



Supplementary Figure 4 Rhapsody Pathogenicity landscape

Pathogenicity values obtained by *in silico* saturation mutagenesis of apoA-I structure using the Rhapsody package. Mutation introduced is depicted in the Y axis. Scales at the right indicate pathogenicity probability (1 more pathogenic, 0 less pathogenic and 0.5 for mutations introducing the same residue present in the wild type sequence).