



Supporting Online Material for

Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes

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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).

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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 $p\text{-value} = 0.001$ with 10,000 permutations, the estimate of the $p\text{-value}$ is 0.001 ± 0.00032 (mean \pm 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 $p\text{-value}$ is $P = 0.001 \pm 0.00014$. 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 significant 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
ASAH1	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
CCND1BP1	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

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

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

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

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
WBSR27	GI_30795189-S	rs8629	7	72690170	3632	14.2531	0.6478	6.75	5.45	4.16	3.38	CEU
WVVOX	GI_18860883-I	rs6564520	16	76863720	6316	7.7879	0.4212	7.51	5.9	4.8	4.01	CEU
XRR1A1	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

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
CRIP1	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

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	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

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

WBSR27	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
XRR1	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

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
FGFR10P	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
GNPMB	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

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

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

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

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
WBCSCR27	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
ASAH1	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	4.74	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

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

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 significant 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
DAAAM2	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

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	Ilumina Gene_ID	clone_Label	chromosome	Distance probe to CNV_start	Distance probe to CNV_end	-log10(p-value)	Adjusted_R^2	slope	postng slope	population	clone_midpoint B35	probe_midpoint B35	distance clone midpoint-probe midpoint	CNV_ID	CNV_class	CNV Frequency in Z70 HapMap Individuals	CNV_start B35	CNV_end B35	probe in CNV?	Distance from probe to CNV
AP2S1	GI_11038644-I	Chr19p-3A4	19	514566	682687	3.5605	0.2046	-1.6672 -	CEU	52633457	52033313	600144	Chr19_9	del	3	52549596	52717317	out	516283	
ARL8	GI_31341468-S	Chr10p-1H10	10	1775769	1931816	3.2798	0.1804	-0.8988 -	CEU	20860591	19006798	1853793	Chr10_6	del	54	20726725	20838614	out	1719927	
CGI-96	GI_25092724-S	Chr22p-8C6	22	-7936	93355	4.2056	0.2338	2.277 +	CEU	41275994	41233284	42710	Chr22_26	dup	25	41091699	41407604	inside	0	
CHL1	GI_27694375-S	Chr3p-4B4	3	-90713	93983	6.1255	0.3451	5.6742 +	CEU	425974	424339	1655	Chr3_25	complex	3	46156	775003	inside	0	
CTNNA2	GI_7656988-S	Chr2p-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	Chr22p-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_31742465-S	Chr17p-2D11	14	-1535518	-1377556	3.585	0.2209	-5.498 -	CEU	32007212	33463749	1456537	Chr14_6	dup	4	31928231	320086193	out	1377566	
FLJ22795	GI_13443001-S	Chr15p-4E11	15	148042	334921	4.2608	0.2334	0.6684 +	CEU	81014141	80772659	241482	Chr15_2	del/dup	32	80676701	81107580	inside	0	
FLJ43692	GI_38348301-S	Chr7p-5B10	7	92344	158953	5.7529	0.3206	0.8584 +	CEU	143446262	143320613	125649	Chr7_29	multiallelic	151	142664612	143806296	inside	0	
GBP3	GI_24308156-S	Chr11p-29F3	11	-61102	3882	5.9266	0.3298	5.6887 +	CEU	89156581	89185191	28610	Chr1_31	complex	27	89124089	89272744	inside	0	
GRLF1	GI_25121939-A	Chr19p-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	Chr6p-5C11	6	-215437	-124891	8.5936	0.457	-10.1863 -	CEU	32548671	32718835	170164	Chr6_19	dup	205	32479731	32813412	inside	0	
HLA-DQA2	GI_11095446-S	Chr6p-5C11	6	-317635	-227089	8.0767	0.4343	6.0867 +	CEU	32548671	32821033	272362	Chr6_19	dup	205	32479731	32813412	out	7621	
hmm19553	hmm19553-S	Chr10p-18B5	10	490276	697781	4.4472	0.2479	-0.3448 -	CEU	45529389	44835340	594029	Chr10_30	del/dup	2	45341719	47972148	out	406379	
hmm26489	hmm26489-S	Chr11p-25A7	11	-29543	81064	4.1963	0.2297	1.8841 +	CEU	1707122	1681361	25761	Chr1_10	del/dup	19	1651818	1762425	inside	0	
hmm34479	hmm34479-S	Chr8p-3H5	8	-456194	-344557	4.6969	0.2594	0.8407 +	CEU	2256571	2656946	400376	Chr8_24	del/dup	3	2105020	2411266	out	245680	
Hs.150050	Hs.150050-S	Chr22p-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	Chr17p-12C1	17	-18185	175877	6.0349	0.3355	1.1365 +	CEU	41074763	40959917	78846	Chr17_17	dup	2	40977732	41171794	inside	0	
Hs.525661	Hs.525661-S	Chr15p-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	Chr12p-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	Chr3p-18B6	3	1881232	1932759	4.9148	0.2832	0.7938 +	CEU	198797824	196980828	1906996	Chr3_1	del	1	198772060	198823587	out	1881232	
LOC345754	GI_37550208-S	Chr5p-2D2	5	-109545	42089	4.2624	0.2335	0.9682 +	CEU	21497307	21531035	33728	Chr5_4	complex	50	21164910	21748947	inside	0	
LOC347981	GI_30180064-S	Chr6p-2E5	6	16532	37753	6.0065	0.3772	2.2144 +	CEU	29898666	29862543	27143	Chr6_22	complex	21	29800413	30083123	inside	0	
LOC374673	GI_37541248-S	Chr15p-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	Chr15p-7C8	15	-17353	147873	5.6011	0.3125	1.3639 +	CEU	20014944	19949684	65266	Chr15_8	complex	129	18263733	21066294	inside	0	
LOC400543	GI_42686801-S	Chr16p-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_3422200-S	Chr19p-6H5	19	564783	680757	3.3479	0.1817	-0.3942 -	CEU	55288809	54864039	622770	Chr19_3	complex	136	55228822	55344796	out	564783	

