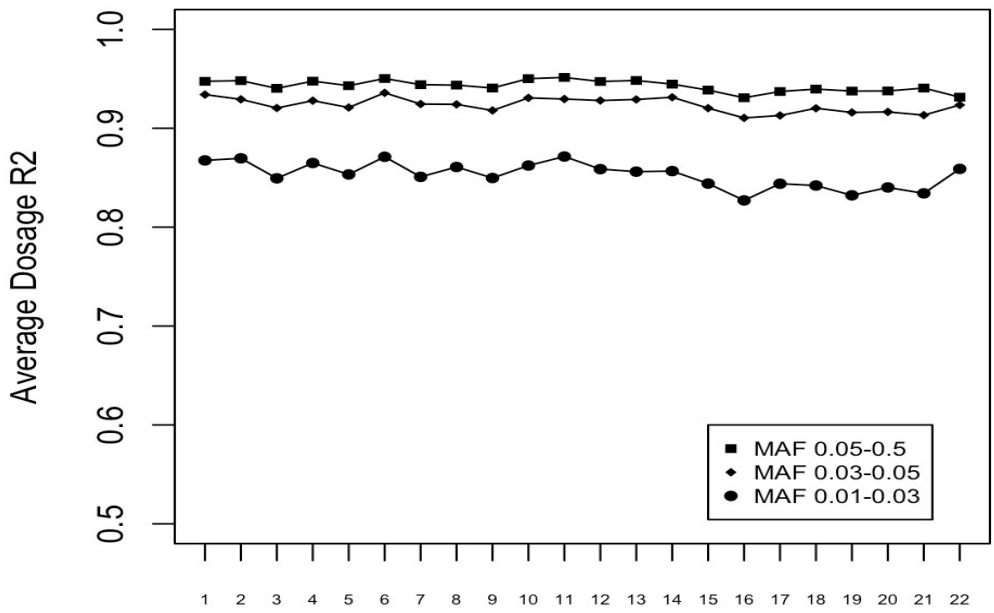
Figure S1

A



B

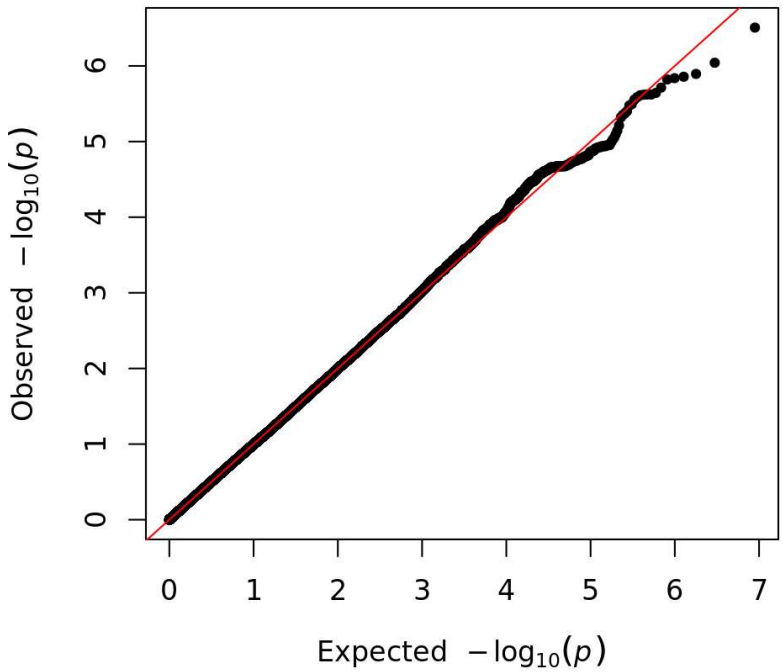


Figure S1. (A) Imputation accuracy measured as average dosage R^2 for 235,942 type 2 variants filtered for an information metric >0.4 and genotype probability call > 0.90. Data shown separately by chromosome and for different minor allele frequency (MAF) ranges, as indicated in the key . (B) Quantile-quantile plot of GWAS p-values.

