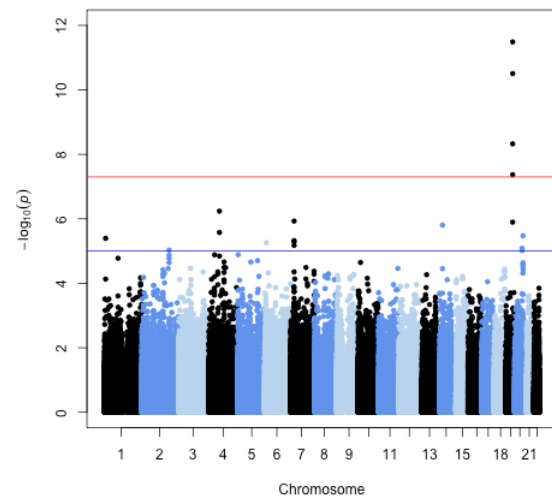
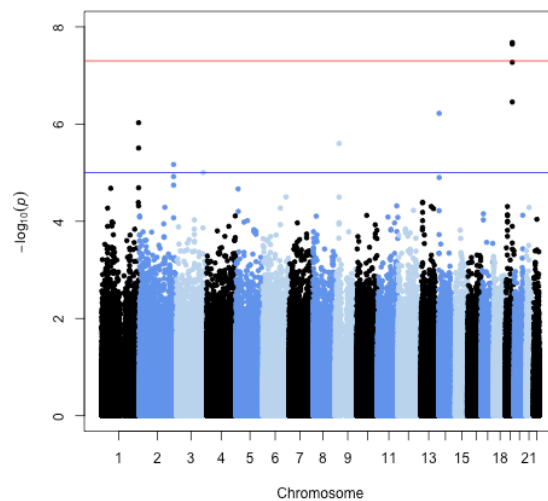


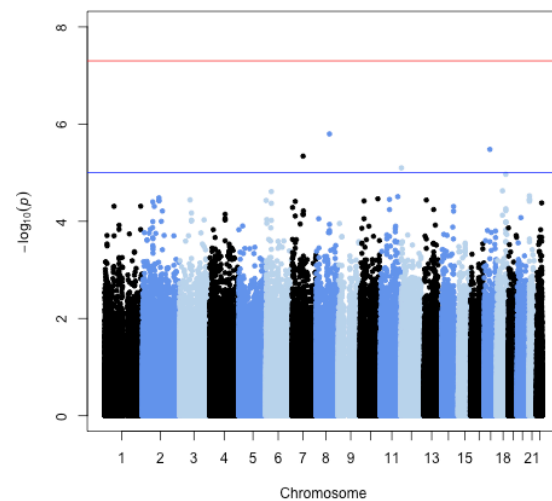
A. IR-L



C. rDR-L



B. IR-C



D. rDR-C

Fig S6. Plots show p-values for all SNP associations for the meta-analysis, 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 $p = -\log(5.0 \times 10^{-8})$ and the lower (blue) horizontal line demarcates $p = -\log(1 \times 10^{-5})$ for SNPs based on their chromosomal position (x-axis).