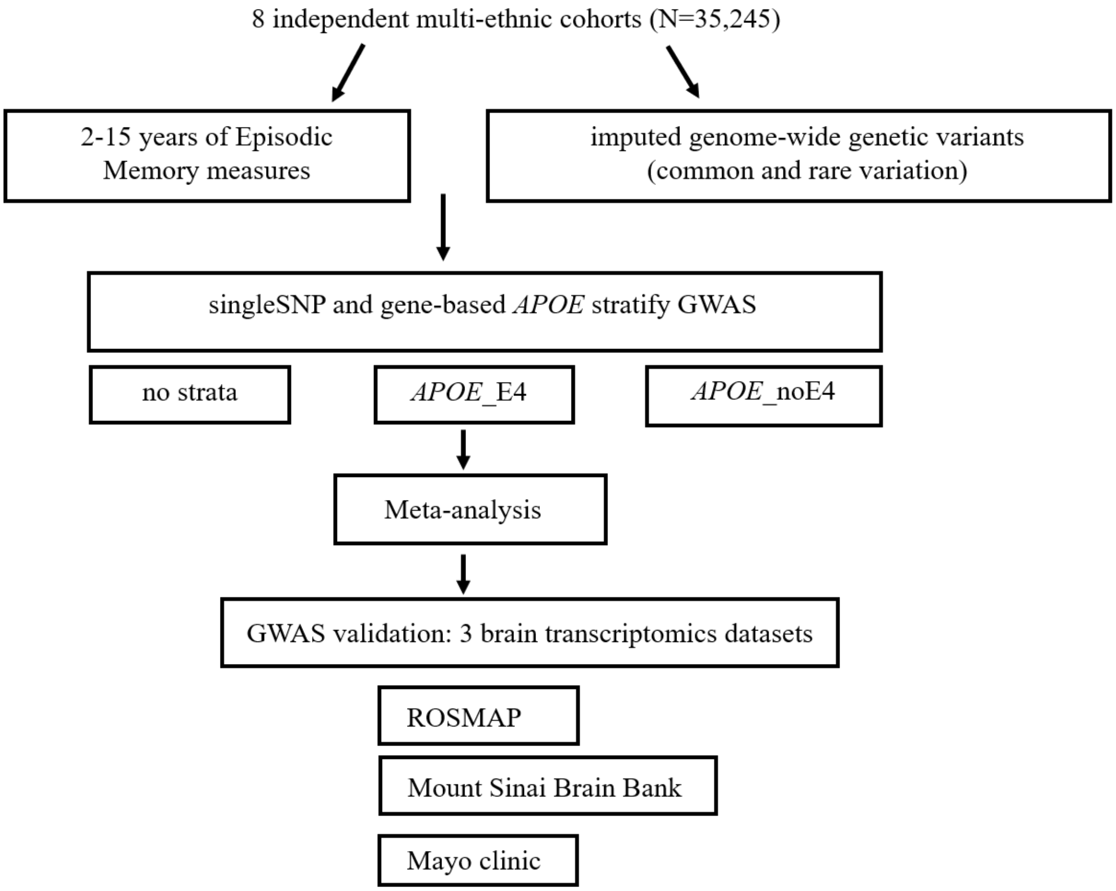
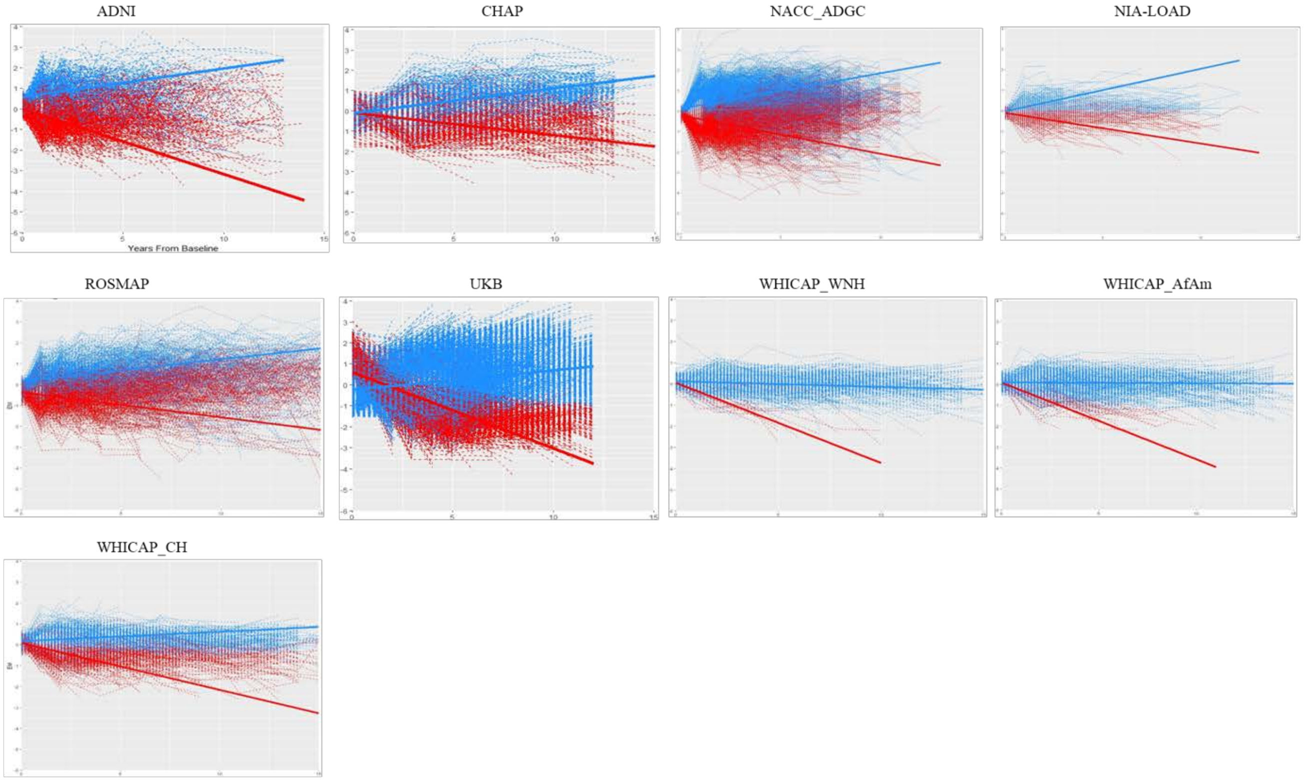
Supplemental Figure 1. Overview of the study design.

