**DIAGRAM 1000G GWAS meta-analysis Stage 1 Summary statistics 31 May 2017**

This file contains association summary statistics for the DIAGRAM 1000 Genomes – imputed GWAS meta-analysis, as published in Scott et al. (Diabetes, May 2017; db161253. https://doi.org/10.2337/db16-1253).

The stage 1 analyses comprised a total of 26,676 T2D cases and 132,532 control participants from 18 GWAS. Samples were typed with a range of GWAS genotyping products. Sample and SNP quality control (QC) were undertaken within each study. We imputed autosomal and X chromosome SNVs using the all ancestries 1000 Genomes Project (1000G) reference panel (1,092 individuals from Africa, Asia, Europe, and the Americas [March, 2012 release]). Full details of genotyping, QC and imputation for each study are presented in Supplementary Table 1 of Scott et al. (Diabetes, 2017).

In stage 1, in each study we performed logistic regression association analysis of T2D with genotype dosage using an additive genetic model including as covariates age, sex and principal components derived from the genetic data to account for population stratification. Fifteen of the 18 studies repeated analyses also adjusting for body mass index (BMI). We further applied genomic control (GC) correction to study-level association summary statistics to correct for residual population structure not accounted for by principal components adjustment. We combined the association results using inverse variance-weighted fixed effect meta-analysis. The stage 1 meta-analysis focussed on SNVs that (1) had a total minor allele count >5, and (2) were present in ≥3 studies.

**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 $\lambda$=1.08.

**For each SNP, we have provided the following information:**
1. Chromosome and position (build 37, bp)
2. Allele 1 and Allele 2 (aligned to the forward strand)
3. P-value for association
4. Effect for the Allele 1 and corresponding Standard Error
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.

Please refer any queries to:
Inga Prokopenko
Mark McCarthy
Michael Boehnke