594 | 0.4098 | 7.06 | 5.77 | 4.52 | 4.52 | YRI |
| TRIT1 | GI_32306540-S | rs11811998 | 1 | 40027819 | 51512 | 8.7858 | 0.4652 | 7.92 | 5.5 | 4.39 | 4.39 | YRI |
| TRNT1 | GI_41281989-I | rs1705805 | 3 | 3164279 | 1184 | 6.6835 | 0.3634 | 7.85 | 6.18 | 4.98 | 4.98 | YRI |
| TSG101 | GI_18765712-S | rs3925781 | 11 | 18481066 | 21289 | 10.3534 | 0.5217 | 6.21 | 5.32 | 4.53 | 4.53 | YRI |
| TSGA10 | GI_41281983-I | rs10181422 | 2 | 99017488 | 198939 | 8.113 | 0.4303 | 7.02 | 5.74 | 4.49 | 4.49 | YRI |
| UBE2L3 | GI_38157977-A | rs878825 | 22 | 20306803 | 4036 | 7.795 | 0.416 | 6.88 | 5.95 | 4.72 | 4.72 | YRI |
| UGT2B11 | GI_4507822-S | rs3100645 | 4 | 69671954 | 575169 | 6.8276 | 0.3756 | 7.55 | 6.26 | 4.82 | 4.82 | YRI |
| UGT2B7 | GI_4507824-S | rs3100645 | 4 | 69671954 | 487102 | 6.5765 | 0.3632 | 8.53 | 6.31 | 4.85 | 4.85 | YRI |
| USP36 | GI_35250685-S | rs6501248 | 17 | 74267767 | 27506 | 8.3585 | 0.4411 | 6.26 | 5.67 | 4.68 | 4.68 | YRI |
| USP52 | GI_41281526-S | rs10747749 | 12 | 54065470 | 931663 | 6.4451 | 0.3516 | 6.49 | 5.45 | 4.5 | 4.5 | YRI |
| VPS11 | GI_17978476-S | rs4614 | 11 | 118457581 | 24 | 7.0093 | 0.3793 | 6.57 | 5.69 | 4.61 | 4.61 | YRI |
| VRK3 | GI_31982928-S | rs11881272 | 19 | 55360157 | 188512 | 6.2868 | 0.3436 | 7.01 | 5.41 | 4.59 | 4.59 | YRI |
| WBSCR27 | GI_30795189-S | rs13232463 | 7 | 72693950 | 148 | 8.8484 | 0.462 | 6.29 | 5.26 | 4.19 | 4.19 | YRI |
| WDR20 | GI_31317273-I | rs7141129 | 14 | 101835084 | 75543 | 5.9266 | 0.3251 | 6.95 | 5.59 | 4.57 | 4.57 | YRI |
| WINS1 | GI_32454732-I | rs8451 | 15 | 98927200 | 2936 | 6.1762 | 0.338 | 6.66 | 5.64 | 4.7 | 4.7 | YRI |
| XRRA1 | GI_42659736-S | rs4944950 | 11 | 74159279 | 70714 | 9.8259 | 0.5015 | 8.08 | 5.74 | 4.67 | 4.67 | YRI |
| ZCCHC9 | GI_14150026-S | rs10035917 | 5 | 81058250 | 413952 | 5.667 | 0.3115 | 6.17 | 5.49 | 4.47 | 4.47 | YRI |
| ZFP100 | GI_27485310-S | rs10409482 | 19 | 55189890 | 53734 | 14.893 | 0.6847 | 7.88 | 5.9 | 4.7 | 4.7 | YRI |
| ZFP161 | GI_19923241-S | rs2789 | 18 | 5279887 | 241 | 5.924 | 0.3498 | 6.38 | 5.72 | 4.76 | 4.76 | YRI |
| ZFYVE21 | GI_20070329-S | rs4983582 | 14 | 104062516 | 793012 | 5.7789 | 0.3174 | 6.23 | 5.5 | 4.51 | 4.51 | YRI |
| ZNF160 | GI_38788301-I | rs329719 | 19 | 58280861 | 5653 | 6.5546 | 0.3571 | 7.1 | 5.84 | 4.77 | 4.77 | YRI |
| ZNF211 | GI_38569444-S | rs9749218 | 19 | 62834703 | 11033 | 6.9201 | 0.375 | 6.13 | 5.43 | 4.55 | 4.55 | YRI |
| ZNF213 | GI_32698677-S | rs2238378 | 16 | 3133218 | 715 | 9.1925 | 0.4762 | 6.66 | 5.63 | 4.59 | 4.59 | YRI |
| ZNF230 | GI_5454181-S | rs1060880 | 19 | 49207192 | 13 | 12.4103 | 0.5929 | 6.12 | 5.62 | 4.51 | 4.51 | YRI |
| ZNF237 | GI_7657706-S | rs7320086 | 13 | 19231071 | 79964 | 7.995 | 0.425 | 6.36 | 5.64 | 4.44 | 4.44 | YRI |
| ZNF253 | GI_10567821-S | rs7254125 | 19 | 19897615 | 33001 | 6.1635 | 0.3374 | 8.07 | 5.81 | 4.47 | 4.47 | YRI |
| ZNF266 | GI_37622342-A | rs1347166 | 19 | 9348808 | 35532 | 9.7934 | 0.5003 | 7.02 | 5.66 | 4.57 | 4.57 | YRI |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZNF30 | GI_34996520-S | rs1053213 | 19 | 40127616 | 21 | 9.4699 | 0.4875 | 6.79 | 5.98 | 4.54 | 4.54 | YRI |
| ZNF34 | GI_31543141-S | rs7829752 | 8 | 145996305 | 26858 | 5.5976 | 0.3078 | 6.11 | 5.33 | 4.33 | 4.33 | YRI |
| ZNF363 | GI_24308060-S | rs2126854 | 4 | 76810328 | 45413 | 5.4243 | 0.2986 | 7.56 | 5.38 | 4.41 | 4.41 | YRI |
| ZNF493 | GI_40255231-S | rs6511239 | 19 | 21380966 | 19788 | 7.2256 | 0.3949 | 7.32 | 5.36 | 4.16 | 4.16 | YRI |
| ZNF557 | GI_13236592-S | rs2115475 | 19 | 7039333 | 5026 | 6.568 | 0.3627 | 7.52 | 6.05 | 4.61 | 4.61 | YRI |
| ZNF85 | GI_4508038-S | rs10454111 | 19 | 20904788 | 20413 | 12.0409 | 0.581 | 6.7 | 5.48 | 4.5 | 4.5 | YRI |
| ZNFN1A1 | GI_31657112-S | rs7792486 | 7 | 50260518 | 16155 | 6.181 | 0.3431 | 8.21 | 5.56 | 4.63 | 4.63 | YRI |
| ZNRD1 | GI_25777705-A | rs11755984 | 6 | 30061014 | 76988 | 7.2064 | 0.3887 | 7.31 | 5.79 | 4.52 | 4.52 | YRI |