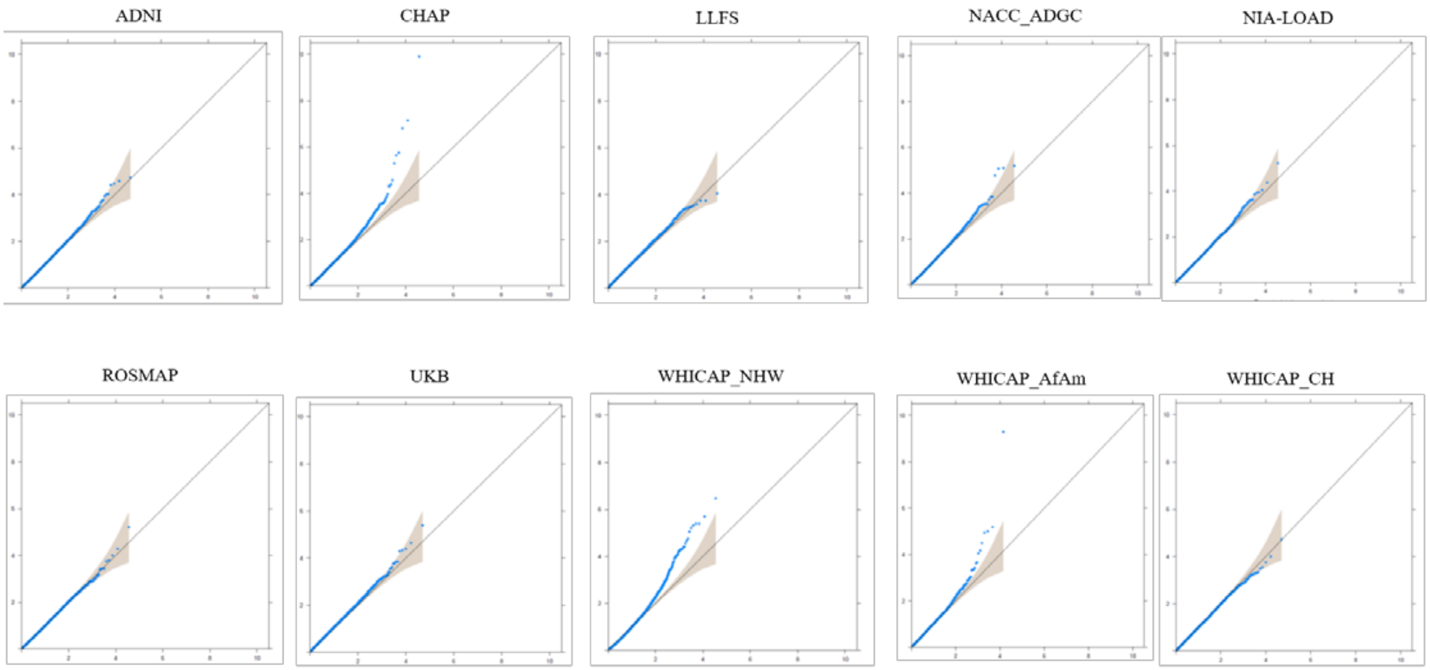


Supplemental Figure 2. Episodic memory trajectories considering all subjects at baseline within each of the study cohorts.



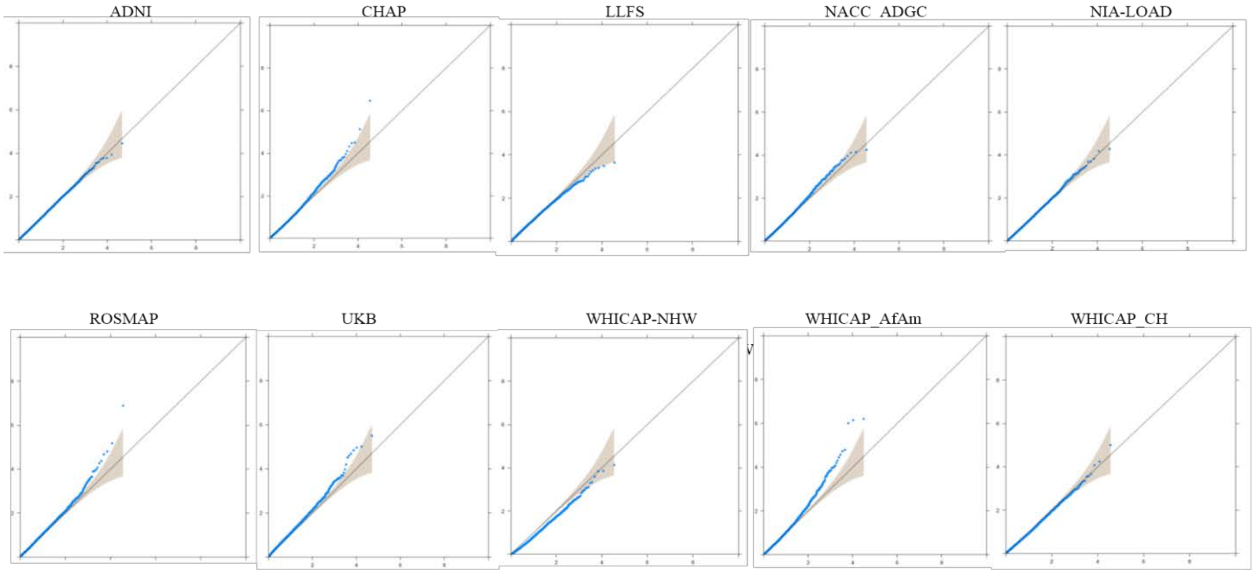
NHW: Non-Hispanic Whites; AfAm: African-Americans ; CH: Caribbean-Hispanics. The X-axis correspond to the time of follow-up in years (ranging from O to 15); the Y-axis correspond to the residual episodic memory score (ranging from -6 to 4) after being adjusted for sex, age, education, episodic memory scores at baseline and total years of follow-up (truncated to a maximum of 15 years

Supplemental Figure 3. QQ-plots of genome-wide gene-based analysis in the non-stratified sample.



