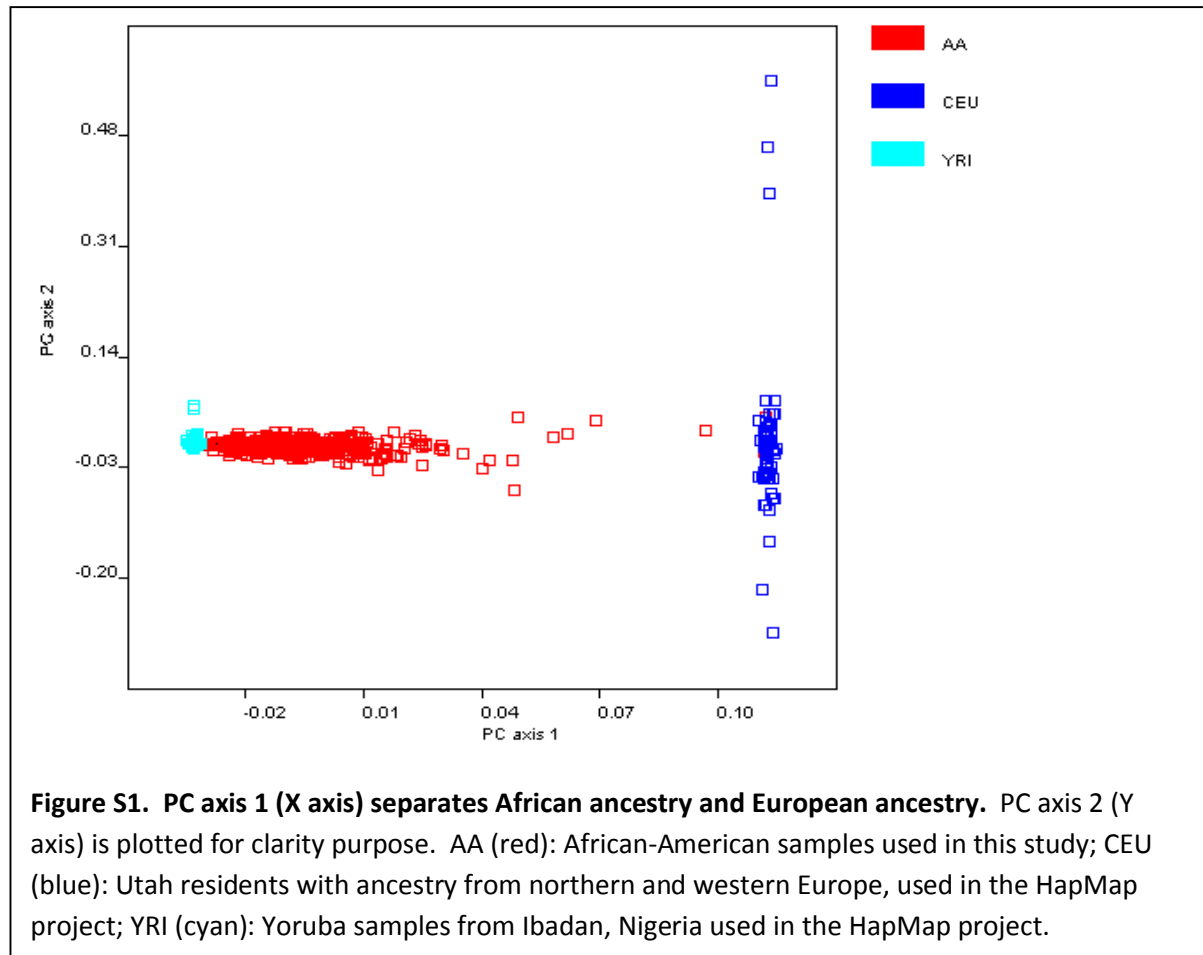


## Supplementary Materials

To further demonstrate the separation of African and European ancestries in the admixed African American population used in this study, we added parental population samples into the EIGENSTRAT analysis. The added seed populations included 60 HapMap CEU samples and 60 HapMap YRI samples into the EIGENSTRAT analysis. Figure S1 shows that PC1 separates African and European ancestries.



