Supplementary Information

Supplementary Research Support Information:

ARIC: A collaborative study supported by the National Heart, Lung and Blood Institute contracts N01-HC-55015, N01-HC-55016, N01-HC-55018, N01-HC-55019, N01-HC-55020, N01-HC-55021, N01-HC-55022 and R01HL087641; National Human Genome Research Institute award U01HG004402; NIH Intramural Research award ZIAEY000426 from the National Eye Institute; and National Institutes of Health contract HHSN268200625226C. Infrastructure was partly supported by Grant Number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research. The authors thank the staff and participants of the ARIC study for their important contributions.

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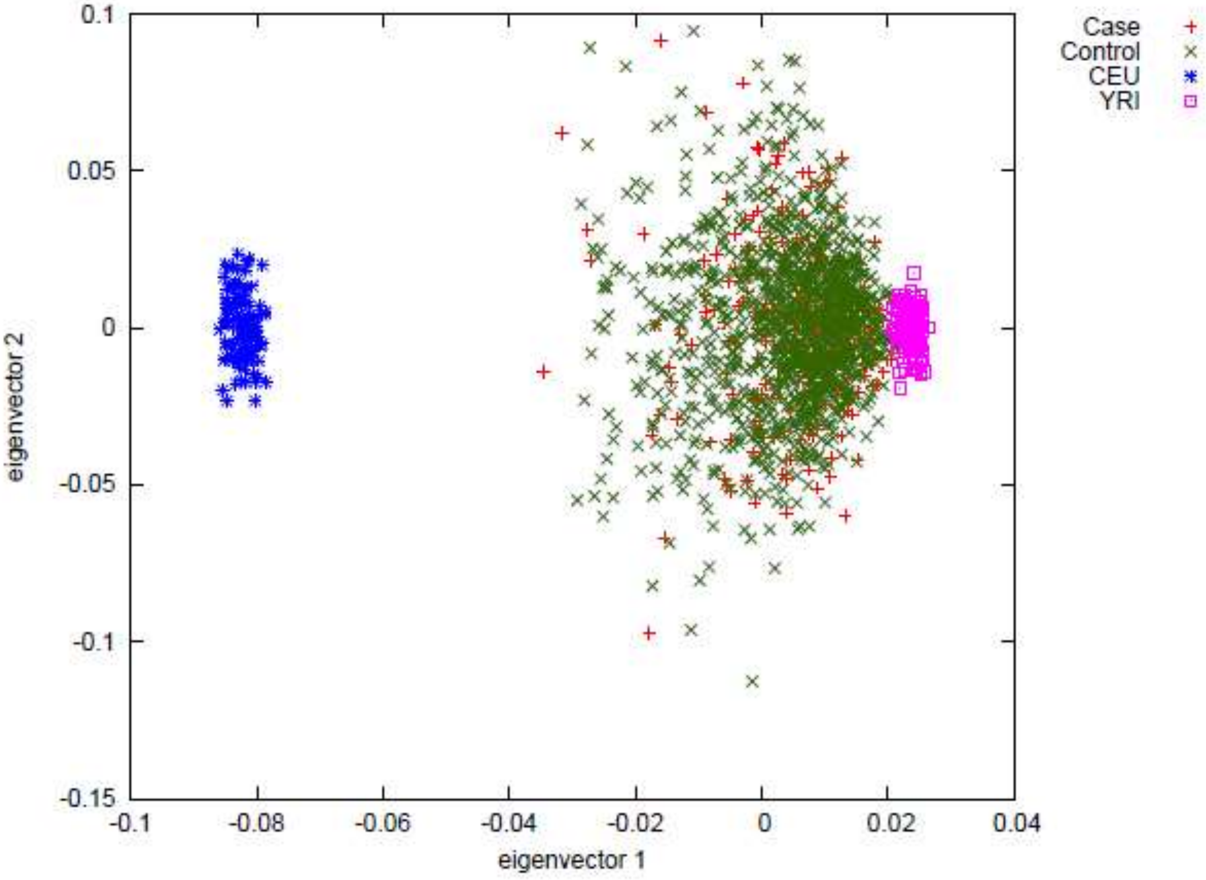
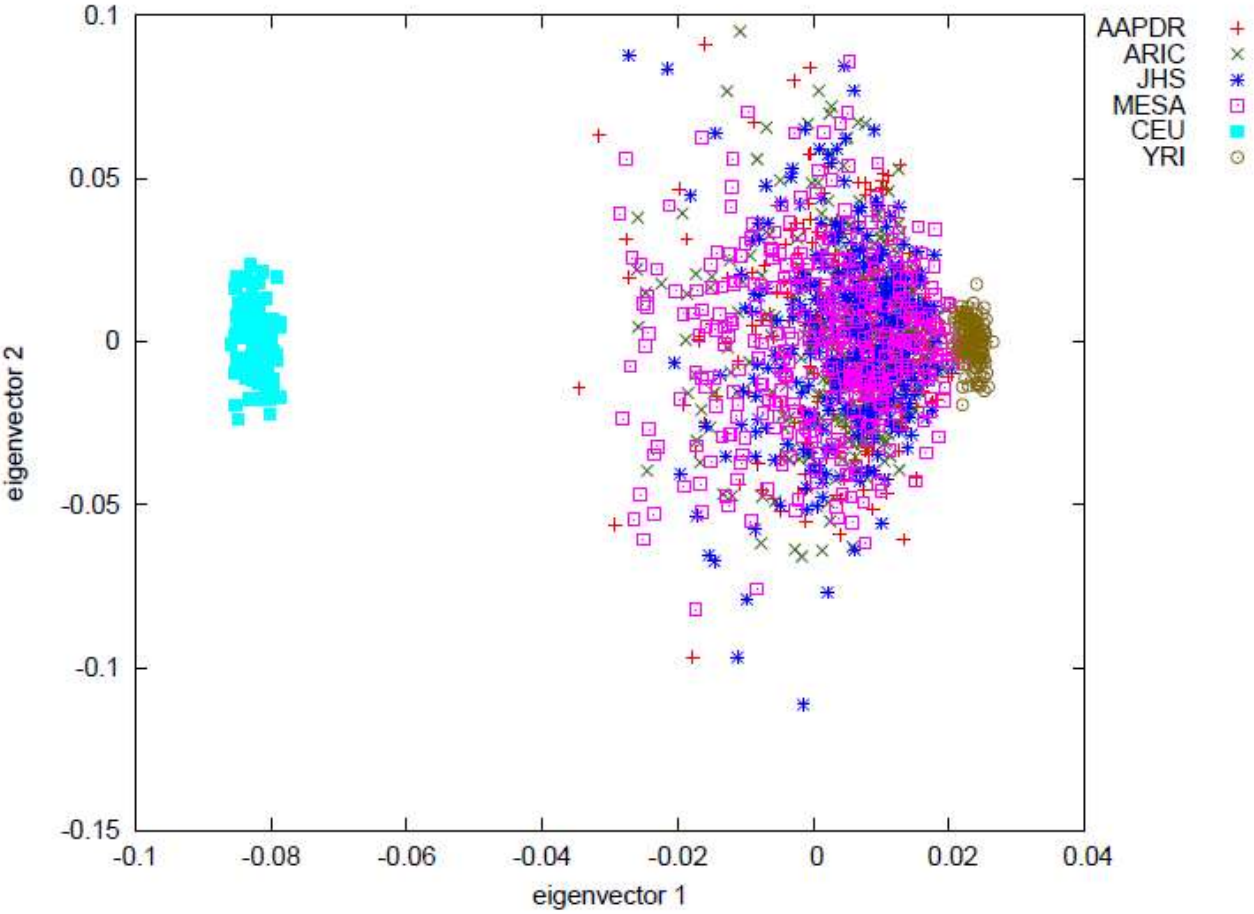
Supplementary Figure S1. Plot of first two principal components of HapMap YRI (Yoruban African) and CEU (European) samples and participants by (A) Case-Control Status and (B) Cohort Study

A.



B.



AAPDR +
ARIC ×
JHS ✱
MESA ⊡
CEU ■
YRI ⊙
0.1
0.05
0
-0.05
-0.1
-0.15
eigenvector 2
-0.1
-0.08
-0.06
-0.04
-0.02
0
0.02
0.04
eigenvector 1

Supplementary Figure S2. Genome-wide admixture mapping scan for loci associated with diabetic retinopathy in the African American Proliferative Diabetic Retinopathy Study where controls all had type 2 diabetes for at least 10 years and no proliferative diabetic retinopathy. The maximum locus genome statistic score was 2.67 on chromosome 14 which did not meet genome-wide statistical significance. The dashed line indicates the level of genome wide significance (locus genome statistic score of 5).