

SI figures

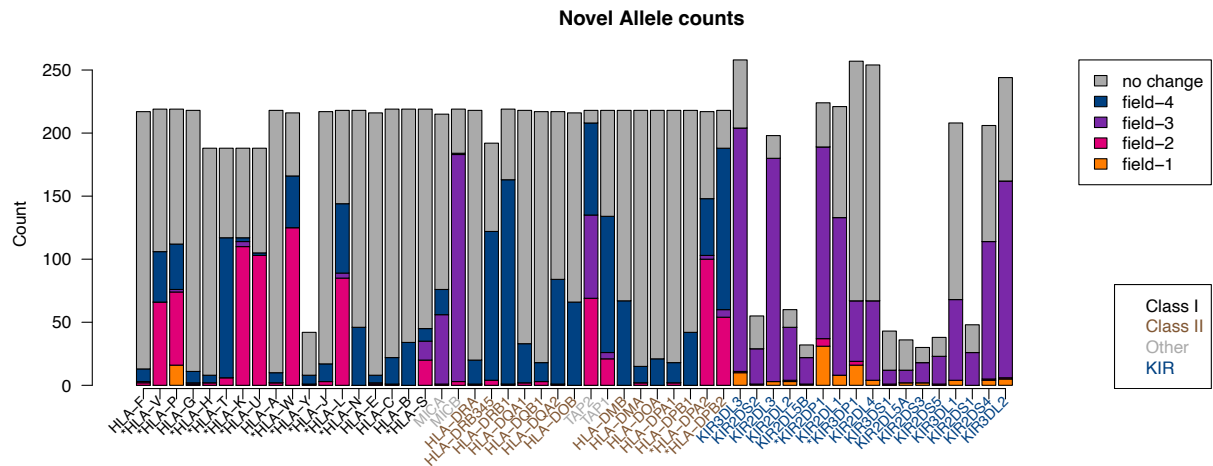


Figure S1: Novel allele distribution regarding to the naming field changes.

