Supplementary Appendix

Supplement to: Plenge RM, Seielstad M, Padyukov L, et al. *TRAF1–C5* as a risk locus for rheumatoid arthritis — a genomewide study. N Engl J Med 2007;357:1199-209.

SUPPLEMENTAL INFORMATION

Subjects

For SONORA, NICRAP and WRDBB, subjects were categorized according to standard broad racial categories (e.g. White, Black, Asian). For the NARAC family collection, a questionnaire detailing ancestry was administered to probands (see "Ethnicity Data Questionnaire", Supplemental Table 2). For the purposes of this study, mixed racial membership excluded subjects from being considered in the "white" group. Participation rates in these studies are not available.

Genotyping (NARAC)

All Illumina genotyping was performed at the Feinstein Institute for Medical Research Samples according to the Illumina Infinium 2 assay manual (Illumina, San Diego), as previously described [31]. All case samples and most controls were genotyped with the HumanHap550K beadchip; some of the controls samples were genotyped with the Illumina HumanHap300 and HumanHap240S beadchips, and the genotype files merged. We found no evidence of systematic difference in genotype call rates for SNPs genotyped with the three different Illumina beadchips by comparing plate membership to the top 10 principal components generated in EIGENSTRAT. To assess Illumina 550K genotype accuracy for the SNPs advanced to replication, a subset of the samples (n=405 cases, 133 controls) were re-genotyped using a different genotyping platform (Sequenom iPLEX Gold at the Broad Institute). We observed 99.605% concordance between the two genotyping platforms. NARAC-2 samples were genotyped using the Sequenom iPLEX GOLD platform at the Broad Institute.

Genotyping (EIRA)

Genotyping of EIRA-I with the Illumina Human Hap300 v.1.0 chip containing probes for 317,503 SNPs was performed at the Genome Institute of Singapore. Samples included for analysis had call-rates > 96%, and more than 93% of samples had a SNP call-rate greater than 99% (mean = 99.7% for all completed samples). Forty-one samples were genotyped twice, with a mean concordance prior to any SNP QC filtering of 99.96% (median: 99.98%; min.: 99.24%; max.: 100%). EIRA-II samples were genotyped using the Sequenom iPLEX GOLD platform at the Genome Institute of Singapore.

Quality control filtering for NARAC-1 and EIRA-1.

All genotype data was processed using the statistical software package PLINK [23]. We filtered the NARAC-1 and EIRA-1 datasets individually, and then merged the files for our final analysis. Each dataset was filtered as follows (see Table below for specific numbers): individuals with >5% missing genotypes, and SNPs with >5% missing data, control HWE p-values <0.00001, and MAF <0.01 were excluded. Next, we screened for sample contamination, evaluated related status, and removed individuals who appeared as genetic outliers using identity-by-state (IBS) sharing methods implemented in PLINK. We removed samples with excess sharing across all pairs of individuals, as this pattern is consistent with DNA sample contamination; we also removed one individual from any pair who appeared as first-degree relatives. We removed individuals if the nearest neighbor was >4 SD from the mean ("gross population stratification"). We used pairwise IBS values to define case-control clusters within NARAC-1 and EIRA-1 separately; some samples failed to cluster with another sample ("IBS singletons"). This set of samples and SNPs was merged to form the final dataset. There were 18,776 SNPs that passed QC filters in EIRA-1 that failed in NARAC-1, for a final set of 297,086 SNPs. We manually-reviewed all SNPs advanced to replication in our study to confirm quality of the genotype clusters.

Quality control filtering for NARAC-2 and EIRA-2.

The NARAC-2 and EIRA-2 datasets were filtered individually based on SNP genotype call rates (<95% completeness), minor allele frequency (MAF<0.01) and Hardy-Weinberg Equilibrium (*P*<0.01); we removed individuals with >5% missing genotypes. A total of 485 cases and 1,282 controls (NARAC-2) and 568 cases and 516 controls (EIRA-2) were available for final analysis. For these samples, the call rates of the 9 tag SNPs were ≥99.1% for NARAC-2 and EIRA-2 (except for rs7026551, which had call rate of 97.6% in EIRA-2). A subset of the samples genotyped as part of the Illumina GWA scan (NARAC: n=405 cases, 133 controls; EIRA: n=588 cases, 603 controls) was re-genotyped using Sequenom. We observed 99.605% concordance between the Illumina and Sequenom genotype platforms (NARAC) and 99.722% in EIRA. A total of 4 tagging SNPs from the *TRAF1-C5* locus (rs10985095, rs12338903, rs10985097, rs2900180) were

NARAC-1 - samples	**case**	**controls**
initial set	908	1,260
>5% missing genotypes	22	29
possible contamination	0	0
cryptic family relationship	4	6
gross population stratification	9	29
IBS singletons	10	14
FINAL SET	**863**	**1182**

NARAC-1 - SNPs	
initial set	545,080
>5% missing genotypes	18,707
HWE (<0.0001)	2,778
MAF (<0.01)	22,851
FINAL SET	**502,757**

EIRA-1 - samples	**case**	**controls**
initial set	660	663
>5% missing genotypes	0	0
possible contamination	0	0
cryptic family relationship	3	2
gross population stratification	11	4
IBS singletons	14	4
FINAL SET	**632**	**653**

EIRA-1 - SNPs	
initial set	317,503
>5% missing genotypes	911
HWE (<0.0001)	259
MAF (<0.01)	297
FINAL SET	**316,036**

genotyped by Sequenom iPLEX Gold in both the EIRA-1 and EIRA-2 sets, as these SNPs were not on the HumanHap300 array.

Statistical analysis in NARAC-1 and EIRA-1.

Prior to combining the NARAC-1 and EIRA-1 datasets, we first conducted an association study in each collection separately. We present our statistical methods here; results for specific SNPs are shown in Supplemental Table 1.

Statistical analysis in NARAC-1. We conducted a genomewide association study of SNP allele frequency by affected status using unrelated case-control samples. Prior to any correction for population stratification, the inflation factor parameter λ=1.43 (standard Pearson's chi-square test for contingency tables). To correct for population stratification, we first removed genetic outliers, as described above, and then applied two distinct methods, a structured association method within homogenous clusters (Cochran-Mantel-Haenszel (CMH) meta-analysis implemented in PLINK) [23], and a principal components method (implemented in EIGENSTRAT [22]). For the former, clusters were based on IBS methods (PLINK command line options: --ppc 0.05, --cc). Based on these constraints, 10 cases and 14 controls formed individual clusters, and were thus removed from downstream analysis. The association test was conducted within each cluster, and combined using Cochran-Mantel-Haenszel meta-analysis. We observed modest inflation (λ_{GC} = 1.20) after implementing this method. We applied this λ_{GC} correction to the chi-square value of each SNP to arrive at a final p-value for association. Limiting analysis to 148, 262 with no missing genotype data only reduced λ_{GC} to 1.17, indicating that genotyping artifact (as estimated by missing data) was not a major contributing factor to inflation in our study.

In our analysis with EIGENSTRAT, we first removed additional outliers (sigma 6.0, 5 iterations; n=7 individuals removed), and corrected along the top 3 statistically significant principal components that correlated with presumed population ancestry using all SNPs and samples that passed our QC criteria. We noted that the 3rd and 4th eigenvector localized to a region on chromosome 8p23 with a known inversion polymorphism [48], as all 854 SNPs correlated (>6 SD from the mean) with these two eigenvectors localized to a 3.8 Mb region on 8p23. For the purpose of our analysis, we excluded SNPs from this region when determining eigenvectors. We also excluded SNPs within the MHC region when determining eigenvectors, to avoid bias that may be introduced by the strong association to RA susceptibility attributable to this region. To calculate the correlation and statistical significance of specific SNPs to each eigenvector, we performed simple linear regression (Pearson's r) for each eigenvector coordinate x individual genotype in control samples using the R statistical software package (www.r-project.org).

