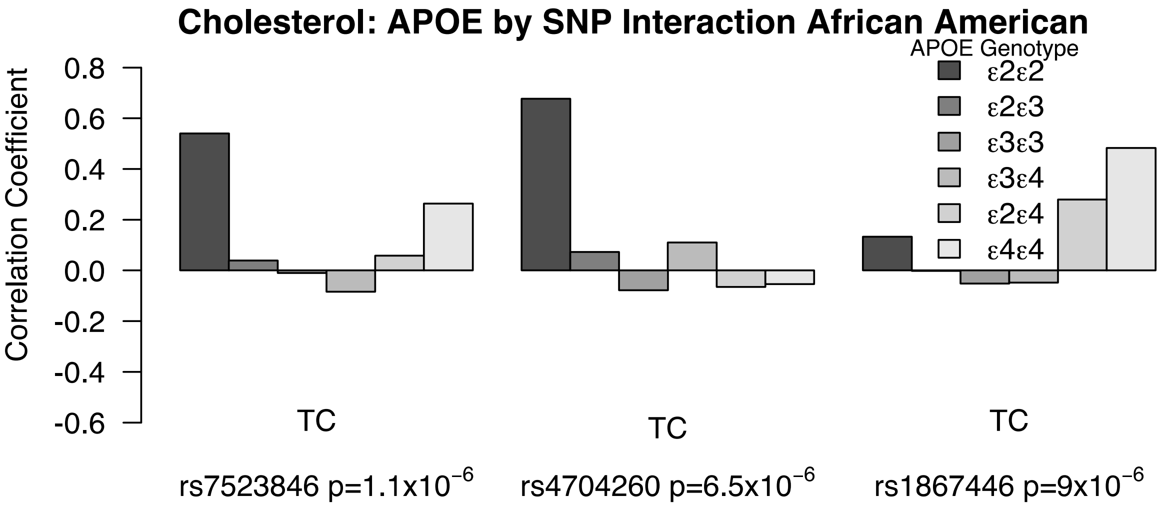


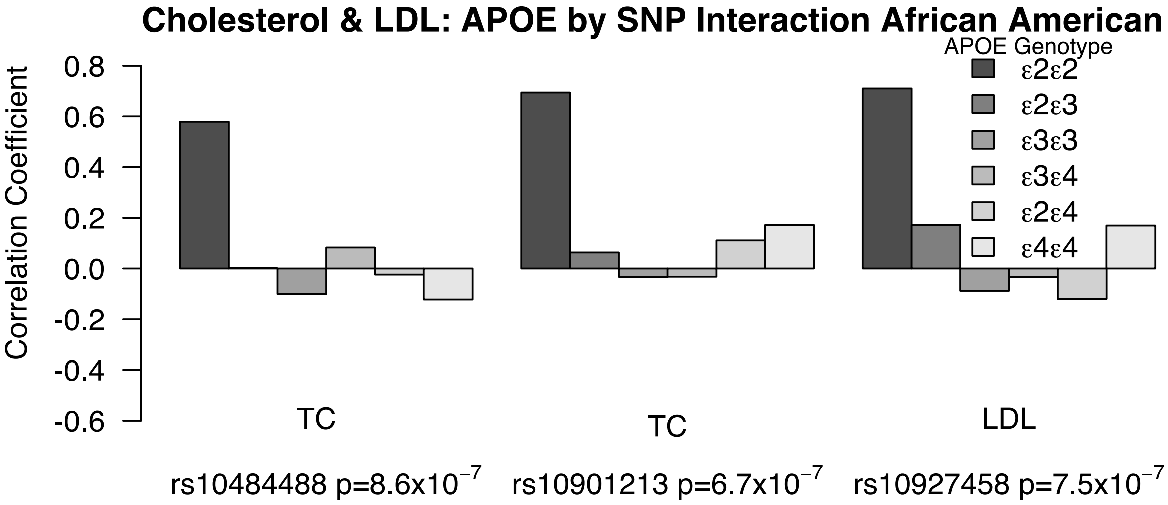
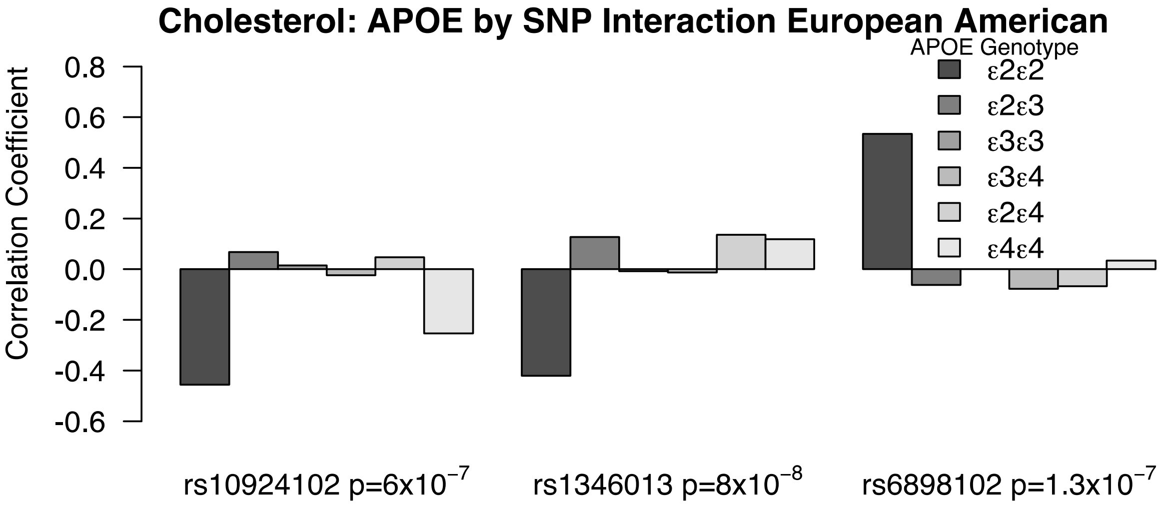


