**2018 Exome Array Summary Statistics**

**Height Exome Array 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.

**Column headers:**

1. CHR: chromosome

2. POS: position of the variant (hg19)

3. REF: reference allele (hg19 + strand)

4. ALT: alternate allele (hg19 + strand)

5. SNPNAME: dbSNP name of the genetic marker

6. (one among these)

GMAF: Non-reference allele and frequency of existing variant in 1000 Genomes

AFR\_MAF: Non-reference allele and frequency of existing variant in 1000 Genomes combined African population

AMR\_MAF: Non-reference allele and frequency of existing variant in 1000 Genomes combined American population

EUR\_MAF: Non-reference allele and frequency of existing variant in 1000 Genomes combined European population

EAS\_MAF: Non-reference allele and frequency of existing variant in 1000 Genomes combined East Asian population

SAS\_MAF: Non-reference allele and frequency of existing variant in 1000 Genomes combined South Asian population

7. (one among these)

ExAC\_MAF: Frequency of existing variant in ExAC combined population

ExAC\_AFR\_MAF: Frequency of existing variant in ExAC African/American population

ExAC\_AMR\_MAF: Frequency of existing variant in ExAC American population

ExAC\_EAS\_MAF: Frequency of existing variant in ExAC East Asian population

ExAC\_NFE\_MAF: Frequency of existing variant in ExAC Non-Finnish European population

ExAC\_SAS\_MAF: Frequency of existing variant in ExAC South Asian population

8. beta: beta

9. se: standard error

10. Pvalue: p-value after meta-analysis using regression coefficients (beta and standard error)