MGCC41943	GI_34222265-S	Chr7p-5B10	7	624842	691451	8.2551	0.4422	0.6558 +	CEU	143446262	142788115	658147	Chr7_29	multiallelic	151	142664612	143806286	inside	0
MRFPS26	GI_39812071-S	Chr20p-4A10	20	-1551652	-1436175	3.8084	0.2134	0.9804 +	CEU	1482520	2976433	1493914	Chr20_5	dup	78	1424781	1627256	out	1349177
NOLA	GI_32493373-S	Chr20p-4A10	20	-1162200	-1046723	9.1326	0.1854	1.4409 +	CEU	1482520	2968981	1104462	Chr20_5	dup	78	1424781	1627256	out	989725
PDR	GI_32261325-S	Chr19p-9C8	16	-62302	118293	9.1347	0.4798	2.0465 +	CEU	68769426	68752430	27986	Chr16_21	complex	19	68412623	68870723	inside	0
PPP5C	GI_20127496-S	Chr19p-3A4	19	963821	1131542	3.38	0.193	-1.5748 -	CEU	52633457	51585775	1047682	Chr19_9	del	3	52549596	52717317	out	963821
SIGLEC5	GI_4502698-S	Chr19p-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	Chr5p-3F4	5	825985	1016855	5.6857	0.3125	3.0261 +	CEU	70330033	69408613	921420	Chr5_29	multiallelic	37	70072978	70425468	out	664365
TIMEPAI	GI_40317614-A	Chr22p-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	Chr17p-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	Chr4p-1F2	4	-802255	-648609	5.2344	0.311	5.9275 +	CEU	69152824	69877256	724432	Chr4_9	dup	54	68998845	69296476	out	580780
UGT2B11	GI_4507822-S	Chr4p-23H10	4	-1120655	-950647	14.7246	0.8671	5.3223 +	CEU	69211472	70247123	1035851	Chr4_9	dup	102	68998845	69296476	out	950647
UGT2B17	GI_4507820-S	Chr4p-23H10	4	-105361	64647	15.0078	0.6746	6.3701 +	CEU	69211472	69231829	20357	Chr4_9	dup	102	68998845	69296476	inside	0
UGT2B7	GI_4507824-S	Chr4p-23H10	4	-1032588	-862590	13.9271	0.6451	4.7684 +	CEU	69211472	70159056	947584	Chr4_9	dup	102	68998845	69296476	out	862590
BIRC1	GI_4759751-S	Chr5p-3A5	5	60291	224986	5.3367	0.3755	0.5983 +	CHB	69567951	69425312	142639	Chr5_51	complex	142	69109876	70831640	inside	0
CGI96	GI_25092724-S	Chr22p-9C6	22	-7636	93355	5.2361	0.3759	1.8544 +	CHB	41275994	41233284	42710	Chr22_26	dup	25	41091689	41407694	inside	0
CHL1	GI_27894375-S	Chr3p-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	Chr11p-3B1	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	Chr6p-5C11	6	-317635	-227089	11.5728	0.6759	7.6617 +	CHB	32548671	32821033	272362	Chr6_19	dup	205	32479731	32813412	out	7621
HLA-DRE5	GI_26665992-S	Chr6p-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	Chr16p-9F3	16	-67323	114166	4.134	0.2989	0.8413 +	CHB	14860002	14856580	23422	Chr16_6	del/dup	19	14529556	15133811	inside	0
Hs.490862	Hs.490862-S	Chr8p-13F3	8	1620253	1796445	4.0778	0.3071	0.9122 +	CHB	3843330	2134981	1708349	Chr8_47	dup	3	3866932	5909600	out	1451951
KIAA0220	GI_42660866-S	Chr16p-8B1	16	48560	224778	7.1145	0.4977	1.0834 +	CHB	22591701	22455032	136869	Chr16_20	del/dup	162	22201625	22679810	inside	0
LOC283820	GI_27734708-S	Chr16p-6D2	16	1812140	1997169	4.9039	0.3604	1.6957 +	CHB	18200678	16296023	1904655	Chr16_18	del/dup	17	18036757	19066807	out	1740734
LOC339088	GI_37541953-S	Chr16p-3A9	16	736563	917563	4.9573	0.3572	1.1873 +	CHB	30200281	29373218	827063	Chr16_30	dup	12	29981456	30290781	out	608238
LOC374673	GI_37541248-S	Chr15p-2D4	15	215922	364619	3.9765	0.2932	1.2506 +	CHB	80812826	80522555	290271	Chr15_2	del/dup	40	80675701	81107580	out	154146
LOC375133	GI_40786633-S	Chr22p-7B3	22	-1399415	-1355688	4.4607	0.329	1.1848 +	CHB	17385275	18762766	1377552	Chr22_17	complex	48	17363351	17436267	out	1326499
LOC378157	GI_37539180-S	Chr7p-13D1	7	-71619	32633	4.3686	0.3223	3.4743 +	CHB	43777905	43797398	19493	Chr7_2	dup	52	43725779	438330031	inside	0
LOC380077	GI_41150141-S	Chr15p-7C8	15	-17353	147873	6.8608	0.4672	1.4305 +	CHB	20014944	19949684	65260	Chr15_8	complex	129	18263733	21066294	inside	0
LOC388440	GI_42661316-S	Chr17p-11A1	17	-145880	11455	5.2236	0.3681	3.467 +	CHB	31388006	31455278	67213	Chr17_14	complex	126	31309398	31981395	inside	0
LOC400543	GI_42660801-S	Chr16p-4B1	16	101320	277538	7.0287	0.4929	0.9031 +	CHB	22591701	22402272	189429	Chr16_20	del/dup	162	22201625	22679810	inside	0
MGC212760	GI_34147433-S	Chr11p-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_44888613-S	Chr9p-3D7	9	648876	836181	3.8841	0.2803	1.0448 +	CHB	64979103	64238674	742429	Chr9_16	del/dup	27	64135929	66383081	inside	0
MGC41943	GI_34222265-S	Chr7p-7H4	7	495012	625041	4.7936	0.3459	0.5695 +	CHB	143348142	142788115	560027	Chr7_29	multiallelic	150	142664612	143806286	inside	0
MGC5178	GI_30089844-A	Chr16p-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	Chr16p-9F3	16	61772	243261	5.4541	0.3902	1.1639 +	CHB	14880002	14727485	152517	Chr16_6	del/dup	19	14525556	15133811	inside	0
PDRP	GI_3261325-S	Chr16p-9C8	16	-62302	118293	11.4405	0.8688	2.4144 +	CHB	68760426	68752430	27986	Chr16_21	complex	19	68412623	68870723	inside	0
PM5	GI_10947030-S	Chr16p-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_41281988-S	Chr5p-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	Chr5p-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	Chr5p-2H6	5	664365	788891	9.3678	0.5994	3.0755 +	CHB	70135141	69408613	726528	Chr5_29	multiallelic	2	70072978	70425468	out	664365