## Table S3: Most singificant associations of CGH-clones with gene expression at 0.001

| Gene_label | Illumina Gene_ID | clone_Label | clone_start B35 | clone_end B35 | Chromosome | Distance probe to CNV_start | Distance probe to CNV_end | -log10(p-value) | Adjusted_R^2 | permutation threshold 10-4 | permutation threshold 10-3 | permutation threshold 10-2 | permutation threshold 0.05 | population |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B3GTL | GI_34996530-S | Chr13tp-4C1 | 32572851 | 32739179 | 13 | 1769296 | 1935624 | 4.5095 | 0.2555 | 5.0934 | 4.494 | 3.6349 | 2.823 | CEU |
| B4GALT1 | GI_13929461-S | Chr9tp-2B9 | 32990076 | 33141107 | 9 | -110842 | 40189 | 6.1114 | 0.3494 | 5.3819 | 4.54 | 3.5263 | 2.759 | CEU |
| BBX | GI_18378730-S | Chr3tp-15B10 | 110121124 | 110248865 | 3 | 1114068 | 1241809 | 5.1429 | 0.2833 | 6.1958 | 4.738 | 3.6527 | 2.942 | CEU |
| C13orf12 | GI_21361533-S | Chr13tp-4D6 | 28033029 | 28199094 | 13 | -117167 | 48898 | 5.2186 | 0.2874 | 5.4241 | 4.537 | 3.5703 | 2.809 | CEU |
| CHL1 | GI_27894375-S | Chr3tp-4B4 | 333626 | 518322 | 3 | -90713 | 93983 | 6.1255 | 0.3451 | 4.6709 | 4.338 | 3.2133 | 2.566 | CEU |
| CPNE8 | GI_38683845-S | Chr12tp-20G1 | 38760988 | 38939322 | 12 | 1428015 | 1606349 | 6.083 | 0.3332 | 5.8267 | 4.477 | 3.4242 | 2.725 | CEU |
| CREB5 | GI_4758499-A | Chr7tp-19C7 | 28147859 | 28305298 | 7 | -484872 | -327433 | 10.838 | 0.5654 | 5.7886 | 4.59 | 3.6306 | 2.834 | CEU |
| CTNNA2 | GI_7656998-S | Chr2tp-3G4 | 80574566 | 80754119 | 2 | -212771 | -33218 | 7.1119 | 0.3949 | 5.1611 | 4.53 | 3.5535 | 2.837 | CEU |
| CTNS | GI_4826681-S | Chr17tp-2G2 | 3350005 | 3512944 | 17 | -161419 | 1520 | 4.5975 | 0.2567 | 4.796 | 4.448 | 3.5621 | 2.779 | CEU |
| CYP7B1 | GI_13787190-S | Chr8tp-4C6 | 65866085 | 66009709 | 8 | 194143 | 337767 | 5.5115 | 0.3033 | 5.4029 | 4.754 | 3.4807 | 2.818 | CEU |
| DKFZp434O0213 | GI_32698823-S | Chr22tp-8G4 | 23976814 | 24145392 | 22 | -95275 | 73303 | 6.9669 | 0.3772 | 6.0092 | 4.535 | 3.4894 | 2.728 | CEU |
| EPS8 | GI_34222299-S | Chr12tp-19C8 | 16129779 | 16284706 | 12 | 465004 | 619931 | 4.7655 | 0.2623 | 5.1345 | 4.56 | 3.6387 | 2.924 | CEU |
| EXT1 | GI_4557570-S | Chr8tp-9D4 | 119317502 | 119493081 | 8 | 436446 | 612025 | 4.4679 | 0.2454 | 5.2771 | 4.438 | 3.5152 | 2.826 | CEU |
| FLJ13614 | GI_20589960-S | Chr4tp-9F11 | 83621297 | 83819983 | 4 | -1118764 | -920078 | 4.7637 | 0.2622 | 5.6739 | 4.612 | 3.5457 | 2.863 | CEU |
| FLJ23403 | GI_13384601-S | Chr18tp-1G12 | 11162286 | 11327785 | 18 | 501298 | 666797 | 6.1652 | 0.3374 | 5.9305 | 4.475 | 3.5489 | 2.79 | CEU |
| FLJ43692 | GI_38348301-S | Chr7tp-5B10 | 143412957 | 143479566 | 7 | 92344 | 158953 | 5.7529 | 0.3206 | 5.9335 | 4.679 | 3.5176 | 2.78 | CEU |
| GAP43 | GI_28872807-S | Chr3tp-22E12 | 115673746 | 115809745 | 3 | -1248997 | -1112998 | 5.4795 | 0.306 | 6.5077 | 5.239 | 3.9314 | 3.09 | CEU |
| GBP3 | GI_24308156-S | Chr1tp-29F3 | 89124089 | 89189073 | 1 | -61102 | 3882 | 5.9266 | 0.3298 | 6.6323 | 4.666 | 3.5825 | 2.849 | CEU |
| GNAI3 | GI_5729849-S | Chr1tp-19B2 | 108167908 | 108334093 | 1 | -1680262 | -1514077 | 5.8833 | 0.3275 | 5.1829 | 4.56 | 3.5102 | 2.829 | CEU |
| GNE | GI_38788307-S | Chr9tp-10A8 | 37215146 | 37385618 | 9 | 1010384 | 1180856 | 5.2378 | 0.2971 | 6.1792 | 4.591 | 3.4585 | 2.738 | CEU |
| HLA-DQA1 | GI_18426974-S | Chr6tp-5C11 | 32503398 | 32593944 | 6 | -215437 | -124891 | 8.5936 | 0.457 | 5.6812 | 4.642 | 3.6019 | 2.834 | CEU |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 32503398 | 32593944 | 6 | -317635 | -227089 | 8.0767 | 0.4343 | 5.8121 | 4.876 | 3.5655 | 2.884 | CEU |
| hmm21257 | hmm21257-S | Chr12tp-20G1 | 38760988 | 38939322 | 12 | -143618 | 34716 | 7.2319 | 0.3899 | 5.6729 | 4.561 | 3.551 | 2.846 | CEU |
| hmm23540 | hmm23540-S | Chr17tp-12F12 | 10352771 | 10550785 | 17 | -2061574 | -1863560 | 4.565 | 0.2548 | 5.3132 | 4.5 | 3.5333 | 2.786 | CEU |
| hmm30810 | hmm30810-S | Chr5tp-11F2 | 55081994 | 55272500 | 5 | 327516 | 518022 | 4.7812 | 0.2632 | 5.432 | 4.659 | 3.5661 | 2.9 | CEU |
| hmm34479 | hmm34479-S | Chr8tp-3H5 | 2200752 | 2312389 | 8 | -456194 | -344557 | 4.6969 | 0.2584 | 5.4331 | 4.591 | 3.5922 | 2.821 | CEU |
| hmm34958 | hmm34958-S | Chr8tp-4F7 | 89032945 | 89202820 | 8 | -1806247 | -1636372 | 4.4988 | 0.263 | 5.3408 | 4.432 | 3.5887 | 2.858 | CEU |
| Hs.150050 | Hs.150050-S | Chr22tp-8G4 | 23976814 | 24145392 | 22 | -264495 | -95917 | 4.9706 | 0.2738 | 6.1695 | 4.669 | 3.5088 | 2.732 | CEU |
| Hs.243596 | Hs.243596-S | Chr13tp-4D6 | 28033029 | 28199094 | 13 | -1641996 | -1475931 | 5.3649 | 0.2954 | 5.4522 | 4.529 | 3.5117 | 2.772 | CEU |
| Hs.269958 | Hs.269958-S | Chr7tp-4H1 | 40054910 | 40234347 | 7 | 1512324 | 1691761 | 5.9997 | 0.3435 | 5.9025 | 4.82 | 3.5693 | 2.828 | CEU |
| Hs.463184 | Hs.463184-S | Chr17tp-12C1 | 40977732 | 41171794 | 17 | -18185 | 175877 | 6.0349 | 0.3355 | 6.3022 | 4.637 | 3.4836 | 2.796 | CEU |
| Hs.464547 | Hs.464547-S | Chr1tp-25E8 | 11182270 | 11282168 | 1 | -1063429 | -963531 | 5.7153 | 0.3186 | 5.5366 | 4.359 | 3.6052 | 2.848 | CEU |
| Hs.476851 | Hs.476851-S | Chr3tp-26G11 | 76747210 | 76935064 | 3 | 60551 | 248405 | 5.9081 | 0.3242 | 5.7532 | 5.272 | 4.1617 | 3.266 | CEU |
| Hs.478669 | Hs.478669-S | Chr3tp-25A11 | 191281358 | 191439015 | 3 | 10725 | 168382 | 5.7154 | 0.3141 | 5.64 | 4.652 | 3.7181 | 2.925 | CEU |
| Hs.495422 | Hs.495422-S | Chr9tp-11C4 | 131717143 | 131863140 | 9 | -1506331 | -1360334 | 4.3928 | 0.2448 | 5.6016 | 4.266 | 3.3934 | 2.646 | CEU |
| Hs.498648 | Hs.498648-S | Chr10tp-7E12 | 12085124 | 12274940 | 10 | 737444 | 927260 | 5.1675 | 0.2846 | 8.4037 | 4.345 | 3.453 | 2.778 | CEU |
| Hs.507644 | Hs.507644-S | Chr13tp-7A11 | 30326059 | 30502988 | 13 | 407908 | 584837 | 5.0464 | 0.278 | 5.7354 | 4.918 | 3.5359 | 2.817 | CEU |
| Hs.525661 | Hs.525661-S | Chr15tp-7C8 | 19932331 | 20097557 | 15 | 801991 | 967217 | 4.7152 | 0.2634 | 4.3978 | 3.923 | 3.103 | 2.347 | CEU |
| IL1R1 | GI_27894331-S | Chr2tp-24A2 | 102122465 | 102306835 | 2 | -131935 | 52435 | 6.4423 | 0.3667 | 5.8498 | 4.736 | 3.486 | 2.769 | CEU |
| IL6ST | GI_28610146-I | Chr5tp-16D7 | 55205360 | 55361836 | 5 | -83462 | 73014 | 4.5954 | 0.2605 | 4.8874 | 4.461 | 3.5968 | 2.858 | CEU |
| IL7 | GI_28610152-S | Chr8tp-7E5 | 80578436 | 80736765 | 8 | 767139 | 925468 | 5.5842 | 0.3071 | 5.4261 | 4.511 | 3.4615 | 2.752 | CEU |
| IPO7 | GI_5453997-S | Chr11tp-2A3 | 10375098 | 10531604 | 11 | 951480 | 1107986 | 4.6081 | 0.2573 | 5.3987 | 4.44 | 3.4583 | 2.764 | CEU |
| ITIH4 | GI_40288189-S | Chr3tp-19E2 | 53282205 | 53439842 | 3 | 459729 | 617366 | 4.9027 | 0.27 | 4.9427 | 4.681 | 3.5395 | 2.886 | CEU |
| KLF12 | GI_21071073-I | Chr13tp-3D12 | 73413445 | 73578554 | 13 | 254972 | 420081 | 5.4055 | 0.3019 | 5.5353 | 4.448 | 3.4348 | 2.802 | CEU |
| LOC151261 | GI_29731277-S | Chr2tp-22E1 | 12733637 | 12937354 | 2 | 511558 | 715275 | 8.3575 | 0.4526 | 5.736 | 4.595 | 3.5282 | 2.812 | CEU |
| LOC255812 | GI_37550242-S | Chr3tp-18B6 | 198772060 | 198823587 | 3 | 1881232 | 1932759 | 4.9148 | 0.2832 | 5.7169 | 4.52 | 3.5952 | 2.828 | CEU |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC347981 | GI_30160064-S | Chr6tp-22E5 | 29979075 | 30000296 | 6 | 16532 | 37753 | 6.0065 | 0.3772 | 6.2417 | 4.635 | 3.6649 | 2.949 | CEU |
| LOC374673 | GI_37541248-S | Chr15tp-4E11 | 80920701 | 81107580 | 15 | 398146 | 585025 | 4.4622 | 0.2451 | 5.2355 | 4.403 | 3.4623 | 2.75 | CEU |
| LOC375508 | GI_37552191-S | Chr6tp-2D2 | 41488763 | 41684723 | 6 | -1530831 | -1334871 | 5.0745 | 0.288 | 5.8439 | 4.714 | 3.552 | 2.836 | CEU |
| LOC377296 | GI_37550226-S | Chr5tp-10D12 | 118758898 | 118939349 | 5 | -152109 | 28342 | 4.4885 | 0.2466 | 5.5963 | 4.467 | 3.5766 | 2.931 | CEU |
| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 19932331 | 20097557 | 15 | -17353 | 147873 | 5.6011 | 0.3125 | 5.6223 | 4.415 | 3.3144 | 2.551 | CEU |
| LOC389609 | GI_41148493-S | Chr8tp-3G10 | 2414807 | 2583462 | 8 | -126885 | 41770 | 5.494 | 0.3067 | 5.6249 | 4.689 | 3.5523 | 2.84 | CEU |
| LOC402472 | GI_42658251-S | Chr7tp-19C7 | 28147859 | 28305298 | 7 | -75575 | 81864 | 6.1995 | 0.3593 | 6.6019 | 5.52 | 4.2173 | 3.184 | CEU |
| MAP3K1 | GI_37550278-S | Chr5tp-16D7 | 55205360 | 55361836 | 5 | -1022144 | -865668 | 5.3563 | 0.3037 | 6.136 | 4.708 | 3.6061 | 2.875 | CEU |
| MGC10871 | GI_32306518-S | Chr11tp-3F10 | 68042930 | 68231187 | 11 | 1853623 | 2041880 | 4.9551 | 0.277 | 6.2863 | 4.724 | 3.5973 | 2.8 | CEU |
| MGC41943 | GI_34222265-S | Chr7tp-5B10 | 143412957 | 143479566 | 7 | 624842 | 691451 | 8.2551 | 0.4422 | 5.7044 | 4.455 | 3.4557 | 2.79 | CEU |
| MGC72075 | GI_40217629-S | Chr7tp-4E8 | 23171705 | 23350234 | 7 | -332731 | -154202 | 4.5861 | 0.2522 | 7.2445 | 4.45 | 3.5063 | 2.822 | CEU |
| MLAT4 | GI_27764881-S | Chr3tp-25A11 | 191281358 | 191439015 | 3 | 123745 | 281402 | 5.6998 | 0.3133 | 6.5443 | 4.732 | 3.5731 | 2.897 | CEU |
| MYO6 | GI_4826845-S | Chr6tp-12E12 | 76960072 | 77052124 | 6 | 277962 | 370014 | 5.4732 | 0.3012 | 5.5246 | 4.605 | 3.5586 | 2.825 | CEU |
| NR2F2 | GI_31377723-S | Chr15tp-1A12 | 94219335 | 94391192 | 15 | -463311 | -291454 | 5.7068 | 0.3229 | 5.8242 | 4.622 | 3.4907 | 2.723 | CEU |
| PARD3 | GI_21361830-S | Chr10tp-8G5 | 34331883 | 34471421 | 10 | -108407 | 31131 | 8.1555 | 0.4322 | 5.2362 | 4.821 | 3.6779 | 2.923 | CEU |
| PDGFD | GI_15451920-A | Chr11tp-2C9 | 103571728 | 103753945 | 11 | 288170 | 470387 | 5.1246 | 0.2823 | 5.592 | 4.659 | 3.6447 | 2.971 | CEU |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 68690128 | 68870723 | 16 | -62302 | 118293 | 9.1346 | 0.4798 | 5.6945 | 4.585 | 3.4252 | 2.762 | CEU |
| PDZGEF1 | GI_7657260-S | Chr4tp-4A12 | 160580983 | 160741167 | 4 | -57683 | 102501 | 5.1198 | 0.282 | 5.7027 | 5.003 | 3.5669 | 2.837 | CEU |
| PRICKLE2 | GI_38524619-S | Chr3tp-25F4 | 63835343 | 64013188 | 3 | -219441 | -41596 | 7.5696 | 0.4057 | 7.488 | 5.067 | 3.7314 | 2.907 | CEU |
| PTPLA | GI_18104975-S | Chr10tp-10E3 | 18732345 | 18910853 | 10 | 1056006 | 1234514 | 4.3273 | 0.2373 | 5.0961 | 4.297 | 3.4588 | 2.796 | CEU |
| PTPRK | GI_18860901-S | Chr6tp-10H9 | 128448580 | 128633213 | 6 | 116589 | 301222 | 5.2841 | 0.291 | 5.4683 | 4.542 | 3.6061 | 2.894 | CEU |
| RASSF6 | GI_41393612-A | Chr4tp-9D11 | 74797930 | 75012988 | 4 | -18144 | 196914 | 5.0114 | 0.2802 | 6.2163 | 4.94 | 3.5063 | 2.821 | CEU |
