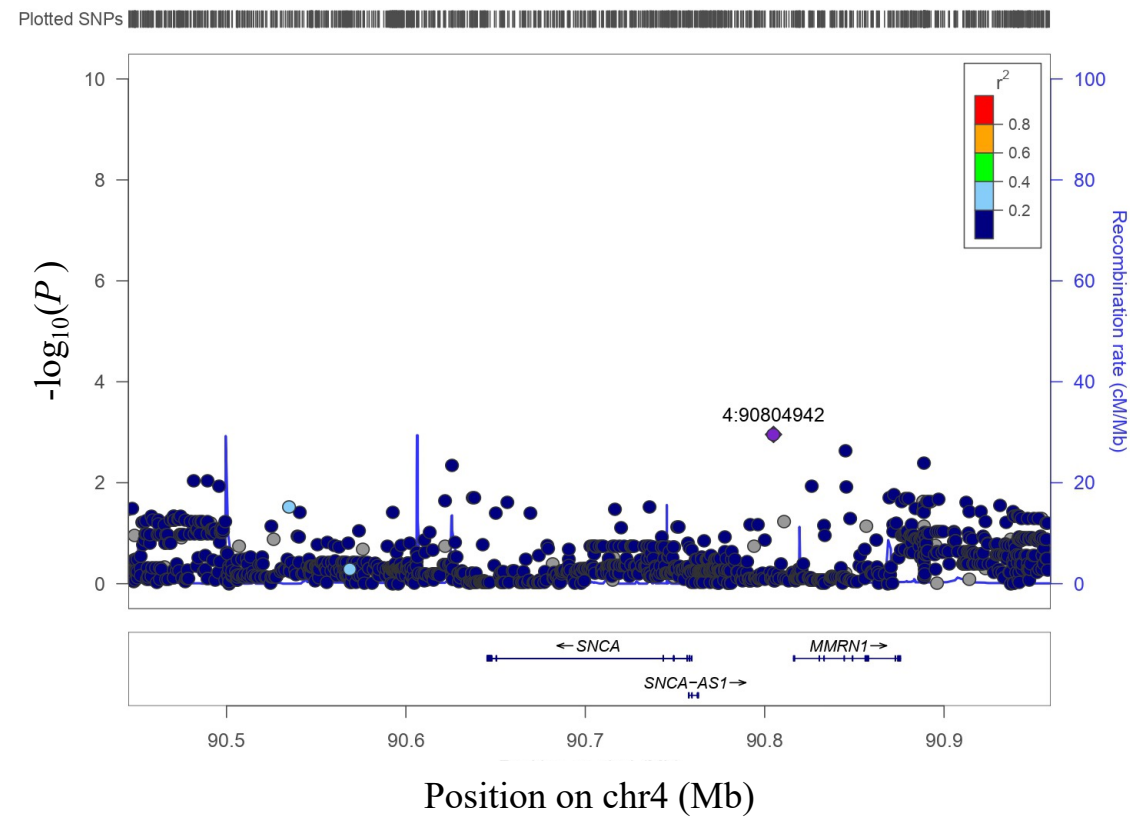
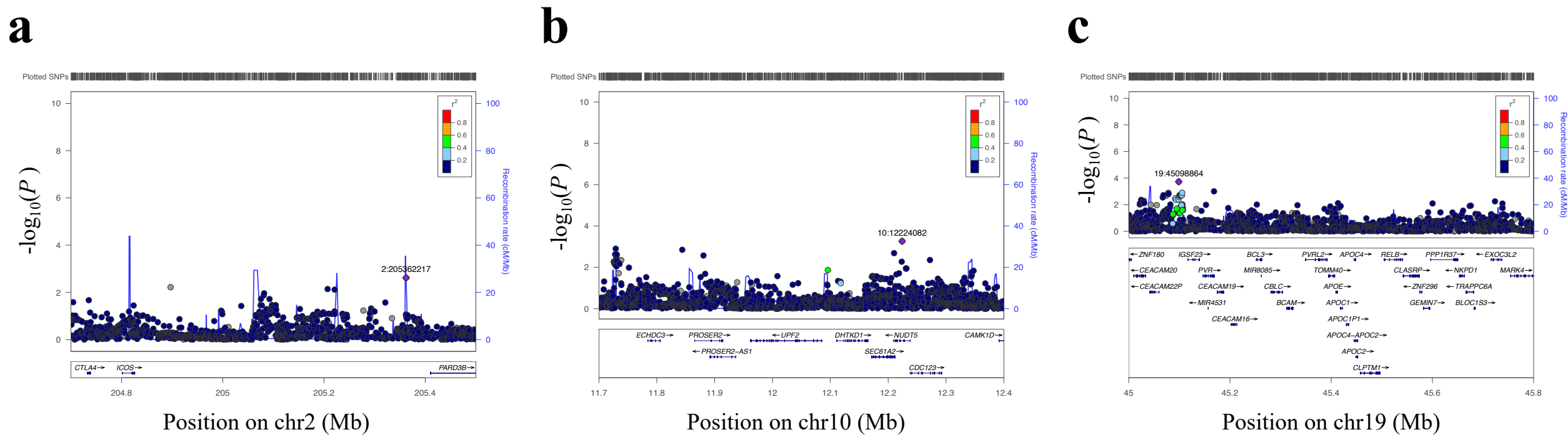


Fig. S2. Regional association plot of *SNCA* locus in Japanese DLB-GWAS.



