DIAGRAMv3 GWAS meta-analysis
6 December 2012

This file contains association summary statistics for the DIAGRAMv3 GWAS meta-analysis, as published in Morris et al. (2012).

The meta-analysis consists of 12,171 T2D cases and 56,862 controls across 12 GWAS from European descent populations. Samples were typed with a range of GWAS genotyping products. Sample and SNP quality control (QC) were undertaken within each study. Each GWAS was then imputed at up to 2.5M SNPs using CEU samples from Phase II of the International HapMap Project. Each SNP with MAF>1% passing QC was tested for association with T2D under an additive model after adjustment for study-specific covariates including indicators of population structure. Full details of genotyping, QC and imputation for each study are presented in Supplementary Table 1 of Morris et al. (2012).

The results of each GWAS were corrected for residual population structure using the genomic control inflation factor, as reported in Supplementary Table 1 of Morris et al. (2012). Association summary statistics were then combined via fixed-effects inverse-variance weighted meta-analysis.

Please note that the summary statistics presented in this file have not been corrected for a second round of genomic control after meta-analysis. Should you wish to "double genomic control" the association summary statistics, the inflation factor from the meta-analysis is $\lambda=1.10$.

For each SNP, we have provided the following information:
1. Chromosome and position (build 36, bp)
2. Risk and other allele (aligned to the forward strand)
3. P-value for association
4. Odds ratio for the risk allele and corresponding 95% confidence limits
5. Number of cases and controls reported

The sample size and precision of the data presented should preclude de-identification of any individual subject. However, in downloading these data, you undertake:
- not to attempt to de-identify individual subjects;
- not to repost these data to a third party website.

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