

GWAS summary statistics for type 2 diabetes

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This file contains association summary statistics for the meta-analysis of type 2 diabetes (T2D), published in Xue *et al.* (Nature Communications, 2018).

We conducted a meta-analysis of genome-wide association studies (GWAS) with ~16 million genetic variants in 62,892 T2D cases and 596,424 controls of European ancestry, by combining three GWAS data sets: DIAbetes Genetics Replication And Meta-analysis (DIAGRAM), Genetic Epidemiology Research on Aging (GERA) and the full cohort release of the UK Biobank (UKB). Full details of genotyping, QC, association analysis for each study are provided in the Methods section of Xue *et al.* Nature Communications, 2018. Here, we provided the meta-analysis results for ~5.1 million common SNPs.

For each SNP, we have provided the following information:

- CHR: Chromosome
- BP: Base-pairs position (build 37)
- SNP: rsID
- A1: minor allele
- A2: major allele
- Frq_A1: allele frequency of A1
- b: effect size of A1
- se: standard error of b
- P: p-value
- N: sample size

Reference: Xue A, *et al.* (2018). Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. *Nature Communications*. 2018 (accepted).

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