DIAGRAM meta-analysis of type 2 diabetes (T2D) based on the GoT2D integrated haplotypes.

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This file contains association summary statistics for the DIAGRAM meta-analysis of 13 cohorts imputed from the GoT2D reference panel, published in Fuchsberger et al. (2016).

We carried out genotype imputation into 44,414 individuals (11,645 T2D cases and 32,769 controls) from 13 studies using the GoT2D integrated haplotypes as reference panel. Each study performed its own sample- and variant-based QC. In each study, SNVs with minor allele count (MAC)≥1 passing QC were tested for T2D association assuming an additive genetic model adjusting for study-specific covariates. Association testing was performed using logistic regression Firth bias-corrected, likelihood ratio, or score tests as implemented in EPACTS (genome.sph.umich.edu/wiki/EPACTS) or SNPTEST. To account for related samples in the Framingham Heart Study, generalized estimating equations (GEE) were used, as implemented in R. Residual population stratification for each study was accounted for using genomic control. We then carried out fixed-effects sample-size weighted meta-analysis as implemented in METAL.

For each SNP, we have provided the following information:

1. Chromosome and position (build 37, base-pairs).
2. Allele 1 and Allele 2 (aligned to the forward strand).
3. Allele 1 frequency.
4. P-value for association.
5. Total reported effective sample size.

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.

Reference: Fuchsberger C, et al. (2016). The genetic architecture of type 2 diabetes. Nature (in press).

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