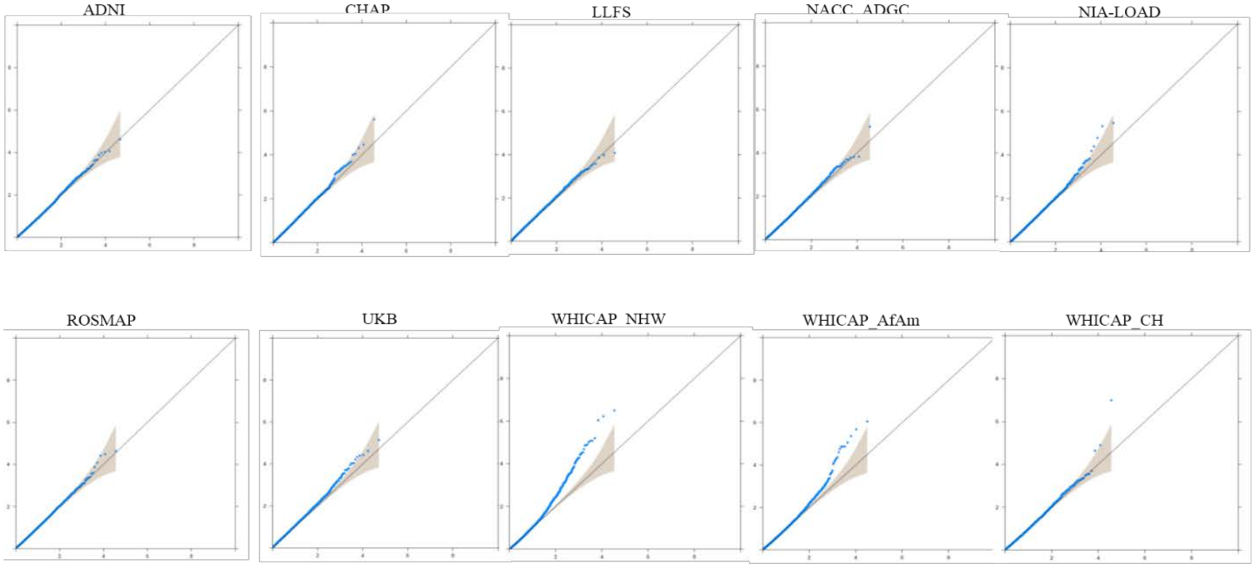
The x axis displays the expected p-values from a theoretical normal distribution ; the y-axis represents the dataset observed p-values.

Supplemental Figure 4. qqplots of genome-wide gene-based analysis in APOE-E4 strata



