

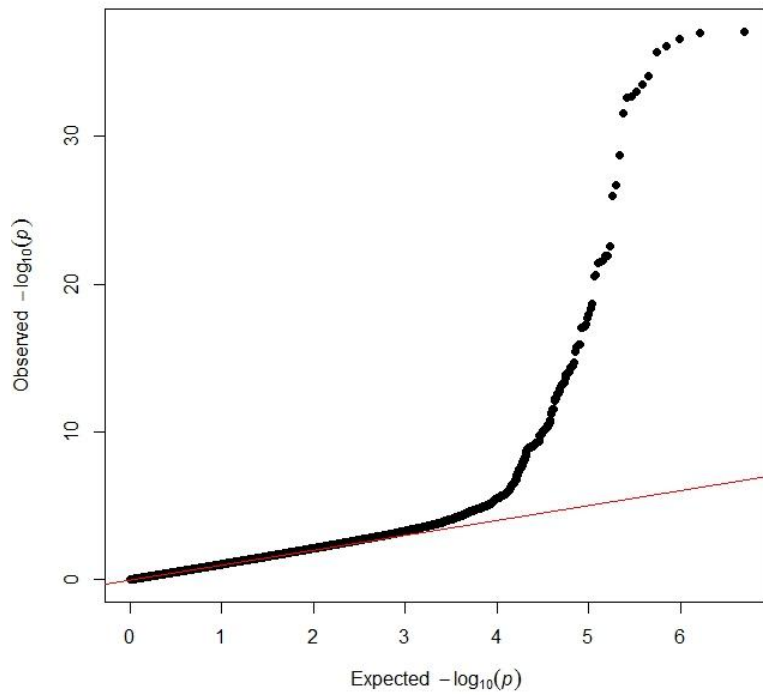
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Supplemental Data

**Genome-wide Association and Population Genetic
Analysis of C-Reactive Protein in African American
and Hispanic American Women**

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African Americans



Hispanic Americans

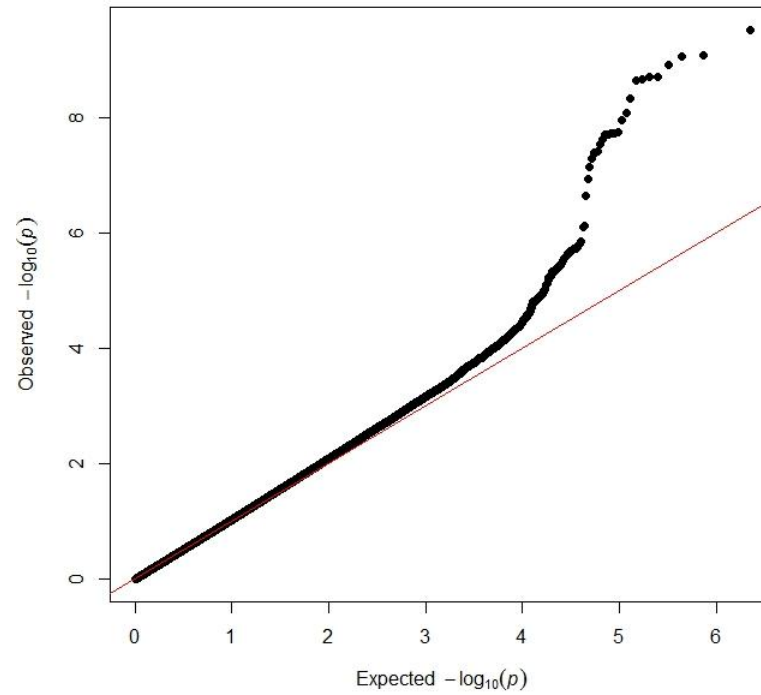


Figure S1. QQ Plot for Association of CRP in African Americans and Hispanic Americans

The inflation factors (λ_{GC}) were 1.053 for African Americans and 1.036 for Hispanic Americans, suggesting that the genome-wide association results were not markedly inflated by population stratification or other confounding factors.