| RGNEF | GI_37550356-S | Chr5tp-20B6 | 73002547 | 73197422 | 5 | -270933 | -76058 | 4.8891 | 0.2692 | 5.6798 | 4.56 | 3.5703 | 2.886 | CEU |
| SIGLEC5 | GI_4502658-S | Chr19tp-7A10 | 56783548 | 56958512 | 19 | -23686 | 151278 | 4.692 | 0.2703 | 5.2413 | 4.547 | 3.3199 | 2.687 | CEU |
| SLC2A13 | GI_16418394-S | Chr12tp-2E5 | 38991138 | 39141490 | 12 | 551941 | 702293 | 7.2523 | 0.3909 | 6.4456 | 4.821 | 3.6189 | 2.867 | CEU |
| SMN2 | GI_13259530-A | Chr5tp-3F4 | 70234598 | 70425468 | 5 | 825985 | 1016855 | 5.6857 | 0.3125 | 5.0157 | 4.448 | 3.3641 | 2.674 | CEU |
| SNRPB2 | GI_38149980-A | Chr20tp-6C10 | 16170259 | 16336536 | 20 | -495767 | -329490 | 5.666 | 0.3115 | 5.7404 | 5.053 | 3.8076 | 2.956 | CEU |
| SNRPD1 | GI_28416941-S | Chr18tp-3B2 | 18532199 | 18719572 | 18 | 1068365 | 1255738 | 4.308 | 0.2598 | 5.5867 | 4.241 | 3.2985 | 2.629 | CEU |
| STEAP | GI_22027487-S | Chr7tp-23B4 | 89160969 | 89355308 | 7 | -277662 | -83323 | 6.2721 | 0.3429 | 5.3442 | 4.599 | 3.5779 | 2.869 | CEU |
| STEAP2 | GI_25092600-S | Chr7tp-23B4 | 89160969 | 89355308 | 7 | -350142 | -155803 | 7.4433 | 0.3998 | 6.5135 | 4.824 | 3.5565 | 2.866 | CEU |
| TMPIT | GI_13994299-S | Chr7tp-17H6 | 75169293 | 75327473 | 7 | -91866 | 66314 | 4.4778 | 0.246 | 5.9645 | 4.418 | 3.302 | 2.671 | CEU |
| TNFRSF11B | GI_22547122-S | Chr8tp-5B6 | 120020198 | 120167611 | 8 | 14463 | 161876 | 6.7894 | 0.3737 | 6.1499 | 4.648 | 3.6132 | 2.813 | CEU |
| TOX | GI_42658956-S | Chr8tp-3E1 | 60223828 | 60381578 | 8 | 343129 | 500879 | 5.6795 | 0.3122 | 6.4618 | 4.586 | 3.5761 | 2.878 | CEU |
| UBE2E2 | GI_22749326-S | Chr3tp-22C11 | 23991826 | 24167234 | 3 | 384915 | 560323 | 4.7944 | 0.2639 | 5.9614 | 4.516 | 3.6421 | 2.882 | CEU |
| UCHL5 | GI_7706752-S | Chr1tp-10F8 | 190899097 | 191041651 | 1 | 1182121 | 1324675 | 4.8727 | 0.2683 | 5.4862 | 4.435 | 3.4676 | 2.786 | CEU |
| UGT2B10 | GI_27552756-S | Chr4tp-1F2 | 69075001 | 69230647 | 4 | -802255 | -646609 | 5.2344 | 0.311 | 5.9642 | 4.227 | 3.4391 | 2.768 | CEU |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1120655 | -950647 | 14.7246 | 0.6671 | 5.8267 | 4.565 | 3.5246 | 2.772 | CEU |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -105361 | 64647 | 15.0078 | 0.6746 | 5.364 | 4.524 | 3.5444 | 2.874 | CEU |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1032588 | -862580 | 13.9271 | 0.6451 | 5.6211 | 4.482 | 3.5341 | 2.754 | CEU |
| AGPAT3 | GI_41327762-S | Chr21tp-3B9 | 44273354 | 44465672 | 21 | 46626 | 238944 | 5.2365 | 0.3831 | 5.3572 | 4.631 | 3.3816 | 2.623 | CHB |
| AIP | GI_4502008-S | Chr11tp-2H4 | 66670500 | 66843551 | 11 | -344542 | -171491 | 4.6304 | 0.3346 | 5.0452 | 4.393 | 3.4765 | 2.79 | CHB |
| BIRC1 | GI_4758751-S | Chr5tp-3A5 | 69485603 | 69650298 | 5 | 60291 | 224986 | 5.3367 | 0.3755 | 5.4139 | 4.631 | 3.3567 | 2.678 | CHB |
| BUB1B | GI_20149508-S | Chr15tp-5C7 | 38061792 | 38223585 | 15 | -238443 | -76650 | 5.0035 | 0.3535 | 5.8117 | 4.314 | 3.5684 | 2.843 | CHB |
| C14orf110 | GI_7661757-S | Chr14tp-11E8 | 104367765 | 104533191 | 14 | -1090365 | -924939 | 3.997 | 0.2888 | 4.9369 | 3.772 | 2.7291 | 1.994 | CHB |
| C14orf116 | GI_20127573-S | Chr14tp-11E4 | 89100485 | 89263148 | 14 | 408005 | 570668 | 5.9495 | 0.4215 | 5.7411 | 4.988 | 3.6323 | 2.883 | CHB |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 41225348 | 41326639 | 22 | -7936 | 93355 | 5.2361 | 0.3759 | 5.6491 | 5.05 | 3.9356 | 3.061 | CHB |
| CHES1 | GI_4885136-S | Chr14tp-11E4 | 89100485 | 89263148 | 14 | 402549 | 565212 | 5.4908 | 0.3925 | 6.813 | 4.501 | 3.5511 | 2.833 | CHB |
| COX7A2L | GI_18105036-S | Chr2tp-29D3 | 41557419 | 41714286 | 2 | -932337 | -775470 | 5.0276 | 0.3551 | 5.103 | 4.536 | 3.5652 | 2.844 | CHB |
| FLJ20442 | GI_32261290-S | Chr3tp-22G12 | 155783429 | 155942113 | 1 | -781889 | -623205 | 4.3848 | 0.3235 | 5.3022 | 4.359 | 3.4656 | 2.779 | CHB |
| FLJ45909 | GI_38348205-S | Chr1tp-7F8 | 148862241 | 149032869 | 1 | 731345 | 901973 | 4.5211 | 0.3205 | 5.7251 | 4.303 | 3.4968 | 2.777 | CHB |
| GTF2E1 | GI_5031726-S | Chr3tp-5F1 | 120684354 | 120844091 | 3 | -1299796 | -1140059 | 4.9976 | 0.3531 | 5.6214 | 4.685 | 3.7568 | 2.987 | CHB |
| HIST1H4B | GI_21166392-S | Chr6tp-2A12 | 24146928 | 24331276 | 6 | -1988457 | -1804109 | 4.8964 | 0.353 | 5.9421 | 4.747 | 3.618 | 2.844 | CHB |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 32503398 | 32593944 | 6 | -317635 | -227089 | 11.5728 | 0.6759 | 4.7611 | 4.016 | 3.1718 | 2.501 | CHB |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C11 | 32503398 | 32593944 | 6 | -89827 | 719 | 7.4891 | 0.5011 | 5.4316 | 4.349 | 3.2159 | 2.505 | CHB |
| hmm28653 | hmm28653-S | Chr2tp-19A8 | 209447808 | 209628092 | 2 | -666939 | -486655 | 5.1026 | 0.367 | 6.6172 | 4.483 | 3.4576 | 2.779 | CHB |
| hmm29193 | hmm29193-S | Chr3tp-28E4 | 70463875 | 70639306 | 3 | -1165545 | -990114 | 4.5188 | 0.3267 | 5.7504 | 4.462 | 3.5699 | 2.903 | CHB |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Hs.287709 | Hs.287709-S | Chr22tp-8E4 | 37493053 | 37629009 | 22 | 731047 | 867003 | 4.7152 | 0.334 | 5.5718 | 4.517 | 3.5315 | 2.862 | CHB |
| KIAA0220 | GI_42660956-S | Chr16tp-8B1 | 22503592 | 22679810 | 16 | 48560 | 224778 | 7.1145 | 0.4977 | 5.2218 | 4.361 | 3.4305 | 2.765 | CHB |
| LMAN1 | GI_10862689-S | Chr18tp-9D2 | 53998291 | 54169211 | 18 | -1150071 | -979151 | 4.9322 | 0.3554 | 5.2811 | 4.526 | 3.4642 | 2.788 | CHB |
| LOC149603 | GI_37548531-S | Chr1tp-35G3 | 225050847 | 225160564 | 1 | 63328 | 173045 | 4.9043 | 0.3469 | 5.3396 | 4.504 | 3.5861 | 2.868 | CHB |
| LOC283820 | GI_27734708-S | Chr16tp-6D2 | 18108163 | 18293192 | 16 | 1812140 | 1997169 | 4.9039 | 0.3604 | 5.7175 | 4.087 | 3.4814 | 2.765 | CHB |
| LOC339088 | GI_37541953-S | Chr16tp-3A9 | 30109781 | 30290781 | 16 | 736563 | 917563 | 4.9573 | 0.3572 | 6.4029 | 4.407 | 3.4075 | 2.727 | CHB |
| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 19932331 | 20097557 | 15 | -17353 | 147873 | 6.8608 | 0.4672 | 5.0463 | 4.085 | 3.3407 | 2.553 | CHB |
| LOC388440 | GI_42661316-S | Chr17tp-11A1 | 31309398 | 31466733 | 17 | -145880 | 11455 | 5.2236 | 0.3681 | 5.3829 | 4.503 | 3.597 | 2.863 | CHB |
| LOC392218 | GI_41148741-S | Chr8tp-17A3 | 48525949 | 48706581 | 8 | -1460144 | -1279512 | 4.6498 | 0.3295 | 5.3675 | 4.441 | 3.578 | 2.842 | CHB |
| LOC400543 | GI_42660801-S | Chr16tp-8B1 | 22503592 | 22679810 | 16 | 101320 | 277538 | 7.0287 | 0.4929 | 5.1864 | 4.443 | 3.4898 | 2.739 | CHB |
| MGC12760 | GI_34147433-S | Chr1tp-25H8 | 16637922 | 16784062 | 1 | -52396 | 93744 | 8.0881 | 0.5488 | 6.0214 | 4.685 | 3.683 | 2.852 | CHB |
| MGC26717 | GI_34222236-S | Chr3tp-27A3 | 87431797 | 87596645 | 3 | -856734 | -691886 | 4.82 | 0.3412 | 6.0931 | 4.621 | 3.4966 | 2.844 | CHB |
| MGC41943 | GI_34222265-S | Chr7tp-7H4 | 143283127 | 143413156 | 7 | 495012 | 625041 | 4.7936 | 0.3459 | 5.879 | 4.509 | 3.5508 | 2.823 | CHB |
| MGC45491 | GI_23397533-S | Chr6tp-3B11 | 42815771 | 42914110 | 6 | -1265048 | -1166709 | 4.6421 | 0.3637 | 5.7331 | 4.575 | 3.5734 | 2.855 | CHB |
| MGC5178 | GI_30089944-A | Chr16tp-9D2 | 29248712 | 29449523 | 16 | -128220 | 72591 | 4.5664 | 0.3301 | 5.6629 | 4.468 | 3.4693 | 2.771 | CHB |
| NDUFB4 | GI_40806201-S | Chr3tp-5F1 | 120684354 | 120844091 | 3 | -1113553 | -953816 | 5.429 | 0.3814 | 5.9631 | 4.813 | 3.7308 | 2.973 | CHB |
| NMNAT3 | GI_31342325-S | Chr3tp-5B8 | 140942616 | 141096384 | 3 | 180753 | 334521 | 5.0202 | 0.3614 | 5.7614 | 4.884 | 3.8354 | 3.031 | CHB |
| NPIP | GI_5902013-S | Chr16tp-9F3 | 14789257 | 14970746 | 16 | 61772 | 243261 | 5.4541 | 0.3902 | 6.7094 | 4.827 | 3.7193 | 2.941 | CHB |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 68690128 | 68870723 | 16 | -62302 | 118293 | 11.4405 | 0.6888 | 6.2231 | 5.029 | 3.7497 | 2.95 | CHB |
| PM5 | GI_10947030-S | Chr16tp-9F3 | 14789257 | 14970746 | 16 | -108109 | 73380 | 5.6759 | 0.4044 | 7.2742 | 4.449 | 3.495 | 2.781 | CHB |
| SMN1 | GI_13259511-A | Chr5tp-2H6 | 70072978 | 70197304 | 5 | 663882 | 788208 | 7.9531 | 0.5333 | 4.8908 | 4.444 | 3.4571 | 2.703 | CHB |
| SMN2 | GI_13259530-A | Chr5tp-2H6 | 70072978 | 70197304 | 5 | 664365 | 788691 | 9.3678 | 0.5994 | 6.2077 | 4.527 | 3.5195 | 2.777 | CHB |
| SULT1A3 | GI_29550920-A | Chr16tp-3A9 | 30109781 | 30290781 | 16 | 726249 | 907249 | 5.6374 | 0.4019 | 5.6376 | 4.474 | 3.5115 | 2.772 | CHB |
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -750788 | -580780 | 7.5642 | 0.5308 | 5.1892 | 4.377 | 3.4914 | 2.774 | CHB |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1120655 | -950647 | 14.9269 | 0.7971 | 6.2696 | 4.666 | 3.5649 | 2.756 | CHB |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -105361 | 64647 | 15.7922 | 0.8163 | 5.8966 | 4.547 | 3.6106 | 2.823 | CHB |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1032588 | -862580 | 14.1214 | 0.7776 | 5.1428 | 4.354 | 3.4034 | 2.73 | CHB |
| APOBEC3B | GI_22907024-S | Chr22tp-2A6 | 37604699 | 37805841 | 22 | -105332 | 95810 | 5.0251 | 0.3618 | 5.0295 | 4.578 | 3.5463 | 2.927 | JPT |
| ATP5A1 | GI_23346425-S | Chr18tp-1F6 | 42005019 | 42163425 | 18 | 84822 | 243228 | 4.6171 | 0.3272 | 4.8094 | 4.323 | 3.5462 | 2.802 | JPT |
| BYSL | GI_15208644-S | Chr6tp-6H11 | 41696767 | 41807431 | 6 | -311709 | -201045 | 4.187 | 0.3028 | 4.9837 | 4.11 | 3.4359 | 2.783 | JPT |
| CENPA | GI_4585861-S | Chr2tp-20B5 | 27972987 | 28136281 | 2 | 1044204 | 1207498 | 4.7281 | 0.3349 | 6.8115 | 4.274 | 3.3786 | 2.754 | JPT |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 41225348 | 41326639 | 22 | -7936 | 93355 | 6.1055 | 0.4234 | 5.9416 | 4.978 | 3.6217 | 2.912 | JPT |
| COPZ1 | GI_7706336-S | Chr12tp-11C6 | 53033144 | 53231483 | 12 | 1581 | 199920 | 5.012 | 0.3679 | 5.0924 | 4.358 | 3.5238 | 2.844 | JPT |
| DEDD | GI_14670395-A | Chr1tp-8C10 | 156169069 | 156313869 | 1 | -1735521 | -1590721 | 4.4998 | 0.3191 | 6.3865 | 4.489 | 3.436 | 2.727 | JPT |
| DKFZP572C163 | GI_42822888-S | Chr9tp-2A1 | 41194015 | 41282840 | 9 | -1021083 | -932258 | 5.7335 | 0.4007 | 4.5863 | 3.98 | 2.9101 | 2.225 | JPT |
| DMPK | GI_4758173-S | Chr19tp-4E7 | 49484154 | 49639855 | 19 | -1480803 | -1325102 | 4.4958 | 0.3188 | 7.1089 | 4.33 | 3.3458 | 2.638 | JPT |
| FBXO2 | GI_15812197-S | Chr1tp-23D2 | 11639235 | 11815970 | 1 | -3689 | 173046 | 5.0459 | 0.3632 | 5.7104 | 4.535 | 3.5063 | 2.816 | JPT |
| FLJ00332 | GI_38348347-S | Chr11tp-14A2 | 65980446 | 66140055 | 11 | -953527 | -793918 | 4.3998 | 0.3182 | 6.086 | 4.383 | 3.5094 | 2.834 | JPT |