Figure S2

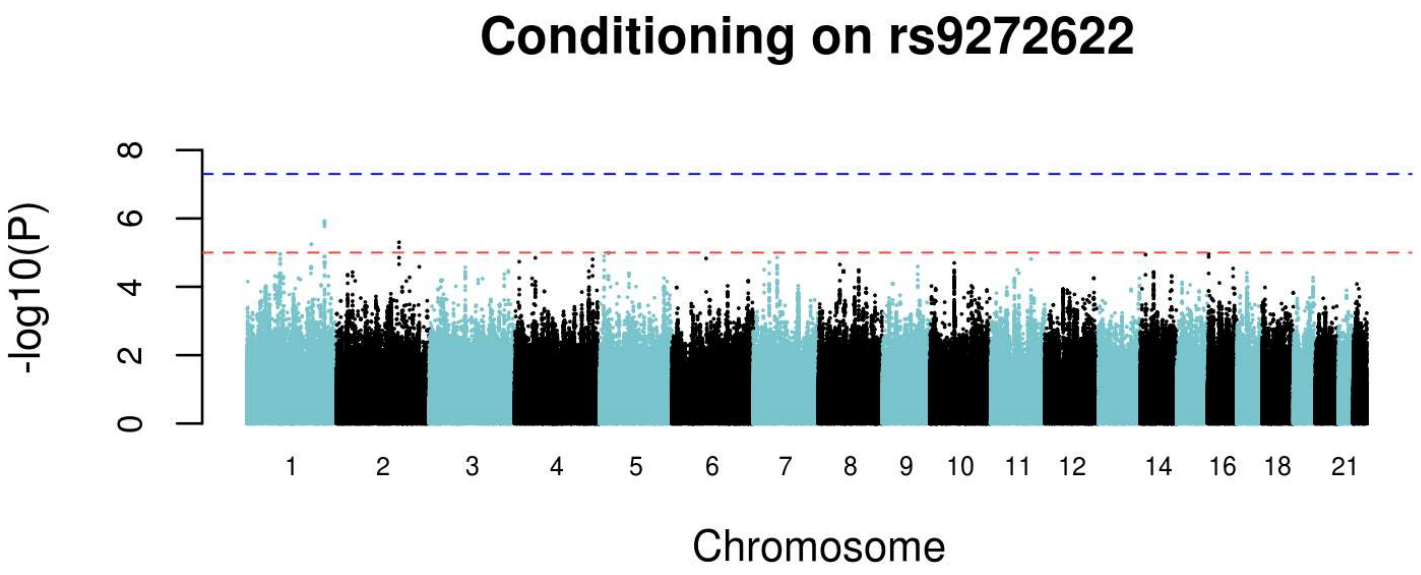


Figure S2. Manhattan plots of GWAS results for the 4.46M high quality 1000G imputed SNP variants after conditioning on the top SNP rs9272622. Data are for analysis in FastLMM looking for association between SNPs and RHD.

