

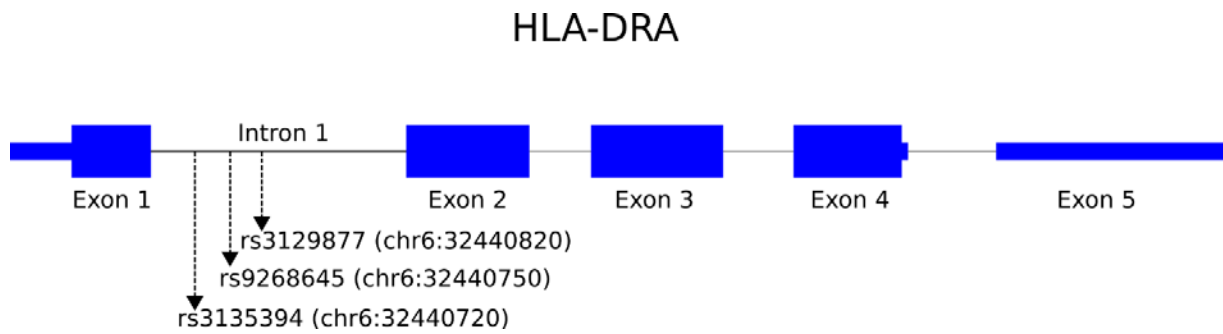
SUPPLEMENTARY DATA

Supplementary Table 1. High risk and low risk haplotype distributions within the BDD samples. Samples were stratified based on the geographical location as being from the Skåne region (where control samples were obtained) and Swedish locations north of Skåne. Risk haplotype frequencies are not significantly different between the strata ($p = 0.75$, Fisher's exact test).

Haplotype	Skåne	North of Skåne
101	152 (68.4%)	40 (71.4%)
010	70 (31.6%)	16 (28.5%)

SUPPLEMENTARY DATA

Supplementary Figure 1. Diagrammatic representation of the *HLA-DRA* gene on chromosome 6, showing the location of the three SNPs in the T1D risk haplotype (not to scale).



SUPPLEMENTARY DATA

Supplementary Figure 2. Expression of class II genes in cells from 93 individuals selected from the 1000 Genomes Project samples, grouped by tri-SNP haplotype. Expression was measured by RNA-sequencing of samples prepared from EBV-transformed lymphocytes, performed as described in Results. RPKM, Reads Per Kilobase Million. Two-way analysis of variance showed that both the class II antigen ($p < 0.0001$) and the tri-SNP haplotype ($p = 0.0061$) significantly contributed to the variance seen in these samples. Dunnett's multiple comparisons test gave $010/010 > 010/101 > 101/101$ for HLA-DQB1 ($p < 0.001$).