Figure S1 A plot similar to **Figure 2** in the main text for each of the SNPs in **Table S1** that interact with APOE to affect TC and LDL in African Americans. These tests were significant with the parametric test yet dropped below significance after calculating empirical p-values with 100 million parametric bootstrap replicate for each SNP. Plots are based on *within* APOE genotype models after adjusting for covariates while the p-values are based on the APOE*SNP interaction in the full model where the APOE genotypes are treated as factors and the SNP is treated as a (0,1,2) additive variable. The beta coefficients from the linear model provide the same story but the correlation coefficient is easier to visualize.



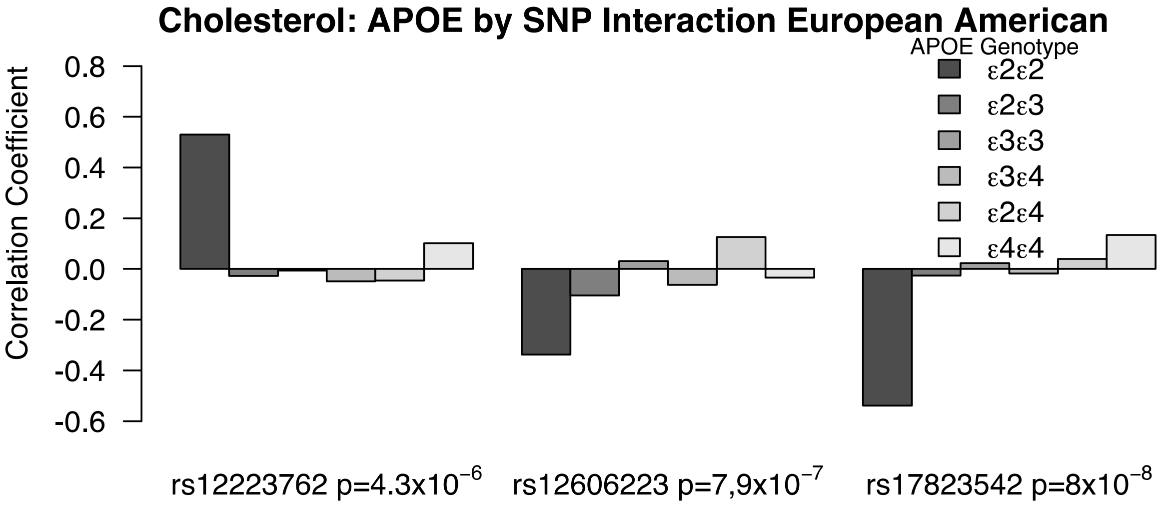
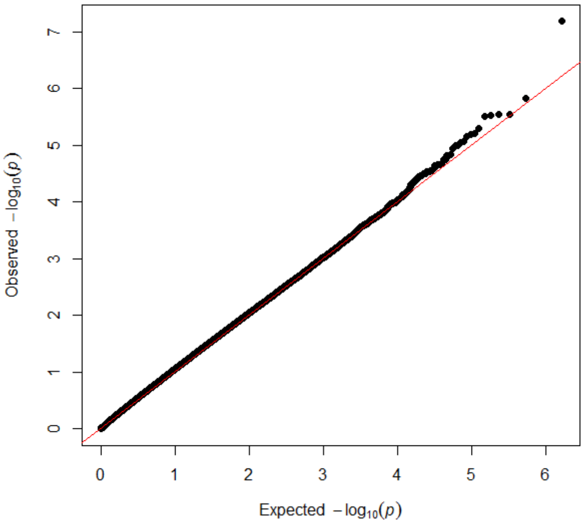
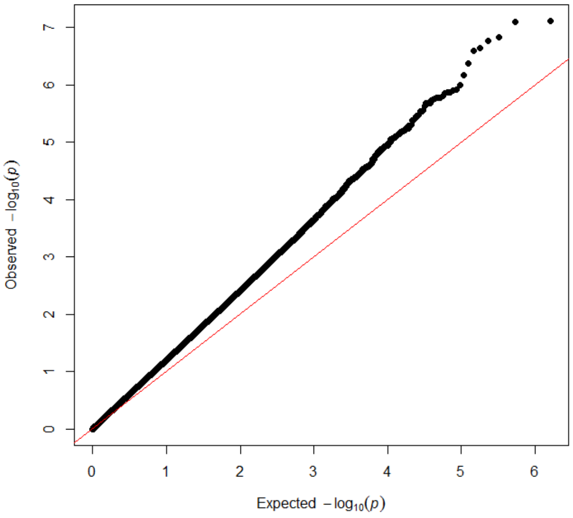