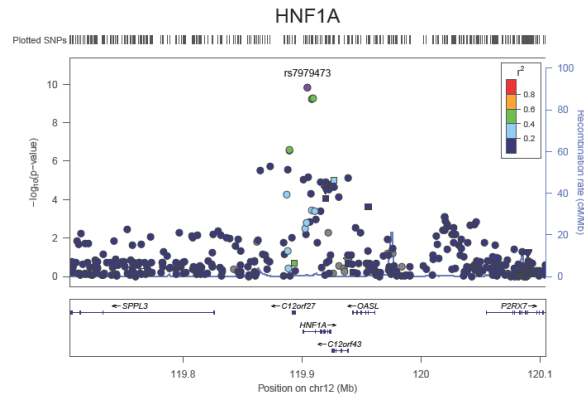
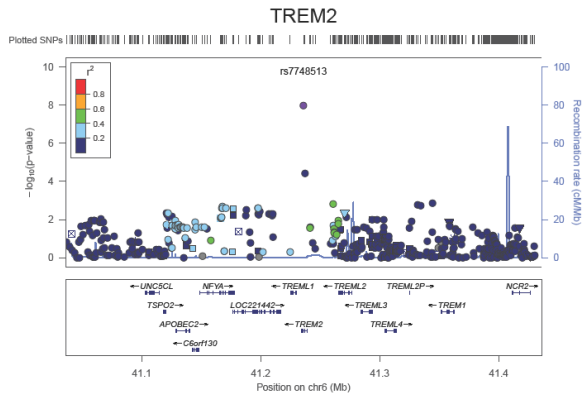
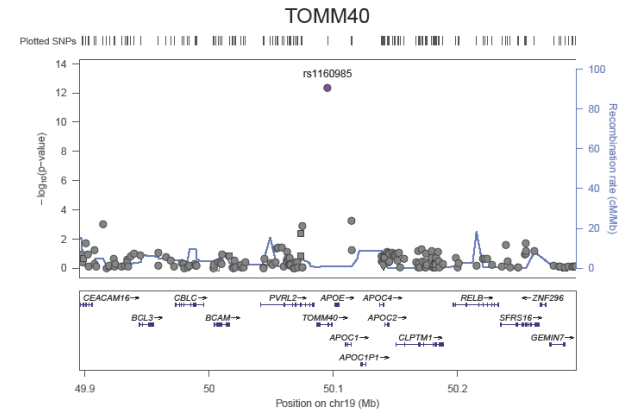
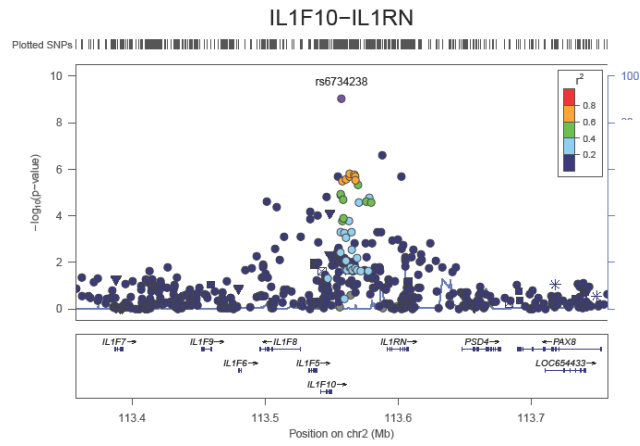
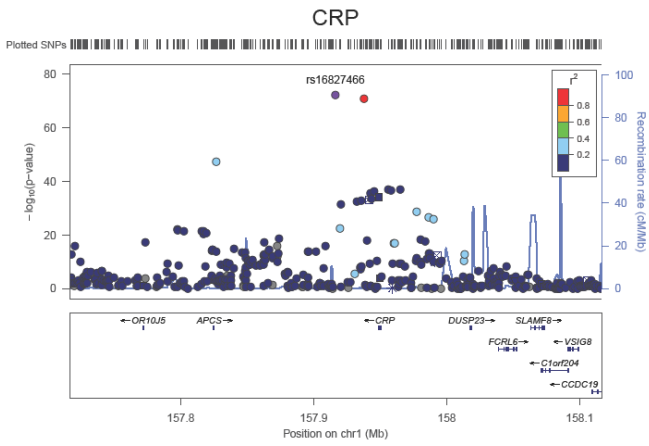


Figure S2. LD Regional Association Plots for CRP in African Americans

Shown are regional association plots generated using LocusZoom for the genome-wide significant regions (*CRP*, *IL1F10-IL1RN*, *TREM2*, *HNF1A*, and *TOMM40*). The index SNP in region is shown in purple. The color of the remaining SNPs indicates the level of pair-wise linkage disequilibrium (LD) based on r -squared relative to the index SNP. r -squared values were calculated from HapMap2 YRI. SNPs with missing LD information are shown in grey.

