We have highlighted in bold and underlined the candidate genes that we are sceptical about due to the lack of functional support and the known functional consequences at these loci. Although the cis-eQTLs for these genes are classified as statistically having the same underlying causal variant as the disease association — our functional genomic data do not robustly support these genes as likely to be involved in pathogenesis. It is possible that these effects are secondary to the pathogenic effect i.e. carried as a passenger on the same functional haplotype but do not contribute to autoimmunity.