Graphical representation of individuals along the top three principal components demonstrated that while the majority of cases and controls overlap, an excess number of controls were found within certain coordinates in principal component space. This observation is consistent with population substructure within individuals of European ancestry. Correcting along the top 3 principal components decreases λ_{GC} from 1.43 to 1.04. We corrected for residual inflation in the structured association method by dividing chi-square values by λ_{GC}. SNPs linked to the lactase (*LCT*) persistence allele, whose frequency is known to vary greatly across European subgroups [49], are no longer significant in analysis of case-control status after implementing CMH or EIGENSTRAT. Thus, λ_{GC} inflation in the NARAC-1 study was likely due to population stratification, but we were able to correct for it using CMH or EIGENSTRAT.

Statistical analysis in EIRA-1. We implemented the same two methods to correct for population stratification in analysis of the EIRA-1 data. Prior to any attempt to correct for stratification (including removal of genetic outliers), we observed $\lambda_{GC} = 1.075$ for 315,967 SNPs that passed our initial QC filters. After removing outliers, as described above, λ_{GC} decreased to 1.057. We generated IBS clusters, using the identical methods as described for NARAC, and λ_{GC} decreased to 1.034.

We implemented EIGENSTRAT on the same set of samples used in our CMH analysis. We first removed additional outliers (sigma 6.0, 5 iterations; n=25 additional individuals removed), and corrected along the top principal component. We observed a decrease in λ_{GC} from 1.051 to 1.022 after EIGENSTRAT correction.

Combined NARAC-1 and EIRA-1 analysis. Association analysis in the 297,086 SNPs in 1,522 cases and 1,850 controls using Pearson's chi-square test for contingency tables yielded $\lambda_{GC} = 1.41$. We used the IBS clusters generated in NARAC-1 and EIRA-1 in our combined analysis, as described above. Consequently, the NARAC cases were clustered with NARAC controls, and the EIRA cases were clustered with EIRA controls, and the association statistics combined across clusters with CMH (as implemented in PLINK). There were a total of 397 case-control clusters, although 24 NARAC samples and 18 EIRA samples failed to cluster with another sample (IBS singletons). We observed $\lambda_{GC} = 1.14$ in this analysis ($\lambda_{GC} = 1.13$ after removing SNPs across the extended MHC region). We use CMH as our primary analysis, and all *P*-values reported have been corrected for residual inflation by λ_{GC}.

As a secondary analysis of the combined NARAC-1 and EIRA-1 dataset, we ran EIGENSTRAT, as described above. We removed additional outliers with the identical methods (sigma 6.0, 5 iterations); n=12 EIRA samples and 5 NARAC samples were removed. Based on our analysis in NARAC-1 and EIRA-1, we corrected along the 5 top principal components, and observed λ_{GC} decrease from 1.40 to 1.086; correcting along the top 10 principal components had little effect on λ_{GC} (1.076). We report our EIGENSTRAT results in Supplemental Table 1, and a Q-Q plot in Supplemental Figure 1.

Combining results obtained from Stages 1 and 2

Results were combined across all samples (NARAC-1, NARAC-2, EIRA-1, EIRA-2) in three ways. First, we calculated a P-value and odds ratio based on allele counts using a Mantel-Haenszel (MH) method, fixed-effects model (*P*=0.10 for heterogeneity across the four sample collections for rs3761847) in the statistical package R. Second, we combined P-values obtained from structured association within the NARAC-EIRA genome scan (IBS CMH) with P-values obtained using 2-by-2 contingency tables of allele frequencies in our replication samples (NARAC-2 and EIRA-2) using Fisher's method. Not all replication SNPs were genotyped in the original GWA scan in EIRA, preventing us from performing this method of combining results for all 9 tag SNPs. Third, we combined all genotype data from NARAC-1, -2 and EIRA-1, -2 to conduct an omnibus (or global) test of haplotypes defined by 9 tag SNPs, and to conduct logistic regression analysis conditional on each SNP. These analyses were performed with statistical software package WHAP [37]. The final p-value and odds ratio we report in the abstract and in Figure 2 are based on Mantel-Haenszel method of combining allele counts.

Combining results with WTCCC

The WTCCC recently reported "moderate" evidence of association for 11 non-MHC SNPs. To determine if these 11 SNPs, which were genotyped as part of the Affymetrix 500K array, had evidence of association in the combined NARAC-EIRA genomewide association study, we identified the best Illumina SNP-proxy for each of the 11 SNPs based on r^2 with CEU HapMap. We report association statistics, together with r^2 between the Affymetrix and Illumina SNPs in CEU HapMap, in Supplemental Table 3.

Supplemental Table 1A: SNPs with P<0.0001(non MHC). We provide results from analysis with structured association (CMH) and principal components (EIGENSTRAT). All p values have been corrected for residual inflation by λ_{GC} (corr). We also report results from a similar analysis in NARAC alone and EIRA alone.

Supplemental Table 1B: SNPs with p<0.0001 (including MHC). The chi-square (CHISQ) statistic is from CMH and corrected for residual inflation by λ_{GC} (corr). The P value is derived from the corrected chi square. The allele frequency in cases (affected) and controls (unaffected) is resported as F_A and F_U, respectively. The odds ratio (OR) is calculated from CMH.

SupplmentalTable 2: Ethnicity Questionnaire used for NARAC.

Supplemental Table 3: WTCCC SNPs in NARAC-1 and EIRA-1

Suplementary Figure 1: Q-Q plot of combined NARAC and EIRA analysis using EIGENSTRAT.