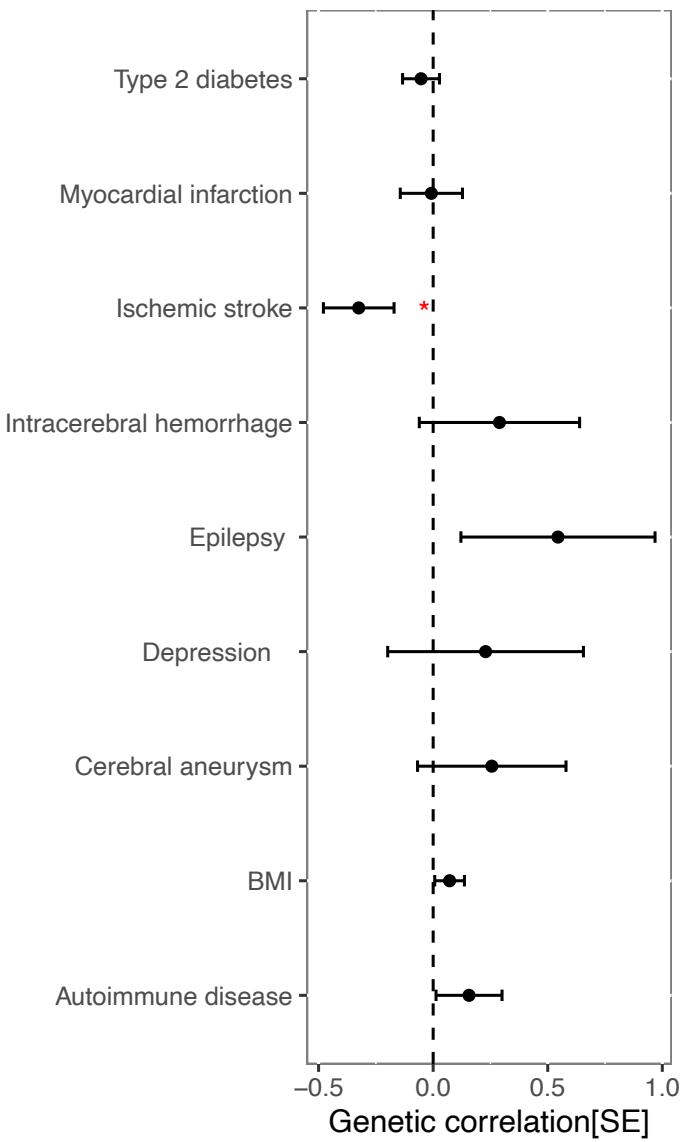
Regional association plot of well-known DLB-risk *SNCA* locus on chromosome 4 reported in Caucasian GWAS.

Fig. S3. Conditional analysis for loci identified in Japanese DLB-GWAS.



