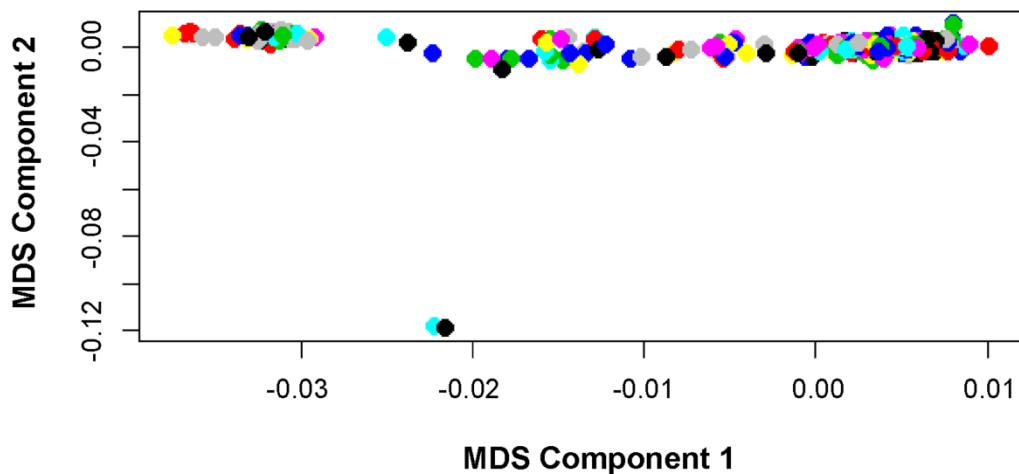
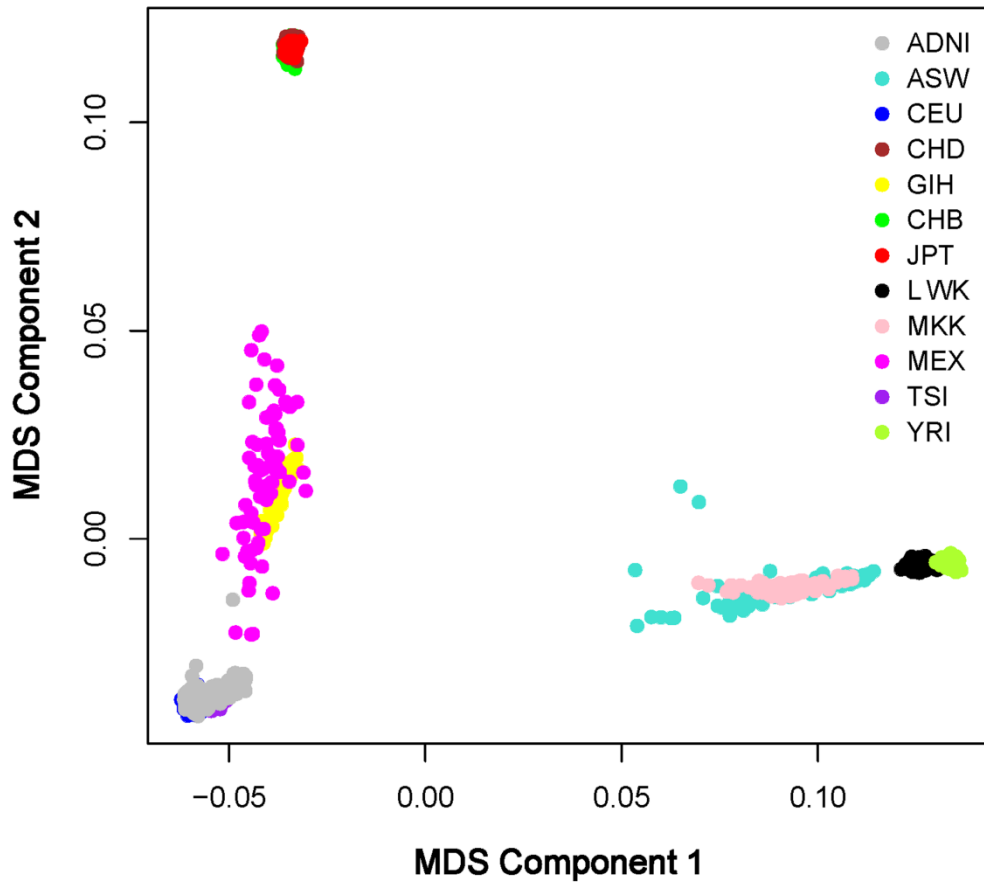