Supplemental Tables 1A and 1B

Table 1A

CHR	SNP	POS	GENE	CHISQ_CMH_corr	P_CMH_corr	F_A	F_U	OR_CMH	CHISQ_EIGEN_corr	P_EIGEN_corr	P_NARAC_CMH_corr	P_NARAC_eigen_corr	P_EIRA_CMH_corr	P_EIRA_eigen_corr
1	rs6429822	14087653	PRDM2	15.4	9E-05	0.131	0.167	0.74	16.3	5E-05	2E-04	1E-03	1E-01	8E-02
1	rs593461	35378870	ZMYM4	18.2	2E-05	0.050	0.026	1.85	16.4	5E-05	5E-03	2E-02	1E-03	2E-04
1	rs953035	35748601	PSMB2	15.1	1E-04	0.054	0.029	1.71	18.4	2E-05	4E-02	5E-02	5E-04	4E-05
1	rs883220	38285964	FHL3-UTP11L-POU3F1	15.4	9E-05	0.211	0.253	0.78	9.7	2E-03	3E-03	8E-03	1E-02	5E-02
1	*rs4839335*	*113945913*	*PTPN22*	*16.7*	*4E-05*	*0.293*	*0.245*	*1.29*	*16.1*	*6E-05*	*1E-03*	*1E-02*	*1E-02*	*2E-03*
1	*rs1230647*	*113965681*	*PTPN22*	*16.5*	*5E-05*	*0.292*	*0.244*	*1.28*	*15.8*	*7E-05*	*1E-03*	*9E-03*	*2E-02*	*2E-03*
1	*rs2797409*	*114042244*	*PTPN22*	*17.2*	*3E-05*	*0.293*	*0.245*	*1.29*	*16.4*	*5E-05*	*9E-04*	*9E-03*	*1E-02*	*2E-03*
1	***rs2476601***	***114089610***	***PTPN22***	***44.9***	***2E-11***	***0.162***	***0.097***	***1.72***	***38.2***	***6E-10***	***4E-09***	***2E-08***	***5E-04***	***2E-04***
1	*rs1217407*	*114105790*	*PTPN22*	*16.5*	*5E-05*	*0.291*	*0.244*	*1.29*	*15.7*	*7E-05*	*1E-03*	*1E-02*	*1E-02*	*2E-03*
2	rs3768984	101009505	NPAS2	15.6	8E-05	0.210	0.263	0.77	15.1	1E-04	6E-04	2E-04	4E-02	3E-02
3	rs10510852	60591830	FHIT	16.2	6E-05	0.214	0.253	0.77	13.9	2E-04	1E-03	8E-03	2E-02	1E-01
4	rs3924900	47390633	ATP10D	17.1	3E-05	0.190	0.232	0.76	17.5	3E-05	2E-03	3E-03	7E-03	2E-02
4	rs6838613	48317467	SLC10A4	15.2	1E-04	0.430	0.485	0.81	14.4	2E-04	2E-04	1E-03	1E-01	7E-02
4	rs13145689	111466624	ELOVL6	15.9	7E-05	0.339	0.288	1.26	14.5	1E-04	8E-05	7E-04	1E-01	1E-01
4	rs10516614	123331298	TRPC3-FSA	15.3	9E-05	0.049	0.070	0.63	9.8	2E-03	1E-04	3E-03	2E-01	5E-01
4	rs1490568	157760127	*none*	17.1	4E-05	0.521	0.459	1.25	14.4	2E-04	3E-05	1E-05	2E-01	2E-01
6	rs4715102	9645597	MRDS1	16.0	6E-05	0.343	0.395	0.80	16.9	4E-05	1E-02	2E-02	7E-04	1E-03
6	rs9349607	9675327	MRDS1	15.4	9E-05	0.363	0.413	0.80	17.5	3E-05	6E-03	1E-02	4E-03	6E-03
6	rs9296264	38908879	DNAH8	17.1	3E-05	0.271	0.317	0.78	15.0	1E-04	1E-03	1E-02	1E-02	1E-02
9	rs1412224	81421590	TLE1	16.4	5E-05	0.292	0.242	1.28	16.3	5E-05	4E-04	2E-04	4E-02	8E-02
9	*rs1953126*	*120720054*	*TRAF1-C5*	*26.8*	*2E-07*	*0.404*	*0.332*	*1.34*	*23.2*	*1E-06*	*1E-06*	*6E-06*	*3E-02*	*2E-02*
9	*rs10985073*	*120723409*	*TRAF1-C5*	*27.9*	*1E-07*	*0.491*	*0.414*	*1.34*	*24.7*	*7E-07*	*5E-06*	*2E-05*	*6E-03*	*4E-03*
9	*rs881375*	*120732452*	*TRAF1-C5*	*28.3*	*1E-07*	*0.408*	*0.333*	*1.35*	*24.1*	*9E-07*	*8E-07*	*5E-06*	*2E-02*	*1E-02*
9	***rs3761847***	***120769793***	***TRAF1-C5***	***30.8***	***3E-08***	***0.487***	***0.407***	***1.36***	***27.0***	***2E-07***	***1E-06***	***4E-06***	***5E-03***	***4E-03***
9	*rs7026551*	*120812687*	*TRAF1-C5*	*22.5*	*2E-06*	*0.238*	*0.181*	*1.37*	*20.5*	*6E-06*	*1E-03*	*1E-03*	*3E-04*	*2E-04*
9	*rs2269066*	*120816572*	*TRAF1-C5*	*17.9*	*2E-05*	*0.131*	*0.094*	*1.44*	*14.4*	*1E-04*	*9E-03*	*2E-02*	*4E-04*	*8E-04*
9	*rs7037673*	*120820038*	*TRAF1-C5*	*20.3*	*7E-06*	*0.380*	*0.444*	*0.78*	*20.4*	*6E-06*	*3E-04*	*7E-04*	*8E-03*	*4E-03*
9	*rs2416810*	*120864754*	*TRAF1-C5*	*15.7*	*7E-05*	*0.213*	*0.167*	*1.31*	*13.6*	*2E-04*	*2E-03*	*2E-03*	*2E-02*	*9E-03*
10	rs1913517	49789060	LRRC18	18.1	2E-05	0.408	0.475	0.79	12.3	4E-04	2E-04	3E-05	3E-02	4E-02
10	rs12252317	64316874	EGR2	19.3	1E-05	0.086	0.059	1.60	20.7	5E-06	6E-05	9E-04	5E-02	4E-02
10	rs7068751	64367154	EGR2	17.1	4E-05	0.083	0.058	1.56	19.8	9E-06	1E-04	2E-03	8E-02	5E-02
10	rs2935689	123476616	ATE1	17.7	3E-05	0.165	0.123	1.38	13.8	2E-04	6E-05	3E-04	7E-02	5E-02
10	rs4271313	134773476	GPR123	18.1	2E-05	0.484	0.430	1.26	14.8	1E-04	3E-04	9E-04	2E-02	7E-02
11	rs2714078	122875449	CR599196-GRAMD1B	16.4	5E-05	0.278	0.319	0.79	13.8	2E-04	9E-05	8E-03	1E-01	9E-02
12	rs941152	130516217	LOC338797-SFRS8	17.6	3E-05	0.273	0.336	0.78	14.9	1E-04	2E-03	7E-04	5E-03	9E-03
14	rs12885166	92195035	RIN3	15.5	8E-05	0.373	0.316	1.25	12.4	4E-04	3E-05	4E-05	3E-01	4E-01
14	rs11160325	95808257	BDKRB1	16.5	5E-05	0.520	0.463	1.24	12.6	4E-04	1E-03	3E-03	1E-02	1E-02
14	rs945034	95809627	BDKRB1	19.5	1E-05	0.461	0.398	1.27	16.1	6E-05	3E-04	8E-04	1E-02	7E-03
14	rs11851852	104239473	C14orf151	15.5	8E-05	0.055	0.084	0.64	14.8	1E-04	2E-05	1E-04	3E-01	3E-01
15	rs11852946	36975713	FLJ35695	18.1	2E-05	0.074	0.109	0.66	20.1	7E-06	4E-04	2E-04	1E-02	2E-02
16	rs4924	54953987	AMFR	15.2	1E-04	0.446	0.491	0.81	17.3	3E-05	2E-05	7E-04	4E-01	5E-01
16	rs2440468	54978095	AMFR	15.7	7E-05	0.446	0.490	0.81	17.2	3E-05	2E-05	8E-04	3E-01	5E-01
17	rs212470	29748906	17q cytokine cluster	17.0	4E-05	0.268	0.213	1.30	18.2	2E-05	5E-03	2E-03	2E-03	2E-03
17	rs8069038	59564896	ERN1-TEX2	16.3	5E-05	0.048	0.071	0.62	17.3	3E-05	4E-04	9E-03	3E-02	2E-02
17	rs3924958	68157041	SLC39A11	15.5	8E-05	0.082	0.109	0.70	15.4	9E-05	2E-02	7E-02	5E-04	9E-04
19	rs8104309	36858686	*none*	15.1	1E-04	0.184	0.142	1.33	13.1	3E-04	6E-05	2E-05	2E-01	3E-01
20	rs6074022	44173603	CD40	21.5	4E-06	0.216	0.269	0.74	18.9	1E-05	7E-04	2E-03	1E-03	3E-03
20	rs1569723	44175471	CD40	22.0	3E-06	0.215	0.270	0.74	20.1	8E-06	5E-04	1E-03	1E-03	3E-03
20	rs4811846	55430874	RBM38	16.0	6E-05	0.342	0.290	1.26	13.7	2E-04	6E-04	2E-03	3E-02	4E-02
20	rs1182531	57826397	PHACTR3	21.1	4E-06	0.154	0.205	0.72	19.3	1E-05	4E-07	2E-06	4E-01	3E-01