SULT1A3	GI_29550920-A	Chr16p-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	Chr4p-23H10	4	-750788	-580780	7.5842	0.5308	2.1606	+	CHB	69211472	69877256	665784	Chr4_9	dup	102	68998845	69296476	out	580780
UGT2B11	GI_4507822-S	Chr4p-23H10	4	-1120655	-950647	14.9289	0.7971	7.2275	+	CHB	69211472	70247123	10359557	Chr4_9	dup	102	68998845	69296476	out	950647
UGT2B17	GI_4507820-S	Chr4p-23H10	4	-1053361	64647	16.7922	0.8163	8.4857	+	CHB	69211472	69231829	20357	Chr4_9	dup	102	68998845	69296476	inside	0
UGT2B7	GI_4507824-S	Chr4p-23H10	4	-1032588	-862580	14.1214	0.7776	6.8692	+	CHB	69211472	70159056	947584	Chr4_9	dup	102	68998845	69296476	out	862580
C19orf6	GI_34089836-S	Chr19p-8D4	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	Chr22p-8C6	22	-7936	93355	6.1055	0.4234	1.5548	+	JPT	41275994	41233284	42710	Chr22_26	dup	25	41091699	41407604	inside	0
DKFZ572C16GI_4282288-S	Chr8p-2A1	Chr8p-2A1	8	-1021083	-932258	5.7335	0.4007	1.0346	+	JPT	41239428	42215098	976671	Chr8_3	complex	79	38557168	44769175	inside	0
DKFZ762C18 GI_22062495-S	Chr11p-2F4	Chr11p-2F4	11	199812	362282	3.2931	0.2299	4.2008	+	JPT	65397704	65116657	281047	Chr11_16	dup	2	65316469	65478939	out	199812
E1F3S8	GI_5579497-S	Chr19p-11B1	16	-43171	97279	4.1549	0.2945	2.7349	+	JPT	28671174	28654120	17054	Chr16_13	del	3	28590949	28751472	inside	0
FLJ00058	GI_32698768-S	Chr19p-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	Chr10p-7D2	10	-168080	-405	2.9484	0.2116	3.8222	+	JPT	5760949	5845191	84243	Chr10_18	dup	2	5677111	5844786	out	405
GBF3	GI_24308156-S	Chr11p-2F3	11	-61102	3882	6.474	0.4452	5.6194	+	JPT	89156581	89185191	28610	Chr1_31	complex	27	89124089	89272744	inside	0
GTF2H2	GI_31747973-S	Chr5p-13C10	5	634966	793009	4.601	0.3261	1.1155	+	JPT	69831862	68917859	714003	Chr5_51	complex	130	69109876	70831640	out	192017
HDAC5	GI_41237396-A	Chr17p-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	Chr6p-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_26665992-S	Chr6p-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	Chr22p-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	Chr8p-2E3	8	1795976	1974709	5.8012	0.4049	0.8569	+	JPT	16741923	14856580	1885343	Chr16_34	del/dup	21	16092718	16831289	out	1236138
KIAA0220	GI_42668056-S	Chr8p-12F7	16	-1046969	-895826	6.5711	0.4587	2.387	+	JPT	21483635	22455032	971398	Chr16_11	del/dup	70	21241957	21833734	out	621298
LOC263820	GI_27734708-S	Chr19p-6G1	16	1812140	1997169	5.8283	0.4065	1.891	+	JPT	18200678	16296023	1904655	Chr16_18	del/dup	10	18036757	19068607	out	1740734
LOC286088	GI_37552972-S	Chr8p-3B9	8	-1416943	-1255764	4.1142	0.2916	-3.7425	-	JPT	384740	1721103	1336364	Chr8_27	dup	3	59932	484890	out	1236213
LOC375249	GI_37547210-S	Chr2p-12B8	2	-117350	73704	3.7456	0.2698	6.1814	+	JPT	97209441	97230264	21823	Chr2_48	del	7	96992983	97492237	inside	0
LOC378157	GI_37539180-S	Chr7p-13D1	7	-71619	32633	10.0615	0.6196	3.4778	+	JPT	43777905	43797398	19493	Chr7_2	dup	52	43725779	43830031	inside	0
LOC388077	GI_41150141-S	Chr15p-7C8	15	-17353	147873	8.1058	0.5324	1.3723	+	JPT	20014944	19949684	65260	Chr15_9	complex	129	18263733	21066294	inside	0
LOC400543	GI_42668001-S	Chr19p-8B1	16	101320	277538	4.2276	0.2997	0.7196	+	JPT	22591701	22402272	189429	Chr16_20	del/dup	182	22201625	22679810	inside	0
LOC402488	GI_42658295-S	Chr7p-13D1	7	-73281	30971	7.8345	0.5189	2.2701	+	JPT	43777905	43799060	21155	Chr7_2	dup	52	43725779	43830031	inside	0
LPHN3	GI_14149676-S	Chr4p-17H8	4	-1143011	-969700	3.3296	0.2427	-0.5935	-	JPT	61710287	62766622	1056356	Chr4_27	dup	7	61623611	61796922	out	969700
MGC12760	GI_34147433-S	Chr11p-25H9	1	62560	180646	6.958	0.4726	1.2497	+	JPT	16811931	16690318	121613	Chr1_15	del/dup	93	16509639	17229287	inside	0
MGC16824	GI_31543158-S	Chr19p-12A1	16	1889590	2055794	3.9098	0.2766	-0.4427	-	JPT	21592230	19819538	1972692	Chr16_11	del/dup	74	21241957	21833734	out	1622419
MGC3130	GI_31543178-S	Chr17p-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	Chr9p-13D1	9	-1547928	-1270095	6.2612	0.4327	0.5567	+	JPT	42789454	44198465	1409012	Chr9_3	complex	1	38557168	44769175	inside	0
MGC5356	GI_15011895-S	Chr20p-6G1	20	538477	718364	3.9929	0.2885	-0.6717	-	JPT	62286696	61659275	628421	Chr20_14	complex	5	62108666	62435964	out	450391
MTVR1	GI_22779872-S	Chr11p-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	Chr19p-8D4	19	-893061	-728252	3.5177	0.2752	0.9102	+	JPT	1413529	2224185	101657	Chr19_6	del	1	1331124	1495933	out	728252
OTUB1	GI_8923113-S	Chr11p-2F4	11	1794138	1956808	3.1233	0.2186	3.3809	+	JPT	65397704	65322331	1875373	Chr11_16	dup	2	65316469	65478939	out	1794138
PDPK	GI_32261325-S	Chr19p-9C8	16	-62302	118293	4.2263	0.2997	1.6147	+	JPT	68769426	68752430	27698	Chr16_21	complex	19	68412623	68870723	inside	0
PM5	GI_10947000-S	Chr16p-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	Chr5p-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	Chr5p-2H6	5	664365	788891	6.9629	0.4728	2.3194	+	JPT	70135141	69408613	726528	Chr5_29	multiallelic	2	70072978	70425468	out	664365