| GBP3 | GI_24308156-S | Chr1tp-29F3 | 89124089 | 89189073 | 1 | -61102 | 3882 | 6.474 | 0.4452 | 5.9659 | 4.665 | 3.5973 | 2.917 | JPT |
| GTF2H2 | GI_31747573-S | Chr5tp-13C10 | 69552855 | 69710868 | 5 | 634996 | 793009 | 4.601 | 0.3261 | 6.7346 | 4.539 | 3.4011 | 2.701 | JPT |
| HAN11 | GI_5031728-S | Chr17tp-2C9 | 60529898 | 60693483 | 17 | 1509665 | 1673250 | 4.8487 | 0.3431 | 5.7882 | 4.685 | 3.5645 | 2.857 | JPT |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 32503398 | 32593944 | 6 | -317635 | -227089 | 9.1094 | 0.5794 | 5.0611 | 4.197 | 3.1648 | 2.498 | JPT |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C11 | 32503398 | 32593944 | 6 | -89827 | 719 | 5.6106 | 0.393 | 6.3063 | 4.195 | 3.2272 | 2.559 | JPT |
| hmm21257 | hmm21257-S | Chr12tp-20B2 | 38644006 | 38815857 | 12 | -260600 | -88749 | 5.0927 | 0.3663 | 6.1368 | 4.865 | 3.6278 | 2.858 | JPT |
| hmm35285 | hmm35285-S | Chr5tp-20C10 | 812176 | 991126 | 9 | -564233 | -385283 | 4.6086 | 0.333 | 5.5329 | 4.409 | 3.4516 | 2.711 | JPT |
| Hs.137868 | Hs.137868-S | Chr5tp-20C5 | 116721255 | 116886886 | 5 | -419087 | -253456 | 5.0253 | 0.355 | 5.4226 | 4.331 | 3.6141 | 2.924 | JPT |
| Hs.460059 | Hs.460059-S | Chr16tp-2E3 | 16652556 | 16831289 | 16 | 1795976 | 1974709 | 5.8012 | 0.4049 | 6.7408 | 5.54 | 4.166 | 3.114 | JPT |
| Hs.489160 | Hs.489160-S | Chr7tp-4B2 | 95703082 | 95756209 | 7 | 1392536 | 1445663 | 4.7342 | 0.3556 | 5.5807 | 4.502 | 3.5832 | 2.858 | JPT |
| Hs.495177 | Hs.495177-S | Chr14tp-12C8 | 21867480 | 22006855 | 14 | 126519 | 265894 | 4.3875 | 0.3111 | 6.2287 | 4.123 | 3.3225 | 2.665 | JPT |
| KIAA0220 | GI_42660956-S | Chr16tp-12F7 | 21408063 | 21559206 | 16 | -1046969 | -895826 | 6.5711 | 0.4587 | 6.1212 | 4.361 | 3.5263 | 2.811 | JPT |
| KIAA1093 | GI_27501258-S | Chr22tp-10B2 | 37049837 | 37145940 | 22 | -1993880 | -1897777 | 5.1509 | 0.3633 | 6.45 | 4.8 | 3.579 | 2.909 | JPT |
| LOC283820 | GI_27734708-S | Chr16tp-6G1 | 18108163 | 18293192 | 16 | 1812140 | 1997169 | 5.8283 | 0.4065 | 5.4582 | 4.95 | 3.6738 | 2.849 | JPT |
| LOC347981 | GI_30160064-S | Chr6tp-5H5 | 29767504 | 29916283 | 6 | -195039 | -46260 | 6.4983 | 0.4466 | 5.4728 | 4.395 | 3.2969 | 2.557 | JPT |
| LOC374395 | GI_37541013-S | Chr11tp-16B4 | 63724994 | 63889434 | 11 | 1411569 | 1576009 | 4.799 | 0.3463 | 5.2915 | 4.491 | 3.5746 | 2.815 | JPT |
| LOC375418 | GI_40786421-S | Chr4tp-16B12 | 157403341 | 157547216 | 4 | 1801845 | 1945720 | 6.4303 | 0.4427 | 5.201 | 4.606 | 3.5207 | 2.818 | JPT |
| LOC378157 | GI_37539180-S | Chr7tp-13D1 | 43725779 | 43830031 | 7 | -71619 | 32633 | 10.0615 | 0.6196 | 5.6432 | 4.678 | 3.5369 | 2.811 | JPT |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 19932331 | 20097557 | 15 | -17353 | 147873 | 8.1058 | 0.5324 | 6.4667 | 4.717 | 3.3907 | 2.66 | JPT |
| LOC388457 | GI_42661337-S | Chr18tp-3G7 | 3109560 | 3288371 | 18 | 418806 | 597617 | 5.8139 | 0.4057 | 6.1445 | 4.709 | 3.6828 | 2.917 | JPT |
| LOC400566 | GI_42661283-S | Chr17tp-3G4 | 1335634 | 1530629 | 17 | 1070992 | 1265987 | 4.0212 | 0.3383 | 4.4672 | 3.971 | 3.0686 | 2.386 | JPT |
| LOC402488 | GI_42658295-S | Chr7tp-13D1 | 43725779 | 43830031 | 7 | -73281 | 30971 | 7.8345 | 0.5189 | 5.2606 | 4.475 | 3.5474 | 2.809 | JPT |
| LOC55871 | GI_13236498-S | Chr9tp-4C8 | 356138 | 537316 | 9 | 244629 | 425807 | 4.5383 | 0.3217 | 7.6292 | 4.08 | 3.2231 | 2.566 | JPT |
| MCOLN1 | GI_10092596-S | Chr19tp-5B1 | 6199888 | 6359433 | 19 | -1304810 | -1145265 | 4.3702 | 0.3161 | 5.1395 | 3.904 | 3.1077 | 2.445 | JPT |
| MGC12760 | GI_34147433-S | Chr1tp-25H9 | 16752898 | 16870964 | 1 | 62580 | 180646 | 6.958 | 0.4726 | 6.8464 | 5.068 | 3.6624 | 2.899 | JPT |
| MGC1842 | GI_42662435-S | Chr22tp-2D1 | 24269780 | 24491286 | 22 | 1008619 | 1230125 | 5.106 | 0.3672 | 5.0939 | 4.365 | 3.424 | 2.672 | JPT |
| MGC42630 | GI_31341689-S | Chr9tp-13D1 | 42650537 | 42928370 | 9 | -1547928 | -1270095 | 6.2612 | 0.4327 | 6.1683 | 4.467 | 3.1576 | 2.28 | JPT |
| NMT1 | GI_39725674-S | Chr17tp-3F3 | 40552637 | 40737608 | 17 | 10961 | 195932 | 6.3393 | 0.4788 | 5.1297 | 4.248 | 3.3791 | 2.721 | JPT |
| Nup37 | GI_34222120-S | Chr12tp-5B6 | 99810968 | 100007844 | 12 | -1159664 | -962788 | 4.7761 | 0.3382 | 5.0175 | 4.547 | 3.5807 | 2.917 | JPT |
| PM5 | GI_10947030-S | Chr16tp-2E3 | 16652556 | 16831289 | 16 | 1755190 | 1933923 | 5.8061 | 0.4052 | 6.2469 | 4.655 | 3.5927 | 2.86 | JPT |
| POLR1C | GI_42560249-A | Chr6tp-6H11 | 41696767 | 41807431 | 6 | -1899677 | -1789013 | 4.4886 | 0.3245 | 5.8111 | 4.451 | 3.5335 | 2.799 | JPT |
| RAD9A | GI_19924112-S | Chr11tp-2F7 | 66841191 | 66872614 | 11 | -80933 | -49510 | 5.2194 | 0.3972 | 5.7707 | 4.537 | 3.5281 | 2.807 | JPT |
| RPL36 | GI_16117795-A | Chr19tp-5C2 | 4739180 | 4897550 | 19 | -903435 | -745065 | 4.4185 | 0.326 | 6.7085 | 4.033 | 3.0967 | 2.324 | JPT |
| SCNM1 | GI_13128997-S | Chr1tp-31C6 | 149067874 | 149151422 | 1 | 1114099 | 1197647 | 4.8816 | 0.3453 | 5.7685 | 4.453 | 3.4639 | 2.73 | JPT |
| SDHC | GI_9257243-S | Chr1tp-8C10 | 156169069 | 156313869 | 1 | -1976781 | -1831981 | 6.6654 | 0.4562 | 5.3767 | 4.452 | 3.4556 | 2.776 | JPT |
| SENP3 | GI_21361498-S | Chr17tp-4B11 | 7042348 | 7223586 | 17 | -373379 | -192141 | 6.4006 | 0.4567 | 6.3244 | 4.545 | 3.4803 | 2.822 | JPT |
| SMN1 | GI_13259511-A | Chr5tp-2H6 | 70072978 | 70197304 | 5 | 663882 | 788208 | 5.3414 | 0.3758 | 5.2103 | 4.414 | 3.3782 | 2.659 | JPT |
| SMN2 | GI_13259530-A | Chr5tp-2H6 | 70072978 | 70197304 | 5 | 664365 | 788691 | 6.9629 | 0.4728 | 7.4926 | 4.586 | 3.5472 | 2.8 | JPT |
| SSNA1 | GI_4505324-S | Chr9tp-3E10 | 136125999 | 136283272 | 9 | -1234420 | -1077147 | 4.5754 | 0.3307 | 5.7194 | 4.07 | 3.273 | 2.594 | JPT |
| TOMM40 | GI_5174722-S | Chr19tp-4E7 | 49484154 | 49639855 | 19 | -614300 | -458599 | 6.0878 | 0.4224 | 5.2396 | 4.196 | 3.401 | 2.682 | JPT |
| UBE2G2 | GI_33359699-A | Chr21tp-1E12 | 46607928 | 46756333 | 21 | 1594331 | 1742736 | 4.9607 | 0.3574 | 5.6648 | 4.082 | 3.1817 | 2.513 | JPT |
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -750788 | -580780 | 14.2091 | 0.7632 | 5.3862 | 4.55 | 3.4658 | 2.76 | JPT |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1120655 | -950647 | 21.039 | 0.8876 | 5.1869 | 4.332 | 3.4551 | 2.72 | JPT |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -105361 | 64647 | 21.7175 | 0.8957 | 5.5734 | 4.516 | 3.5404 | 2.8 | JPT |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1032588 | -862580 | 20.6757 | 0.8831 | 5.2161 | 4.51 | 3.4536 | 2.752 | JPT |
| WDR21 | GI_31317285-A | Chr14tp-2D8 | 74386054 | 74589417 | 14 | 1890400 | 2093763 | 4.731 | 0.3483 | 5.3995 | 4.189 | 3.4407 | 2.812 | JPT |
| XAB1 | GI_14149628-S | Chr2tp-20B5 | 27972987 | 28136281 | 2 | 187859 | 351153 | 4.8347 | 0.3422 | 5.7698 | 4.499 | 3.5036 | 2.785 | JPT |
| AFG3L2 | GI_5802969-S | Chr18tp-4G4 | 13810695 | 13953988 | 18 | 1491313 | 1634606 | 4.9518 | 0.2768 | 5.4651 | 4.591 | 3.5855 | 2.826 | YRI |
| AKR1A1 | GI_24497576-A | Chr1tp-20C5 | 46007370 | 46165931 | 1 | 302623 | 461184 | 4.9097 | 0.2704 | 5.5989 | 4.712 | 3.5537 | 2.807 | YRI |
| AMD1 | GI_5209326-S | Chr6tp-15A3 | 111196247 | 111320737 | 6 | -127026 | -2536 | 4.8594 | 0.2676 | 5.4386 | 4.628 | 3.6001 | 2.859 | YRI |
| AP4B1 | GI_5729741-S | Chr1tp-30F8 | 114433496 | 114570985 | 1 | 283500 | 420989 | 5.9587 | 0.3268 | 6.5679 | 5.635 | 4.776 | 2.464 | YRI |
| ARHA | GI_10835048-S | Chr5tp-17G5 | 47858118 | 48047419 | 3 | -1513741 | -1324440 | 4.4821 | 0.2462 | 6.0643 | 4.43 | 3.4609 | 2.731 | YRI |
| ARL10C | GI_8922600-S | Chr3tp-20D6 | 5027803 | 5180954 | 3 | -169368 | -16217 | 4.798 | 0.2641 | 4.8576 | 4.301 | 3.4139 | 2.799 | YRI |
| ARPC3 | GI_23397667-S | Chr12tp-20D8 | 108015022 | 108199720 | 12 | -1320664 | -1135966 | 5.7499 | 0.33 | 7.1513 | 5.016 | 3.7951 | 2.862 | YRI |
| C14orf123 | GI_40548421-S | Chr14tp-8B2 | 22278362 | 22444232 | 14 | -1470427 | -1304557 | 4.2434 | 0.236 | 5.6853 | 4.178 | 3.3994 | 2.754 | YRI |
| C20orf103 | GI_40804463-S | Chr20tp-6D6 | 9427891 | 9550775 | 20 | -31127 | 91757 | 5.5391 | 0.3092 | 5.2863 | 4.747 | 3.6561 | 2.893 | YRI |
| C6orf69 | GI_40255181-S | Chr6tp-5G5 | 34918527 | 35051474 | 6 | -1647347 | -1514400 | 4.8059 | 0.2686 | 5.4811 | 4.534 | 3.5074 | 2.815 | YRI |
| CDC23 | GI_16554575-S | Chr5tp-22E9 | 137422515 | 137594755 | 5 | -128841 | 43399 | 4.6039 | 0.2532 | 5.6316 | 4.358 | 3.5147 | 2.822 | YRI |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 41225348 | 41326639 | 22 | -7936 | 93355 | 7.9883 | 0.4303 | 7.4911 | 4.726 | 3.6406 | 2.912 | YRI |
| CIRH1A | GI_14249535-S | Chr16tp-11H12 | 66655002 | 66809694 | 16 | -1105281 | -950589 | 5.2456 | 0.2932 | 7.2381 | 4.234 | 3.4214 | 2.729 | YRI |
| CLSPN | GI_21735568-S | Chr1tp-27A6 | 35476101 | 35593060 | 1 | -395522 | -278563 | 5.626 | 0.3233 | 5.9559 | 4.871 | 3.665 | 2.835 | YRI |
| CYB5-M | GI_13385593-S | Chr16tp-11H12 | 66655002 | 66809694 | 16 | -1400032 | -1245340 | 6.6454 | 0.3666 | 5.9232 | 4.494 | 3.4064 | 2.725 | YRI |
| DAAM2 | GI_40548414-S | Chr6tp-4H9 | 39397275 | 39637314 | 6 | -583218 | -343179 | 5.0049 | 0.2798 | 6.4778 | 4.841 | 3.7317 | 2.949 | YRI |
| DHX33 | GI_20336301-S | Chr17tp-2C8 | 3671876 | 3830289 | 17 | -1614776 | -1456363 | 5.6127 | 0.3086 | 5.0002 | 4.43 | 3.5055 | 2.798 | YRI |
| DHX37 | GI_29029600-S | Chr12tp-7D11 | 122098129 | 122246939 | 12 | -1858170 | -1709360 | 4.7337 | 0.2685 | 6.8876 | 4.538 | 3.6046 | 2.811 | YRI |
| DKFZp434N035 | GI_14149994-S | Chr22tp-7B3 | 17363351 | 17407078 | 22 | -2020023 | -1976296 | 6.6283 | 0.3658 | 6.3186 | 4.509 | 3.4139 | 2.697 | YRI |
| DKFZp762C186 | GI_22062495-S | Chr11tp-5B8 | 63363053 | 63569797 | 11 | -1753604 | -1546860 | 4.8092 | 0.2688 | 5.5153 | 4.456 | 3.4763 | 2.727 | YRI |
| EIF3S4 | GI_4503516-S | Chr19tp-5G1 | 8072715 | 8276904 | 19 | -2014668 | -1810479 | 4.7369 | 0.2607 | 5.8574 | 4.544 | 3.2848 | 2.608 | YRI |
| ELKS | GI_38045893-A | Chr12tp-10D8 | 2969428 | 3145565 | 12 | 1496872 | 1673009 | 5.3873 | 0.3101 | 5.4161 | 4.539 | 3.4821 | 2.745 | YRI |
| ETF1 | GI_4759033-S | Chr5tp-22E9 | 137422515 | 137594755 | 5 | -447720 | -275480 | 5.0665 | 0.2791 | 6.0418 | 4.614 | 3.5625 | 2.832 | YRI |
| ETV4 | GI_24307882-S | Chr17tp-2G5 | 38491053 | 38601721 | 17 | -469999 | -359331 | 4.9819 | 0.2744 | 5.6916 | 4.603 | 3.5285 | 2.82 | YRI |
| FCHO1 | GI_29789053-S | Chr19tp-4C8 | 16541755 | 16705788 | 19 | -1218547 | -1054514 | 5.4592 | 0.3004 | 5.3796 | 4.357 | 3.33 | 2.602 | YRI |
