**GIANT Consortium 2010 GWAS Summary Statistics**

Each file consists of the following information for each SNP and its association to the specified trait based on meta-analysis in the respective publication. SNPs where N < 50% of the maximum have been excluded.

**MarkerName:** The [dbSNP](https://www.ncbi.nlm.nih.gov/snp) name of the genetic marker

**Allele1:** The first allele, by definition the trait-increasing allele (hg18 + strand)

**Allele2:** The second allele (hg18 + strand)

**Freq.Allele1.HapMapCEU:** The allele frequency of Allele1 in the [HapMap](https://www.ncbi.nlm.nih.gov/variation/news/NCBI_retiring_HapMap/) CEU population

**P:** P value after meta-analysis using regression coefficients (beta and standard error), and after correction for inflation of test statistics using genomic control both at the individual study level and again after meta-analysis

**N:** Number of observations