UGT2B10	GI_275522766-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	0.8857	8.7412	+	JPT	69211472	69231829	20357	Chr4_9	dup	102	68998845	69296476	inside	0
UGT2B7	GI_4507824-S	Chr4tp-23H10	4	-1032568	-862560	20.6757	0.8831	6.7305	+	JPT	69211472	70150056	947584	Chr4_9	dup	102	68998845	69296476	out	862560
ZNF558	GI_21687263-S	Chr19p-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	Chr22p-8C6	22	-7936	93355	7.9883	0.4303	2.1899	+	YRI	41275994	41233284	42710	Chr22_26	dup	25	41091699	41407604	inside	0
DC6	GI_34222364-S	Chr2tp-22A7	2	1096812	1259913	3.8511	0.2195	0.9066	+	YRI	129719533	128541170	1178363	Chr2_86	complex	50	129581854	12986275	out	1040684
DKFZ434N03	GI_14149894-S	Chr22p-7B3	22	-2020023	-1976296	6.6283	0.3658	1.9718	+	YRI	17385215	19383374	1988160	Chr22_17	complex	48	17363351	17436267	out	1947107
DKFZ434O02	GI_32698823-S	Chr22p-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	142864612	143806286	inside	0
FM04	GI_4503758-S	Chr17p-3IG2	1	-1529056	-1425876	3.5595	0.1918	0.7407	+	YRI	166565254	168042720	1477468	Chr1_7	complex	116	166513664	166616844	out	1425876
GGT1	GI_4885270-A	Chr22p-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_16426974-S	Chr6tp-2E8	6	90564	94577	6.6771	0.4143	31.641	+	YRI	32811416	32718835	92581	Chr6_19	dup	58	32479731	32813412	inside	0
HLA-DRE5	GI_26665892-S	Chr6tp-4E2	6	41581	57379	10.8926	0.5415	-9.8057	-	YRI	32642705	32593225	49480	Chr6_4	complex	6	32634606	32650604	out	41581
Hs.449564	Hs.449564-S	Chr22p-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	Chr17p-2C2	17	-126434	31668	4.9199	0.271	0.7032	+	YRI	18942851	18990234	47383	Chr17_32	complex	96	18771341	19132640	inside	0
Hs.467323	Hs.467323-S	Chr2tp-8F2	2	-728390	-412600	4.7445	0.2611	0.6291	+	YRI	131093675	131664170	570495	Chr2_13	complex	6	130291879	133031735	inside	0
K1A0739	GI_7662275-S	Chr17p-1E4	7	13370	183092	4.1804	0.2287	0.3944	+	YRI	142320407	142822176	98231	Chr7_29	multiallelic	103	142864612	143806286	inside	0
LOC127069	GI_17437031-S	Chr11p-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	Chr10p-14D8	10	-928439	-764035	3.0752	0.162	-1.5632	-	YRI	132203	978440	846237	Chr10_15	dup	2	50001	214405	out	764035
LOC255812	GI_37530242-S	Chr3tp-18B6	3	1881232	1932759	7.1673	0.4089	0.9991	+	YRI	198797824	196890828	1906998	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	Chr22p-7B3	22	-1399415	-1355688	9.9142	0.5111	1.2384	+	YRI	17385215	18762766	1377552	Chr22_17	complex	48	17363351	17436267	out	1326499
LOC375790	GI_375486731-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	438330031	inside	0