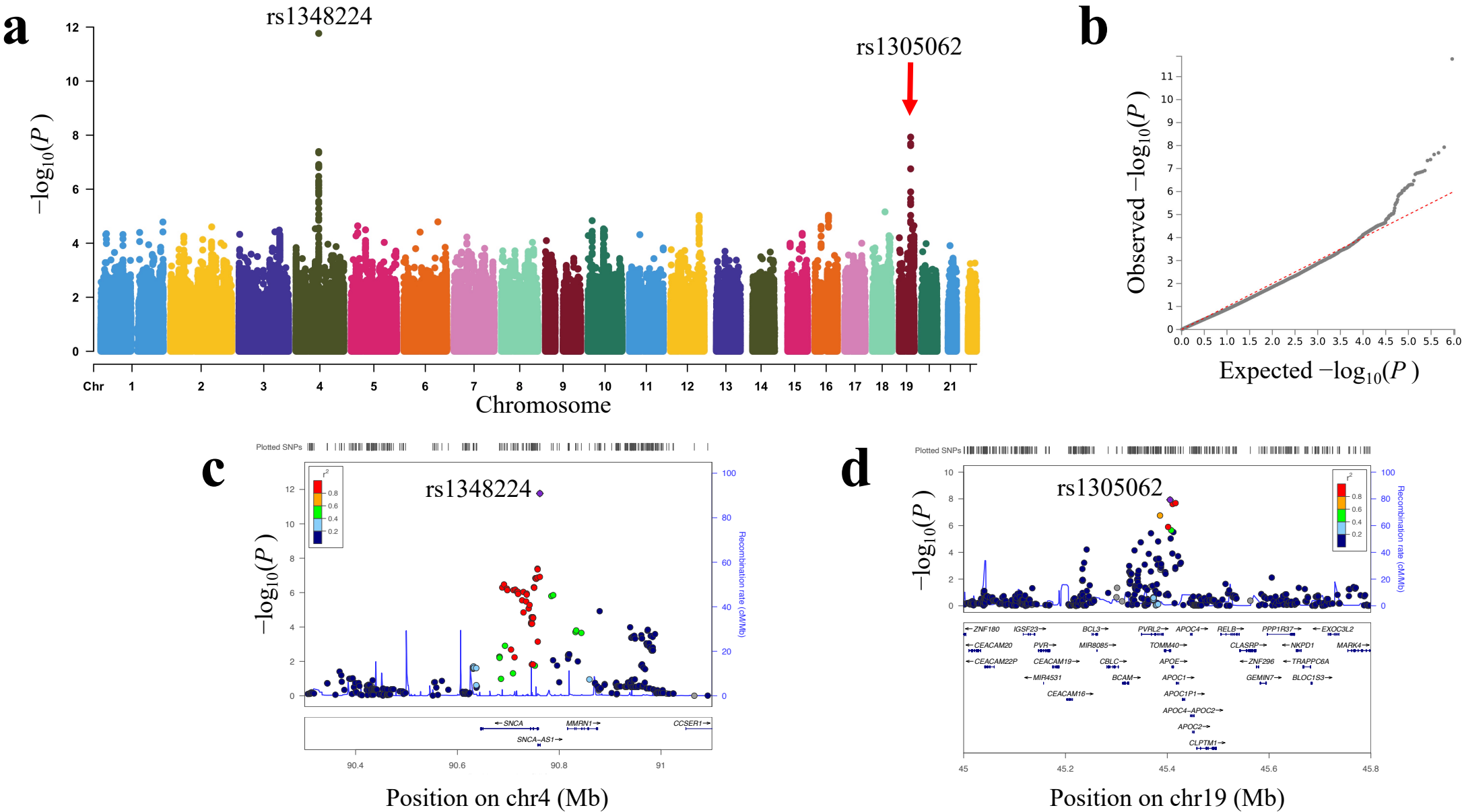
Regional association plots of **a)** rs74866774 on chromosome 2, **b)** rs138587229 on chromosome 10, and **c)** rs111789331 on chromosome 19.

Fig. S4. Genetic correlation analyses.



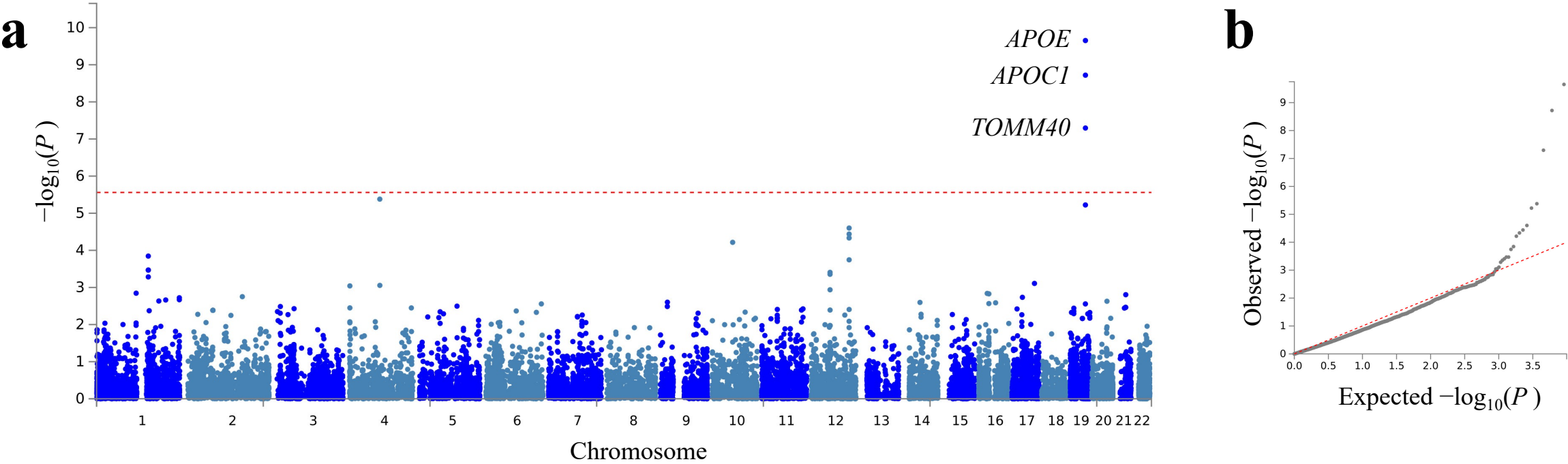
Genetic correlations between DLB and nine phenotypes are shown. Asterisk indicates significant correlation ($P < 0.05$). Error bars indicate standard error (SE).