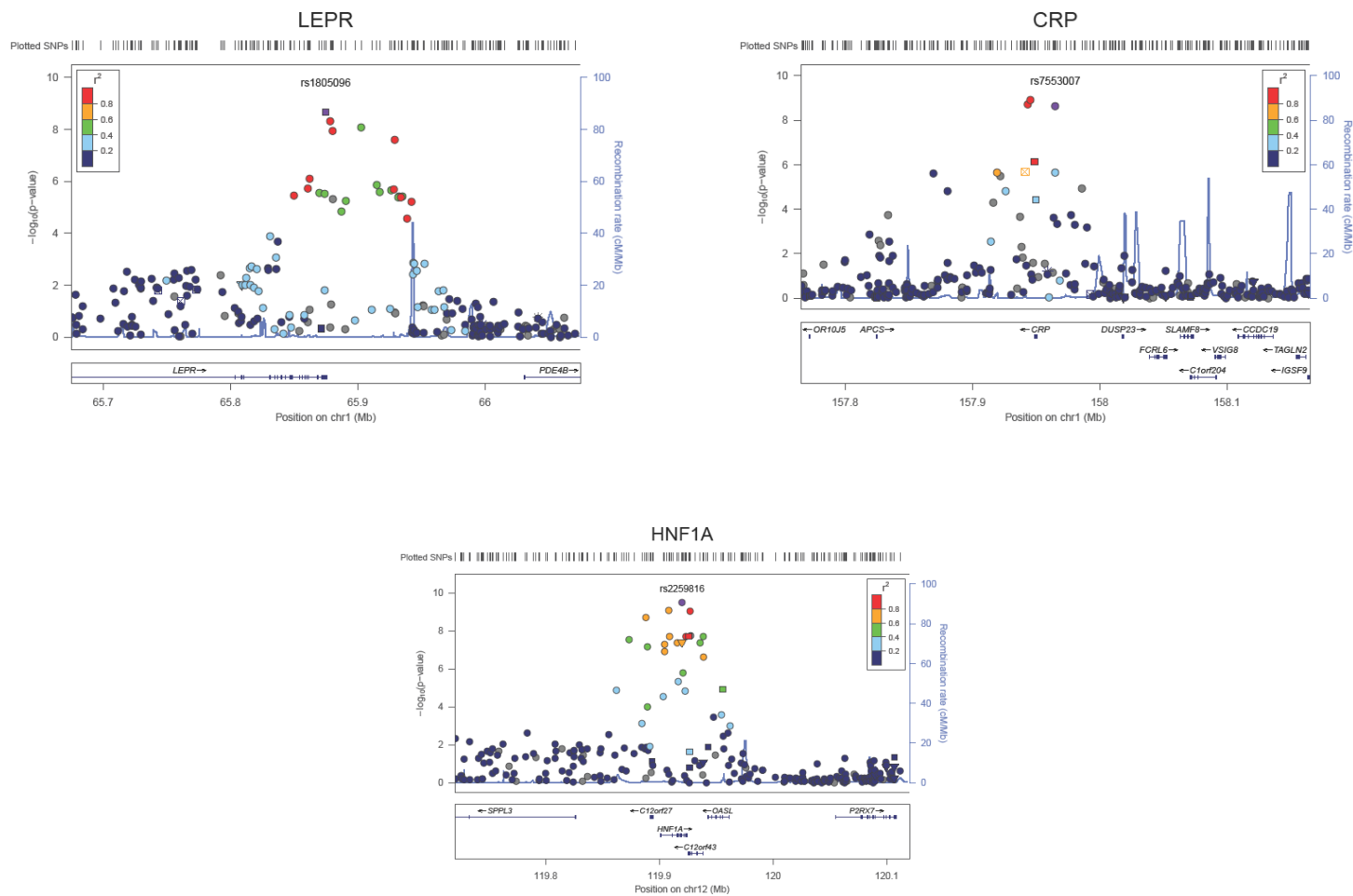


Figure S3. LD Regional Association Plots for CRP in Hispanic Americans

Shown are regional association plots generated using LocusZoom for the genome-wide significant regions (*LEPR*, *CRP*, and *HNF1A*). The index SNP in region is shown in purple. The color of the remaining SNPs indicates the level of pair-wise linkage disequilibrium (LD) based on r-squared relative to the index SNP. r-squared values were calculated from HapMap2 CEU. SNPs with missing LD information are shown in grey.