Table 1B

CHR	SNP	POS	CHISQ	P	F_A	F_U	OR
1	rs6429822	14087653	15.4	9E-05	0.131	0.167	0.74
1	rs593461	35378870	18.2	2E-05	0.050	0.026	1.85
1	rs953035	35748601	15.1	1E-04	0.054	0.029	1.71
1	rs883220	38285964	15.4	9E-05	0.211	0.253	0.78
1	rs4839335	113945913	16.7	4E-05	0.293	0.245	1.29
1	rs1230647	113965681	16.5	5E-05	0.292	0.244	1.28
1	rs2797409	114042244	17.2	3E-05	0.293	0.245	1.29
1	rs2476601	114089610	44.9	2E-11	0.162	0.097	1.72
1	rs1217407	114105790	16.5	5E-05	0.291	0.244	1.29
2	rs3768984	101009505	15.6	8E-05	0.210	0.263	0.77
3	rs10510852	60591830	16.2	6E-05	0.214	0.253	0.77
4	rs3924900	47390633	17.1	3E-05	0.190	0.232	0.76
4	rs6838613	48317467	15.2	1E-04	0.430	0.485	0.81
4	rs13145689	111466624	15.9	7E-05	0.339	0.288	1.26
4	rs10516614	123331298	15.3	9E-05	0.049	0.070	0.63
4	rs1490568	157760127	17.1	4E-05	0.521	0.459	1.25
6	rs4715102	9645597	16.0	6E-05	0.343	0.395	0.80
6	rs9349607	9675327	15.4	9E-05	0.363	0.413	0.80
6	rs3763338	29002290	19.8	9E-06	0.107	0.073	1.53
6	rs2071788	29020286	15.4	9E-05	0.099	0.071	1.47
6	rs9295794	29212914	15.2	1E-04	0.099	0.069	1.47
6	rs4713211	29444033	18.6	2E-05	0.267	0.322	0.77
6	rs2747457	29764396	15.8	7E-05	0.192	0.235	0.77
6	rs3131888	29771868	30.1	4E-08	0.338	0.417	0.73
6	rs7776082	29775252	20.8	5E-06	0.372	0.438	0.78
6	rs2523399	29808058	16.6	5E-05	0.398	0.447	0.80
6	rs2394160	29811241	17.5	3E-05	0.487	0.432	1.26
6	rs1737078	29832918	20.2	7E-06	0.389	0.453	0.78
6	rs1611185	29876323	20.0	8E-06	0.471	0.404	1.28
6	rs1736971	29884301	17.1	4E-05	0.239	0.290	0.77
6	rs1632948	29902028	31.4	2E-08	0.410	0.499	0.73
6	rs1611133	29917361	21.1	4E-06	0.185	0.239	0.73
6	rs2734985	29926641	20.3	7E-06	0.180	0.230	0.73
6	rs2517861	29929961	17.3	3E-05	0.191	0.238	0.76
6	rs2975033	29930240	34.8	4E-09	0.378	0.292	1.41
6	rs1611710	29936895	34.0	5E-09	0.346	0.430	0.72
6	rs1611732	29938987	33.4	7E-09	0.347	0.430	0.72

6	rs3893464	30043229	15.8	7E-05	0.401	0.461	0.80
6	rs2256543	30045812	20.9	5E-06	0.378	0.437	0.78
6	rs2523946	30049922	41.0	1E-10	0.534	0.444	1.42
6	rs6904029	30051046	36.4	2E-09	0.375	0.290	1.42
6	rs166327	30110860	20.1	7E-06	0.370	0.437	0.78
6	rs4711207	30113733	38.6	5E-10	0.368	0.277	1.45
6	rs3807031	30141863	44.3	3E-11	0.292	0.208	1.52
6	rs1150735	30153178	19.0	1E-05	0.319	0.374	0.78
6	rs6909253	30163622	31.7	2E-08	0.513	0.428	1.36
6	rs3132680	30181174	41.5	1E-10	0.426	0.335	1.44
6	rs2844795	30181826	21.0	5E-06	0.538	0.465	1.28
6	rs2523990	30185208	21.3	4E-06	0.380	0.450	0.77
6	rs4959041	30185946	35.5	2E-09	0.384	0.303	1.41
6	rs757262	30222934	55.0	1E-13	0.333	0.235	1.57
6	rs757259	30223521	55.3	1E-13	0.333	0.235	1.57
6	rs2022065	30229439	31.3	2E-08	0.389	0.313	1.38
6	rs9261535	30235302	59.2	1E-14	0.338	0.236	1.59
6	rs929156	30247678	46.9	8E-12	0.345	0.254	1.51
6	rs2844786	30252399	39.6	3E-10	0.374	0.292	1.44
6	rs4711211	30270788	58.3	2E-14	0.339	0.238	1.58
6	rs3129690	30304834	15.1	1E-04	0.503	0.448	1.24
6	rs2844779	30313386	36.4	2E-09	0.372	0.295	1.42
6	rs928822	30383225	31.2	2E-08	0.501	0.420	1.36
6	rs3094054	30441484	15.4	9E-05	0.079	0.106	0.68
6	rs1034323	30476614	40.9	2E-10	0.482	0.400	1.42
6	rs7741364	30480549	38.6	5E-10	0.433	0.353	1.42
6	rs1076832	30527810	48.4	3E-12	0.234	0.156	1.62
6	rs2844729	30530611	17.2	3E-05	0.453	0.398	1.26
6	rs6930977	30543267	47.4	6E-12	0.229	0.153	1.62
6	rs2844713	30627237	24.1	9E-07	0.405	0.338	1.32
6	rs1264432	30670000	30.8	3E-08	0.381	0.305	1.38
6	rs1140809	30719655	61.4	5E-15	0.397	0.513	0.65
6	rs1076828	30736231	35.7	2E-09	0.281	0.355	0.70
6	rs1075496	30766218	21.4	4E-06	0.368	0.435	0.77
6	rs12210947	30843084	28.6	9E-08	0.231	0.165	1.44
6	rs4711235	30876615	16.2	6E-05	0.355	0.297	1.26
6	rs2894046	30890084	17.7	3E-05	0.364	0.304	1.28
6	rs2394412	30890214	17.5	3E-05	0.364	0.304	1.27
6	rs4713391	30900214	53.0	3E-13	0.221	0.135	1.68
6	rs12192704	30900249	51.7	6E-13	0.219	0.134	1.67
6	rs1264344	30908556	32.6	1E-08	0.515	0.441	1.37
6	rs3095352	30913900	18.7	2E-05	0.381	0.437	0.79

