162162

G00002

ABSTRACT

The present invention relates to methods for identifying variations that occur in the human genome and relating these variations to the genetic basis of disease and drug response. In particular, the present invention relates to identifying individual SNPs, determining SNP haplotype blocks and patterns, and, further, using the SNP haplotype blocks and patterns to dissect the genetic bases of disease and drug response. The methods of the present invention are useful in whole genome analysis.