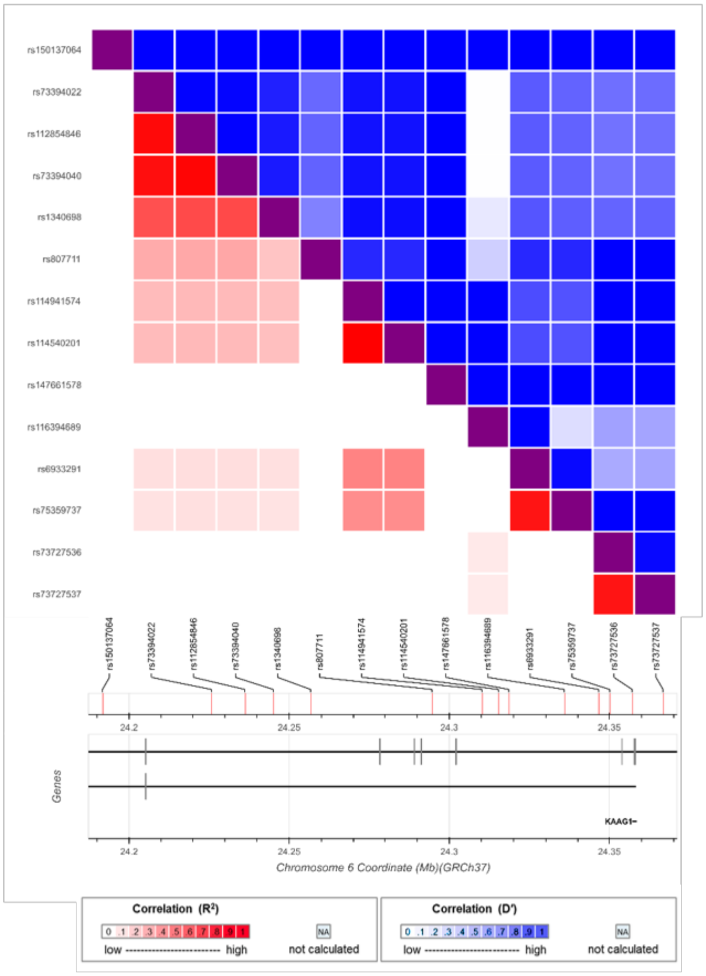
The x axis displays the expected p-values from a theoretical normal distribution ; the y-axis represents the dataset observed p-values

Supplemental Figure 5. qqplots of genome-wide gene-based analysis in APOE-noE4 strata.



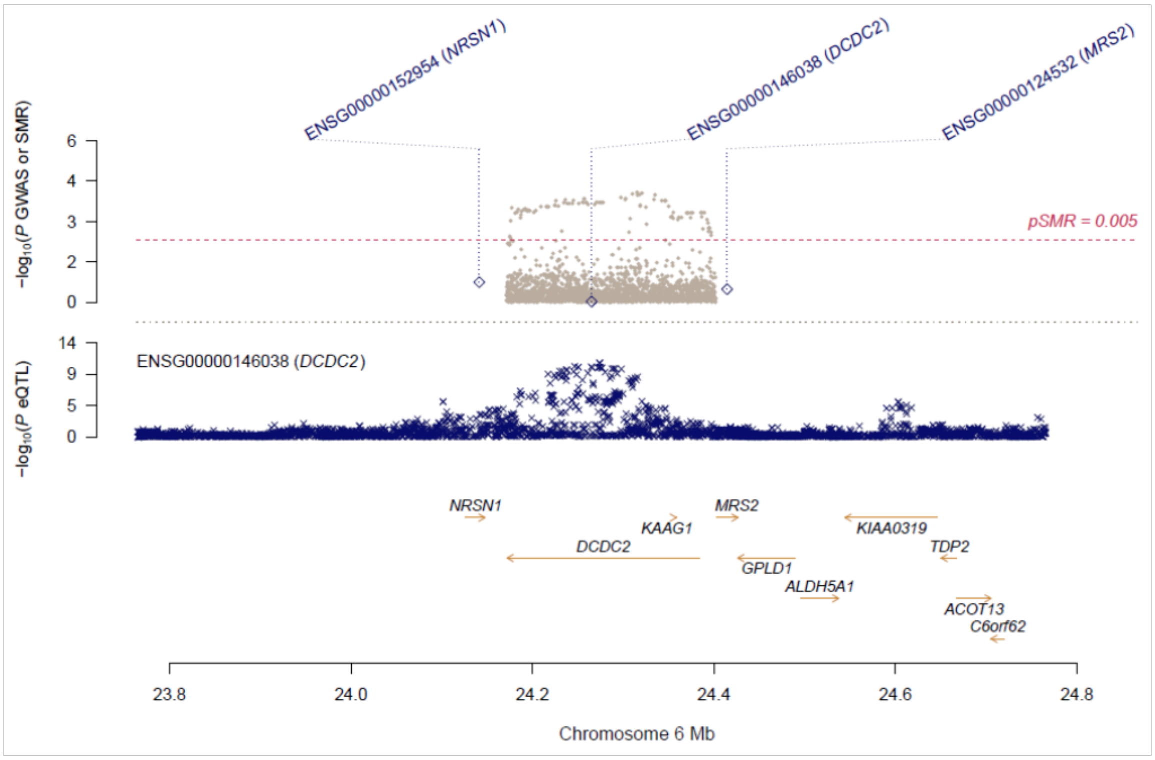
The x axis displays the expected p-values from a theoretical normal distribution ; the y-axis represents the dataset observed p-values.