6	rs2844654	30946667	42.2	8E-11	0.439	0.352	1.44
6	rs1264333	30952293	42.3	8E-11	0.439	0.352	1.44
6	rs1264303	30990492	42.8	6E-11	0.440	0.352	1.44
6	rs1264302	30990613	36.6	1E-09	0.433	0.351	1.41
6	rs2074506	30998462	43.9	4E-11	0.440	0.352	1.45
6	rs753725	30998850	37.0	1E-09	0.391	0.472	0.72
6	rs2532934	31002738	35.1	3E-09	0.395	0.474	0.72
6	rs2240804	31028869	42.0	9E-11	0.440	0.349	1.45
6	rs3095089	31041773	16.4	5E-05	0.138	0.177	0.73
6	rs1634717	31080568	20.8	5E-06	0.362	0.431	0.78
6	rs2523897	31101937	17.8	2E-05	0.122	0.164	0.71
6	rs6933349	31109992	22.8	2E-06	0.257	0.194	1.37
6	rs4248154	31110595	30.4	3E-08	0.245	0.178	1.45
6	rs2523849	31133030	23.0	2E-06	0.104	0.157	0.67
6	rs2428514	31135495	20.3	7E-06	0.073	0.113	0.64
6	rs2517403	31174988	19.4	1E-05	0.282	0.346	0.77
6	rs2844635	31183460	19.3	1E-05	0.283	0.346	0.77
6	rs1265048	31189388	23.4	1E-06	0.412	0.347	1.31
6	rs3815087	31201566	19.4	1E-05	0.136	0.188	0.72
6	rs3130559	31205280	24.0	1E-06	0.268	0.208	1.37
6	rs1966	31215712	29.9	5E-08	0.261	0.189	1.42
6	rs130067	31226490	29.1	7E-08	0.261	0.189	1.42
6	rs1265110	31227401	34.5	4E-09	0.178	0.112	1.58
6	rs3130933	31240064	16.8	4E-05	0.112	0.141	0.71
6	rs3868542	31253818	22.5	2E-06	0.448	0.378	1.30
6	rs9295957	31265572	51.9	6E-13	0.262	0.168	1.62
6	rs4713447	31270942	22.6	2E-06	0.466	0.401	1.30
6	rs3094609	31273545	18.0	2E-05	0.124	0.155	0.72
6	rs3868075	31275794	22.4	2E-06	0.466	0.401	1.30
6	rs4122189	31275906	28.4	1E-07	0.289	0.217	1.40
6	rs3869109	31292175	40.5	2E-10	0.355	0.435	0.70
6	rs7745906	31311987	51.5	7E-13	0.244	0.154	1.63
6	rs2074488	31348410	81.5	2E-19	0.235	0.128	1.90
6	rs7382297	31355046	18.1	2E-05	0.121	0.153	0.71
6	rs2243868	31369255	43.5	4E-11	0.331	0.414	0.69
6	rs3873379	31370148	30.5	3E-08	0.352	0.283	1.38
6	rs2524089	31374501	43.4	4E-11	0.330	0.413	0.69
6	rs9366778	31377152	23.3	1E-06	0.447	0.387	1.31
6	rs6457374	31380240	23.1	2E-06	0.226	0.270	0.74
6	rs3873386	31381724	43.9	3E-11	0.465	0.375	1.45
6	rs2156875	31425326	35.1	3E-09	0.406	0.492	0.72
6	rs2523619	31426123	23.6	1E-06	0.133	0.193	0.70

6	rs2523589	31435313	28.5	1E-07	0.438	0.505	0.74
6	rs2844575	31442924	20.0	8E-06	0.518	0.456	1.28
6	rs2253907	31444849	29.6	5E-08	0.413	0.495	0.74
6	rs2254556	31450610	22.5	2E-06	0.135	0.174	0.70
6	rs9266722	31457901	40.7	2E-10	0.167	0.107	1.66
6	rs2844533	31458781	40.1	2E-10	0.180	0.248	0.65
6	rs2844529	31461572	15.2	1E-04	0.264	0.328	0.79
6	rs2428486	31462083	15.2	1E-04	0.264	0.328	0.79
6	rs2251396	31472686	39.2	4E-10	0.398	0.306	1.43
6	rs2256028	31487177	15.9	7E-05	0.105	0.154	0.72
6	rs2844513	31496193	30.1	4E-08	0.343	0.432	0.73
6	rs2524279	31500885	70.8	4E-17	0.147	0.068	2.12
6	rs2596480	31533964	27.8	1E-07	0.032	0.069	0.50
6	rs2523674	31544768	42.6	7E-11	0.376	0.475	0.70
6	rs2244839	31546347	27.9	1E-07	0.178	0.249	0.70
6	rs1055569	31548061	18.3	2E-05	0.255	0.318	0.77
6	rs2516440	31548476	15.6	8E-05	0.263	0.323	0.79
6	rs2523467	31565557	16.2	6E-05	0.261	0.326	0.78
6	rs3130922	31569068	16.1	6E-05	0.277	0.333	0.79
6	rs2516398	31589505	25.1	5E-07	0.273	0.329	0.74
6	rs2844494	31591394	19.3	1E-05	0.281	0.330	0.77
6	rs3130637	31596124	17.5	3E-05	0.212	0.251	0.76
6	rs3093993	31598704	18.1	2E-05	0.212	0.251	0.76
6	rs3095227	31598979	17.3	3E-05	0.211	0.250	0.76
6	rs2259435	31604894	19.3	1E-05	0.223	0.176	1.35
6	rs2071596	31614670	21.1	4E-06	0.221	0.169	1.37
6	rs2844509	31618903	57.0	4E-14	0.134	0.225	0.58
6	rs2239705	31621381	15.8	7E-05	0.113	0.160	0.72
6	rs6929796	31630648	21.6	3E-06	0.222	0.169	1.37
6	rs2844484	31644203	21.5	4E-06	0.339	0.403	0.77
6	rs2844482	31647746	19.8	8E-06	0.213	0.162	1.37
6	rs3093662	31652168	27.4	2E-07	0.032	0.067	0.50
6	rs2256965	31663109	22.4	2E-06	0.355	0.422	0.77
6	rs2844480	31672800	16.4	5E-05	0.242	0.196	1.30
6	rs2844479	31680935	60.3	8E-15	0.441	0.357	1.55
6	rs2269475	31691910	42.5	7E-11	0.208	0.131	1.60
6	rs2260000	31701455	59.2	1E-14	0.458	0.369	1.53
6	rs3115663	31709822	41.3	1E-10	0.127	0.187	0.61
6	rs2261033	31711570	163.4	2E-37	0.361	0.526	0.49
6	rs9267522	31711749	40.6	2E-10	0.128	0.187	0.62
6	rs3132453	31712023	19.3	1E-05	0.051	0.075	0.61
6	rs1077393	31718508	29.4	6E-08	0.464	0.521	0.74

6	rs2844463	31723146	35.1	3E-09	0.069	0.124	0.56
6	rs3130050	31726740	33.4	8E-09	0.102	0.146	0.62
6	rs3117582	31728499	23.6	1E-06	0.080	0.116	0.64
6	rs3130617	31735502	54.5	2E-13	0.178	0.255	0.61
6	rs805262	31736712	22.7	2E-06	0.458	0.514	0.77
6	rs3130618	31740113	41.0	2E-10	0.128	0.187	0.62
6	rs2280800	31754377	43.0	5E-11	0.209	0.132	1.61
6	rs9267546	31781415	20.9	5E-06	0.052	0.088	0.60
6	rs2242653	31783744	37.7	8E-10	0.221	0.147	1.54
6	rs3749952	31791136	16.0	6E-05	0.010	0.027	0.40
6	rs3131379	31829012	22.0	3E-06	0.084	0.117	0.65
6	rs707939	31834667	113.4	2E-26	0.486	0.355	1.81
6	rs2075800	31885925	111.8	4E-26	0.469	0.340	1.81
6	rs2227956	31886251	43.3	5E-11	0.124	0.178	0.60
6	rs9267649	31932807	41.4	1E-10	0.123	0.176	0.61
6	rs660550	31945256	34.7	4E-09	0.388	0.444	0.72
6	rs644827	31946420	35.0	3E-09	0.387	0.443	0.72
6	rs494620	31946692	84.6	4E-20	0.525	0.420	1.66
6	rs2242665	31947288	34.1	5E-09	0.388	0.444	0.72
6	rs2736428	31951903	100.0	2E-23	0.467	0.345	1.75
6	rs9267658	31953964	36.4	2E-09	0.095	0.138	0.60
6	rs652888	31959213	37.6	9E-10	0.154	0.212	0.65
6	rs535586	31968316	77.1	2E-18	0.245	0.336	0.59
6	rs659445	31972283	77.5	1E-18	0.246	0.337	0.59
6	rs558702	31978305	21.5	4E-06	0.082	0.115	0.65
6	rs2734335	32001923	98.6	3E-23	0.375	0.493	0.58
6	rs1042663	32013109	72.5	2E-17	0.030	0.085	0.34
6	rs550605	32015126	53.5	3E-13	0.039	0.088	0.43
6	rs541862	32024930	55.5	9E-14	0.037	0.087	0.42
6	rs4151657	32025519	109.5	1E-25	0.486	0.356	1.79
6	rs1270942	32026839	24.6	7E-07	0.082	0.118	0.63
6	rs2072633	32027557	159.1	2E-36	0.302	0.451	0.49
6	rs4151672	32027809	16.4	5E-05	0.070	0.043	1.62
6	rs438999	32036285	51.1	9E-13	0.039	0.088	0.44
6	rs437179	32036993	73.6	1E-17	0.225	0.312	0.59
6	rs406936	32041140	46.8	8E-12	0.066	0.122	0.52
6	rs454212	32042351	46.6	9E-12	0.065	0.121	0.52
6	rs389884	32048876	25.4	5E-07	0.081	0.117	0.63
6	rs387608	32049536	45.1	2E-11	0.067	0.122	0.53
6	rs6941112	32054593	97.4	6E-23	0.434	0.314	1.75
6	rs389883	32055439	78.1	1E-18	0.220	0.311	0.57
6	rs12333245	32127747	18.5	2E-05	0.061	0.095	0.64