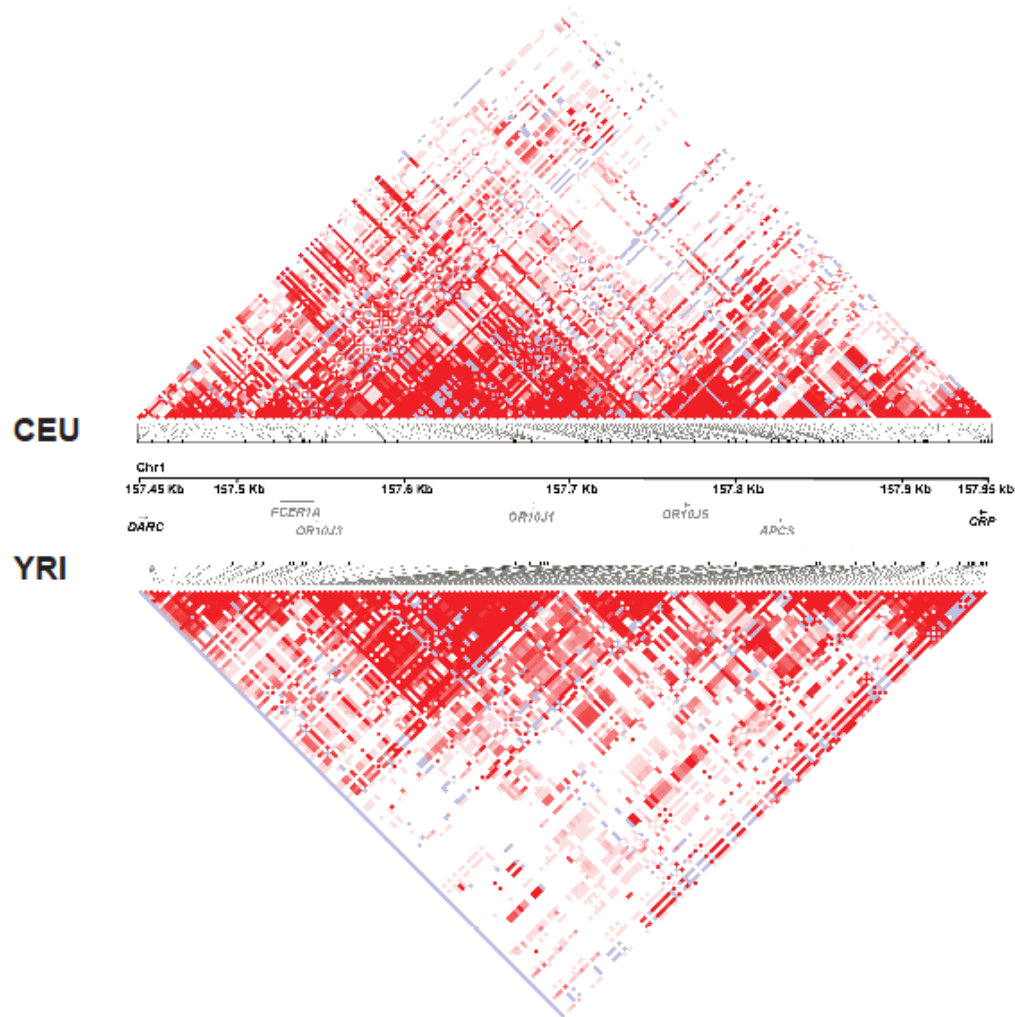


Figure S4. Comparison of Linkage Disequilibrium (LD) between HapMap Populations in the Region of *CRP* and *DARC*

LD plots based on pair-wise r-squared between SNPs were generated separately for CEU and YRI using Haploview.