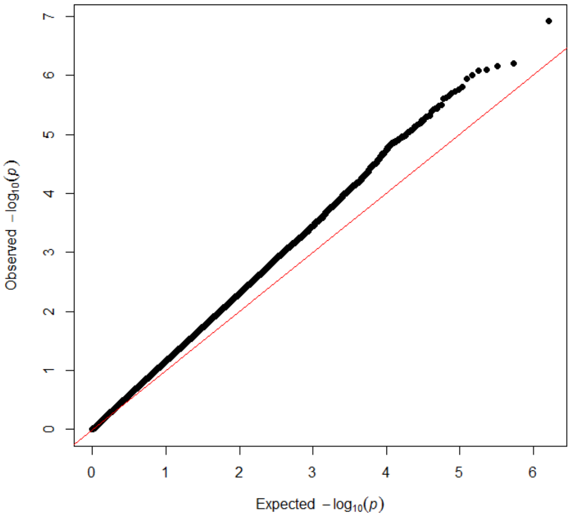
Figure S2 A plot similar to **Figure 2** in the main text for each of the SNPs in **Table S1** that interact with APOE to affect TC in European Americans. These tests were significant with the parametric test yet dropped below significance after calculating empirical p-values with 100 million parametric bootstrap replicate for each SNP. Plots are based on *within* APOE genotype models after adjusting for covariates while the p-values are based on the APOE*SNP interaction in the full model where the APOE genotypes are treated as factors and the SNP is treated as a (0,1,2) additive variable. The beta coefficients from the linear model provide the same story but the correlation coefficient is easier to visualize.