6	rs12198173	32134786	21.2	4E-06	0.048	0.081	0.59
6	rs2269429	32137161	27.0	2E-07	0.050	0.087	0.56
6	rs2239689	32138262	141.7	1E-32	0.478	0.328	1.95
6	rs2071295	32146678	143.3	5E-33	0.478	0.326	1.96
6	rs185819	32158045	52.8	4E-13	0.409	0.496	0.67
6	rs169496	32160961	17.7	3E-05	0.061	0.095	0.65
6	rs204899	32165605	20.3	6E-06	0.058	0.093	0.62
6	rs1150752	32172704	16.0	6E-05	0.077	0.106	0.68
6	rs13199524	32174743	22.0	3E-06	0.046	0.079	0.58
6	rs3134954	32179871	43.1	5E-11	0.099	0.150	0.58
6	rs12153855	32182782	33.6	7E-09	0.052	0.096	0.53
6	rs2269426	32184477	43.5	4E-11	0.462	0.384	1.44
6	rs8111	32191153	99.4	2E-23	0.410	0.289	1.78
6	rs3830076	32204222	80.8	2E-19	0.146	0.066	2.25
6	rs204999	32217957	110.7	7E-26	0.149	0.266	0.48
6	rs2269425	32231617	21.4	4E-06	0.197	0.141	1.40
6	rs3134603	32233980	37.0	1E-09	0.090	0.139	0.59
6	rs3096697	32242488	85.6	2E-20	0.119	0.209	0.49
6	rs3134945	32254470	76.6	2E-18	0.127	0.213	0.52
6	rs3134943	32255739	43.2	5E-11	0.092	0.143	0.57
6	rs2070600	32259421	112.6	3E-26	0.131	0.047	2.87
6	rs204994	32262976	87.0	1E-20	0.127	0.219	0.50
6	rs204991	32269344	70.5	5E-17	0.116	0.197	0.52
6	rs204990	32269408	74.2	7E-18	0.116	0.200	0.52
6	rs2071277	32279661	17.6	3E-05	0.438	0.504	0.80
6	rs3131296	32280971	45.6	1E-11	0.086	0.141	0.55
6	rs2071286	32287874	18.3	2E-05	0.260	0.222	1.31
6	rs206015	32290737	29.2	6E-08	0.157	0.110	1.54
6	rs3132946	32298006	40.3	2E-10	0.090	0.135	0.58
6	rs3830041	32299317	40.1	2E-10	0.033	0.077	0.45
6	rs2267644	32300538	45.0	2E-11	0.084	0.041	2.15
6	rs479536	32301656	55.3	1E-13	0.018	0.057	0.30
6	rs404890	32306845	91.9	9E-22	0.269	0.407	0.57
6	rs2849015	32306914	94.6	2E-22	0.270	0.409	0.57
6	rs9267873	32307330	112.8	2E-26	0.569	0.402	1.79
6	rs3130299	32311515	47.0	7E-12	0.157	0.248	0.62
6	rs382259	32317005	64.6	9E-16	0.147	0.258	0.56
6	rs3115573	32326821	115.5	6E-27	0.552	0.421	1.80
6	rs9267992	32328375	56.4	6E-14	0.088	0.145	0.52
6	rs3130315	32328663	115.8	5E-27	0.552	0.421	1.80
6	rs3130320	32331236	175.6	4E-40	0.221	0.368	0.45
6	rs3130340	32352605	99.9	2E-23	0.135	0.233	0.49

6	rs3115553	32353805	99.7	2E-23	0.135	0.233	0.49
6	rs9268132	32362632	233.2	1E-52	0.590	0.393	2.31
6	rs926070	32365544	41.1	1E-10	0.251	0.324	0.68
6	rs6935269	32368328	99.4	2E-23	0.135	0.233	0.49
6	rs7775397	32369230	46.4	1E-11	0.067	0.116	0.52
6	rs6457536	32381743	86.5	1E-20	0.134	0.224	0.51
6	rs547261	32390011	232.6	2E-52	0.590	0.393	2.31
6	rs6910071	32390832	408.4	8E-91	0.473	0.205	3.29
6	rs498422	32394739	29.7	5E-08	0.024	0.059	0.44
6	rs547077	32397296	238.4	9E-54	0.595	0.396	2.34
6	rs10484560	32406115	20.0	8E-06	0.133	0.093	1.46
6	rs9405090	32406350	233.5	1E-52	0.590	0.393	2.31
6	rs1003878	32407800	101.4	8E-24	0.121	0.224	0.47
6	rs1033500	32415360	232.9	1E-52	0.591	0.391	2.33
6	rs2076537	32425613	49.2	2E-12	0.288	0.373	0.67
6	rs2395150	32434023	79.9	4E-19	0.307	0.421	0.60
6	rs9268368	32441933	231.9	2E-52	0.590	0.393	2.31
6	rs9268384	32444564	235.1	5E-53	0.590	0.393	2.33
6	rs3129939	32444744	73.4	1E-17	0.103	0.178	0.50
6	rs3129941	32445664	127.7	1E-29	0.118	0.231	0.43
6	rs3129943	32446673	106.1	7E-25	0.149	0.260	0.49
6	rs2050190	32447054	112.7	2E-26	0.187	0.321	0.50
6	rs2050189	32447625	15.2	1E-04	0.188	0.231	0.77
6	rs2395157	32456123	277.4	3E-62	0.494	0.274	2.58
6	rs4424066	32462406	274.0	2E-61	0.340	0.568	0.40
6	rs3117098	32466491	89.7	3E-21	0.178	0.295	0.54
6	rs3817973	32469089	274.9	1E-61	0.340	0.568	0.40
6	rs1980493	32471193	108.8	2E-25	0.078	0.165	0.40
6	rs2076530	32471794	268.2	3E-60	0.338	0.564	0.40
6	rs3817963	32476065	263.7	3E-59	0.500	0.286	2.50
6	rs3763305	32477466	27.7	1E-07	0.095	0.052	1.74
6	rs3806156	32481676	153.8	2E-35	0.538	0.367	1.98
6	rs3763309	32483951	407.6	1E-90	0.479	0.217	3.28
6	rs3129963	32488186	128.6	8E-30	0.088	0.189	0.39
6	rs6932542	32488240	274.5	1E-61	0.265	0.484	0.38
6	rs9268542	32492699	263.8	3E-59	0.574	0.369	2.45
6	rs2395163	32495787	433.6	3E-96	0.481	0.212	3.42
6	rs3135363	32497626	149.5	2E-34	0.142	0.286	0.43
6	rs3135353	32500855	95.8	1E-22	0.075	0.154	0.42
6	rs9501626	32508322	72.1	2E-17	0.046	0.109	0.39
6	rs3135338	32509195	182.1	2E-41	0.171	0.326	0.41
6	rs7356880	32509305	18.3	2E-05	0.025	0.046	0.53