We then repeated the association analysis using this newly generated PC1. This new PC1 including parental seed populations is in high correlation with the previous PC1 without seed populations ( $r^2=0.9958$ , Figure S2). All the previous reported negative findings remain unchanged with similar P values (Table S1).

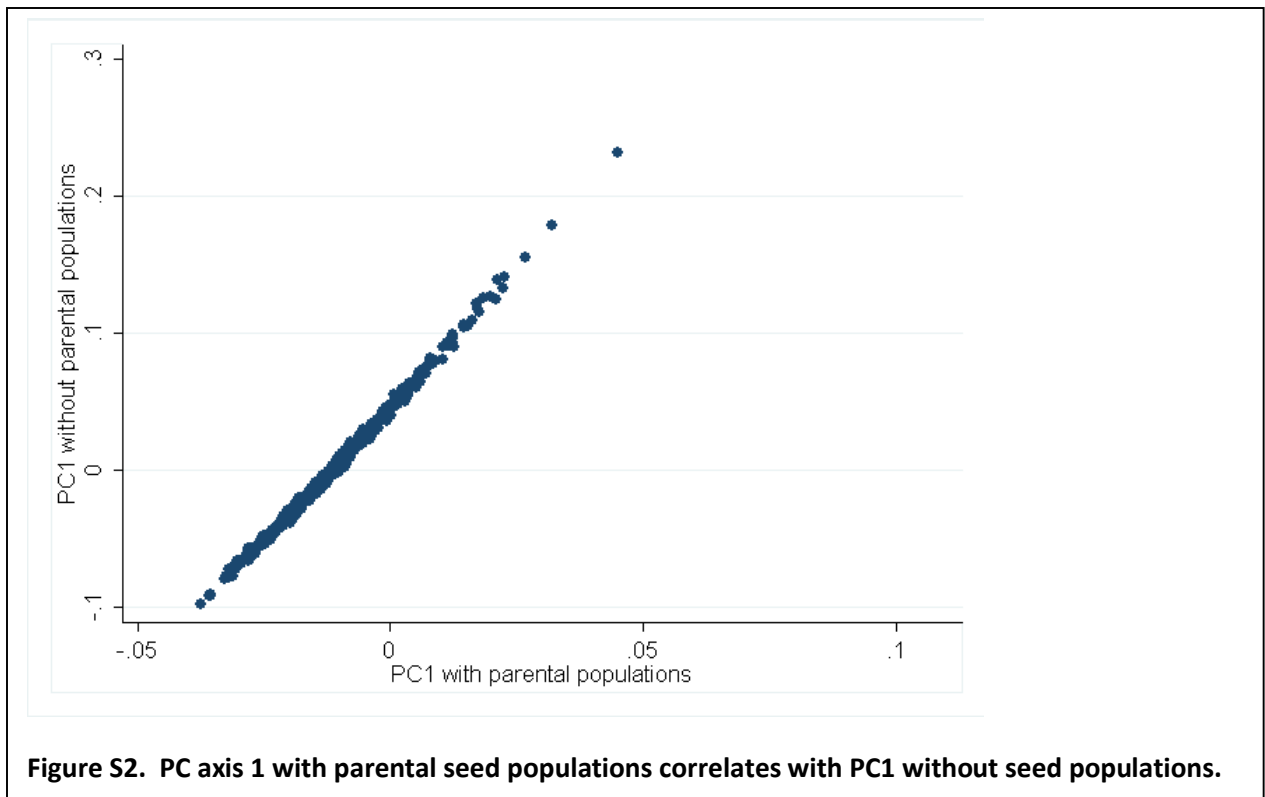


Table S1. Association results corrected for PC1 with or without parental seed populations

Phenotype / Test	P value corrected for PC1 without parental seed populations	P value corrected for PC1 with parental seed populations
Viral load/Linear regression	0.524	0.689
Progression (with HARRT as time varying variable) / Cox proportional-hazards regression	0.191	0.178
HIV infection status/Logistic regression	0.555	0.486