Table S1. Transferability of Previously Identified European and Asian CRP Loci to African American and Hispanic American Women in WHI-SHARE

Discovery Population [Ref.]	Chromosome	Locus	Lead SNP	Original GWAS (in EA or Asians)			WHI-SHARE African Americans		WHI-SHARE Hispanics	
				Effect Allele	EAF	Beta (SE)	EAF	BETA ± SE (P-value)	EAF	BETA ± SE (P-value)
European [12]	1q23.2	<i>CRP</i>	rs2794520	T	0.34	-0.160 (0.006)	0.22	-0.275 ± 0.021 (3.8x10 ⁻³⁷)	0.35	-0.158 ± 0.026 (1.2x10 ⁻⁹)
European [15]	19q13.32	<i>APOC1</i>	rs4420638	G	0.20	-0.236 (0.009)	0.20	-0.045 ± 0.023 (0.047)	0.19	-0.171 ± 0.040 (1.8x10 ⁻⁵)
European [15]	12q24.31	<i>HNF1A</i>	rs1183910	T	0.33	-0.149 (0.006)	0.13	-0.119 ± 0.026 (6.5x10 ⁻⁶)	NA	NA
European [15]	1p31.3	<i>LEPR</i>	rs4420065	T	0.39	-0.090 (0.005)	0.41	-0.079 ± 0.019 (2.7x10 ⁻⁵)	0.44	-0.145 (0.026) (2.6x10 ⁻⁵)
European [15]	1q21.3	<i>IL6R</i>	rs4129267	T	0.40	-0.079 (0.005)	0.15	-0.110 ± 0.025 (1.8x10 ⁻⁵)	0.48	-0.087 ± 0.025 (4.3x10 ⁻⁴)
European [15]	2q13	<i>GCKR</i>	rs1260326	T	0.41	0.072 (0.005)	0.17	0.058 ± 0.025 (0.019)	0.36	0.098 ± 0.026 (2.0x10 ⁻⁴)
European [15]	1q44	<i>NLRP3</i>	rs12239046	T	0.39	-0.047 (0.006)	0.50	-0.050 ± 0.018 (0.0047)	0.38	-0.055 ± 0.025 (0.031)
European [15]	2p23.3	<i>IL1F10</i>	rs6734238	G	0.42	0.050 (0.006)	0.44	0.108 ± 0.018 (1.4 x10 ⁻⁹)	0.36	0.065 ± 0.026 (0.0097)
European [15]	8p23.1	<i>PPP1R3B</i>	rs9987289	A	0.10	-0.069 (0.011)	0.19	-0.094 ± 0.024 (8.3 x10 ⁻⁵)	NA	NA
European [15]	12q23.2	<i>ASCL1</i>	rs10745954	A	0.50	0.039 (0.006)	0.22	0.049 ± 0.022 (0.027)	NA	NA
European [15]	20q13.12	<i>HNF4A</i>	rs1800961	T	0.05	-0.088 (0.015)	0.008	-0.248 ± 0.100 (0.013)	0.04	-0.268 ± 0.061 (7.7 x10 ⁻⁶)
European [15]	15q22.2	<i>RORA</i>	rs340029	C	0.38	-0.032 (0.006)	0.18	-0.021 ± 0.024 (0.38)	0.37	-0.033 ± 0.026 (0.18)
European [15]	16q12.1	<i>SALL1</i>	rs10521222	T	0.06	-0.104 (0.015)	NA	NA	0.03	-0.224 ± 0.108 (0.039)
European [15]	1p32.4	<i>PABPC4</i>	rs12037222	A	0.24	0.045 (0.007)	NA	NA	NA	NA
European [15]	7q11.23	<i>BCL7B</i>	rs13233571	T	0.14	-0.054 (0.009)	0.05	-0.079 ± 0.041 (0.057)	0.07	-0.038 ± 0.048 (0.43)
European [15]	21q22.2	<i>PSMG1</i>	rs2836878	A	0.28	-0.032 (0.006)	0.12	-0.129 ± 0.041 (0.0017)	0.26	-0.055 ± 0.032 (0.089)
European [15]	14q24.2	<i>RGS6</i>	rs4903031	G	0.21	0.032 (0.007)	0.15	0.007 ± 0.029 (0.81)	0.20	0.053 ± 0.032 (0.095)
Japanese	7p15	<i>IL6</i>	rs2097677	A	0.19	0.101 (0.015)	0.20	0.0124 ± 0.022 (0.58)	NA	NA

EAF = effect allele frequency. EA = European Americans.

Genomic positions and annotations are given using NCBI build 36.1. Effect allele is always on the forward strand. Effect size (BETA) and standard error (SE) are given a natural log-transformed CRP. NA indicates genotype data not available due to QC or imputation failure.

Based on the number of SNPs tested, the Bonferroni-corrected significance threshold is $P < 0.0028$.