DIAGRAM Metabochip meta-analysis
18 April 2013

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

Stage 1 of 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. The results of the Stage 1 meta-analysis were then corrected for residual inflation using the genomic control inflation factor.

Stage 2 of the meta-analysis consists of 22,669 cases and 58,119 controls genotyped with Metabochip, primarily from European descent populations, but including 1,178 cases and 2,472 controls of Pakistani descent (PROMIS). Samples were typed with the Metabochip. Sample and SNP QC were undertaken within each study. 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 study were corrected for residual population structure using QT interval SNPs, 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. The results of the Stage 2 meta-analysis were then corrected for residual inflation using the genomic control inflation factor from QT interval SNPs.

Association summary statistics for Metabochip SNPs for the two stages were then combined via fixed-effects inverse-variance weighted meta-analysis, and adjusted for a final round of QT interval SNP correction for residual inflation.

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. Total effective sample size.

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.

Please refer any queries to:

Andrew Morris
Mark McCarthy