Fig S4. Plots show p-values for all 1,204,603 SNP associations for the ELSA replication sample, for all phenotypes: (A) immediate recall level (IR-L) and (B) immediate recall change (IR-C) and (C) residual delayed recall level (rDR-L) and (D) residual delayed recall change (rDR-C). The upper (red) horizontal line demarcates the threshold of $p = \log(5.0 \times 10^{-08})$ and the lower (blue) horizontal line demarcates $p = \log(1 \times 10^{-05})$ for SNPs based on their chromosomal position (x-axis).