Trans-ethnic T2D GWAS meta-analysis
14 October 2014

This file contains association summary statistics for the trans-ethnic T2D GWAS meta-analysis as published in Mahajan *et al*. (2014).

Ancestry-specific meta-analyses were previously performed by: the DIAGRAM Consortium (12,171 cases and 56,862 controls, European ancestry); the AGEN-T2D Consortium (6,952 cases and 11,865 controls, East Asian ancestry); the SAT2D Consortium (5,561 cases and 14,458 controls, South Asian ancestry); and the MAT2D Consortium (1,804 cases and 779 controls, Mexican and Mexican American ancestry). Further details of the samples and methods employed within each ancestry group are presented in the corresponding consortium papers (see references). Briefly, individuals were assayed with a range of genotyping products, with sample and SNP quality control (QC) undertaken within each individual study. Each GWAS scaffold was imputed up to 2.5 million autosomal SNPs using reference panels from Phase II/III HapMap. Each SNP with MAF>1%, (except MAF>5% in the Mexican and Mexican American ancestry GWAS due to smaller sample size), and passing QC, was tested for association with T2D under an additive model after adjustment for study-specific covariates. The results of each GWAS were corrected for population structure with genomic control (unless λ_{GC}<1). Association summary statistics from GWAS within each ancestry group were then combined via fixed-effects meta-analysis. The results of each ancestry meta-analysis were then corrected by a second round of genomic control: European ancestry (λ_{GC}=1.10); East Asian ancestry (λ_{GC}=1.05); South Asian ancestry (λ_{GC}=1.02); Mexican and Mexican American ancestry (λ_{GC}=1.01).

Association summary statistics from each ancestry-specific meta-analysis were combined via fixed-effects inverse-variance weighted meta-analysis (in a total of 26,488 cases and 83,964 controls). The association results of the trans-ethnic meta-analysis were corrected by a final round of genomic control (λ_{GC}=1.05).

Note that association summary statistics have been through three rounds of genomic control: at the cohort level, after ethnic-specific meta-analysis, and finally after trans-ethnic meta-analysis.

For each SNP, we have provided the following information:
1. Chromosome and position (build 36, base-pairs)
2. Risk and other allele (aligned to the forward strand)
3. Odds ratio for the risk allele and corresponding 95% confidence limits
4. P-value for association
5. Total sample size reported
6. Direction of effects in ethnic-specific meta-analyses: DIAGRAM (European), SAT2D (South Asian), MAT2D (Mexican and Mexican American), and AGEN-T2D (East Asian)

The sample size and precision of the statistics presented should preclude identification of any individual subject. **However, in downloading these data, you undertake not to attempt to de-identify individual subjects.**

Please refer any queries to:
Andrew Morris (apmorris@liverpool.ac.uk)
Mark McCarthy (mark.mccarthy@drl.ox.ac.uk)