Figure S3

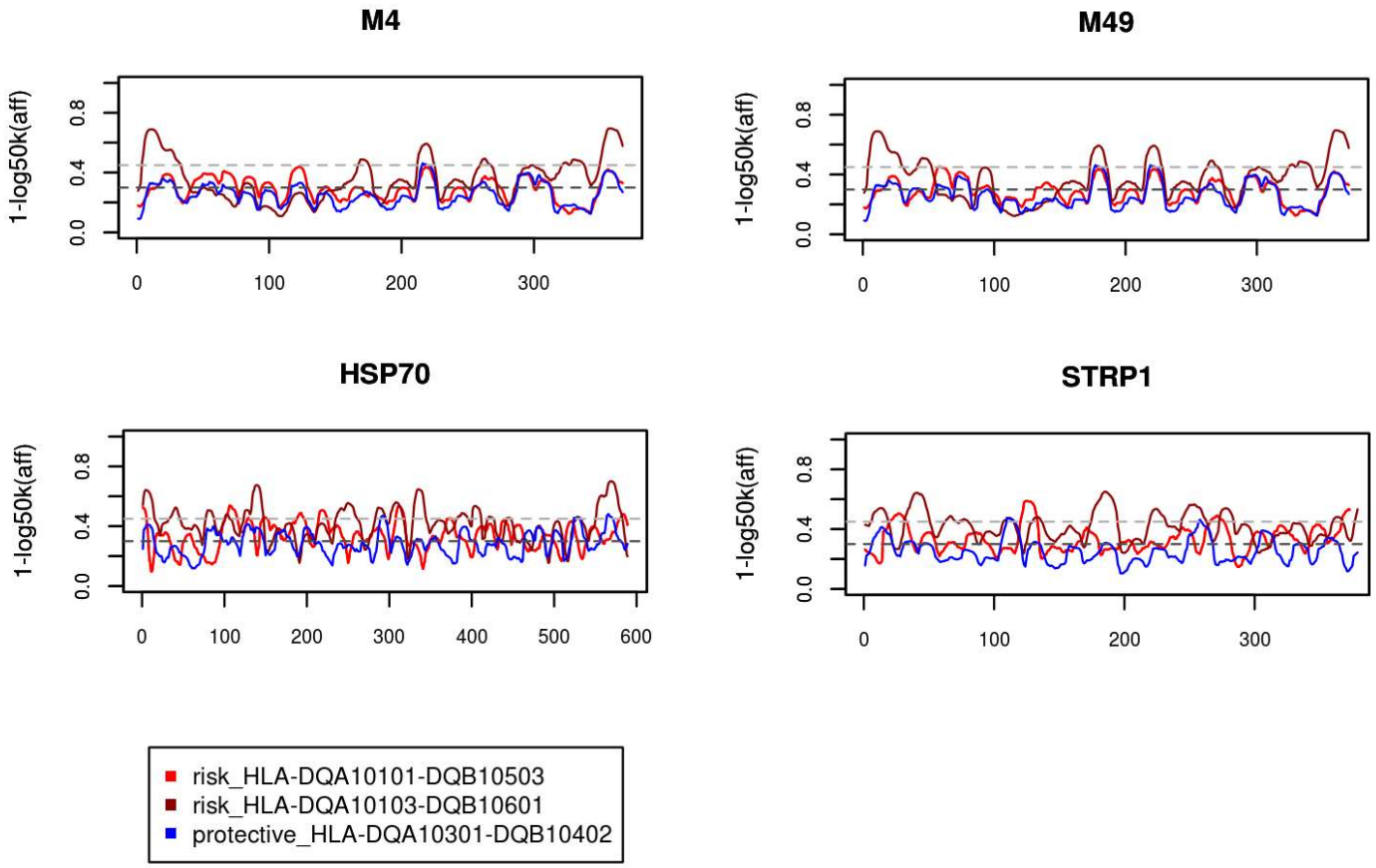


Figure S3. Plots showing binding affinities for predicted epitopes of GAS M proteins recognised by HLA DQ-DB heterodimers. Epitope binding predictions were performed in NetMHCIIPan3.1. The y-axis shows the relative binding affinity (expressed as 1-$\log_{50,000}$ of the nM binding affinity) for heterodimers formed from risk (red, brown) and protective (blue) DQ_DB haplotypes (see key); the x-axis indicates the amino acid sequence locations for mature proteins, also equivalent to the start position of overlapping 20mers (1-mer sliding window) in non-rheumatogenic GAS M4 (Accession number CAA33269) and M49 (Accession number AAA26868.1) sequences, GAS HSP70 (Accession number AAB39223.1) and GAS STRP1 (Accession number AAA26987.1) sequences. Horizontal lines indicate 500nM (upper) and 1000nM (lower) binding affinities.