*DNA Collection, Genotyping, and Quality Control*

DNA was extracted from whole blood samples using the PUREGENE® DNA Isolation Kit (Gentra Systems, Inc., Minneapolis, MN). DNA concentrations were quantified using UV spectrophotometry (DU® 530 Spectrophotometer, Beckman Coulter, Fullerton, CA). A total of 37 SNPs in 1,456 individuals were genotyped using competitive allele-specific PCR based KASPTM genotyping assays (LGC Genomics, Beverly, MA). Duplicate quality control (QC) samples from 102 individuals were placed randomly throughout each of the 96-well plates. The genotype concordance rate was 99.73%. All discordant genotypes were set to missing. To assess the potential for sample mislabeling, concordance was also assessed with previous genotyping that included three overlapping variants (rs7412 and rs429358 in apolipoprotein E(*APOE*), and rs6656401 in *CR1*) in 1,152 individuals. Six genotypes were discordant in six different individuals, who were removed from further analyses.

Further QC was conducted using PLINK v1.07 (Purcell, et al. 2007). Five individuals were excluded due to high missingness of alleles (>10%). No SNPs were excluded due to low call rates (<95%), however, 4 SNPs were excluded as a result of being monomorphic in our sample (rs4819 in *PLD3*, and rs63750847 in *APP*, and 2 SNPs from an African-American GWAS meta-analysis (Reitz, et al. 2013): rs145848414 (an intergenic SNP on chromosome 5) and rs6973770 in *EPHA1-AS1*). Hardy-Weinberg equilibrium (HWE) was assessed among a subset of 1,120 unrelated individuals using a Bonferroni adjusted p-value threshold of .05/33=.0015. One SNP failed HWE (p=.00104) but was retained due to the negligible difference from the p-value threshold (rs28834970 in *PTK2B*). A total of 1,451 individuals and 33 SNPs remained after the completion of all QC procedures.