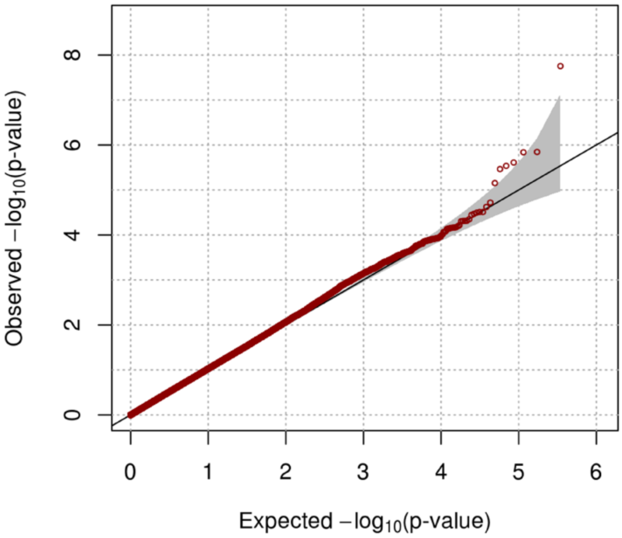
Supplementary Fig. 1. Results of single-SNP analysis for 344,893 SNPs in KARE data. (A) QQ plot of p-values derived from linear regression with adjustments for sex, age, and area. The 95% confidence interval around the null hypothesis is displayed as the shaded portion. (B) Manhattan plot of the single-SNP analysis. The red dotted line marks the threshold for genome-wide significance ($p = 1.45 \times 10^{-07}$). SNP, single-nucleotide polymorphism; KARE, Korea Association Resource; QQ, quantile-quantile.

(A)



(B)