| FLJ11286 | GI_8922978-S | Chr19tp-5G1 | 8072715 | 8276904 | 19 | -1992142 | -1787953 | 4.7771 | 0.263 | 6.2737 | 4.701 | 3.377 | 2.613 | YRI |
| FLJ12455 | GI_11545792-S | Chr1tp-26E12 | 28184670 | 28217009 | 1 | 1283510 | 1315849 | 7.0497 | 0.3865 | 6.0523 | 4.923 | 3.6382 | 2.851 | YRI |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FLJ14466 | GI_38016942-S | Chr12tp-12C7 | 120538520 | 120689076 | 12 | -3794 | 146762 | 5.0278 | 0.2853 | 4.994 | 4.448 | 3.4962 | 2.773 | YRI |
| FLJ25059 | GI_21450678-S | Chr11tp-4F9 | 64563983 | 64751916 | 11 | 1407603 | 1595536 | 5.296 | 0.2959 | 6.6229 | 4.797 | 3.5115 | 2.829 | YRI |
| FLJ43692 | GI_38348301-S | Chr7tp-7H4 | 143283127 | 143413156 | 7 | -37486 | 92543 | 5.6868 | 0.3171 | 5.8276 | 4.499 | 3.4513 | 2.734 | YRI |
| GCNT1 | GI_34485725-S | Chr9tp-2D2 | 76595419 | 76758995 | 9 | 244101 | 407677 | 6.1957 | 0.3438 | 5.8374 | 4.664 | 3.4787 | 2.747 | YRI |
| GMEB1 | GI_13435374-A | Chr1tp-26F6 | 27386878 | 27464199 | 1 | -1474877 | -1397556 | 6.6993 | 0.3693 | 5.6555 | 4.473 | 3.57 | 2.769 | YRI |
| GTF2E1 | GI_5031726-S | Chr3tp-19D12 | 123673731 | 123823998 | 3 | 1689581 | 1839848 | 5.5197 | 0.3037 | 5.752 | 4.666 | 3.6837 | 2.96 | YRI |
| HARS | GI_18201902-S | Chr5tp-19B6 | 139516108 | 139694346 | 5 | -517611 | -339373 | 5.0563 | 0.2785 | 5.3644 | 4.521 | 3.5679 | 2.797 | YRI |
| HEM1 | GI_34485726-S | Chr12tp-17C10 | 51985795 | 52180082 | 12 | -1237121 | -1042834 | 5.0951 | 0.2982 | 6.2778 | 4.811 | 3.5496 | 2.886 | YRI |
| HLA-DQA1 | GI_18426974-S | Chr6tp-22E8 | 32809419 | 32813412 | 6 | 90584 | 94577 | 6.6771 | 0.4143 | 6.1176 | 4.898 | 3.6055 | 2.891 | YRI |
| HLA-DRB5 | GI_26665892-S | Chr6tp-4E2 | 32634806 | 32650604 | 6 | 41581 | 57379 | 10.8926 | 0.5415 | 5.4195 | 4.571 | 3.6035 | 2.869 | YRI |
| HPS6 | GI_31881784-S | Chr10tp-1H2 | 104340398 | 104506997 | 10 | 522794 | 689393 | 4.9283 | 0.2714 | 5.4104 | 4.507 | 3.4879 | 2.735 | YRI |
| Hs.105147 | Hs.105147-S | Chr17tp-6E1 | 5331201 | 5506598 | 17 | 1213010 | 1388407 | 6.6369 | 0.3611 | 5.7289 | 4.578 | 3.5389 | 2.797 | YRI |
| Hs.135624 | Hs.135624-S | Chr3tp-6F2 | 178755570 | 178931836 | 3 | -1816190 | -1639924 | 4.8907 | 0.2693 | 5.486 | 4.751 | 3.6804 | 2.899 | YRI |
| Hs.449564 | Hs.449564-S | Chr22tp-6B8 | 20693407 | 20733158 | 22 | -11926 | 27825 | 6.4528 | 0.352 | 7.4914 | 5.342 | 3.7554 | 2.76 | YRI |
| Hs.462423 | Hs.462423-S | Chr17tp-2C2 | 18863800 | 19021902 | 17 | -126434 | 31668 | 4.9199 | 0.271 | 5.402 | 4.441 | 3.4653 | 2.771 | YRI |
| Hs.468488 | Hs.468488-S | Chr10tp-4A6 | 126760588 | 126955018 | 10 | 323990 | 518420 | 4.671 | 0.257 | 6.5086 | 4.456 | 3.4907 | 2.79 | YRI |
| Hs.473730 | Hs.473730-S | Chr21tp-1H8 | 36765627 | 36936688 | 21 | 280448 | 451509 | 5.2371 | 0.2971 | 5.0234 | 4.541 | 3.4575 | 2.8 | YRI |
| Hs.485352 | Hs.485352-S | Chr1tp-6G9 | 110647995 | 110811836 | 1 | 632727 | 796568 | 4.8381 | 0.2704 | 5.952 | 4.608 | 3.6521 | 2.968 | YRI |
| Hs.487323 | Hs.487323-S | Chr2tp-8F2 | 130935780 | 131251570 | 2 | -728390 | -412600 | 4.7445 | 0.2611 | 4.8779 | 4.224 | 3.4558 | 2.728 | YRI |
| Hs.523150 | Hs.523150-S | Chr1tp-27C12 | 40360418 | 40487326 | 1 | 659187 | 786095 | 4.7705 | 0.2626 | 5.6001 | 4.666 | 3.4963 | 2.819 | YRI |
| IAN4L1 | GI_28416948-S | Chr7tp-16B1 | 149327158 | 149384711 | 7 | -550972 | -493419 | 4.8398 | 0.2665 | 6.0589 | 4.516 | 3.497 | 2.857 | YRI |
| JAM3 | GI_21704285-S | Chr11tp-2A2 | 133022689 | 133217958 | 11 | -504047 | -308778 | 6.7403 | 0.3662 | 9.0656 | 6.068 | 4.3316 | 3.095 | YRI |
| KIAA0252 | GI_34222098-S | Chr15tp-5D2 | 38766143 | 38944390 | 15 | -795993 | -617746 | 4.8173 | 0.2692 | 5.1675 | 4.684 | 3.521 | 2.753 | YRI |
| LOC126598 | GI_37546761-S | Chr1tp-5F6 | 92783031 | 92966868 | 1 | 530069 | 713906 | 4.5545 | 0.2504 | 5.2885 | 4.471 | 3.614 | 2.87 | YRI |
| LOC151963 | GI_31341922-S | Chr3tp-22A11 | 194016261 | 194212650 | 3 | 18694 | 215083 | 5.0469 | 0.278 | 5.5269 | 4.471 | 3.4349 | 2.858 | YRI |
| LOC155340 | GI_37538348-S | Chr7tp-21E5 | 5845548 | 6028567 | 7 | -822428 | -639409 | 4.5443 | 0.2536 | 6.2794 | 4.481 | 3.5262 | 2.767 | YRI |
| LOC255812 | GI_37550242-S | Chr3tp-18B6 | 198772060 | 198823587 | 3 | 1881232 | 1932759 | 7.1673 | 0.4089 | 5.0103 | 4.407 | 3.5933 | 2.853 | YRI |
| LOC347981 | GI_30160064-S | Chr6tp-22A4 | 29900413 | 29981074 | 6 | -62130 | 18531 | 6.4796 | 0.4036 | 5.5303 | 4.455 | 3.6215 | 2.944 | YRI |
| LOC375133 | GI_40786533-S | Chr22tp-7B3 | 17363351 | 17407078 | 22 | -1399415 | -1355688 | 9.9142 | 0.5111 | 6.021 | 4.389 | 3.4702 | 2.75 | YRI |
| LOC378157 | GI_37539180-S | Chr7tp-13D1 | 43725779 | 43830031 | 7 | -71619 | 32633 | 9.6845 | 0.5146 | 4.9606 | 4.558 | 3.5487 | 2.836 | YRI |
| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 19932331 | 20097557 | 15 | -17353 | 147873 | 5.8149 | 0.3386 | 5.1493 | 4.173 | 3.2954 | 2.593 | YRI |
| LOC388673 | GI_41115452-S | Chr1tp-31B7 | 145043332 | 145140950 | 1 | -1346096 | -1248478 | 5.5127 | 0.3078 | 7.2725 | 4.582 | 3.4063 | 2.7 | YRI |
| LOC390113 | GI_41201035-S | Chr11tp-13C10 | 46216957 | 46379340 | 11 | -2025656 | -1863273 | 5.6452 | 0.3195 | 6.012 | 4.65 | 3.6277 | 2.854 | YRI |
| LOC402488 | GI_42658295-S | Chr7tp-13D1 | 43725779 | 43830031 | 7 | -73281 | 30971 | 9.1073 | 0.491 | 5.863 | 4.533 | 3.5641 | 2.808 | YRI |
| LOC51249 | GI_24475971-S | Chr1tp-20C5 | 46007370 | 46165931 | 1 | 178590 | 337151 | 4.4107 | 0.2421 | 5.1927 | 4.381 | 3.498 | 2.786 | YRI |
| LOC55831 | GI_8923856-S | Chr3tp-10B12 | 10137483 | 10347535 | 3 | 156621 | 366673 | 4.3991 | 0.2451 | 5.1645 | 4.34 | 3.4664 | 2.74 | YRI |
| LOC90987 | GI_29734344-S | Chr8tp-18A7 | 144355201 | 144524781 | 8 | -1563059 | -1393479 | 4.5619 | 0.2546 | 6.4604 | 4.43 | 3.3161 | 2.469 | YRI |
| MASA | GI_10864016-S | Chr4tp-13H7 | 83714295 | 83899208 | 4 | -24783 | 160130 | 4.7482 | 0.2653 | 5.1107 | 4.721 | 3.6356 | 2.857 | YRI |
| MGC12760 | GI_34147433-S | Chr1tp-25H8 | 16637922 | 16784062 | 1 | -52396 | 93744 | 13.3699 | 0.6355 | 6.1935 | 4.753 | 3.6522 | 2.861 | YRI |
| MGC31967 | GI_28316809-S | Chr9tp-5D9 | 34758158 | 34919696 | 9 | -890547 | -729009 | 4.6108 | 0.2536 | 5.268 | 4.442 | 3.5561 | 2.818 | YRI |
| MRPS22 | GI_16554602-S | Chr3tp-10C7 | 140849541 | 141009102 | 3 | 291013 | 450574 | 4.6585 | 0.2563 | 5.3519 | 4.529 | 3.5772 | 2.873 | YRI |
| MTVR1 | GI_22779872-S | Chr11tp-5B8 | 63363053 | 63569797 | 11 | -1734991 | -1528247 | 4.58 | 0.2556 | 5.2754 | 4.447 | 3.4929 | 2.721 | YRI |
| NASP | GI_27262629-A | Chr1tp-27E10 | 44959288 | 45130943 | 1 | -794223 | -622568 | 4.7908 | 0.2637 | 6.2405 | 4.523 | 3.5335 | 2.821 | YRI |
| NDUFB10 | GI_4758773-S | Chr16tp-1G7 | 3800356 | 3965551 | 16 | 1848795 | 2013990 | 6.1779 | 0.3429 | 6.5913 | 4.879 | 3.4885 | 2.68 | YRI |
| NIF3L1BP1 | GI_13376622-S | Chr3tp-20B4 | 65182251 | 65361126 | 3 | 1387405 | 1566280 | 4.805 | 0.2685 | 6.4545 | 4.434 | 3.5779 | 2.846 | YRI |
| NME6 | GI_38564323-S | Chr3tp-26F2 | 49955698 | 50112586 | 3 | 1644718 | 1801606 | 4.3947 | 0.2412 | 5.3973 | 4.353 | 3.298 | 2.66 | YRI |
| NT5C2 | GI_20149601-S | Chr10tp-1E10 | 102751071 | 102953191 | 10 | -2087204 | -1885084 | 4.5539 | 0.2503 | 5.273 | 4.508 | 3.5017 | 2.734 | YRI |
| PARD3 | GI_21361830-S | Chr10tp-4F9 | 34455689 | 34621117 | 10 | 15399 | 180827 | 5.341 | 0.2984 | 5.8674 | 4.816 | 3.6299 | 2.936 | YRI |
| PDF | GI_11641242-S | Chr16tp-11H12 | 66655002 | 66809694 | 16 | -1266494 | -1111802 | 5.4287 | 0.3032 | 5.4723 | 4.484 | 3.4341 | 2.766 | YRI |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 68690128 | 68870723 | 16 | -62302 | 118293 | 14.5848 | 0.6765 | 5.4666 | 4.459 | 3.4897 | 2.746 | YRI |
| RAB10 | GI_33695094-S | Chr2tp-13B3 | 27274856 | 27470373 | 2 | 1003049 | 1198566 | 4.5047 | 0.2475 | 5.5601 | 4.29 | 3.455 | 2.79 | YRI |
| RAB8B | GI_7706562-S | Chr15tp-10G9 | 62785585 | 62962963 | 15 | 1442549 | 1619927 | 4.8866 | 0.2691 | 5.369 | 4.39 | 3.5254 | 2.846 | YRI |
| RG9MTD1 | GI_8923404-S | Chr3tp-7H10 | 101385631 | 101585598 | 3 | -1381667 | -1181700 | 5.2077 | 0.2955 | 5.5501 | 4.528 | 3.606 | 2.891 | YRI |
| RIOK1 | GI_23510357-A | Chr6tp-7B2 | 8428714 | 8532326 | 6 | 1065985 | 1169597 | 6.0384 | 0.3456 | 8.525 | 4.664 | 3.5717 | 2.874 | YRI |
| RNF122 | GI_38045930-S | Chr8tp-16E12 | 33802163 | 33956976 | 8 | 277264 | 432077 | 5.3974 | 0.2971 | 5.6556 | 4.642 | 3.6396 | 2.902 | YRI |
| RNGTT | GI_4506562-S | Chr6tp-9D8 | 88286018 | 88456272 | 6 | -1090799 | -920545 | 4.9128 | 0.2788 | 5.6281 | 4.707 | 3.7204 | 2.979 | YRI |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RNPS1 | GI_18379333-A | Chr16tp-1G7 | 3800356 | 3965551 | 16 | 1556572 | 1721767 | 4.5633 | 0.2547 | 5.9791 | 4.267 | 3.4185 | 2.629 | YRI |
| SAMSN1 | GI_21361921-S | Chr21tp-2F5 | 14448525 | 14618661 | 21 | -331691 | -161555 | 5.8211 | 0.3243 | 5.6841 | 4.693 | 3.4363 | 2.71 | YRI |
| SFRS9 | GI_38016912-S | Chr12tp-1F2 | 120246649 | 120419203 | 12 | 884024 | 1056578 | 5.9492 | 0.331 | 6.6093 | 4.362 | 3.5095 | 2.834 | YRI |
| SIAT8A | GI_28373095-S | Chr12tp-1H8 | 22333762 | 22472221 | 12 | 87977 | 226436 | 14.7398 | 0.6675 | 6.4653 | 5.15 | 3.7744 | 2.992 | YRI |
| SIGLEC5 | GI_4502658-S | Chr19tp-7A10 | 56783548 | 56958512 | 19 | -23686 | 151278 | 5.3744 | 0.3094 | 5.4547 | 4.494 | 3.3275 | 2.641 | YRI |
| SLC2A13 | GI_16418394-S | Chr12tp-19E9 | 38449595 | 38641367 | 12 | 10398 | 202170 | 5.1673 | 0.2932 | 5.8112 | 4.465 | 3.5723 | 2.841 | YRI |
| SUHW2 | GI_38202248-S | Chr22tp-6B8 | 20693407 | 20733158 | 22 | -470451 | -430700 | 6.103 | 0.3343 | 8.8075 | 6.009 | 4.3078 | 2.841 | YRI |
| TCEB3 | GI_4507388-S | Chr1tp-26D1 | 24514712 | 24618461 | 1 | 683167 | 786916 | 5.0591 | 0.2787 | 6.1699 | 4.835 | 3.6751 | 2.889 | YRI |
| UBAP2 | GI_22325365-A | Chr9tp-5D9 | 34758158 | 34919696 | 9 | 846421 | 1007959 | 4.3566 | 0.239 | 5.4601 | 4.335 | 3.4624 | 2.776 | YRI |
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -750788 | -580780 | 4.7695 | 0.2665 | 5.5891 | 4.577 | 3.4286 | 2.746 | YRI |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1120655 | -950647 | 11.4101 | 0.566 | 6.2463 | 4.833 | 3.6682 | 2.888 | YRI |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -105361 | 64647 | 10.4865 | 0.5329 | 6.6359 | 5.408 | 3.791 | 2.985 | YRI |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 69126468 | 69296476 | 4 | -1032588 | -862580 | 11.0417 | 0.5531 | 5.8227 | 4.708 | 3.7028 | 2.913 | YRI |

