SUPPLEMENTARY MATERIAL

Principal Component Analysis

We conducted Principal Component Analysis (PCA) using PLINK software on our GWAS data, generating principal component scores and eigenvalues. To determine the optimal number of components, we created a Scree Plot, identifying 'elbow' points after the 6th and 10th components (Figure S5). Quantitatively, the first 6 components explained 43% of variance, and the first 10 explained 61.1%. To balance dimensionality reduction and information preservation, we retained 10 components, aligning with best practices in exploratory analyses. Our genomic inflation est. lambda is 1.04787.

GWAS Power Calculations

Chi-squared power calculations for GWAS were performed using R software, with a total case-control sample size of 1679, a local disease prevalence of 0.1310 (Cheok et al., 2018), a statistical significance level of 5×10^{-8}, and an effect size of 0.5306 calculated from the OR of 1.70 for AD-only genome-wide association studies (Arehart et al., 2022). Based on these parameters, our study was calculated to possess sufficient statistical power, with power = 1.

doi: 10.18176/jiaci.0978

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