6	rs2395173	32512837	186.3	2E-42	0.173	0.331	0.41
6	rs2395174	32512856	19.9	8E-06	0.257	0.302	0.76
6	rs2395175	32513004	486.5	8E-108	0.452	0.166	3.85
6	rs3129871	32514320	217.6	3E-49	0.183	0.357	0.39
6	rs3129882	32517508	148.4	4E-34	0.248	0.412	0.49
6	rs2239804	32519501	172.9	2E-39	0.407	0.564	0.49
6	rs7192	32519624	297.6	1E-66	0.215	0.417	0.35
6	rs2395182	32521295	103.1	3E-24	0.127	0.226	0.47
6	rs3129890	32522251	166.8	4E-38	0.141	0.281	0.41
6	rs9268832	32535767	296.0	2E-66	0.220	0.425	0.35
6	rs6903608	32536263	162.7	3E-37	0.145	0.296	0.42
6	rs2395185	32541145	330.8	7E-74	0.549	0.309	2.76
6	rs2516049	32678378	314.2	3E-70	0.536	0.300	2.70
6	rs660895	32685358	490.6	1E-108	0.503	0.210	3.62
6	rs9271366	32694832	69.8	7E-17	0.084	0.150	0.49
6	rs3129763	32698903	103.1	3E-24	0.117	0.235	0.47
6	rs2187668	32713862	57.2	4E-14	0.067	0.125	0.48
6	rs1063355	32735692	66.6	3E-16	0.317	0.418	0.63
6	rs9275141	32759095	151.8	7E-35	0.369	0.521	0.51
6	rs9275184	32762692	263.1	4E-59	0.288	0.107	3.24
6	rs7775228	32766057	85.0	3E-20	0.053	0.127	0.38
6	rs5000634	32771542	269.0	2E-60	0.595	0.382	2.46
6	rs6457617	32771829	441.4	5E-98	0.230	0.496	0.29
6	rs2647012	32772436	301.4	2E-67	0.197	0.399	0.34
6	rs9357152	32772938	25.5	4E-07	0.281	0.239	1.37
6	rs9275312	32773706	209.6	2E-47	0.316	0.145	2.59
6	rs1794282	32774504	57.4	4E-14	0.061	0.115	0.47
6	rs9275390	32777134	274.5	1E-61	0.490	0.267	2.56
6	rs2856705	32778934	74.2	7E-18	0.033	0.095	0.34
6	rs9275572	32786977	325.2	1E-72	0.218	0.430	0.34
6	rs7745656	32788948	106.1	7E-25	0.123	0.251	0.47
6	rs2858331	32789255	18.8	1E-05	0.299	0.375	0.78
6	rs3873444	32790702	68.6	1E-16	0.040	0.102	0.38
6	rs3892710	32790840	23.6	1E-06	0.234	0.175	1.39
6	rs3916765	32793528	128.0	1E-29	0.245	0.122	2.24
6	rs12177980	32794062	28.4	1E-07	0.458	0.395	1.34
6	rs9461799	32797507	28.3	1E-07	0.458	0.395	1.34
6	rs2239800	32821245	16.1	6E-05	0.060	0.090	0.65
6	rs2071800	32822121	50.2	1E-12	0.115	0.064	2.01
6	rs7756516	32831895	26.1	3E-07	0.468	0.523	0.76
6	rs7774954	32832167	34.1	5E-09	0.026	0.061	0.44
6	rs719653	32860544	28.4	1E-07	0.240	0.298	0.72

6	rs7762279	32863268	43.6	4E-11	0.061	0.110	0.52
6	rs7758736	32866372	63.5	2E-15	0.110	0.185	0.54
6	rs2621330	32889502	17.9	2E-05	0.012	0.030	0.42
6	rs2856997	32889754	22.7	2E-06	0.483	0.417	1.30
6	rs7383287	32891064	52.5	4E-13	0.140	0.221	0.59
6	rs2071554	32892654	84.2	4E-20	0.123	0.053	2.50
6	rs2857107	32893493	43.4	4E-11	0.048	0.099	0.48
6	rs10484565	32903010	98.9	3E-23	0.178	0.082	2.27
6	rs241437	32905662	43.5	4E-11	0.304	0.394	0.69
6	rs3819721	32912776	145.1	2E-33	0.401	0.241	2.03
6	rs9357155	32917826	44.4	3E-11	0.191	0.121	1.66
6	rs2071543	32919607	36.1	2E-09	0.199	0.134	1.56
6	rs241407	32970718	54.9	1E-13	0.174	0.101	1.81
6	rs154981	32988971	20.5	6E-06	0.424	0.491	0.78
6	rs151719	33011878	23.8	1E-06	0.178	0.227	0.72
6	rs1480380	33021224	37.5	9E-10	0.049	0.089	0.51
6	rs194682	33022591	22.6	2E-06	0.412	0.349	1.31
6	rs209474	33032562	17.5	3E-05	0.484	0.428	1.26
6	rs3130597	33049169	15.8	7E-05	0.064	0.084	0.66
6	rs620202	33049888	20.2	7E-06	0.360	0.299	1.30
6	rs565876	33058028	21.0	5E-06	0.461	0.395	1.29
6	rs3135034	33059640	69.0	1E-16	0.153	0.083	2.04
6	rs2395300	33076254	24.2	9E-07	0.267	0.342	0.75
6	rs172274	33077435	28.6	9E-08	0.272	0.355	0.73
6	rs206762	33078428	20.5	6E-06	0.508	0.432	1.28
6	rs2581	33082379	34.0	6E-09	0.528	0.439	1.37
6	rs381218	33085398	26.6	3E-07	0.326	0.250	1.36
6	rs429916	33086565	36.6	1E-09	0.037	0.076	0.48
6	rs2395309	33134224	50.6	1E-12	0.098	0.168	0.56
6	rs3077	33141000	49.7	2E-12	0.100	0.169	0.56
6	rs9277341	33147603	20.7	5E-06	0.235	0.298	0.76
6	rs987870	33150858	34.2	5E-09	0.076	0.130	0.59
6	rs9277535	33162839	41.0	2E-10	0.164	0.231	0.64
6	rs9277554	33163516	54.6	1E-13	0.205	0.288	0.63
6	rs9277565	33164875	19.7	9E-06	0.159	0.201	0.73
6	rs3128917	33167974	40.7	2E-10	0.188	0.255	0.66
6	rs3117222	33168927	41.0	2E-10	0.188	0.255	0.66
6	rs2064478	33180244	26.0	3E-07	0.166	0.217	0.70
6	rs3130215	33182941	32.8	1E-08	0.501	0.414	1.37
6	rs3117230	33183613	25.6	4E-07	0.166	0.216	0.71
6	rs1883414	33194426	19.4	1E-05	0.243	0.297	0.76
6	rs6901221	33206254	19.2	1E-05	0.126	0.164	0.71