LOC388077	GI_41150141-S	Chr19p-7C8	15	-17353	147873	5.8149	0.3386	1.1983	+	YRI	20014944	19949684	65260	Chr15_8	complex	129	18263733	21066294	inside	0
LOC388873	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	Chr12p-4B7	12	-75735	67053	3.7973	0.2093	0.5611	+	YRI	8239207	8243548	4341	Chr12_4	complex	23	7748086	8515254	inside	0
MGC12760	GI_34147433-S	Chr7tp-13D1	7	-73281	30971	9.1073	0.491	2.2705	+	YRI	43777905	43799060	21155	Chr7_2	dup	52	43725779	438330031	inside	0
MGC5178	GI_42658295-S	Chr7tp-25H8	1	-52396	93744	13.3699	0.6355	1.8406	+	YRI	16710992	16690318	20674	Chr7_15	del/dup	60	16508639	17229287	inside	0
MGC71969	GI_42476196-S	Chr19p-3A9	16	732849	913849	4.2287	0.2316	2.0264	+	YRI	30200281	29374681	825800	Chr16_30	dup	12	29981456	30290781	out	606775
PDPFR	GI_32261325-S	Chr17p-11E5	17	-1662645	-1509032	3.723	0.2048	-1.7982	-	YRI	55437138	55022976	1585839	Chr17_2	complex	31	55350429	55513944	out	1509032
SGLECS	GI_4502688-S	Chr19p-9C8	16	-62302	118293	14.5848	0.6765	1.8497	+	YRI	68760426	68752430	27996	Chr16_21	complex	19	68412623	68870723	inside	0
SLC20A1	GI_31543629-S	Chr2tp-2E12	2	-23866	151278	5.3744	0.3094	-0.8369	-	YRI	56871030	56807234	63796	Chr19_11	del	15	56683708	56958512	inside	0
SM44	GI_41281988-S	Chr5tp-9E3	5	138171	292973	3.8824	0.2145	0.4489	+	YRI	112016780	113137232	1120472	Chr2_28	del/dup	13	11616014	112463168	out	674064
SUNHW2	GI_38202248-S	Chr5tp-6B8	22	-470451	-430700	6.103	0.3343	2.58	+	YRI	69187277	68971705	215572	Chr5_10	dup	1	69109876	69264678	out	138171
TBCD	GI_41350323-S	Chr17p-3H2	17	-1732788	-1560057	3.3925	0.1938	-1.2951	-	YRI	20713283	21163858	450576	Chr22_10	del	5	20693407	20733158	out	430700
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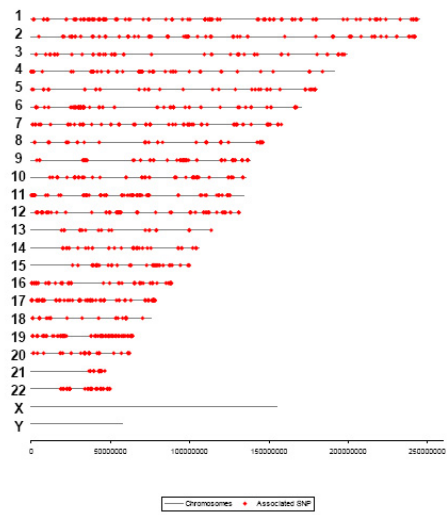
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UGT2B11	GI_4507822-S	Chr4p-23H10	4	-1120655	-950647	11.4101	0.566	4.3649 +	YRI	89211472	70247123	1035651	Chr4_9	dup	102	68998845	69296476	out	950647
UGT2B17	GI_4507820-S	Chr4p-23H10	4	-105361	64647	10.4865	0.5329	4.6238 +	YRI	69211472	69231829	20357	Chr4_9	dup	102	68998845	69296476	inside	0
UGT2B7	GI_4507824-S	Chr4p-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	Chr22p-4F6	22	-1507386	-1465764	3.6564	0.1976	1.4189 +	YRI	47115941	48602516	1486575	Chr22_14	dup	7	47095130	47136752	out	1465764
ZNF265	GI_42741881-S	Chr1p-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	Chr19p-5H2	19	-22902	51275	3.0914	0.1712	-0.5779 -	YRI	8795759	8781572	14167	Chr19_1	complex	128	8758670	8832847	inside	0