Fig. S5. Trans-ethnic meta-analysis of DLB.



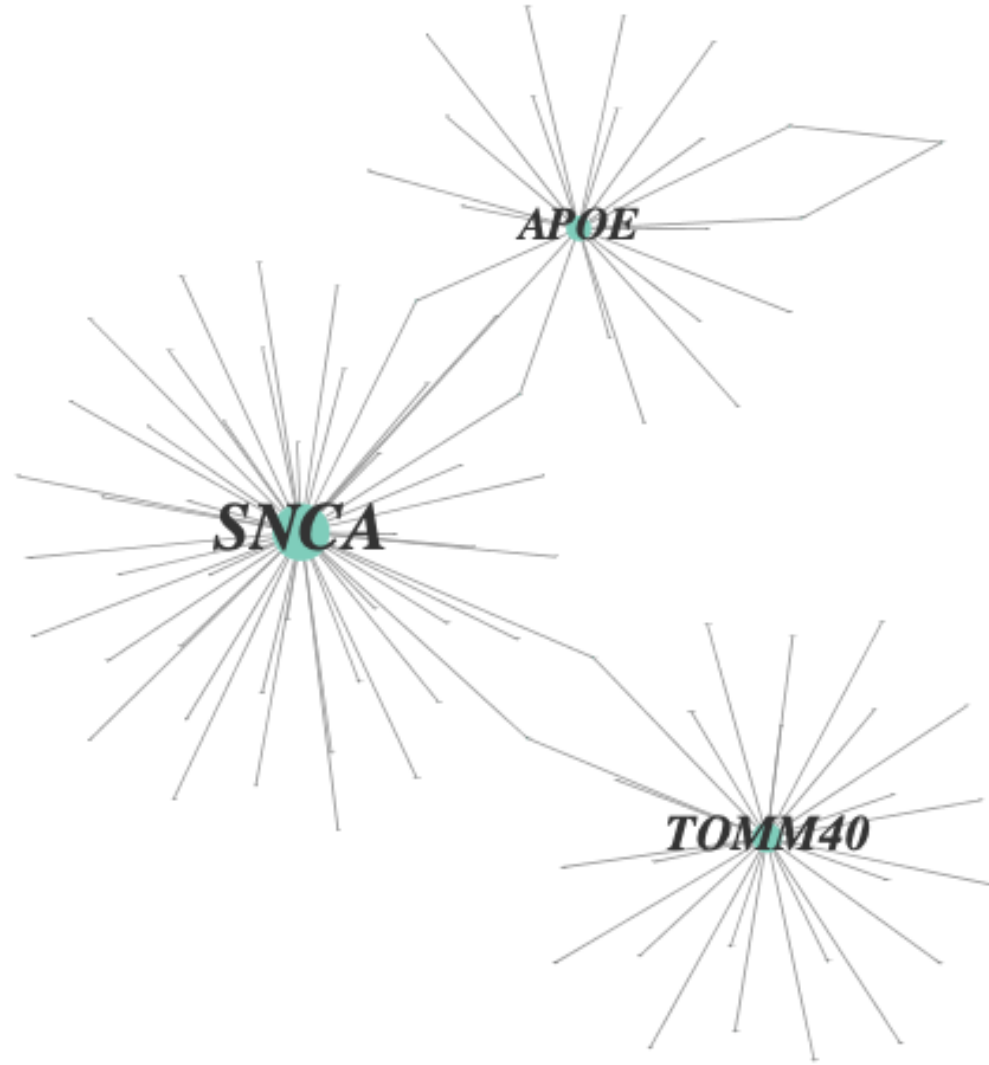
a) Manhattan plot. **b)** Quantile–quantile plot. **c,d)** Regional plots of **(c)** the *SNCA* locus and **(d)** the *APOE* locus.

Fig. S6. Gene-based association analysis using trans-ethnic meta-GWAS data.



a) Manhattan plot. Red line indicates the Bonferroni-corrected P -value threshold. **b)** Quantile-quantile plot.

Fig. S7. PPI network analysis based on the 5 candidate genes identified in gene-based association analysis.



PPI network was visualized in Cytoscape. Gene symbols are displayed for nodes with degree of centrality > 20.