## Table S4: Most significant associations of CNV-clones with gene expression at 0.001

| Gene_label | Illumina Gene_ID | clone_Label | chromosome | Distance probe to CNV_start | Distance probe to CNV_end | -log10(p-value) | Adjusted_R^2 | slope | pos/neg slope | population | clone_midpoint B35 | probe_midpoint B35 | distance clone midpoint-probe midpoint | CNV_ID | CNV_class | CNV Frequency in 270 HapMap individuals | CNV_start B35 | CNV_end B35 | probe in CNV? | Distance from probe to CNV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AP2S1 | GI_11038644-I | Chr19tp-3A4 | 19 | 514966 | 682687 | 3.5605 | 0.2046 | -1.6672 | - | CEU | 52633457 | 52033313 | 600144 | Chr19_9 | del | 3 | 52549596 | 52717317 | out | 516283 |
| ARL8 | GI_31341468-S | Chr10tp-1H10 | 10 | 1775769 | 1931816 | 3.2798 | 0.1804 | -0.8988 | - | CEU | 20860591 | 19006798 | 1853793 | Chr10_6 | del | 54 | 20726725 | 20938614 | out | 1719927 |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 22 | -7936 | 93355 | 4.2056 | 0.2338 | 2.277 | + | CEU | 41275994 | 41233284 | 42710 | Chr22_26 | dup | 25 | 41091699 | 41407804 | inside | 0 |
| CHL1 | GI_27894375-S | Chr3tp-4B4 | 3 | -90713 | 93983 | 6.1255 | 0.3451 | 5.6742 | + | CEU | 425974 | 424339 | 1635 | Chr3_25 | complex | 3 | 46156 | 773503 | inside | 0 |
| CTNNA2 | GI_7656998-S | Chr2tp-3G4 | 2 | -212771 | -33218 | 7.1119 | 0.3949 | 9.949 | + | CEU | 80664343 | 80787337 | 122995 | Chr2_10 | del | 2 | 80312976 | 80754119 | out | 33218 |
| DKFZp434O02 | GI_32698823-S | Chr22tp-8G4 | 22 | -95275 | 73303 | 6.9669 | 0.3772 | 1.8491 | + | CEU | 24061103 | 24072089 | 10986 | Chr22_24 | del/dup | 27 | 23691355 | 24281461 | inside | 0 |
| EGLN3 | GI_31742485-S | Chr14tp-2D11 | 14 | -1535518 | -1377556 | 3.585 | 0.2209 | -5.498 | - | CEU | 32007212 | 33463749 | 1456537 | Chr14_6 | dup | 4 | 31928231 | 32086193 | out | 1377556 |
| FLJ22795 | GI_13443001-S | Chr15tp-4E11 | 15 | 148042 | 334921 | 4.2608 | 0.2334 | 0.8684 | + | CEU | 81014141 | 80772659 | 241482 | Chr15_2 | del/dup | 32 | 80676701 | 81107580 | inside | 0 |
| FLJ43692 | GI_38348301-S | Chr7tp-5B10 | 7 | 92344 | 158953 | 5.7529 | 0.3206 | 0.8584 | + | CEU | 143446262 | 143320613 | 125649 | Chr7_29 | multiallelic | 151 | 142664612 | 143806286 | inside | 0 |
| GBP3 | GI_24308156-S | Chr1tp-29F3 | 1 | -61102 | 3882 | 5.9266 | 0.3298 | 5.6887 | + | CEU | 89156581 | 89185191 | 28610 | Chr1_31 | complex | 27 | 89124089 | 89272744 | inside | 0 |
| GRLF1 | GI_25121939-A | Chr19tp-3A4 | 19 | 353163 | 520884 | 3.2638 | 0.1854 | -2.3938 | - | CEU | 52633457 | 52196433 | 437024 | Chr19_9 | del | 3 | 52549596 | 52717317 | out | 353163 |
| HLA-DQA1 | GI_18426974-S | Chr6tp-5C11 | 6 | -215437 | -124891 | 8.5936 | 0.457 | -10.1863 | - | CEU | 32548671 | 32718835 | 170164 | Chr6_19 | dup | 205 | 32479731 | 32813412 | inside | 0 |
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| hmm26489 | hmm26489-S | Chr1tp-25A7 | 1 | -29543 | 81064 | 4.1963 | 0.2297 | 1.8841 | + | CEU | 1707122 | 1681361 | 25761 | Chr1_10 | del/dup | 19 | 1651818 | 1762425 | inside | 0 |
| hmm34479 | hmm34479-S | Chr8tp-3H5 | 8 | -456194 | -344557 | 4.6969 | 0.2584 | 0.8407 | + | CEU | 2256571 | 2656946 | 400376 | Chr8_24 | del/dup | 3 | 2105020 | 2411266 | out | 245680 |
| Hs.150050 | Hs.150050-S | Chr22tp-8G4 | 22 | -264495 | -95917 | 4.9706 | 0.2738 | 0.6043 | + | CEU | 24061103 | 24241309 | 180206 | Chr22_24 | del/dup | 27 | 23691355 | 24281461 | inside | 0 |
| Hs.463184 | Hs.463184-S | Chr17tp-12C1 | 17 | -18185 | 175877 | 6.0349 | 0.3355 | 1.1365 | + | CEU | 41074763 | 40995917 | 78846 | Chr17_17 | dup | 2 | 40977732 | 41171794 | inside | 0 |
| Hs.525661 | Hs.525661-S | Chr15tp-7C8 | 15 | 801991 | 967217 | 4.7152 | 0.2634 | 0.2536 | + | CEU | 20014944 | 19130340 | 884604 | Chr15_8 | complex | 129 | 18263733 | 21066294 | inside | 0 |
| LOC196394 | GI_37543779-S | Chr12tp-7F5 | 12 | -699189 | -528324 | 3.6695 | 0.2016 | 2.2924 | + | CEU | 31102167 | 31715923 | 613757 | Chr12_16 | del/dup | 10 | 31016734 | 31382371 | out | 333552 |
| LOC255812 | GI_37550242-S | Chr3tp-18B6 | 3 | 1881232 | 1932759 | 4.9148 | 0.2832 | 0.7938 | + | CEU | 198797824 | 196890828 | 1906996 | Chr3_1 | del | 1 | 198772060 | 198823587 | out | 1881232 |
| LOC345754 | GI_37550208-S | Chr5tp-2D2 | 5 | -109545 | 42089 | 4.2624 | 0.2335 | 0.9662 | + | CEU | 21497307 | 21531035 | 33728 | Chr5_4 | complex | 50 | 21184910 | 21748947 | inside | 0 |
| LOC347981 | GI_30160064-S | Chr6tp-22E5 | 6 | 16532 | 37753 | 6.0065 | 0.3772 | 2.2144 | + | CEU | 29989686 | 29962543 | 27143 | Chr6_22 | complex | 21 | 29900413 | 30083123 | inside | 0 |
| LOC374673 | GI_37541248-S | Chr15tp-4E11 | 15 | 398146 | 585025 | 4.4622 | 0.2451 | 1.2832 | + | CEU | 81014141 | 80522555 | 491586 | Chr15_2 | del/dup | 32 | 80676701 | 81107580 | out | 154146 |
| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 15 | -17353 | 147873 | 5.6011 | 0.3125 | 1.3639 | + | CEU | 20014944 | 19949684 | 65260 | Chr15_8 | complex | 129 | 18263733 | 21066294 | inside | 0 |
| LOC400543 | GI_42660801-S | Chr16tp-12F7 | 16 | -994209 | -843066 | 4.1915 | 0.2404 | 1.5906 | + | CEU | 21483635 | 22402272 | 918638 | Chr16_11 | del/dup | 70 | 21241957 | 21833734 | out | 568538 |
| MGC10204 | GI_34222200-S | Chr19tp-6H5 | 19 | 564783 | 680757 | 3.3479 | 0.1817 | -0.3942 | - | CEU | 55286809 | 54664039 | 622770 | Chr19_3 | complex | 136 | 55228822 | 55344796 | out | 564783 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MGC41943 | GI_34222265-S | Chr7tp-5B10 | 7 | 624842 | 691451 | 8.2551 | 0.4422 | 0.6558 | + | CEU | 143446262 | 142788115 | 658147 | Chr7_29 | multiallelic | 151 | 142664612 | 143806286 | inside | 0 |
| MRPS26 | GI_39812071-S | Chr20tp-4A10 | 20 | -1551652 | -1436175 | 3.8084 | 0.2134 | 0.9804 | + | CEU | 1482520 | 2976433 | 1493914 | Chr20_5 | dup | 78 | 1424781 | 1627256 | out | 1349177 |
| NOL5A | GI_32483373-S | Chr20tp-4A10 | 20 | -1162200 | -1046723 | 3.3275 | 0.1834 | 1.4409 | + | CEU | 1482520 | 2586981 | 1104462 | Chr20_5 | dup | 78 | 1424781 | 1627256 | out | 959725 |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 16 | -62302 | 118293 | 9.1346 | 0.4798 | 2.0465 | + | CEU | 68780426 | 68752430 | 27996 | Chr16_21 | complex | 19 | 68412623 | 68870723 | inside | 0 |
| PPP5C | GI_20127496-S | Chr19tp-3A4 | 19 | 963821 | 1131542 | 3.38 | 0.193 | -1.5748 | - | CEU | 52633457 | 51585775 | 1047682 | Chr19_9 | del | 3 | 52549596 | 52717317 | out | 963821 |
| SIGLEC5 | GI_4502658-S | Chr19tp-7A10 | 19 | -23686 | 151278 | 4.692 | 0.2703 | -1.0019 | - | CEU | 56871030 | 56807234 | 63796 | Chr19_11 | del | 15 | 56683708 | 56958512 | inside | 0 |
| SMN2 | GI_13259530-A | Chr5tp-3F4 | 5 | 825985 | 1016855 | 5.6857 | 0.3125 | 3.0261 | + | CEU | 70330033 | 69408613 | 921420 | Chr5_29 | multiallelic | 37 | 70072978 | 70425468 | out | 664365 |
| TMEPAI | GI_40317614-A | Chr20tp-6F1 | 20 | -52910 | 84183 | 3.7237 | 0.2049 | 2.9585 | + | CEU | 55672731 | 55657094 | 15637 | Chr20_18 | del | 35 | 55604184 | 56121677 | inside | 0 |
| TOM1L1 | GI_4885638-S | Chr17tp-7C4 | 17 | -1966752 | -1836886 | 3.8046 | 0.2238 | -3.4675 | - | CEU | 48480141 | 50381960 | 1901819 | Chr17_23 | del | 2 | 48369345 | 48627779 | out | 1754181 |
| UGT2B10 | GI_27552756-S | Chr4tp-1F2 | 4 | -802255 | -646609 | 5.2344 | 0.311 | 5.9275 | + | CEU | 69152824 | 69877256 | 724432 | Chr4_9 | dup | 54 | 68998845 | 69296476 | out | 580780 |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 4 | -1120655 | -950647 | 14.7246 | 0.6671 | 5.3223 | + | CEU | 69211472 | 70247123 | 1035651 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 950647 |
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| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 4 | -1032588 | -862580 | 13.9271 | 0.6451 | 4.7694 | + | CEU | 69211472 | 70159056 | 947584 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 862580 |
| BIRC1 | GI_4758751-S | Chr5tp-3A5 | 5 | 60291 | 224986 | 5.3367 | 0.3755 | 0.5983 | + | CHB | 69567951 | 69425312 | 142639 | Chr5_61 | complex | 142 | 69109876 | 70831640 | inside | 0 |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 22 | -7936 | 93355 | 5.2361 | 0.3759 | 1.8544 | + | CHB | 41275994 | 41233284 | 42710 | Chr22_26 | dup | 25 | 41091699 | 41407804 | inside | 0 |
| CHL1 | GI_27894375-S | Chr3tp-4B4 | 3 | -90713 | 93983 | 4.2427 | 0.3068 | 4.6578 | + | CHB | 425974 | 424339 | 1635 | Chr3_25 | complex | 3 | 46156 | 773503 | inside | 0 |
| GBP3 | GI_24308156-S | Chr1tp-35B1 | 1 | 1883 | 87553 | 4.2589 | 0.3276 | 5.6114 | + | CHB | 89229909 | 89185191 | 44718 | Chr1_31 | complex | 27 | 89124089 | 89272744 | inside | 0 |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 6 | -317635 | -227089 | 11.5728 | 0.6759 | 7.6617 | + | CHB | 32548671 | 32821033 | 272362 | Chr6_19 | dup | 205 | 32479731 | 32813412 | out | 7621 |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C11 | 6 | -89827 | 719 | 7.4891 | 0.5011 | 7.9969 | + | CHB | 32548671 | 32593225 | 44554 | Chr6_19 | dup | 205 | 32479731 | 32813412 | inside | 0 |
| Hs.460059 | Hs.460059-S | Chr16tp-9F3 | 16 | -67323 | 114166 | 4.134 | 0.2989 | 0.8413 | + | CHB | 14880002 | 14856580 | 23422 | Chr16_6 | del/dup | 19 | 14529556 | 15133811 | inside | 0 |
| Hs.490862 | Hs.490862-S | Chr8tp-13F3 | 8 | 1620253 | 1796445 | 4.0778 | 0.3071 | 0.9122 | + | CHB | 3843330 | 2134981 | 1708349 | Chr8_47 | dup | 3 | 3586932 | 5909600 | out | 1451951 |
| KIAA0220 | GI_42660956-S | Chr16tp-8B1 | 16 | 48560 | 224778 | 7.1145 | 0.4977 | 1.0834 | + | CHB | 22591701 | 22455032 | 136669 | Chr16_20 | del/dup | 162 | 22201625 | 22679810 | inside | 0 |
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| LOC339088 | GI_37541953-S | Chr16tp-3A9 | 16 | 736563 | 917563 | 4.9573 | 0.3572 | 1.1873 | + | CHB | 30200281 | 29373218 | 827063 | Chr16_30 | dup | 12 | 29981456 | 30290781 | out | 608238 |
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| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 15 | -17353 | 147873 | 6.8608 | 0.4672 | 1.4305 | + | CHB | 20014944 | 19949684 | 65260 | Chr15_8 | complex | 129 | 18263733 | 21066294 | inside | 0 |
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| LOC400543 | GI_42660801-S | Chr16tp-8B1 | 16 | 101320 | 277538 | 7.0287 | 0.4929 | 0.9031 | + | CHB | 22591701 | 22402272 | 189429 | Chr16_20 | del/dup | 162 | 22201625 | 22679810 | inside | 0 |
| MGC12760 | GI_34147433-S | Chr1tp-25H8 | 1 | -52396 | 93744 | 8.0881 | 0.5488 | 2.2552 | + | CHB | 16710992 | 16690318 | 20674 | Chr1_15 | del/dup | 60 | 16509639 | 17229287 | inside | 0 |
| MGC21881 | GI_44888813-S | Chr9tp-3D7 | 9 | 648676 | 836181 | 3.8841 | 0.2803 | 1.0448 | + | CHB | 64979103 | 64236674 | 742429 | Chr9_16 | del/dup | 27 | 64135929 | 68383081 | inside | 0 |
| MGC41943 | GI_34222265-S | Chr7tp-7H4 | 7 | 495012 | 625041 | 4.7936 | 0.3459 | 0.5695 | + | CHB | 143348142 | 142788115 | 560027 | Chr7_29 | multiallelic | 150 | 142664612 | 143806286 | inside | 0 |
| MGC5178 | GI_30089944-A | Chr16tp-9D2 | 16 | -128220 | 72591 | 4.5664 | 0.3301 | 3.4539 | + | CHB | 29349118 | 29374681 | 25564 | Chr16_41 | dup | 13 | 29181449 | 29609853 | inside | 0 |
| NPIP | GI_5902013-S | Chr16tp-9F3 | 16 | 61772 | 243261 | 5.4541 | 0.3902 | 1.1639 | + | CHB | 14880002 | 14727485 | 152517 | Chr16_6 | del/dup | 19 | 14529556 | 15133811 | inside | 0 |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 16 | -62302 | 118293 | 11.4405 | 0.6888 | 2.4144 | + | CHB | 68780426 | 68752430 | 27996 | Chr16_21 | complex | 19 | 68412623 | 68870723 | inside | 0 |
| PM5 | GI_10947030-S | Chr16tp-9F3 | 16 | -108109 | 73380 | 5.6759 | 0.4044 | 1.6182 | + | CHB | 14880002 | 14897366 | 17365 | Chr16_6 | del/dup | 19 | 14529556 | 15133811 | inside | 0 |
| SMA4 | GI_41281598-S | Chr5tp-2H6 | 5 | 1101273 | 1225599 | 4.074 | 0.2945 | 0.595 | + | CHB | 70135141 | 68971705 | 1163436 | Chr5_29 | multiallelic | 2 | 70072978 | 70425468 | out | 1101273 |
| SMN1 | GI_13259511-A | Chr5tp-2H6 | 5 | 663882 | 788208 | 7.9531 | 0.5333 | 1.5541 | + | CHB | 70135141 | 69409096 | 726045 | Chr5_29 | multiallelic | 2 | 70072978 | 70425468 | out | 663882 |
| SMN2 | GI_13259530-A | Chr5tp-2H6 | 5 | 664365 | 788691 | 9.3678 | 0.5994 | 3.0755 | + | CHB | 70135141 | 69408613 | 726528 | Chr5_29 | multiallelic | 2 | 70072978 | 70425468 | out | 664365 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SULT1A3 | GI_29550920-A | Chr16tp-3A9 | 16 | 726249 | 907249 | 5.6374 | 0.4019 | 2.7247 | + | CHB | 30200281 | 29383532 | 816749 | Chr16_30 | dup | 12 | 29981456 | 30290781 | out | 597924 |
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 4 | -750788 | -580780 | 7.5642 | 0.5308 | 2.1606 | + | CHB | 69211472 | 69877256 | 665784 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 580780 |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 4 | -1120655 | -950647 | 14.9269 | 0.7971 | 7.2275 | + | CHB | 69211472 | 70247123 | 1035651 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 950647 |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 4 | -105361 | 64647 | 15.7922 | 0.8163 | 8.4857 | + | CHB | 69211472 | 69231829 | 20357 | Chr4_9 | dup | 102 | 68998845 | 69296476 | inside | 0 |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 4 | -1032588 | -862580 | 14.1214 | 0.7776 | 6.592 | + | CHB | 69211472 | 70159056 | 947584 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 862580 |
| C19orf6 | GI_34098936-S | Chr19tp-6D4 | 19 | 369986 | 534795 | 3.4487 | 0.2694 | 1.1283 | + | JPT | 1413529 | 961138 | 452391 | Chr19_6 | del | 1 | 1331124 | 1495933 | out | 369986 |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 22 | -7936 | 93355 | 6.1055 | 0.4234 | 1.5548 | + | JPT | 41275994 | 41233284 | 42710 | Chr22_26 | dup | 25 | 41091699 | 41407804 | inside | 0 |
| DKFZP572C16 | GI_42822888-S | Chr9tp-2A1 | 9 | -1021083 | -932258 | 5.7335 | 0.4007 | 1.0346 | + | JPT | 41238428 | 42215098 | 976671 | Chr9_3 | complex | 79 | 38557168 | 44769175 | inside | 0 |
| DKFZp762C18 | GI_22062495-S | Chr11tp-2F4 | 11 | 199812 | 362282 | 3.2931 | 0.2299 | 4.2008 | + | JPT | 65397704 | 65116657 | 281047 | Chr11_16 | dup | 2 | 65316469 | 65478939 | out | 199812 |
| EIF3S8 | GI_5579457-S | Chr16tp-11B1 | 16 | -63171 | 97279 | 4.1549 | 0.2945 | 2.7349 | + | JPT | 28671174 | 28654120 | 17054 | Chr16_13 | del | 3 | 28590949 | 28751472 | inside | 0 |
| FLJ00058 | GI_32698768-S | Chr19tp-6D4 | 19 | -1131251 | -966442 | 3.6805 | 0.2886 | 1.9588 | + | JPT | 1413529 | 2462375 | 1048847 | Chr19_6 | del | 1 | 1331124 | 1495933 | out | 966442 |
| FLJ20360 | GI_37620164-S | Chr10tp-7D2 | 10 | -168080 | -405 | 2.9484 | 0.2116 | 3.8222 | + | JPT | 5760949 | 5845191 | 84243 | Chr10_18 | dup | 2 | 5677111 | 5844786 | out | 405 |
| GBP3 | GI_24308156-S | Chr1tp-29F3 | 1 | -61102 | 3882 | 6.474 | 0.4452 | 5.6194 | + | JPT | 89156581 | 89185191 | 28610 | Chr1_31 | complex | 27 | 89124089 | 89272744 | inside | 0 |
| GTF2H2 | GI_31747573-S | Chr5tp-13C10 | 5 | 634996 | 793009 | 4.601 | 0.3261 | 1.1155 | + | JPT | 69631862 | 68917859 | 714003 | Chr5_61 | complex | 130 | 69109876 | 70831640 | out | 192017 |
| HDAC5 | GI_21237796-A | Chr17tp-5C2 | 17 | 1928218 | 2054448 | 3.4697 | 0.2486 | -3.7205 | - | JPT | 41502866 | 39511533 | 1991333 | Chr17_12 | multiallelic | 33 | 41439751 | 42632332 | out | 1928218 |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 6 | -317635 | -227089 | 9.1094 | 0.5794 | 6.1418 | + | JPT | 32548671 | 32821033 | 272362 | Chr6_19 | dup | 205 | 32479731 | 32813412 | out | 7621 |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C11 | 6 | -89827 | 719 | 5.6106 | 0.393 | 5.7606 | + | JPT | 32548671 | 32593225 | 44554 | Chr6_19 | dup | 205 | 32479731 | 32813412 | inside | 0 |
| hmm27235 | hmm27235-S | Chr22tp-7B3 | 22 | 1096475 | 1140202 | 4.4093 | 0.3189 | -0.4264 | - | JPT | 17385215 | 16266876 | 1118339 | Chr22_17 | complex | 48 | 17363351 | 17436267 | out | 1096475 |
| Hs.460059 | Hs.460059-S | Chr16tp-2E3 | 16 | 1795976 | 1974709 | 5.8012 | 0.4049 | 0.8569 | + | JPT | 16741923 | 14856580 | 1885343 | Chr16_34 | del/dup | 21 | 16092718 | 16831289 | out | 1236138 |
| KIAA0220 | GI_42660956-S | Chr16tp-12F7 | 16 | -1046969 | -895826 | 6.5711 | 0.4587 | 2.387 | + | JPT | 21483635 | 22455032 | 971398 | Chr16_11 | del/dup | 70 | 21241957 | 21833734 | out | 621298 |
| LOC283820 | GI_27734708-S | Chr16tp-6G1 | 16 | 1812140 | 1997169 | 5.8283 | 0.4065 | 1.891 | + | JPT | 18200678 | 16296023 | 1904655 | Chr16_18 | del/dup | 10 | 18036757 | 19066807 | out | 1740734 |
| LOC286088 | GI_37552472-S | Chr8tp-3B9 | 8 | -1416943 | -1255784 | 4.1142 | 0.2916 | -3.7425 | - | JPT | 384740 | 1721103 | 1336364 | Chr8_27 | dup | 3 | 59932 | 484890 | out | 1236213 |
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| LOC400543 | GI_42660801-S | Chr16tp-8B1 | 16 | 101320 | 277538 | 4.2276 | 0.2997 | 0.7196 | + | JPT | 22591701 | 22402272 | 189429 | Chr16_20 | del/dup | 162 | 22201625 | 22679810 | inside | 0 |
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| LPHN3 | GI_14149676-S | Chr4tp-17H8 | 4 | -1143011 | -969700 | 3.3296 | 0.2427 | -0.5935 | - | JPT | 61710267 | 62766622 | 1056356 | Chr4_27 | dup | 7 | 61623611 | 61796922 | out | 969700 |
| MGC12760 | GI_34147433-S | Chr1tp-25H9 | 1 | 62580 | 180646 | 6.958 | 0.4726 | 1.2497 | + | JPT | 16811931 | 16690318 | 121613 | Chr1_15 | del/dup | 93 | 16509639 | 17229287 | inside | 0 |
| MGC16824 | GI_31543158-S | Chr16tp-12A1 | 16 | 1889590 | 2055794 | 3.9098 | 0.2766 | -0.4427 | - | JPT | 21592230 | 19619538 | 1972692 | Chr16_11 | del/dup | 74 | 21241957 | 21833734 | out | 1622419 |
| MGC3130 | GI_31543178-S | Chr17tp-5C2 | 17 | 1844433 | 1970663 | 3.2367 | 0.2302 | -4.1774 | - | JPT | 41502866 | 39595318 | 1907548 | Chr17_12 | multiallelic | 33 | 41439751 | 42632332 | out | 1844433 |
| MGC42630 | GI_31341689-S | Chr9tp-13D1 | 9 | -1547928 | -1270095 | 6.2612 | 0.4327 | 0.5567 | + | JPT | 42789454 | 44198465 | 1409012 | Chr9_3 | complex | 1 | 38557168 | 44769175 | inside | 0 |
| MGC5356 | GI_15011885-S | Chr20tp-6G1 | 20 | 538477 | 718364 | 3.9929 | 0.2885 | -0.6717 | - | JPT | 62286696 | 61658275 | 628421 | Chr20_14 | complex | 5 | 62108666 | 62435964 | out | 450391 |
| MTVR1 | GI_22779872-S | Chr11tp-2F4 | 11 | 218425 | 380895 | 4.3057 | 0.3053 | 4.1412 | + | JPT | 65397704 | 65098044 | 299660 | Chr11_16 | dup | 2 | 65316469 | 65478939 | out | 218425 |
| OAZ1 | GI_34486089-S | Chr19tp-6D4 | 19 | -893061 | -728252 | 3.5177 | 0.2752 | 0.9102 | + | JPT | 1413529 | 2224185 | 810657 | Chr19_6 | del | 1 | 1331124 | 1495933 | out | 728252 |
| OTUB1 | GI_8923113-S | Chr11tp-2F4 | 11 | 1794138 | 1956608 | 3.1233 | 0.2166 | 3.3809 | + | JPT | 65397704 | 63522331 | 1875373 | Chr11_16 | dup | 2 | 65316469 | 65478939 | out | 1794138 |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 16 | -62302 | 118293 | 4.2263 | 0.2997 | 1.6147 | + | JPT | 68780426 | 68752430 | 27996 | Chr16_21 | complex | 19 | 68412623 | 68870723 | inside | 0 |
| PM5 | GI_10947030-S | Chr16tp-2E3 | 16 | 1755190 | 1933923 | 5.8061 | 0.4052 | 1.1397 | + | JPT | 16741923 | 14897366 | 1844557 | Chr16_34 | del/dup | 21 | 16092718 | 16831289 | out | 1195352 |
| SMN1 | GI_13259511-A | Chr5tp-2H6 | 5 | 663882 | 788208 | 5.3414 | 0.3758 | 1.0272 | + | JPT | 70135141 | 69409096 | 726045 | Chr5_29 | multiallelic | 2 | 70072978 | 70425468 | out | 663882 |
| SMN2 | GI_13259530-A | Chr5tp-2H6 | 5 | 664365 | 788691 | 6.9629 | 0.4728 | 2.3194 | + | JPT | 70135141 | 69408613 | 726528 | Chr5_29 | multiallelic | 2 | 70072978 | 70425468 | out | 664365 |

