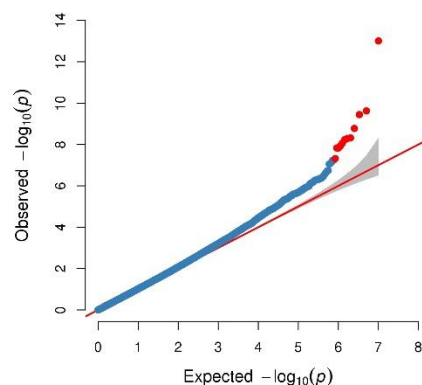
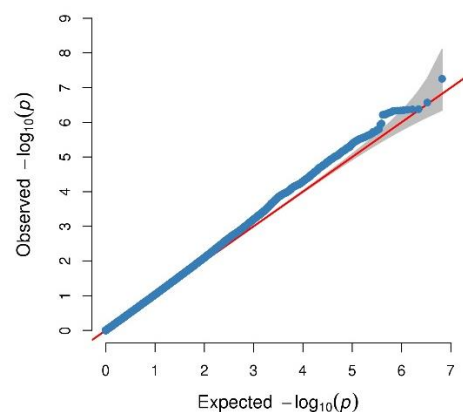


**Supplementary Figure 1.** Quantile-quantile plots for the GWAS in **(A)** African American (AA), **(B)** European ancestry (EA), and **(C)** combined AA and EA datasets. Estimates of p-value inflation ( $\lambda$ ) are 1.020, 1.038, and 1.041 for the GWAS in AAs, EAs and combined population, respectively. Red dots represent the observed genome-wide significant variants.

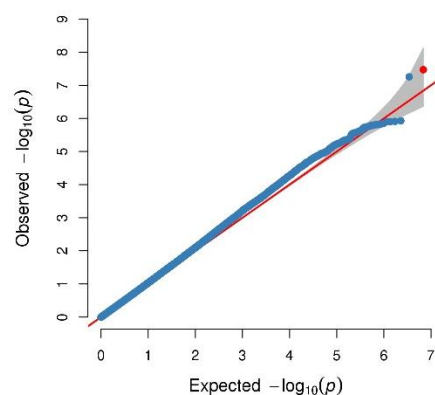
(a)



(b)

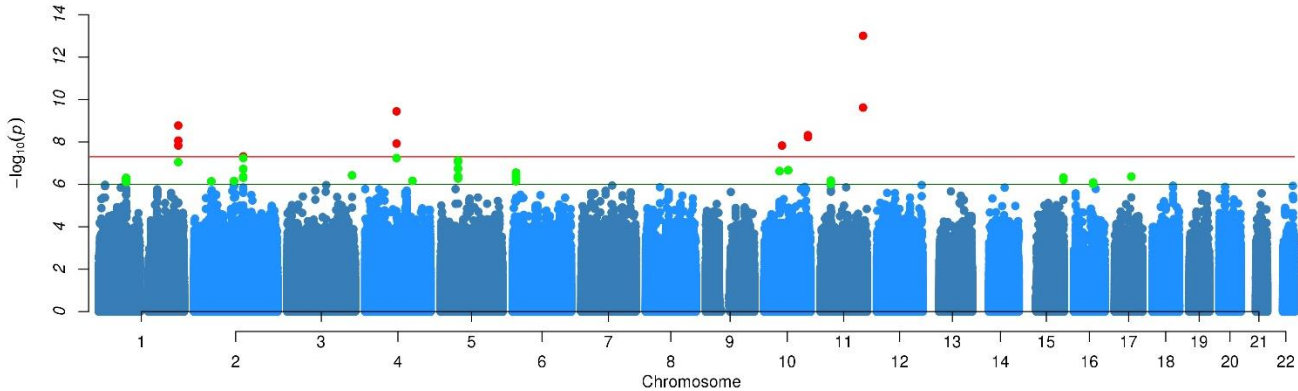


(c)

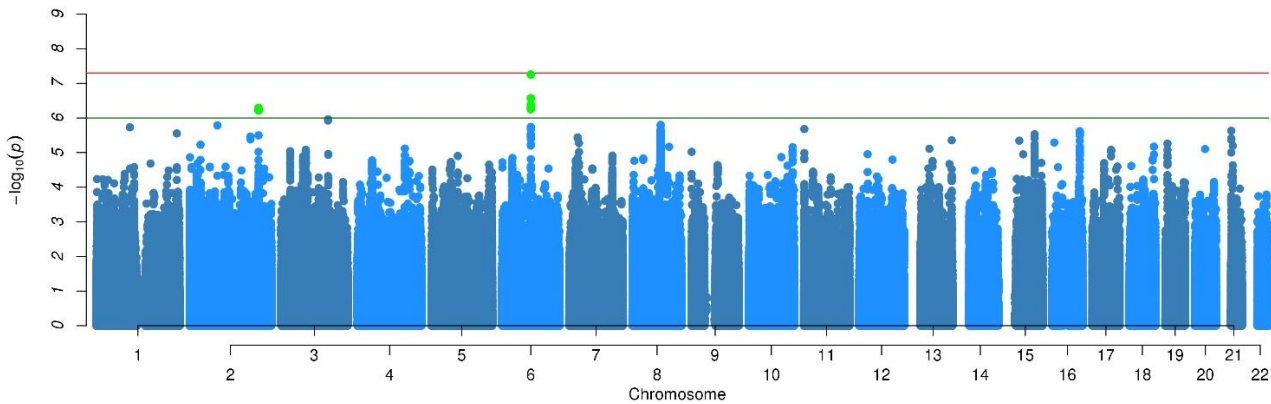


**Supplementary Figure 2.** GWAS results for **(A)** African American (AA), **(B)** European ancestry (EA), and **(C)** combined AA and EA discovery datasets. Red dots represent SNPs that surpassed the genome-wide significant threshold ( $p < 1 \times 10^{-8}$ ) indicated by a red line. Green dots above the green line represent SNPs that showed suggestive evidence for association ( $p < 1 \times 10^{-6}$ ).

**(A)**



**(B)**



**(C)**