Table S5: Associations 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		pvalue	-logp	Adjusted_R^2	Gradient	POP
						om_CNV_start	om_CNV_end					
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

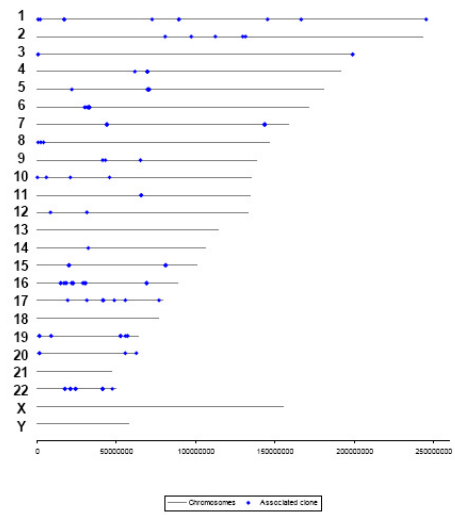


Figure S2A

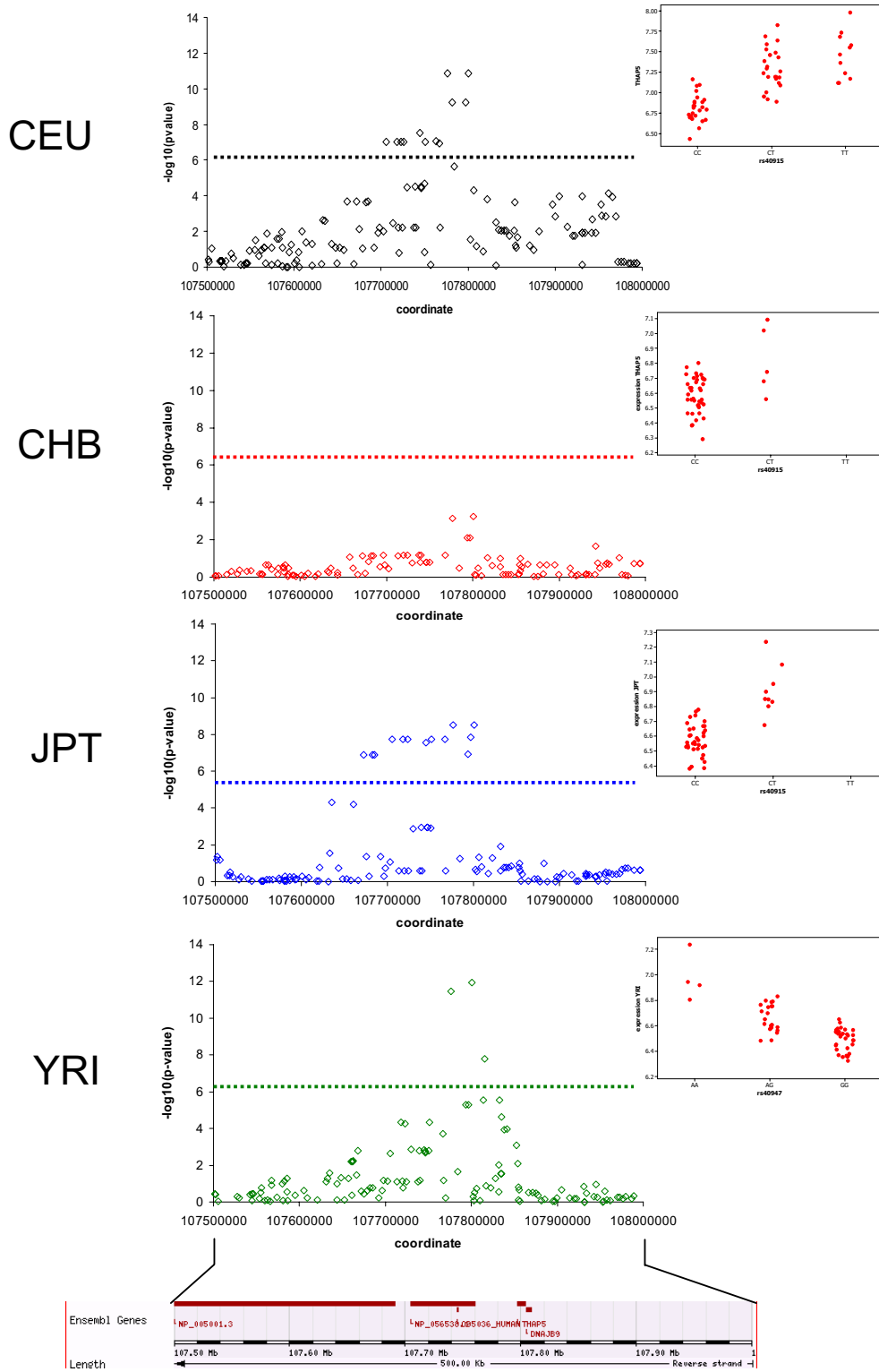