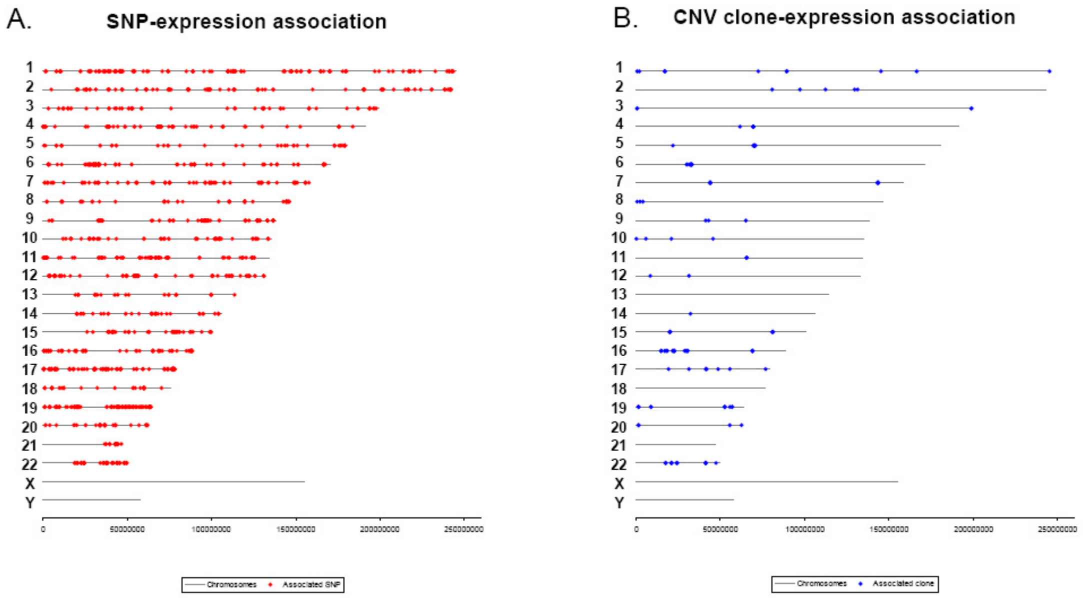
| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 4 | -750788 | -580780 | 14.2091 | 0.7632 | 1.7196 | + | JPT | 69211472 | 69877256 | 665784 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 580780 |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 4 | -1120655 | -950647 | 21.039 | 0.8876 | 7.2871 | + | JPT | 69211472 | 70247123 | 1035651 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 950647 |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 4 | -105361 | 64647 | 21.7175 | 0.8957 | 8.7412 | + | JPT | 69211472 | 69231829 | 20357 | Chr4_9 | dup | 102 | 68998845 | 69296476 | inside | 0 |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 4 | -1032588 | -862580 | 20.6757 | 0.8831 | 6.7305 | + | JPT | 69211472 | 70159056 | 947584 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 862580 |
| ZNF558 | GI_21687263-S | Chr19tp-5H2 | 19 | -22902 | 51275 | 3.6131 | 0.2544 | -0.4341 | - | JPT | 8795759 | 8781572 | 14187 | Chr19_1 | complex | 128 | 8758670 | 8832847 | inside | 0 |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 22 | -7936 | 93355 | 7.9883 | 0.4303 | 2.1899 | + | YRI | 41275994 | 41233284 | 42710 | Chr22_26 | dup | 25 | 41091699 | 41407804 | inside | 0 |
| DC6 | GI_34222364-S | Chr2tp-22A7 | 2 | 1096812 | 1259913 | 3.8511 | 0.2195 | 0.9066 | + | YRI | 129719533 | 128541170 | 1178363 | Chr2_66 | complex | 50 | 129581854 | 129866275 | out | 1040684 |
| DKFZp434N03 | GI_14149994-S | Chr22tp-7B3 | 22 | -2020023 | -1976296 | 6.6283 | 0.3658 | 1.9718 | + | YRI | 17385215 | 19383374 | 1998160 | Chr22_17 | complex | 48 | 17363351 | 17436267 | out | 1947107 |
| DKFZp434O02 | GI_32698823-S | Chr22tp-2A8 | 22 | -197718 | -95176 | 4.3913 | 0.241 | 3.3708 | + | YRI | 23925642 | 24072089 | 146447 | Chr22_24 | del/dup | 22 | 23691355 | 24281461 | inside | 0 |
| FLJ43692 | GI_38348301-S | Chr7tp-7H4 | 7 | -37486 | 92543 | 5.6868 | 0.3171 | 0.5377 | + | YRI | 143348142 | 143320613 | 27529 | Chr7_29 | multiallelic | 150 | 142664612 | 143806286 | inside | 0 |
| FMO4 | GI_4503758-S | Chr1tp-31G2 | 1 | -1529056 | -1425876 | 3.5595 | 0.1918 | 0.7407 | + | YRI | 166565254 | 168042720 | 1477466 | Chr1_7 | complex | 116 | 166513664 | 166616844 | out | 1425876 |
| GGT1 | GI_4885270-A | Chr22tp-6D1 | 22 | -688420 | -648338 | 3.6784 | 0.2087 | -7.6916 | - | YRI | 20646428 | 21314807 | 668379 | Chr22_21 | dup | 2 | 20619657 | 20733158 | out | 581649 |
| GTF2H2 | GI_31747573-S | Chr5tp-3H2 | 5 | 1753019 | 1913781 | 3.7977 | 0.2094 | 3.7004 | + | YRI | 70751259 | 68917859 | 1833400 | Chr5_61 | complex | 34 | 69109876 | 70831640 | out | 192017 |
| HLA-DQA1 | GI_18426974-S | Chr6tp-22E8 | 6 | 90584 | 94577 | 6.6771 | 0.4143 | 31.641 | + | YRI | 32811416 | 32718835 | 92581 | Chr6_19 | dup | 58 | 32479731 | 32813412 | inside | 0 |
| HLA-DRB5 | GI_26665892-S | Chr6tp-4E2 | 6 | 41581 | 57379 | 10.8926 | 0.5415 | -9.8057 | - | YRI | 32642705 | 32593225 | 49480 | Chr6_4 | complex | 6 | 32634806 | 32650604 | out | 41581 |
| Hs.449564 | Hs.449564-S | Chr22tp-6B8 | 22 | -11926 | 27825 | 6.4528 | 0.352 | -13.9622 | - | YRI | 20713283 | 20705333 | 7950 | Chr22_10 | del | 5 | 20693407 | 20733158 | inside | 0 |
| Hs.462423 | Hs.462423-S | Chr17tp-2C2 | 17 | -126434 | 31668 | 4.9199 | 0.271 | 0.7032 | + | YRI | 18942851 | 18990234 | 47383 | Chr17_32 | complex | 96 | 18771341 | 19132640 | inside | 0 |
| Hs.487323 | Hs.487323-S | Chr2tp-8F2 | 2 | -728390 | -412600 | 4.7445 | 0.2611 | 0.6291 | + | YRI | 131093675 | 131664170 | 570495 | Chr2_13 | complex | 6 | 130291879 | 133031735 | inside | 0 |
| KIAA0738 | GI_7662275-S | Chr7tp-1E4 | 7 | 13370 | 183092 | 4.1804 | 0.2287 | 0.3944 | + | YRI | 142920407 | 142822176 | 98231 | Chr7_29 | multiallelic | 103 | 142664612 | 143806286 | inside | 0 |
| LOC127069 | GI_17437031-S | Chr1tp-15A9 | 1 | -69065 | 108799 | 3.5733 | 0.1988 | 0.2765 | + | YRI | 245102483 | 245082616 | 19867 | Chr1_45 | del | 58 | 244826150 | 245191415 | inside | 0 |
| LOC143034 | GI_18575382-S | Chr10tp-14D8 | 10 | -928439 | -764035 | 3.0752 | 0.162 | -1.5632 | - | YRI | 132203 | 978440 | 846237 | Chr10_15 | dup | 2 | 50001 | 214405 | out | 764035 |
| LOC255812 | GI_37550242-S | Chr3tp-18B6 | 3 | 1881232 | 1932759 | 7.1673 | 0.4089 | 0.9991 | + | YRI | 198797824 | 196890828 | 1906996 | Chr3_1 | del | 1 | 198772060 | 198823587 | out | 1881232 |
| LOC282956 | GI_27483210-S | Chr6tp-22C7 | 6 | -129990 | -9794 | 4.1698 | 0.2644 | 1.6168 | + | YRI | 31400659 | 31470551 | 69892 | Chr6_27 | del/dup | 4 | 31338567 | 31605085 | inside | 0 |
| LOC347981 | GI_30160064-S | Chr6tp-22A4 | 6 | -62130 | 18531 | 6.4796 | 0.4036 | 2.4676 | + | YRI | 29940744 | 29962543 | 21800 | Chr6_22 | complex | 21 | 29900413 | 30083123 | inside | 0 |
| LOC375133 | GI_40786533-S | Chr22tp-7B3 | 22 | -1399415 | -1355688 | 9.9142 | 0.5111 | 1.2384 | + | YRI | 17385215 | 18762766 | 1377552 | Chr22_17 | complex | 48 | 17363351 | 17436267 | out | 1326499 |
| LOC375790 | GI_37546731-S | Chr1tp-35F11 | 1 | -673561 | -519913 | 3.9638 | 0.2229 | 2.2767 | + | YRI | 434407 | 1031144 | 596737 | Chr1_32 | complex | 49 | 377 | 852347 | out | 178797 |
| LOC378157 | GI_37539180-S | Chr7tp-13D1 | 7 | -71619 | 32633 | 9.6845 | 0.5146 | 2.63 | + | YRI | 43777905 | 43797398 | 19493 | Chr7_2 | dup | 52 | 43725779 | 43830031 | inside | 0 |
| LOC388077 | GI_41150141-S | Chr15tp-7C8 | 15 | -17353 | 147873 | 5.8149 | 0.3386 | 1.1993 | + | YRI | 20014944 | 19949684 | 65260 | Chr15_8 | complex | 129 | 18263733 | 21066294 | inside | 0 |
| LOC388673 | GI_41115452-S | Chr1tp-31B7 | 1 | -1346096 | -1248478 | 5.5127 | 0.3078 | 0.8178 | + | YRI | 145092141 | 146389428 | 1297287 | Chr1_4 | complex | 22 | 144800023 | 145140950 | out | 1248478 |
| LOC401449 | GI_42658877-S | Chr12tp-4B7 | 12 | -75735 | 67053 | 3.7973 | 0.2093 | 0.5611 | + | YRI | 8239207 | 8243548 | 4341 | Chr12_4 | complex | 23 | 7748086 | 8515254 | inside | 0 |
| LOC402488 | GI_42658295-S | Chr7tp-13D1 | 7 | -73281 | 30971 | 9.1073 | 0.491 | 2.2705 | + | YRI | 43777905 | 43799060 | 21155 | Chr7_2 | dup | 52 | 43725779 | 43830031 | inside | 0 |
| MGC12760 | GI_34147433-S | Chr1tp-25H8 | 1 | -52396 | 93744 | 13.3699 | 0.6355 | 1.8406 | + | YRI | 16710992 | 16690318 | 20674 | Chr1_15 | del/dup | 60 | 16509639 | 17229287 | inside | 0 |
| MGC5178 | GI_30089944-A | Chr16tp-3A9 | 16 | 732849 | 913849 | 4.2287 | 0.2316 | 2.0264 | + | YRI | 30200281 | 29374681 | 825600 | Chr16_30 | dup | 12 | 29981456 | 30290781 | out | 606775 |
| MGC71999 | GI_42476196-S | Chr17tp-11E5 | 17 | -1662645 | -1509032 | 3.723 | 0.2048 | -1.7982 | - | YRI | 55437138 | 57022976 | 1585839 | Chr17_8 | complex | 31 | 55350429 | 55513944 | out | 1509032 |
| PDPR | GI_32261325-S | Chr16tp-9C8 | 16 | -62302 | 118293 | 14.5848 | 0.6765 | 1.8497 | + | YRI | 68780426 | 68752430 | 27996 | Chr16_21 | complex | 19 | 68412623 | 68870723 | inside | 0 |
| SIGLEC5 | GI_4502658-S | Chr19tp-7A10 | 19 | -23686 | 151278 | 5.3744 | 0.3094 | -0.8369 | - | YRI | 56871030 | 56807234 | 63796 | Chr19_11 | del | 15 | 56683708 | 56958512 | inside | 0 |
| SLC20A1 | GI_31543629-S | Chr2tp-2E12 | 2 | -1223303 | -1017641 | 3.7532 | 0.2035 | 2.8865 | + | YRI | 112016760 | 113137232 | 1120472 | Chr2_28 | del/dup | 13 | 111616014 | 112463168 | out | 674064 |
| SMA4 | GI_41281598-S | Chr5tp-9E3 | 5 | 138171 | 292973 | 3.8824 | 0.2145 | 0.4489 | + | YRI | 69187277 | 68971705 | 215572 | Chr5_10 | dup | 1 | 69109876 | 69264678 | out | 138171 |
| SUHW2 | GI_38202248-S | Chr22tp-6B8 | 22 | -470451 | -430700 | 6.103 | 0.3343 | 2.58 | + | YRI | 20713283 | 21163858 | 450576 | Chr22_10 | del | 5 | 20693407 | 20733158 | out | 430700 |
| TBCD | GI_41350332-S | Chr17tp-3H2 | 17 | -1752788 | -1560057 | 3.3925 | 0.1938 | -1.2951 | - | YRI | 76837392 | 78493814 | 1656423 | Chr17_16 | dup | 8 | 76741026 | 76933757 | out | 1560057 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 4 | -750788 | -580780 | 4.7695 | 0.2665 | 1.3933 | + | YRI | 69211472 | 69877256 | 665784 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 580780 |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 4 | -1120655 | -950647 | 11.4101 | 0.566 | 4.3649 | + | YRI | 69211472 | 70247123 | 1035651 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 950647 |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 4 | -105361 | 64647 | 10.4865 | 0.5329 | 4.6238 | + | YRI | 69211472 | 69231829 | 20357 | Chr4_9 | dup | 102 | 68998845 | 69296476 | inside | 0 |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 4 | -1032588 | -862580 | 11.0417 | 0.5531 | 4.0765 | + | YRI | 69211472 | 70159056 | 947584 | Chr4_9 | dup | 102 | 68998845 | 69296476 | out | 862580 |
| ZBED4 | GI_7662217-S | Chr22tp-4F6 | 22 | -1507386 | -1465764 | 3.6564 | 0.1976 | 1.4189 | + | YRI | 47115941 | 48602516 | 1486575 | Chr22_14 | dup | 7 | 47095130 | 47136752 | out | 1465764 |
| ZNF265 | GI_42741681-S | Chr1tp-4C10 | 1 | 1222167 | 1357555 | 3.6414 | 0.2133 | 0.5239 | + | YRI | 72531140 | 71241279 | 1289861 | Chr1_27 | dup | 17 | 72454417 | 72598834 | out | 1213138 |
| ZNF558 | GI_21687263-S | Chr19tp-5H2 | 19 | -22902 | 51275 | 3.0914 | 0.1712 | -0.5779 | - | YRI | 8795759 | 8781572 | 14187 | Chr19_1 | complex | 128 | 8758670 | 8832847 | inside | 0 |

Table S5: Asociations of CNVs with gene expression up to 6Mb at 0.001

| Gene_label | Gene_ID | CNV_Label | Gene_Chromosome | CNV_Chromosome | Gene_distance_from_CNV_start | Gene_distance_from_CNV_end | pvalue | "-logp | Adjusted_R^2 | Gradient | POP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 4 | 4 | -131829 | 568171 | 0 | 16.029 | 0.7066 | 3.7396 | CEU |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 4 | 4 | -1147123 | -447123 | 0 | 13.4627 | 0.6383 | 2.9815 | CEU |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 4 | 4 | -1059056 | -359056 | 0 | 11.656 | 0.581 | 2.591 | CEU |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 6 | 6 | -317635 | -227089 | 0 | 10.3172 | 0.5459 | 3.5736 | CEU |
| Hs.463184 | Hs.463184-S | Chr17tp-2G12 | 17 | 17 | 514083 | 804083 | 0.00002 | 4.6957 | 0.2705 | 0.116 | CEU |
| LOC90786 | GI_14756242-S | Chr12tp-19H4 | 12 | 12 | 4121401 | 4381401 | 9.2E-05 | 4.0357 | 0.2601 | 0.0466 | CEU |
| MRPS26 | GI_39812071-S | Chr20tp-4A10 | 20 | 20 | -1566433 | -1376433 | 0.00052 | 3.2876 | 0.187 | 0.2165 | CEU |
| HLA-DQA1 | GI_18426974-S | Chr6tp-5C11 | 6 | 6 | -215437 | -124891 | 0.00011 | 3.9797 | 0.2311 | -3.8628 | CEU |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C12 | 6 | 6 | -43225 | 66775 | 0.00066 | 3.1792 | 0.1769 | -0.9534 | CEU |
| DKFZp761G2113 | GI_42661165-S | Chr17tp-2G12 | 17 | 17 | 1884370 | 2174370 | 0.00103 | 2.9859 | 0.1643 | 0.1262 | CEU |
| C20orf194 | GI_37556073-S | Chr20tp-4A10 | 20 | 20 | -1769914 | -1579914 | 0.00173 | 2.7626 | 0.1522 | 0.1758 | CEU |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 22 | 22 | -63284 | 136716 | 0.00069 | 3.1614 | 0.1757 | 0.4065 | CEU |
| NOL5A | GI_32483373-S | Chr20tp-4A10 | 20 | 20 | -1176981 | -986981 | 0.00133 | 2.8778 | 0.1599 | 0.3228 | CEU |
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 4 | 4 | -777256 | -77256 | 0.00056 | 3.2558 | 0.1789 | 0.8646 | CEU |
| Hs.428161 | Hs.428161-S | Chr15tp-9C6 | 15 | 15 | -2808207 | -2108207 | 0.00635 | 2.197 | 0.1063 | 0.1162 | CEU |
| UGT2B11 | GI_4507822-S | Chr4tp-23H10 | 4 | 4 | -1147123 | -447123 | 0 | 12.3091 | 0.6026 | 1.2525 | YRI |
| UGT2B7 | GI_4507824-S | Chr4tp-23H10 | 4 | 4 | -1059056 | -359056 | 0 | 11.8636 | 0.588 | 1.1665 | YRI |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C12 | 6 | 6 | -43225 | 66775 | 0 | 11.6926 | 0.6096 | -3.05 | YRI |
| UGT2B17 | GI_4507820-S | Chr4tp-23H10 | 4 | 4 | -131829 | 568171 | 0 | 10.9767 | 0.5572 | 1.3194 | YRI |
| CGI-96 | GI_25092724-S | Chr22tp-8C6 | 22 | 22 | -63284 | 136716 | 0 | 9.743 | 0.5235 | 0.4464 | YRI |
| HLA-DRB5 | GI_26665892-S | Chr6tp-5C11 | 6 | 6 | -89827 | 719 | 0 | 7.5441 | 0.4458 | 3.3835 | YRI |
| UGT2B10 | GI_27552756-S | Chr4tp-23H10 | 4 | 4 | -777256 | -77256 | 3E-06 | 5.4612 | 0.3095 | 0.4182 | YRI |
| LOC388673 | GI_41115452-S | Chr1tp-7D2 | 1 | 1 | -3989428 | -3539428 | 6E-06 | 5.23 | 0.3107 | 0.1098 | YRI |
| HLA-DQA2 | GI_11095446-S | Chr6tp-5C11 | 6 | 6 | -317635 | -227089 | 0.00001 | 5.0017 | 0.3072 | 1.2221 | YRI |
| LOC127069 | GI_17437031-S | Chr1tp-15A9 | 1 | 1 | -132616 | 108799 | 0.00043 | 3.3668 | 0.189 | 0.0722 | YRI |
| ZNF265 | GI_42741681-S | Chr1tp-4C10 | 1 | 1 | 1235858 | 1283182 | 0.00062 | 3.2108 | 0.1883 | 0.0892 | YRI |