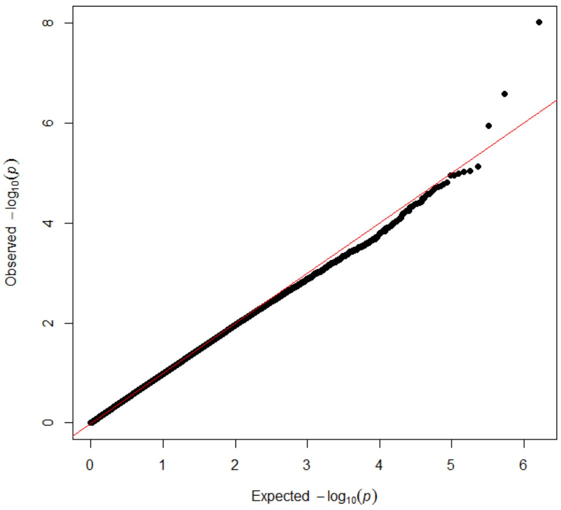
APOExSNP CHD AA



APOExSNP TC AA



APOExSNP LDL AA



APOExSNP HDL AA

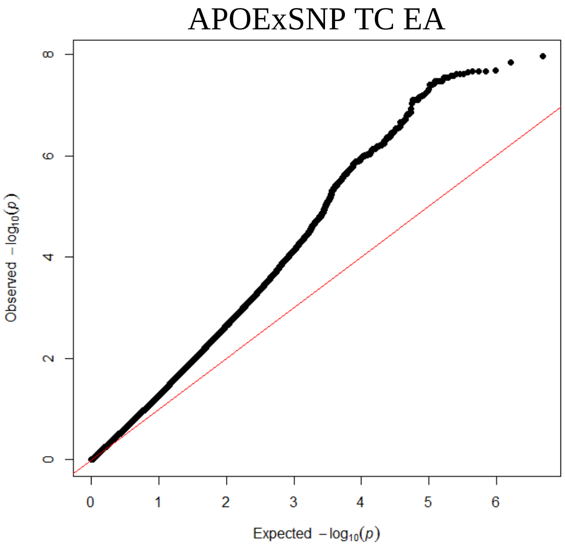
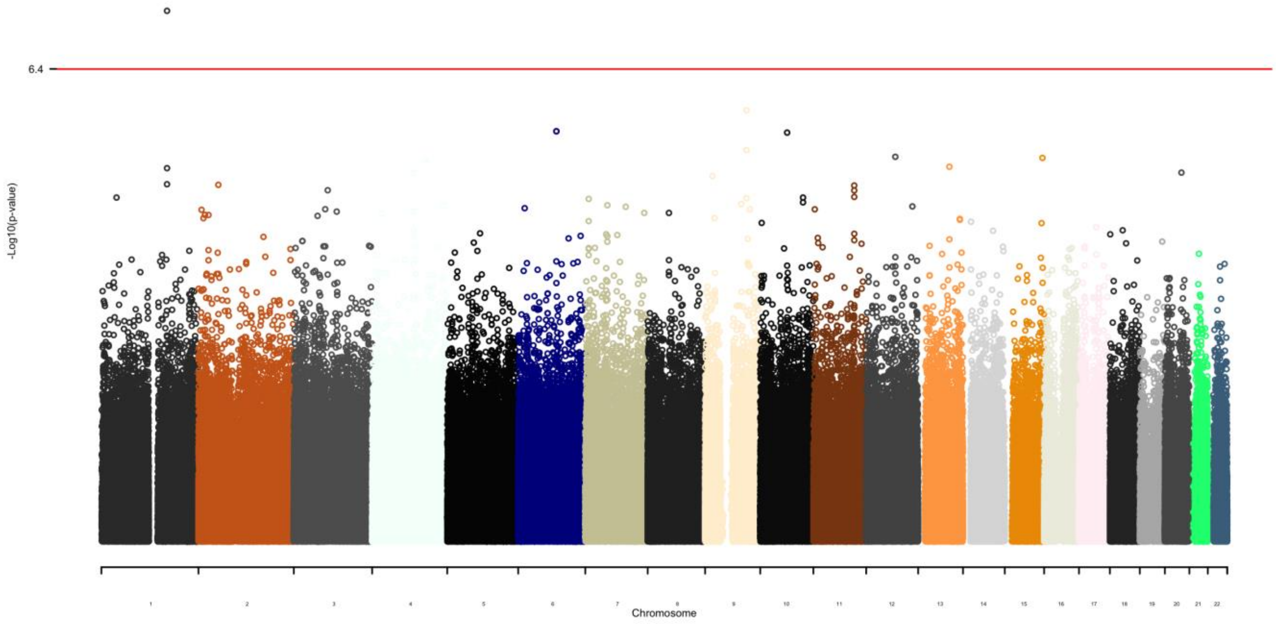
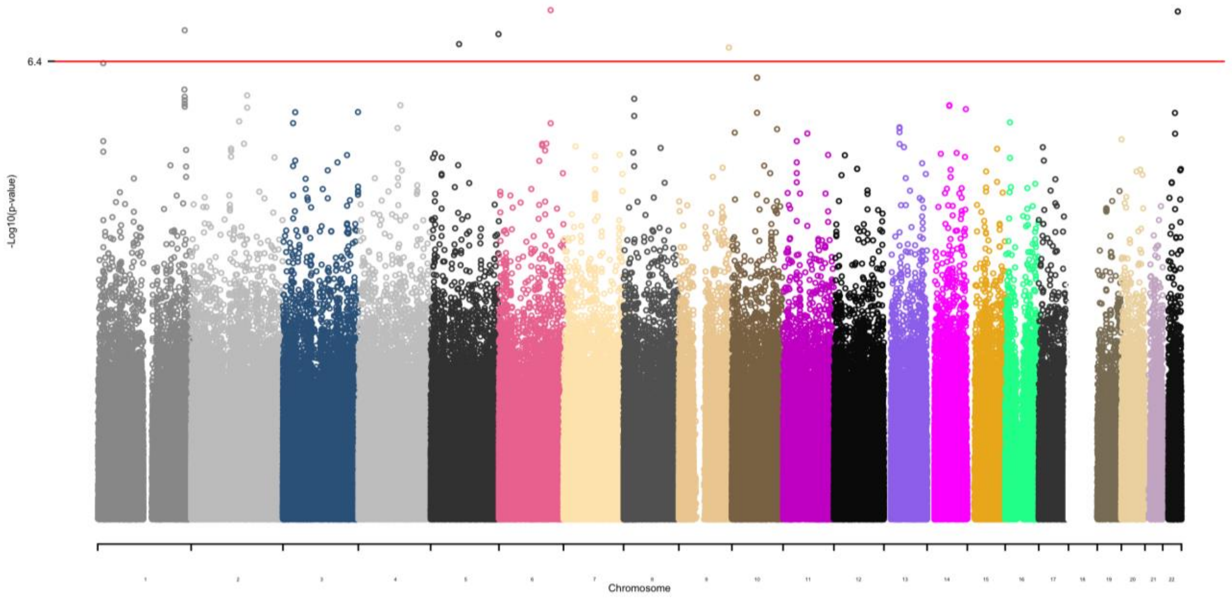