6	rs2395365	33224200	16.8	4E-05	0.354	0.407	0.79
6	rs756441	33230149	16.1	6E-05	0.357	0.409	0.80
6	rs986521	33244123	24.1	9E-07	0.326	0.249	1.34
6	rs439205	33281820	26.5	3E-07	0.173	0.224	0.70
6	rs421446	33282761	32.2	1E-08	0.200	0.265	0.69
6	rs213199	33343733	23.2	1E-06	0.293	0.360	0.76
6	rs2282851	33388287	19.1	1E-05	0.372	0.306	1.28
6	rs3130100	33391744	31.8	2E-08	0.394	0.469	0.73
6	rs2239839	33396053	19.2	1E-05	0.373	0.307	1.28
6	rs3130014	33420286	15.6	8E-05	0.267	0.318	0.79
6	rs211455	33436496	20.4	6E-06	0.232	0.295	0.76
6	rs211452	33438959	27.5	2E-07	0.290	0.362	0.74
6	rs3130276	33444908	18.5	2E-05	0.434	0.367	1.27
6	rs211456	33497359	18.0	2E-05	0.315	0.372	0.79
6	rs2247385	33529555	20.1	7E-06	0.322	0.385	0.78
6	rs6935686	33722105	21.3	4E-06	0.252	0.197	1.36
6	rs4259245	33732199	15.1	1E-04	0.324	0.379	0.80
6	rs4713653	33755572	31.5	2E-08	0.248	0.319	0.71
6	rs4713654	33755629	30.9	3E-08	0.249	0.320	0.72
6	rs3818528	33769069	31.2	2E-08	0.281	0.347	0.72
6	rs594223	33775943	19.4	1E-05	0.105	0.144	0.70
6	rs2281829	33783620	43.7	4E-11	0.548	0.457	1.43
6	rs2966	33797498	41.3	1E-10	0.544	0.457	1.42
6	rs4713668	33798774	43.6	4E-11	0.547	0.458	1.43
6	rs6457740	33805103	31.3	2E-08	0.214	0.274	0.70
6	rs652049	33819398	20.5	6E-06	0.146	0.191	0.72
6	rs9469583	33825748	48.6	3E-12	0.362	0.454	0.68
6	rs1536500	33831361	20.4	6E-06	0.153	0.199	0.72
6	rs6919321	33831982	32.2	1E-08	0.310	0.389	0.72
6	rs9380376	33832772	16.9	4E-05	0.360	0.304	1.27
6	rs2296748	33853049	18.2	2E-05	0.425	0.365	1.27
6	rs3806109	33878348	18.4	2E-05	0.421	0.360	1.27
6	rs9394169	33886942	32.5	1E-08	0.396	0.478	0.73
6	rs1535950	33893805	20.1	7E-06	0.408	0.343	1.28
6	rs9296264	38908879	17.1	3E-05	0.271	0.317	0.78
9	rs1412224	81421590	16.4	5E-05	0.292	0.242	1.28
9	rs1953126	120720054	26.8	2E-07	0.404	0.332	1.34
9	rs10985073	120723409	27.9	1E-07	0.491	0.414	1.34
9	rs881375	120732452	28.3	1E-07	0.408	0.333	1.35
9	rs3761847	120769793	30.8	3E-08	0.487	0.407	1.36
9	rs7026551	120812687	22.5	2E-06	0.238	0.181	1.37
9	rs2269066	120816572	17.9	2E-05	0.131	0.094	1.44

9	rs7037673	120820038	20.3	7E-06	0.380	0.444	0.78
9	rs2416810	120864754	15.7	7E-05	0.213	0.167	1.31
10	rs1913517	49789060	18.1	2E-05	0.408	0.475	0.79
10	rs12252317	64316874	19.3	1E-05	0.086	0.059	1.60
10	rs7068751	64367154	17.1	4E-05	0.083	0.058	1.56
10	rs2935689	123476616	17.7	3E-05	0.165	0.123	1.38
10	rs4271313	134773476	18.1	2E-05	0.484	0.430	1.26
11	rs2714078	122875449	16.4	5E-05	0.278	0.319	0.79
12	rs941152	130516217	17.6	3E-05	0.273	0.336	0.78
14	rs12885166	92195035	15.5	8E-05	0.373	0.316	1.25
14	rs11160325	95808257	16.5	5E-05	0.520	0.463	1.24
14	rs945034	95809627	19.5	1E-05	0.461	0.398	1.27
14	rs11851852	104239473	15.5	8E-05	0.055	0.084	0.64
15	rs11852946	36975713	18.1	2E-05	0.074	0.109	0.66
16	rs4924	54953987	15.2	1E-04	0.446	0.491	0.81
16	rs2440468	54978095	15.7	7E-05	0.446	0.490	0.81
17	rs212470	29748906	17.0	4E-05	0.268	0.213	1.30
17	rs8069038	59564896	16.3	5E-05	0.048	0.071	0.62
17	rs3924958	68157041	15.5	8E-05	0.082	0.109	0.70
19	rs8104309	36858686	15.1	1E-04	0.184	0.142	1.33
20	rs6074022	44173603	21.5	4E-06	0.216	0.269	0.74
20	rs1569723	44175471	22.0	3E-06	0.215	0.270	0.74
20	rs4811846	55430874	16.0	6E-05	0.342	0.290	1.26
20	rs1182531	57826397	21.1	4E-06	0.154	0.205	0.72

Describe your ethnic/racial background - Based on your 4 grandparents

PLEASE CHECK ALL THAT APPLY:

- ☐**White**
  - ☐Northern European (England, Scotland, Wales, Ireland, N. France, Holland, Belgium, Switzerland)
  - ☐Scandinavian (Denmark, Norway, Sweden, Finland)
  - ☐Southern European (Spain, Portugal, Italy, S. France)
  - ☐Central European (Germany, Austria, Hungary)
  - ☐Eastern European (Russia, Poland, Romania, Ukraine, Lithuania, Latvia, Estonia, Czech Republic)
  - ☐East Mediterranean (Greece, Turkey, Croatia, Bosnia, Yugoslavia, Albania)
  - ☐Northern Africa
  - ☐Middle East
  - ☐French Canada
  - ☐South Africa
- ☐ **Jewish**
  - ☐Ashkenazi Jewish
  - ☐Sephardic Jewish
  - ☐Unknown
- ☐**American Indian/Alaska Native**
  - ☐North America
  - ☐South America (includes Central America)
- ☐**Latino/Hispanic**
  - ☐Mexican
  - ☐Central American
  - ☐South American
  - ☐West Indian
  - ☐Dominican
  - ☐Puerto Rican
  - ☐Cuban
- ☐**Native Hawaiian/Pacific Islander**
  - ☐Hawaiian
  - ☐Samoan
  - ☐Guamanian or Chamorro
  - ☐Pacific Islands
- ☐**Black/African-American**
  - ☐African-American
  - ☐African heritage
  - ☐West Indian
- ☐**Asian**
  - ☐Chinese
  - ☐Korean
  - ☐Filipino
  - ☐Pakistani
  - ☐Vietnamese
  - ☐Cambodian
  - ☐Japanese
  - ☐Malaysian
  - ☐Thai
  - ☐ Indian
- ☐**Unknown**

To the best of your knowledge, your 4 Grandparents or their ancestors came from:

Maternal Grandmother ____

Maternal Grandfather ____

Paternal Grandmother ____

Paternal Grandfather ______________________________________ __

GENE	**LOC**	**WTCCC_SNP**	**WTCCC_MAF_con**	**WTCCC_MAF_case**	**ILLUMINA_SNP**
7q32	130.80–130.84	rs11761231	0.38	0.33	rs12536699
10p15	6.07–6.17	rs2104286	0.29	0.25	rs12722561
1p36	2.44–2.77	rs6684865	0.34	0.29	rs3890745
1p31	80.16–80.36	rs11162922	0.07	0.05	rs6424687
4p15	24.99–25.13	rs3816587	0.41	0.43	rs6840622
6q23	138.00–138.06	rs6920220	0.22	0.26	rs2327832
7q32	130.80–130.84	rs11761231	0.38	0.33	rs12536699
10p15	6.07–6.16	rs2104286	0.29	0.24	rs12722561
13q12	19.845–19.855	rs9550642	0.08	0.11	rs4770010
21q22	41.430–41.465	rs2837960	0.17	0.19	rs2837960
22q13	35.870–35.885	rs743777	0.29	0.34	rs929022

r2_CEU	P_corr_NARAC-EIRA
0.65	0.07
0.55	0.80
1.00	0.08
1.00	0.23
0.81	0.75
1.00	0.00013
0.65	0.07
0.55	0.80
0.45	0.76
1.00	0.17
0.96	0.05

Supplemental Figure 1