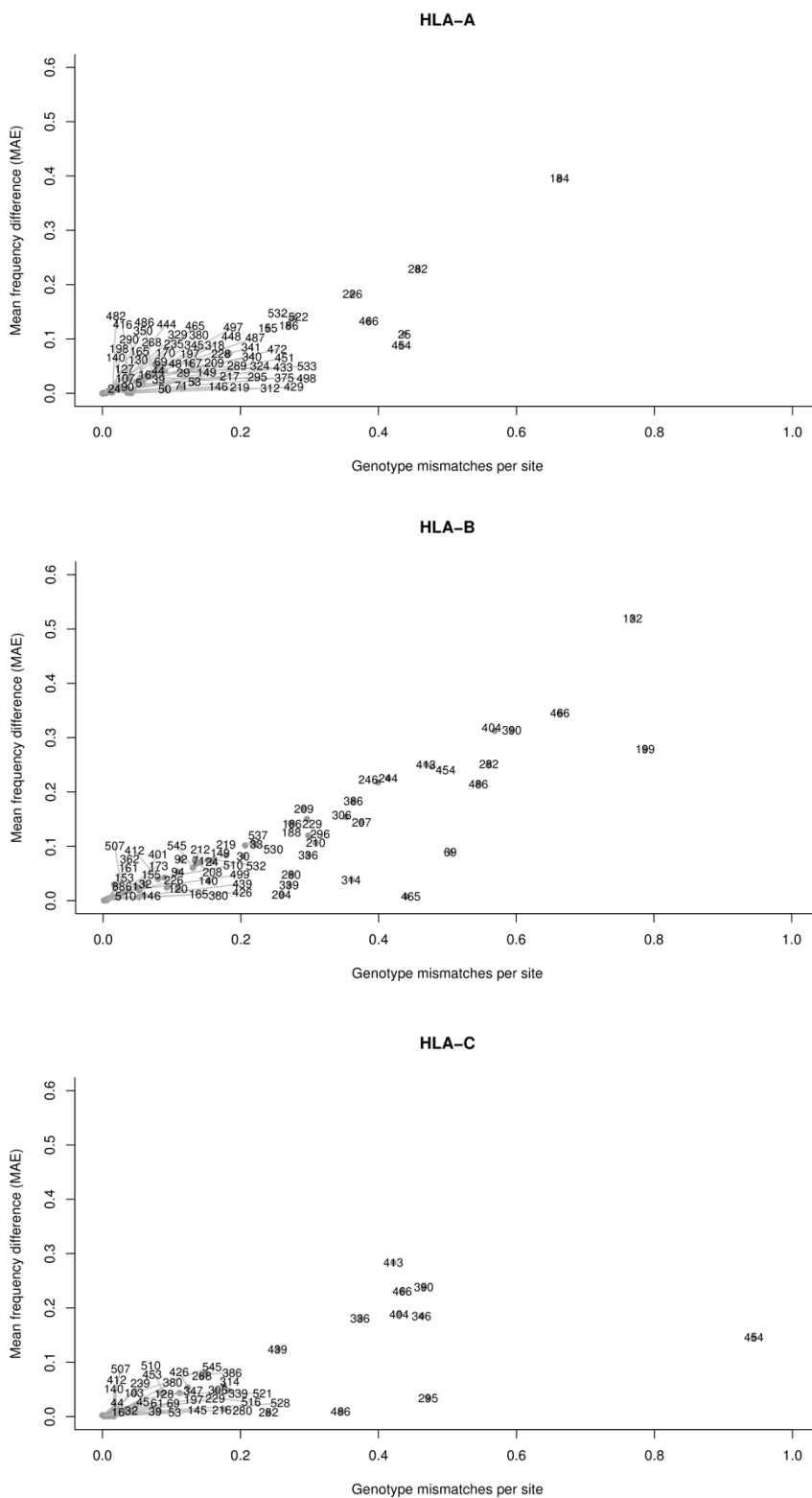


Figure S8



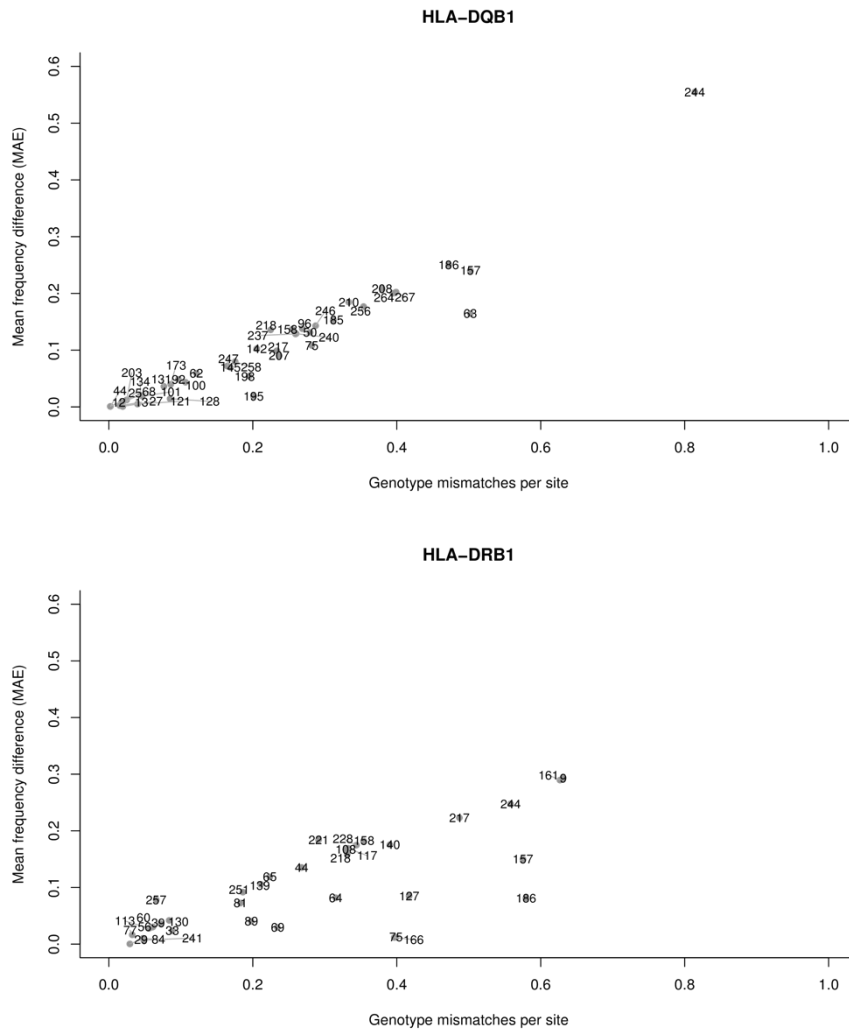


Figure S8 Relationship between proportion of mismatched genotypes per site (considering all individual genotypes) and mean difference in reference allele frequency estimated from the 1000 Genomes NGS data and Gourraud *et al.* (2014) Sanger sequencing data. Numbers indicate site position in ARS exons sequence.