Figure S2B

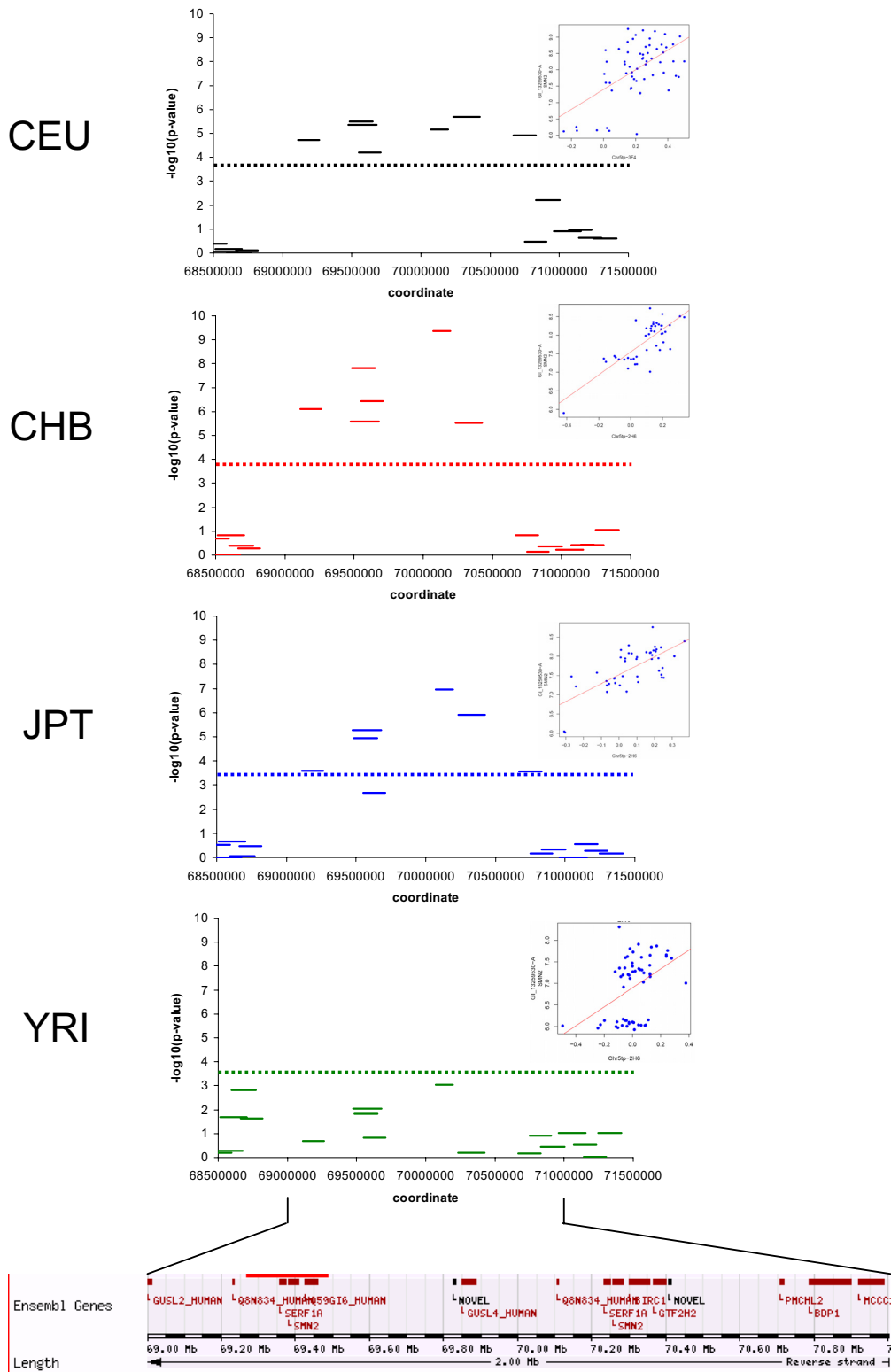


Figure S2C

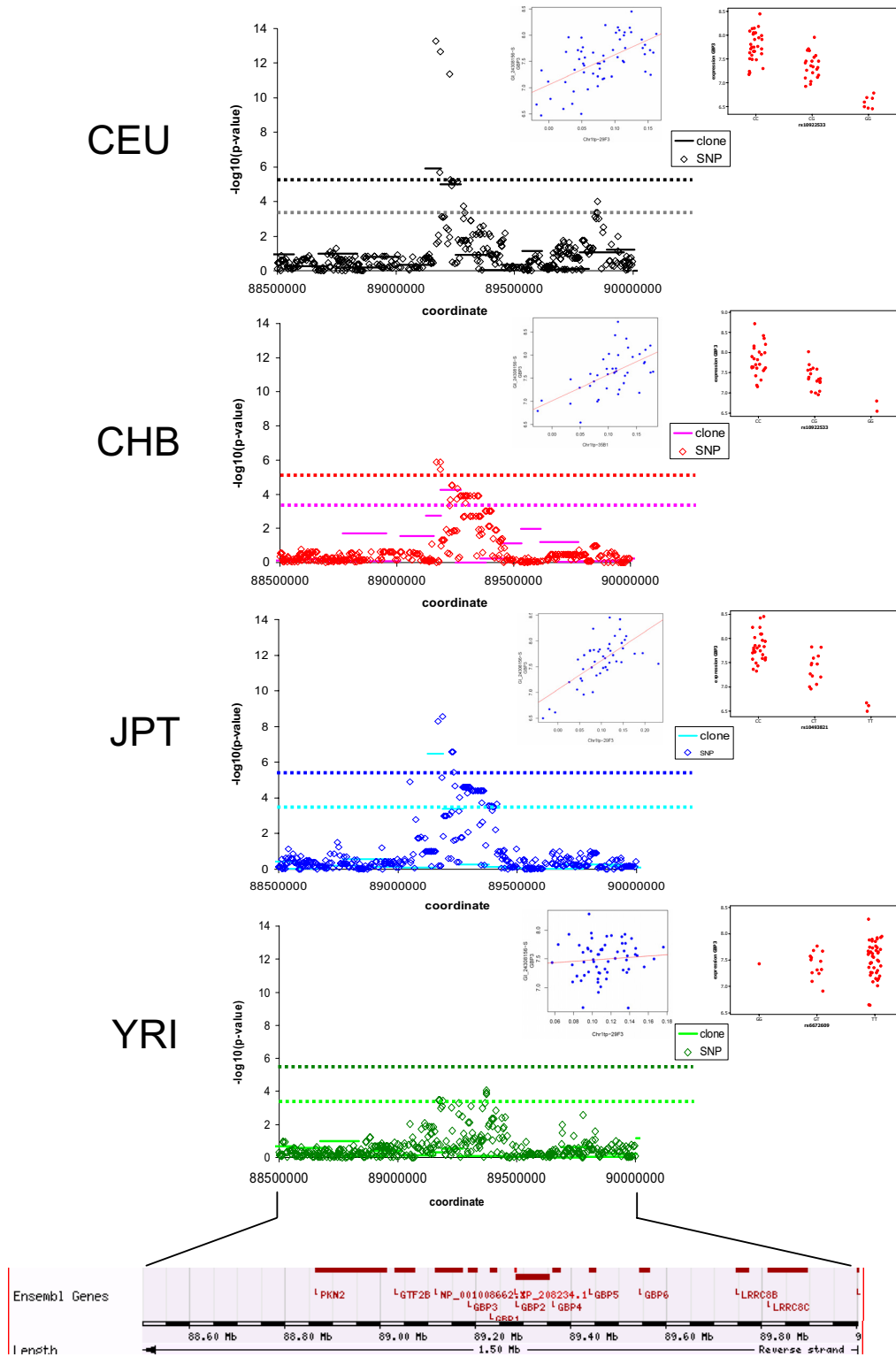


Figure S3. Distribution of p-values for all SNP-expression associations (SNP-probe distance < 1Mb) and all clone-expression associations (clone midpoint-probe distance < 2Mb).