Figure S3 QQ Plots for each of the APOExSNP interaction scans from the parametric tests.

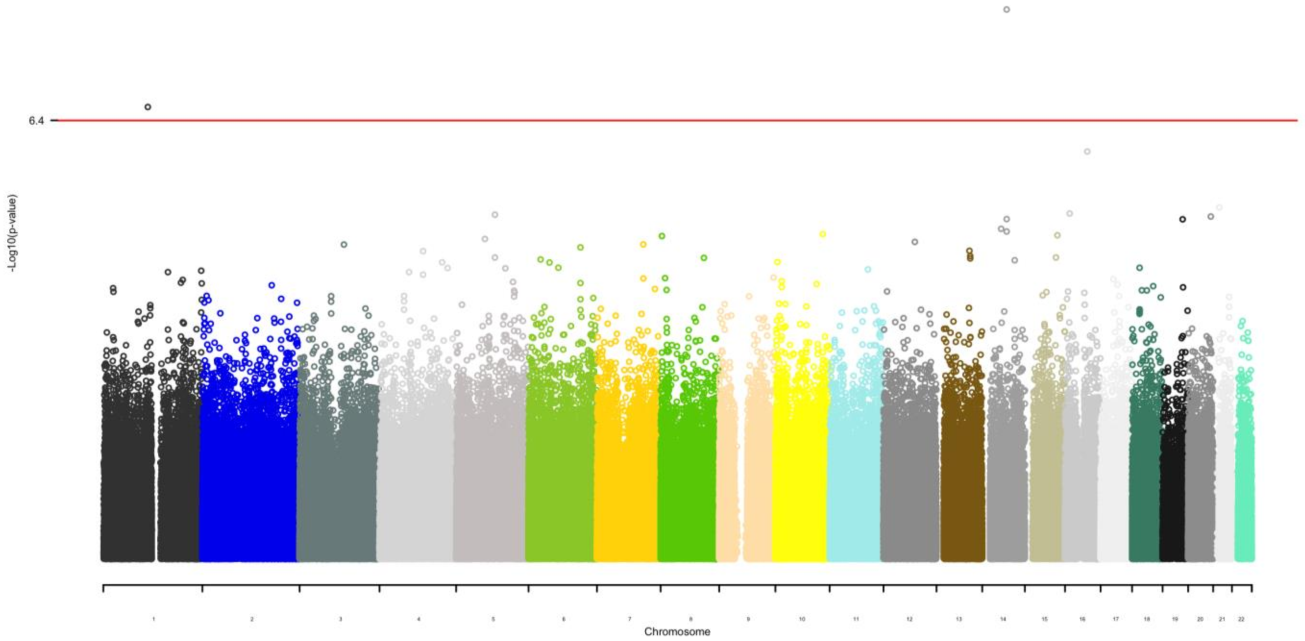
AA APOExSNP Interactions for CHD



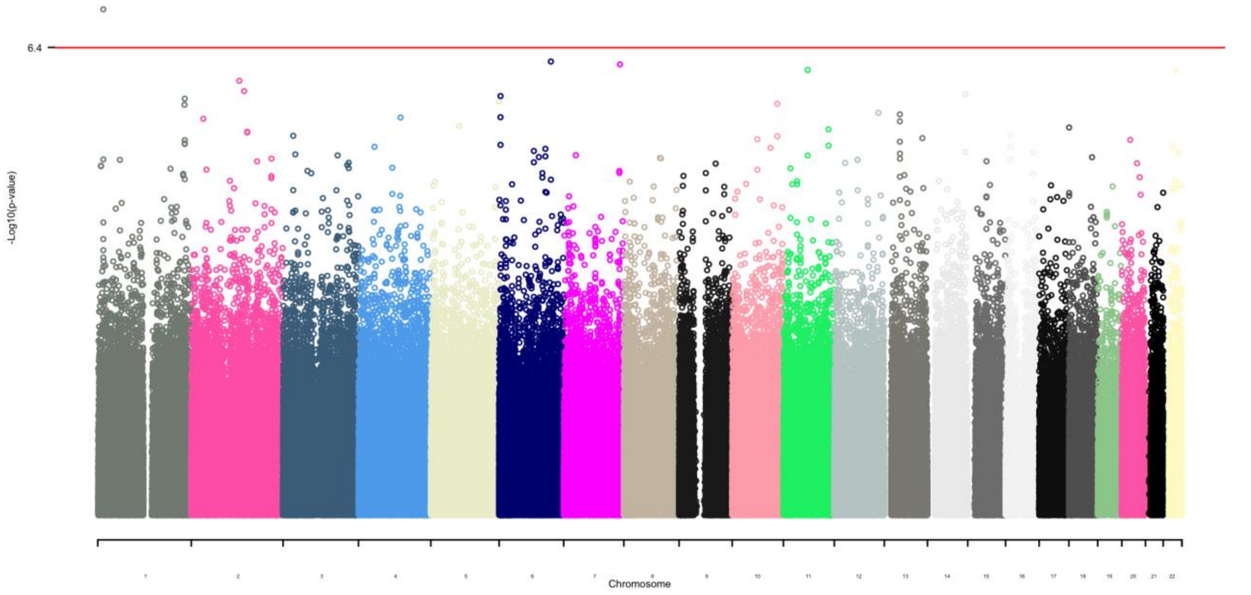
AA APOExSNP Interactions for Total Cholesterol



