

Single nucleotide polymorphism (SNP) tags in these 100 candidate genes were selected to represent the gene and 10 kilobases flanking each side based on the following criteria: 1) Illumina SNP design score  $\geq 0.6$ , 2) reported minor allele frequency  $\geq 0.05$ , 3) 80% coverage of each gene in European and African HapMap samples at a pairwise  $r^2 \geq 0.8$ . SNPs were tagged using the Tagger Server [10] in HapMap's population of European ancestry (CEPH) first to provide coverage for HABC Caucasian participants, then further tagged in HapMap's African population (YRI) to fill in areas of lower linkage disequilibrium (LD) in African Americans. NCBI Build 35 and HapMap release 21 were used for this selection process.

A panel of 1,295 SNPs in 100 candidate genes was genotyped using Illumina BeadArray technology at the Johns Hopkins Core SNP Center. DNA used was whole-genome amplified from 15 ng of genomic DNA prior to PCR in the Johns Hopkins Institute for Genetic Medicine. Allele frequencies were calculated and Hardy-Weinberg equilibrium was tested for each genotyped SNP. Pairwise LD measures ( $D'$  and  $r^2$ ) were calculated for SNPs within each gene.