Extended analysis performed using the output from 4 GWAS in Late-onset Alzheimer’s disease (LOAD) - Reiman et al, Li et al, Beecham et al, Carrasquillo et al - revealed two putative AD candidate genes - tripartite motif-containing protein 15 (TRIM15) and Cytochrome P450 7B1 (CYP7B1).

We have attempted to select genes that merit further study by identifying all SNPs with p-values in range \(5 \times 10^{-5} - 5 \times 10^{-8}\) and determining their effects across all the other studies either directly or by using a proxy when comparing data from different chip platforms.

SNP rs929156 (TRIM15) showed suggestive association with AD giving p-value 1.69E-05 in Beecham et al study, and p-value = 0.04 in Carrasquillo et al study. The odds ratios are consistent indicating an association with risk (OR: 1.1 - 1.5).

SNP rs11998077 (CYP7B1) showed suggestive association with AD in the Li et al GWAS giving a p-value of 4.59E-05; p-value = 0.006 was seen in Reiman et al GWAS. The SNP the odds ratios were all protective (OR 0.6 - 0.9). Deep sequencing of these genes will be undertaken to determine ‘multiple rare variants’ that may be associated with disease.