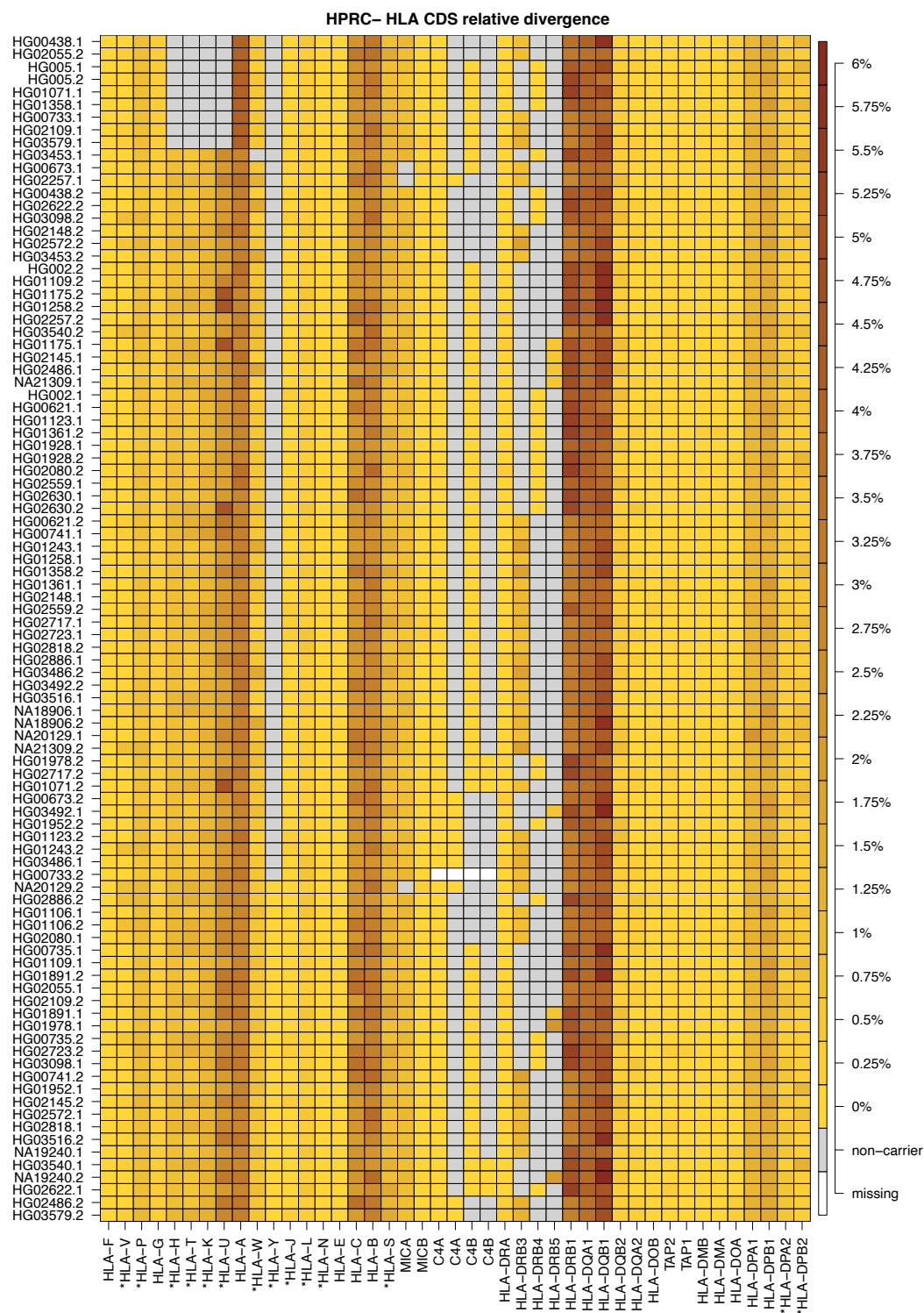


Figure S2: A large version of Figure 3A, with row labels attached (HPRC haplotype id).

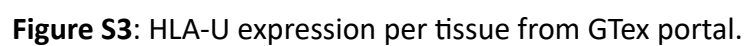


Figure S3: HLA-U expression per tissue from GTex portal.

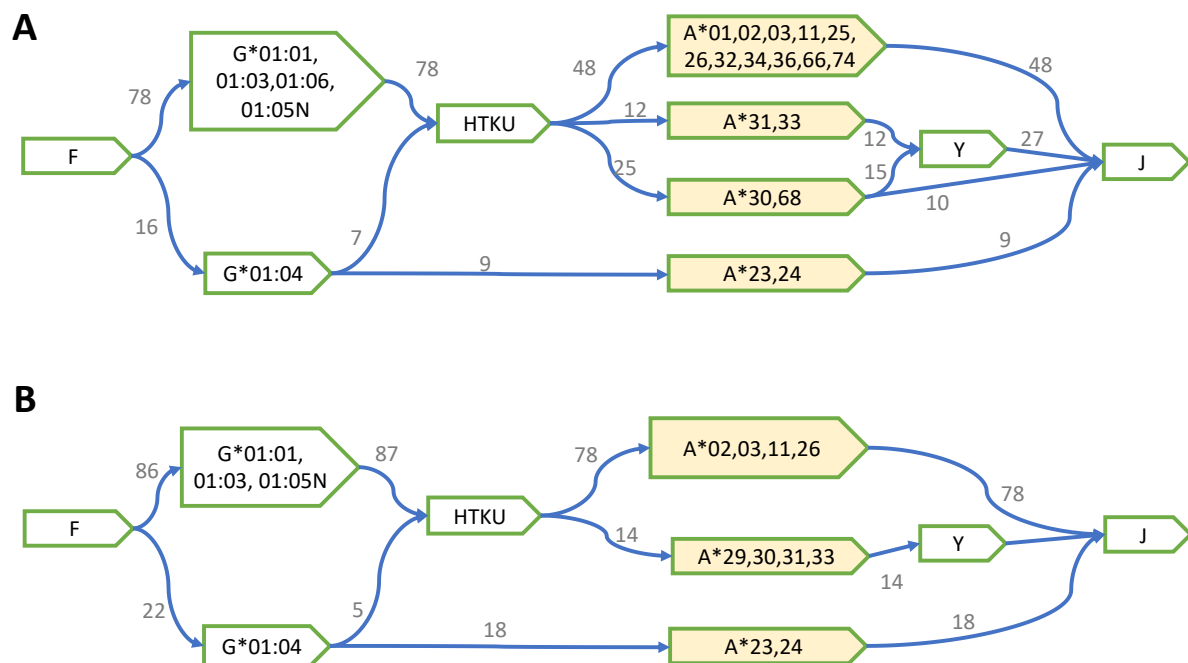


Figure S4: HTKU-del haplotype structure in HPRC (A) and CPC-p1 (B). Counts of edges are labeled.

