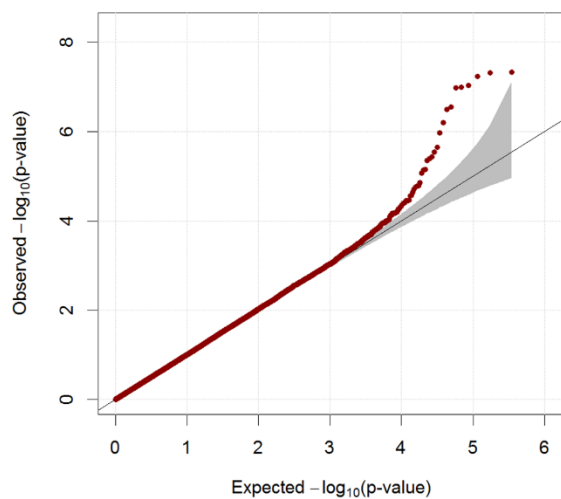


**Supplementary Fig. 1.** Results of single-variant analysis for 344,893 SNPs in KARE cohort.

(A) QQ plot of p-values derived from logistic regression with adjustments for Age, Sex, Area, and BMI. The shaded region represents the 95% confidence interval around the null hypothesis. (B) Manhattan plot of association p-values for T2D. The x-axis indicates the physical position of each genetic variant, and y-axis plots  $-\log_{10}(\text{p-value})$ . The genome-wide significance level is set to  $1.45 \times 10^{-07}$  and is plotted as a red dotted line. SNP, single-nucleotide polymorphism; KARE, Korean Association Resource; QQ, quantile-quantile; BMI, body mass index; T2D, type 2 diabetes.

**(A)**



**(B)**