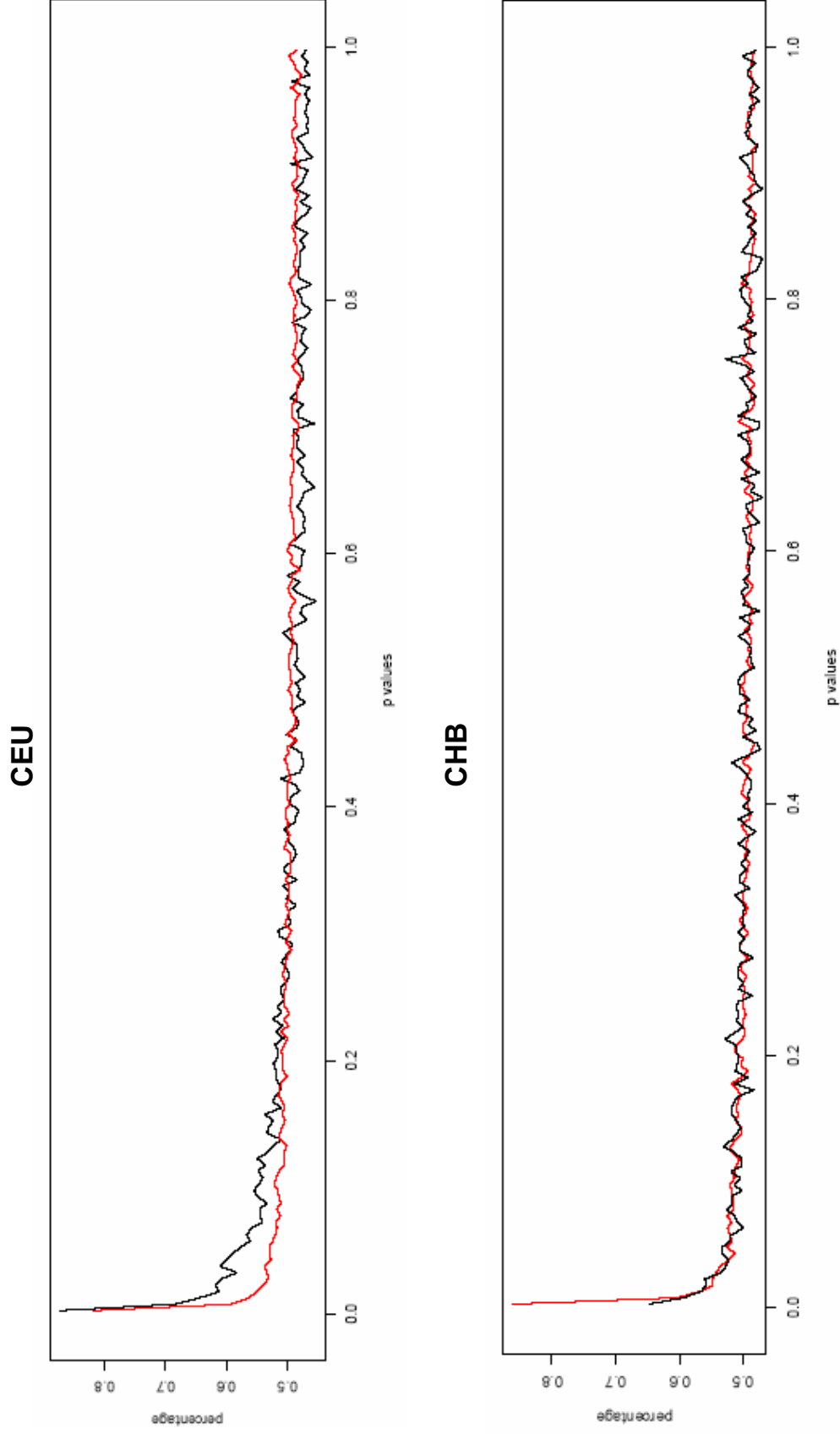
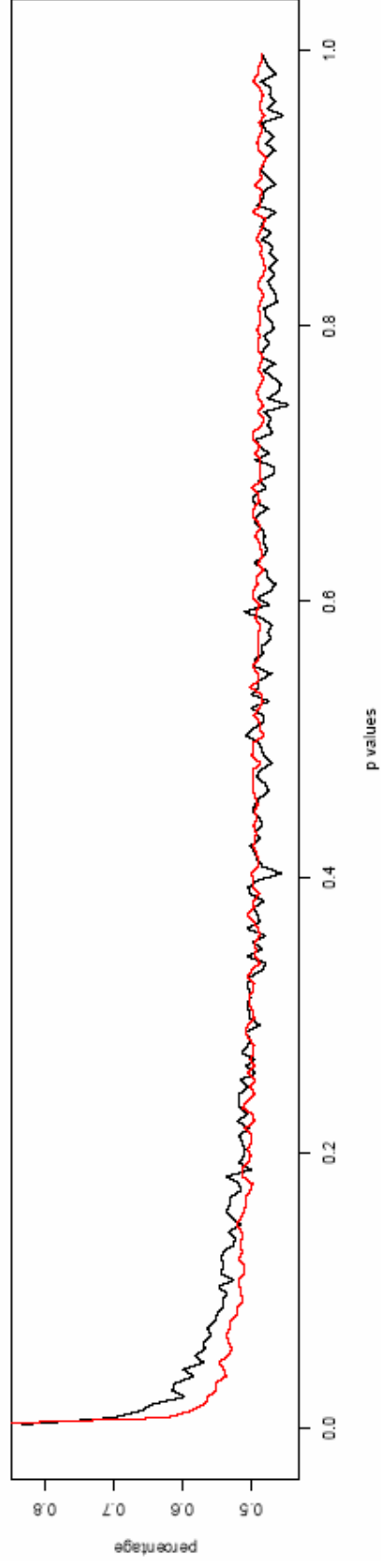


Figure S3 (cont). Distribution of p-values for all SNP-expression associations (SNP-probe distance < 1Mb) and all clone-expression associations (clone midpoint-probe distance < 2Mb).

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YRI

