ExTexT2D Exome Chip meta-analysis of type 2 diabetes

9th April 2018

This file contains association summary statistics for the ExTexT2D exome chip meta-analysis of type 2 diabetes (T2D), published in Mahajan *et al.* (Nature Genetics, 2018; http://dx.doi.org/10.1038/s41588-018-0084-1).

We aggregated T2D association summary statistics in up to 452,244 individuals (effective sample size 228,825) across five ancestry groups, performing both European-specific and trans-ethnic meta-analyses. Sample and variant quality control was performed within each study. Full details of genotyping, QC, association analysis for each study are provided in Supplementary Tables and Methods section of Mahajan *et al*. Nature Genetics, 2018.

The European-specific meta-analyses comprised of a total of 48,286 cases and 250,671 controls. The trans-ethnic meta-analyses aggregated association summary statistics from a total of 81,412 cases and 370,832 controls across all studies. Association analyses were conducted with and without body mass index adjustment.

Association summary statistics across all studies were aggregated under an additive model: (i) effective sample size weighting of *Z*-scores to obtain *p*-values; and (ii) inverse variance weighting for log-odds ratios. At study level, association summary statistics were corrected for residual inflation by means of genomic control. A second round of genomic control correction was then applied to the meta-analyses.

For each SNP, we have provided the following information:

- rsID
- Chromosome and position (build 37, base-pairs).
- Risk and other allele (aligned to the forward strand).
- Risk allele frequency.
- Odds ratio for the risk allele and the corresponding 95% confidence limits.
- P-value for association.
- Total reported effective sample size.

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.

Reference: Mahajan A, *et al*. (2018). Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nat Genet* (in press).

Please refer any queries to: Anubha Mahajan (anubha@well.ox.ac.uk).