AA APOExSNP Interactions for HDL



AA APOExSNP Interactions for LDL



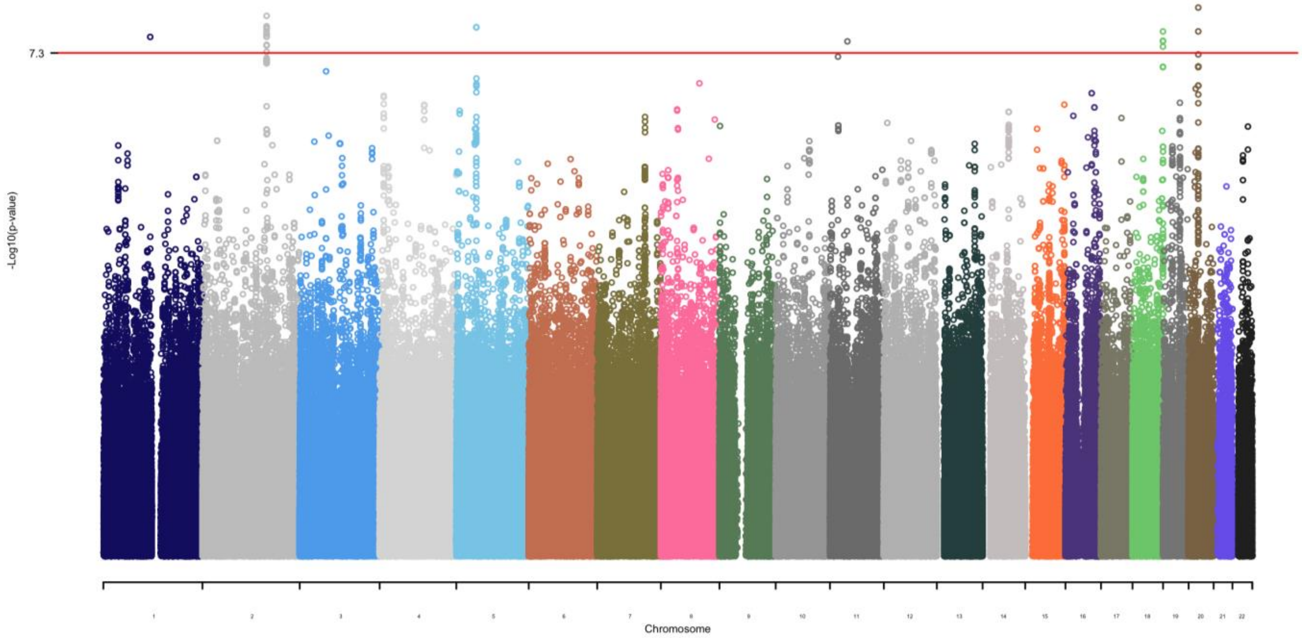

AA APOExSNP Interactions for Total Cholesterol

Figure S4 Manhattan plots for each of the APOExSNP scans. These plots are for the original parametric tests. Note that the SNP density in the European American population is about three times that of the African American population. This would lead to greater clustering around highly significant SNPs.

Table S1 SNPs from the TC and LDL scans initially significant with the parametric test yet dropped below significance after doing 100 million parametric bootstrap replicates.

Population	AA	AA	AA	AA
Trait	TC	TC	TC	TC
SNP	rs7523846	rs4704260	rs1867446	rs10484488
Chromosome	1	5	5	6
Location (build 36.3)	230075483	75223049	179439720	136713787
Maj/Min (MAF)	G/A (0.098)	A/T (0.035)	T/C (0.032)	T/G (0.104)
Parametric p-val	1.47E-07	2.29E-07	1.66E-07	7.69E-08
Par Bootstrap p-val	1.05E-06	6.49E-06	8.99E-06	8.60E-07
Gene	*DISC1* (intron)			*MAP7* (intron)
Left Gene	*DISC2*	*LOC391798*	*RNF130*	*BCLAF1*
Right Gene	*SIPA1L2*	*LOC100132039*	*LOC646058*	*LOC100128745*

Population	AA	AA	EA	EA
Trait	TC	LDL	TC	TC
SNP	rs10901213	rs10927458	rs10924102	rs1346013
Chromosome	9	1	1	2
Location (build 36.3)	132237274	14731263	116832505	160021586
Maj/Min (MAF)	A/C (0.122)	C/A (0.185)	C/T (0.302)	G/A (0.486)
Parametric p-val	2.56E-07	7.50E-07	2.93E-08	1.45E-08
Par Bootstrap p-val	6.70E-07[a]	1.20E-07	6.00E-07	8.00E-08
Gene	*HMCN2* (intron)			*BAZ2B* (intron)
Left Gene	*LOC392395*	*PRDM2*	*LOC148766*	*LOC100127929*
Right Gene	*ASS1*	*RP1-21O18.1*	*CD58*	*LOC728059*

Population	EA	EA	EA	EA
Trait	TC	TC	TC	TC
SNP	rs6898102	rs12223762	rs12606223	rs17823542
Chromosome	5	11	18	20
Location (build 36.3)	49910087	43546197	75914383	24071100
Maj/Min (MAF)	G/A (0.487)	T/A (0.040)	T/G (0.289)	G/C (0.486)
Parametric p-val	2.12E-08	3.40E-08	2.44E-08	1.10E-08
Par Bootstrap p-val	1.30E-07	4.27E-06	7.90E-07	8.00E-08
Gene				
Left Gene	*EMB*	*LOC120449*	*C18orf22*	*POM121L3*
Right Gene	*PARP8*	*LOC100131381*	*ADNP2*	*LOC100128232*

[a] **nominally significant in EA (p=0.008)**