Supplemental Figure 6. Matrix of linkage disequilibrium for topSNPs in the singleSNP based meta-analysis.



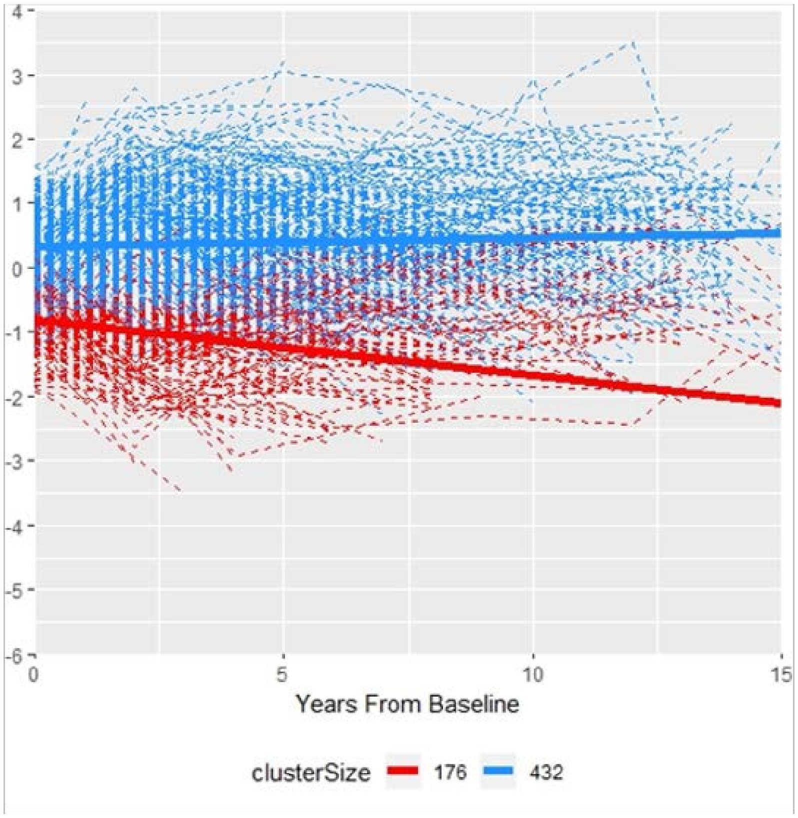
The dimensions of the square plot correspond to the number of SNP variants tested. SNPs are displayed based on their GRCh37 genomic coordinates. Measures of SNP pairwise linkage disequilibrium consisted of D' (blue colored) and R2 (red colored) statistics.

Supplemental Figure 7. Mendelian randomization *DCDC2*-brain eQTLs.



The x-axis displays the position (in Mb) for each of the SNPs tested within chromosomal region 6p22.3. In the top panel, each colored circle represents the -log10 association GWAS p-values for each of the SNPs. The hollow diamonds show the p-values for probes considered in the analyses. The bottom panel displays the eQTLs p-values of the SNPs from Brain-eMeta dataset. The dotted line highlighted in red indicates SMR threshold of significance.

Supplemental Figure 8. Trajectories of language in WHICAP Non-Hispanic Whites study



The X-axis correspond to the time of follow-up in years (ranging from 0 to 15); the Y-axis correspond to the residual episodic memory score (ranging from -6 to 4) after being adjusted for sex, age, education, episodic memory scores at baseline and total years of follow-up (truncated to a maximum of 15 years).