Brief methods:

Fasting proinsulin values (pmol/L) were natural logarithm transformed and adjusted for age, sex, population structure, and natural logarithm of fasting insulin. Covariate adjustment was performed in two steps: first modeling natural logarithm of fasting proinsulin on all covariates, then inverse normal transforming the residuals, and then modeling the inverse normally transformed residuals on the covariates again. We performed a fixed-effects inverse-variance weighted meta-analysis using METAL, and applied double genomic-control (GC). Variants must be represented by at least one quarter of the maximum sample size, in at least two studies, and have an overall MAF > 0.005 for inclusion.

For each variant, we have provided the following information:

- chromosome: the chromosome that the variant is located on
- base_pair_location: the base pair location of the variant based in build 37
- effect_allele: the effect allele of the variant (+ strand)
- other_allele: the non-effect allele (+ strand)
- effect_allele_frequency: frequency of the effect allele in the meta-analysis
- beta: the effect size of the effect allele in the meta-analysis
- standard_error: the standard error of the effect size in the meta-analysis
- p_value: the p-value of the variant/trait association in the meta-analysis
- sample_size: the number of individuals after QC being tested for association at a specific variant
- het_p_value: heterogeneity test p-value