DIAMANTE (European) meta-analysis of type 2 diabetes
5th March 2022

Reference: Mahajan A, *et al*. (2018b). Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics* http://dx.doi.org/10.1038/s41588-018-0241-6.

In this study we aggregated GWAS results for 32 studies for 898,130 individuals (74,124 T2D cases and 824,006 controls) of European ancestry, a 3.2-fold increase in effective sample size from previous studies of T2D risk in Europeans. Imputation was performed using the Haplotype Reference Consortium reference panel for all of the component studies except deCODE GWAS, which was imputed using a population-specific reference panel.

Association summary statistics from sex-combined analyses for each variant across all studies, with and without adjustment for BMI, were aggregated using fixed-effects meta-analysis with inverse-variance weighting of log-ORs. At study level, association summary statistics were corrected for residual inflation by means of genomic control. The BMI unadjusted meta-analysis was subsequently corrected for residual inflation (to account for structure between studies) by means of genomic control. No adjustment was required for the BMI adjusted meta-analysis.

Fine-mapping was performed for 380 independent T2D association signals to generate credible sets of variants that together account for 99% of the posterior probability of driving the association.

The download contains following data sets:

i) The full meta-analysis of all studies to generate associations for *T2D unadjusted for BMI* (**Mahajan.NatGenet2018b.T2D.European.gz**)
ii) The full meta-analysis of all studies to generate associations for *T2D adjusted for BMI* (**Mahajan.NatGenet2018b.T2Dbmiadj.European.gz**)
iii) Summary of T2D associations of HRC variants for *only European UK Biobank subjects* (**Mahajan.NatGenet2018b.UKBB.HRC.T2D.European.gz**). Association analysis was conducted using the UK Biobank resource under application number ***9161 (McCarthy)***.
iv) 99% credible sets of variants for 380 distinct association signals
    a. genetic_credible_sets.tar.gz
    b. functional_credible_sets.tar.gz

v) Summary of sex-specific *T2D* association *unadjusted for BMI*
    a. **Mahajan.NatGenet2018b.T2D.FEMALE.European.txt.gz**
    b. **Mahajan.NatGenet2018b.T2D.MALE.European.txt.gz**

vi) Summary of *T2D association unadjusted for BMI* – ***WITHOUT UK BIOBANK samples***
    a. **Mahajan.NatGenet2018b.T2D-noUKBB.European.gz**

b. **Mahajan.NatGenet2018b.T2D-noUKBB.FEMALE.European.txt.gz**
c. **Mahajan.NatGenet2018b.T2D-noUKBB.MALE.European.txt.gz**

In the summary files, for each SNP, we have provided the following information:

- Chromosome and position (build 37, base-pairs).
- Effect (EA) and non-effect allele (NEA), aligned to the forward strand.
- Effect allele frequency (EAF).
- Log-odds ratio for the effect allele (Beta) and the corresponding standard error (SE).
- P-value for association (Pvalue).
- Total reported effective sample size (Neff) / total sample size for UK Biobank (N).

For credible set of each of the 380 distinct association signal, we provide the following information:

- Index SNP.
- Chromosome and position (build 37, base-pairs) of all variants contained in the 99% credible set.
- Posterior probability of driving the association signal.

The sample size and precision of the statistics 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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