# Figure S1


A.
SNP-expression association
B.
CNV clone-expression association
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
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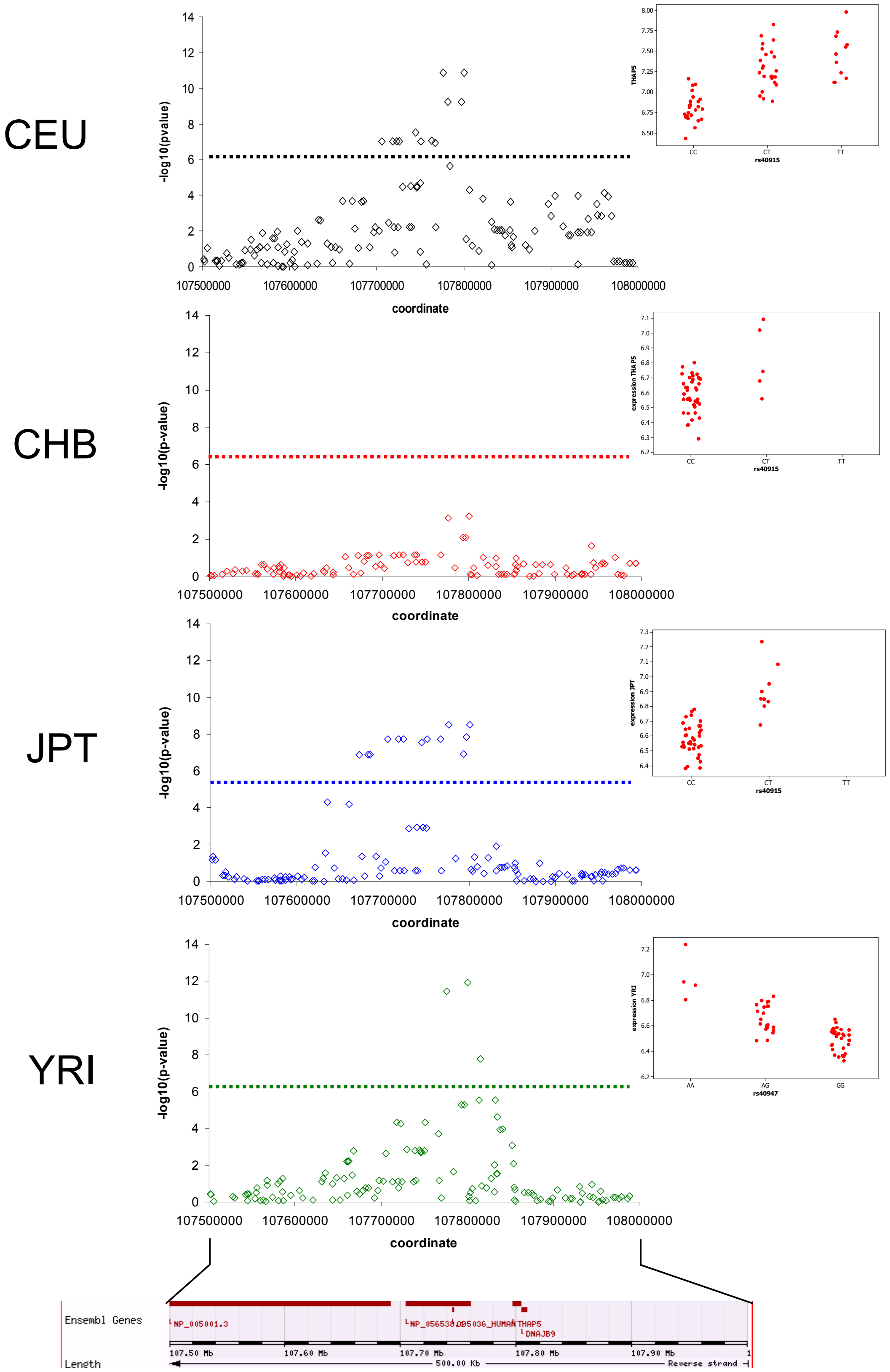
100000000
150000000
200000000
250000000
Chromosomes
Associated SNP
Associated clone

Figure S2A


CEU
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14
12
10
8
6
4
2
0
107500000
107600000
107700000
107800000
107900000
108000000
coordinate
THAP5
8.00
7.75
7.50
7.25
7.00
6.75
6.50
CC
CT
TT
rs40915
CHB
-log10(p-value)
expression THAP5
rs40915
JPT
-log10(p-value)
expression JPT
rs40915
YRI
-log10(p-value)
expression YRI
AA
AG
GG
rs40947
Ensembl Genes
NP_005001.3
NP_056538
O95036_HUMAN
THAP5
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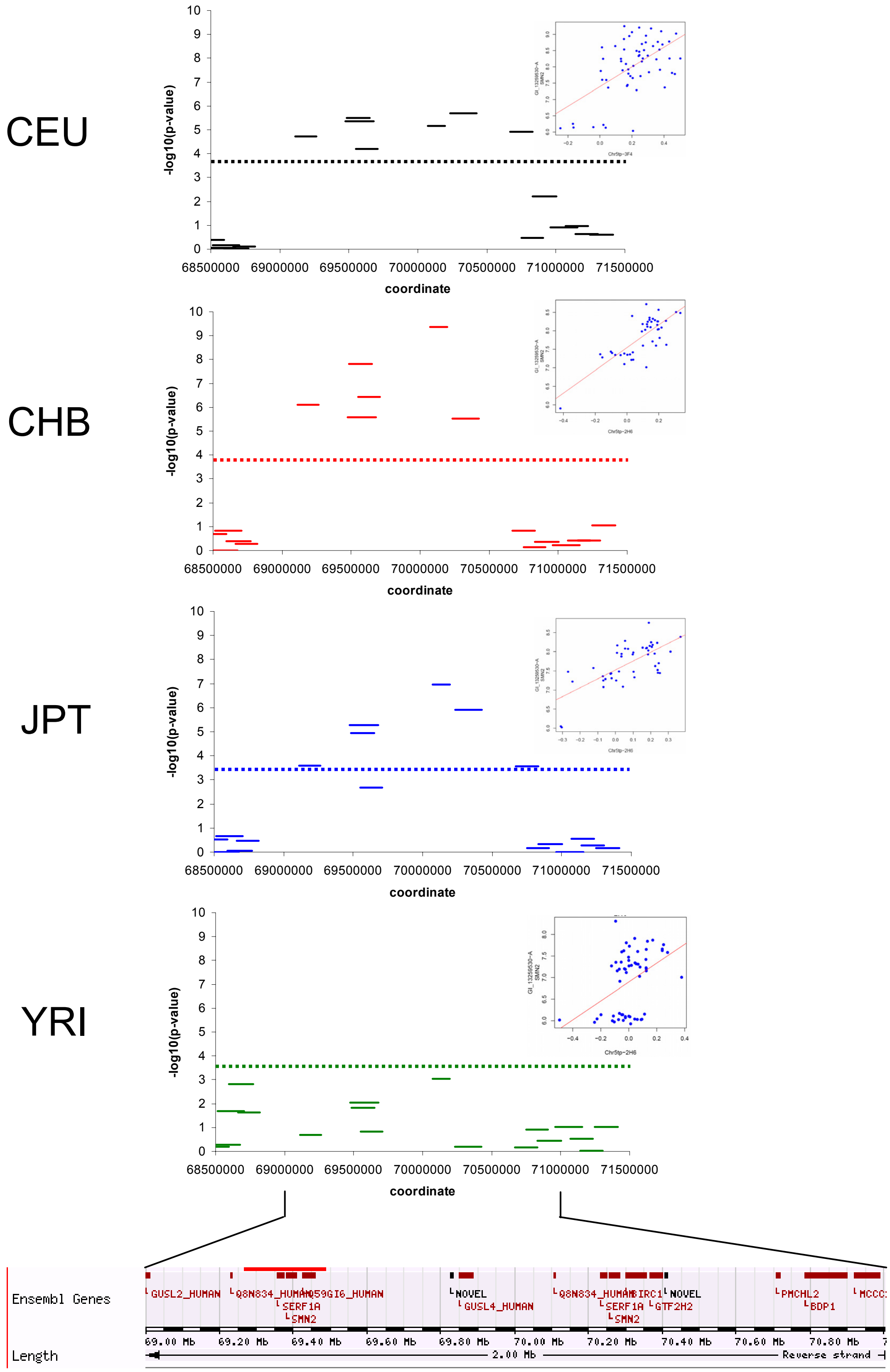
107.60 Mb
107.70 Mb
107.80 Mb
107.90 Mb
Length
500.00 Kb
Reverse strand

Figure S2B



CEU
CHB
JPT
YRI
-log10(p-value)
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1
2
3
4
5
6
7
8
9
10
68500000
69000000
69500000
70000000
70500000
71000000
71500000
coordinate
GI_13259530-A SMN2
Chr5tp-3F4
Chr5tp-2H6
Ensembl Genes
GUSL2_HUMAN
Q8N834_HUMAN
Q59GI6_HUMAN
SERF1A
SMN2
NOVEL
GUSL4_HUMAN
Q8N834_HUMAN
BIRC1
NOVEL
SERF1A
GTF2H2
SMN2
PMCHL2
BDP1
MCCC
Length
69.00 Mb
69.20 Mb
69.40 Mb
69.60 Mb
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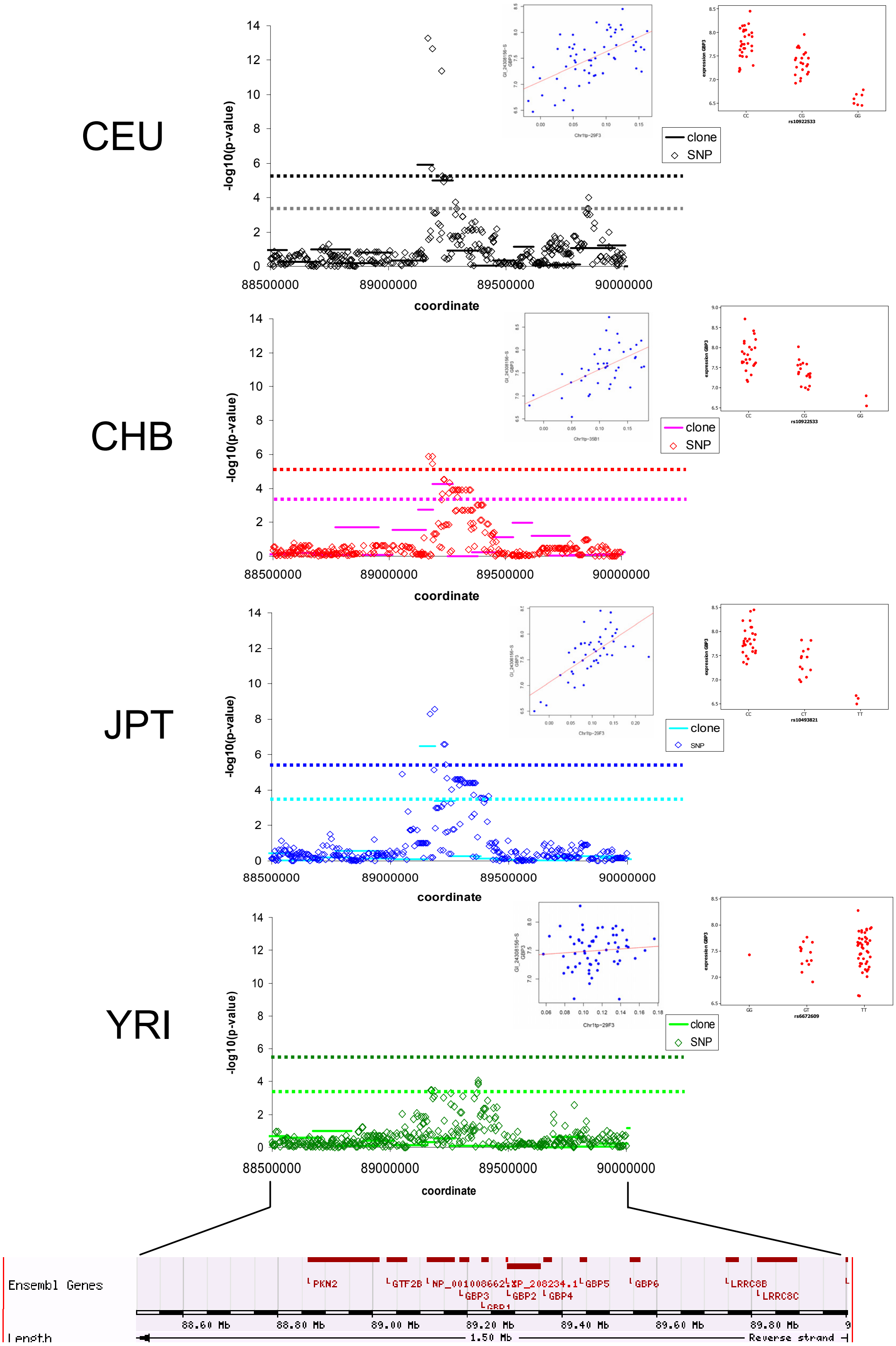
70.20 Mb
70.40 Mb
70.60 Mb
70.80 Mb
2.00 Mb
Reverse strand

Figure S2C



CEU
CHB
JPT
YRI
-log10(p-value)
0
2
4
6
8
10
12
14
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89000000
89500000
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coordinate
clone
SNP
Chr1tp-29F3
Chr1tp-35B1
rs10922533
rs10493821
rs6672609
expression GBP3
CC
CG
GG
CT
TT
GT
Ensembl Genes
PKN2
GTF2B
NP_001008662.1
XP_208234.1
GBP5
GBP6
GBP3
GBP2
GBP4
GBP1
LRRC8B
LRRC8C
88.60 Mb
88.80 Mb
89.00 Mb
89.20 Mb
89.40 Mb
89.60 Mb
89.80 Mb
Length
1.50 Mb
Reverse strand

Figure S3. Distribution of p-values for all SNP-expression associations (SNP-probe distance < 1Mb) and all clone-expression associations (clone midpoint-probe distance < 2Mb).

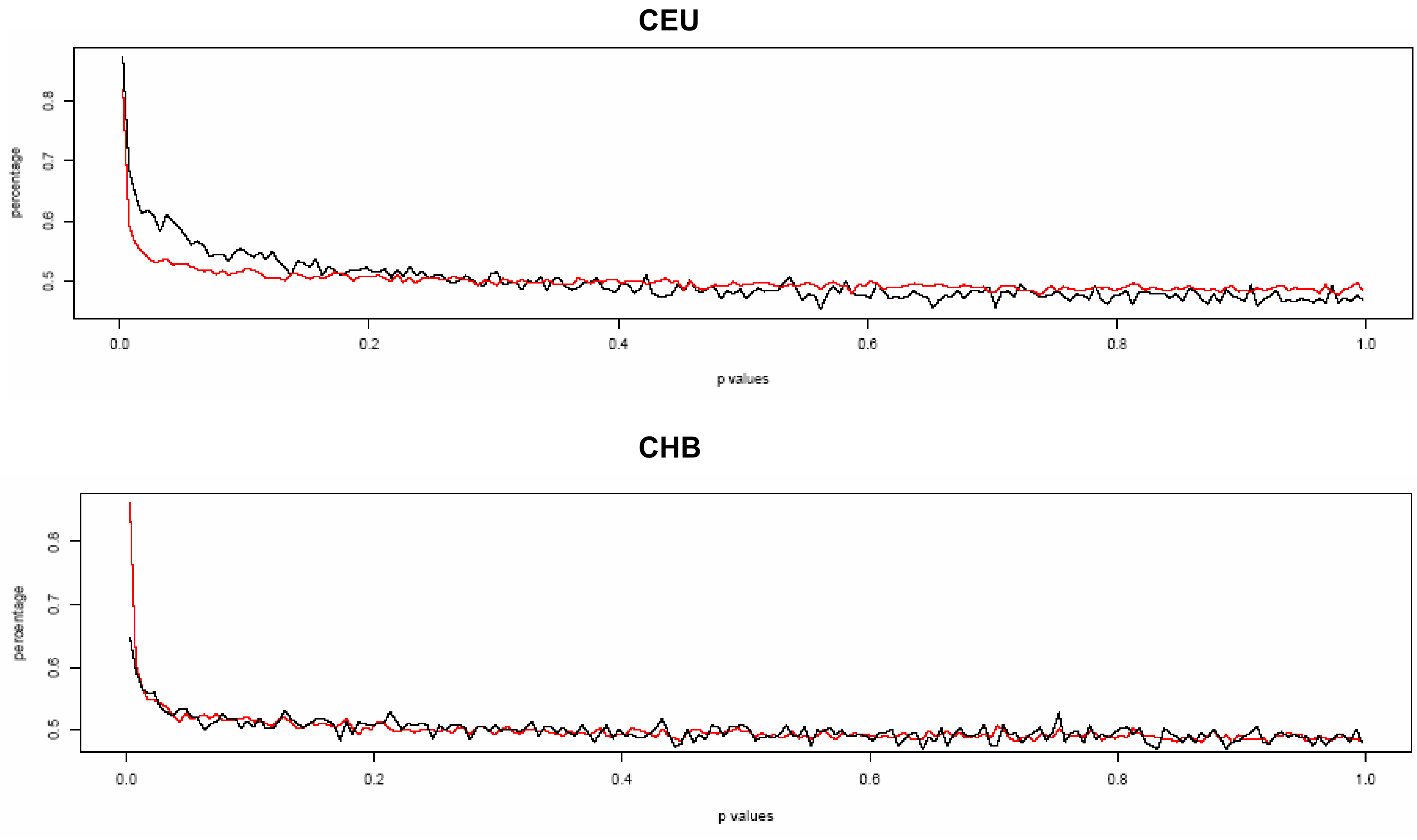

Figure S3 (cont). Distribution of p-values for all SNP-expression associations (SNP-probe distance < 1Mb) and all clone-expression associations (clone midpoint-probe distance < 2Mb).