1. Result file from plink analysis with brain volume
2. File with all of the subject numbers and family ID, and Gender and Alleles at each specific snp
3. A file with the SNP name, Chromosome Number, a useless column and the base pair position
4. A file with the phenotype “brain volume” data for each subject organized in the same sorting order as the genetic file with 3 columns: a unique number for each subject, the subject ID, and the phenotype