**GIANT Consortium 2012-2015 GIANT 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. Significant digits for the p values, betas and standard errors are limited to two digits to further limit the possibility of identifiability.

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

**Allele1:** The first allele (hg19 + strand). Where the regression coefficients (betas) are provided, the first allele is the effect allele. Where betas are not provided (typically the 2010 data), the first allele is the trait-increasing allele.

**Allele2:** The second allele (hg19 + 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

**b:** beta

**SE:** standard error

**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

For the Height DEPICT Gene Set Enrichment Analysis file, the columns are as follows:

**A:** the ID of the predefined gene set (before reconstitution by DEPICT);

**B:** the name of the gene set;

**C:** the DEPICT P-value for enrichment;

**D:** the false discovery rate for enrichment;

**E:** the genes in the gene set that overlap height-associated loci