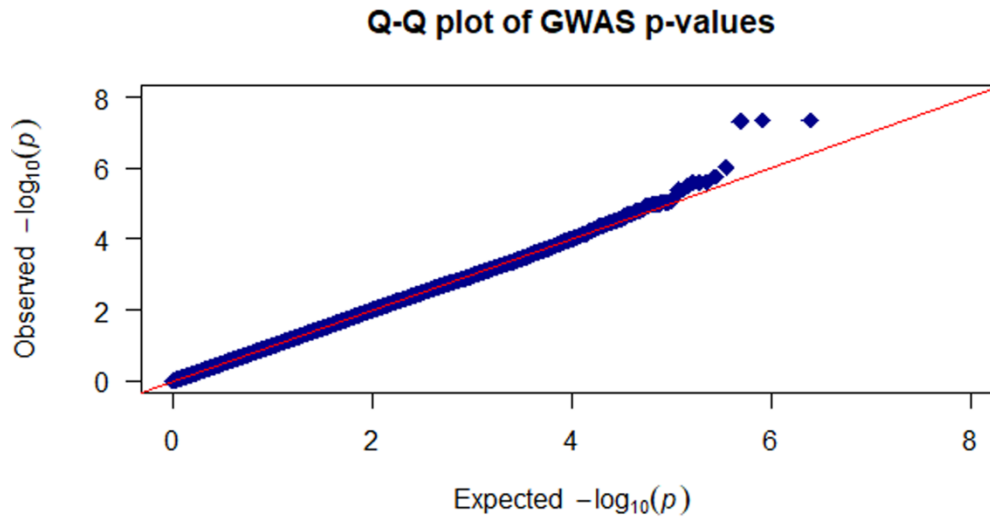
## SUPPLEMENTARY FIGURES



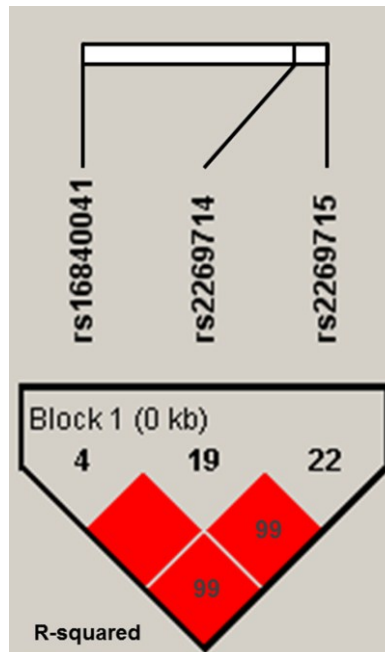
**Supplementary Figure 1. MDS plot of ADNI non-Hispanic Caucasian samples.** Samples seemed to form loose clusters and two samples were outliers based on the second MDS component (at bottom of plot; 031\_S\_4032 and 031\_S\_4203), suggesting potential population substructure. To check for cryptic relatedness, which can confound GWAS studies, pairwise identity-by-descent fraction ( $\pi$ ) between each pair of samples were calculated using PLINK. Three related sample pairs were identified (137\_S\_4466 and 021\_S\_0159,  $\pi = 0.50$ ; 023\_S\_0058 and 023\_S\_4035,  $\pi = 0.48$ ; 024\_S\_2239 and 024\_S\_4084,  $\pi = 0.42$ ), which are probably first-degree relatives. Optionally, we remove one member of each pair. No other cryptic relations were identified from the sample, at a threshold of  $\pi > 0.05$ .



**Supplementary Figure 2. MDS plot of ADNI samples overlaid on HapMap samples.** The ancestry of the HapMap participants is shown by the point color. The outlying point represents Participant 116\_S\_1315 who is likely of mixed ancestry. Abbreviations: MDS, multidimensional scaling; ADNI, Alzheimer’s Disease Neuroimaging Initiative; ASW, African ancestry in Southwest USA; CEU, Utah residents with Northern and Western European ancestry from the CEPH collection; CHB, Han Chinese individuals from Beijing, China; CHD, Chinese in Metropolitan Denver, Colorado; GIH, Gujarati Indians in Houston, Texas; JPT, Tokyo, Japan; LWK, Luhya in Webuye, Kenya; MEX, Mexican ancestry in Los Angeles, California; MKK, Maasai in Kinyawa, Kenya; TSI, Tuscans in Italy; YRI, Yoruba in Ibadan, Nigeria.



Supplementary Figure 3. The quantile-quantile (QQ) plot shows the negative logarithm of the observed and the expected p-value for each SNP.



Supplementary Figure 4. Linkage-disequilibrium (LD) analysis of the variants rs16840041, rs2269714 and rs2269715 in *CD1A*. Pairwise linkage disequilibrium analysis shows  $r^2$  ( $\times 100$ ) values. The LD plots were generated using the Haploview software v4.2.