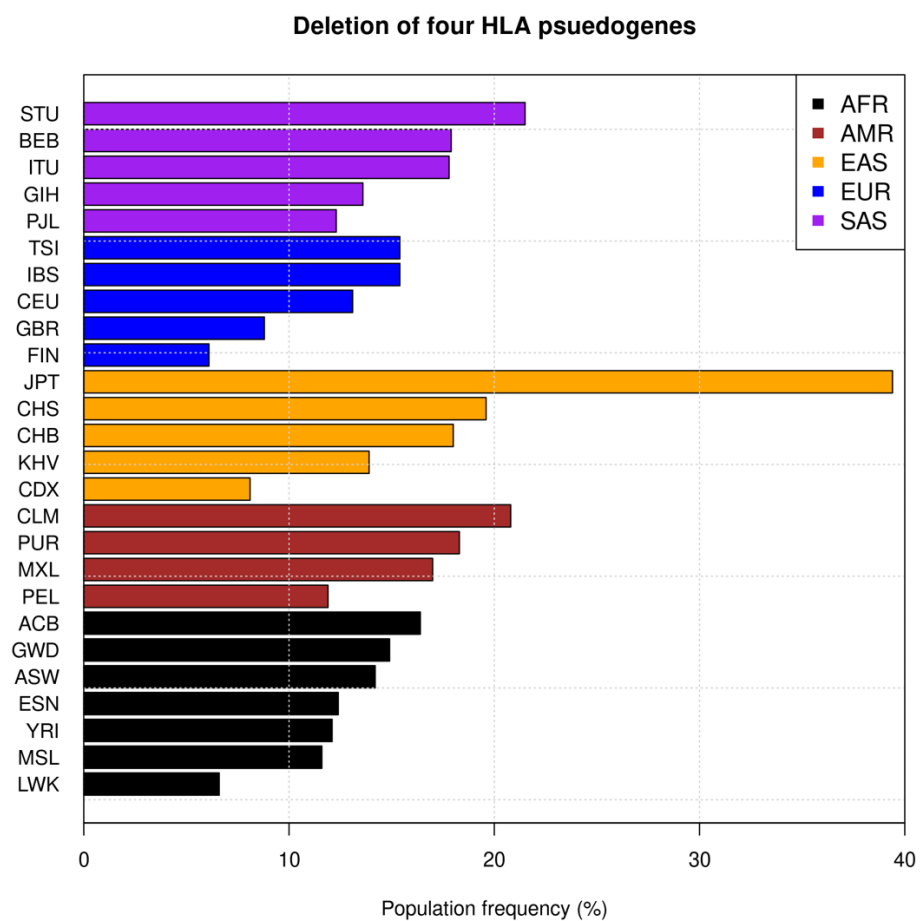


Figure S5: HTKU-del frequency distribution among 1000 genome project populations.

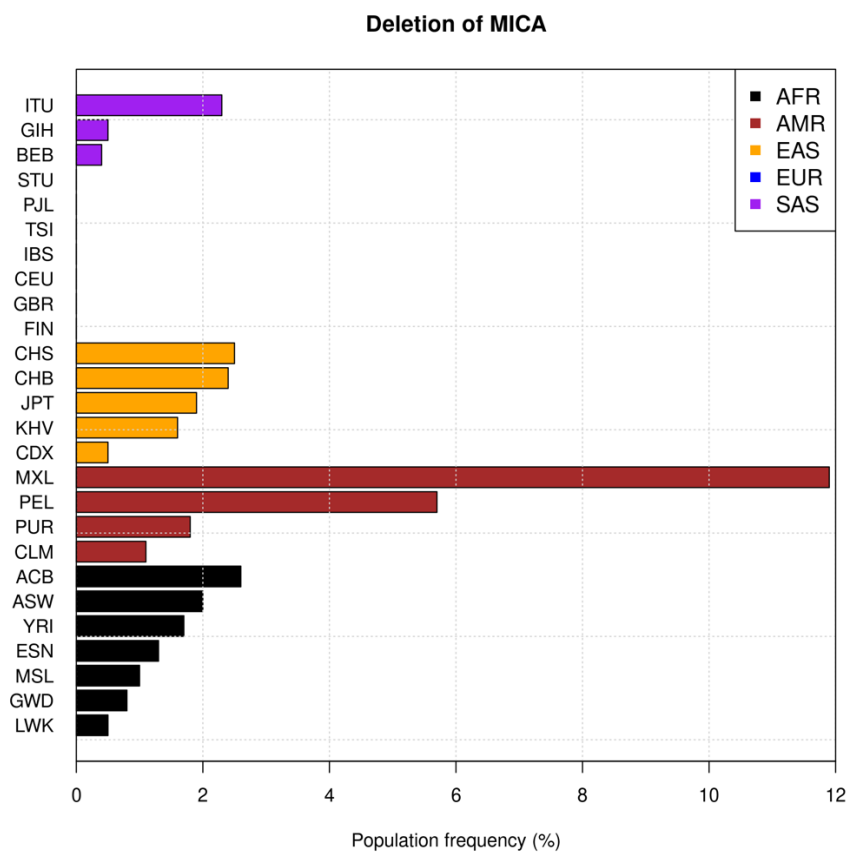


Figure S6: MICA-del frequency distribution among 1000 genome project populations.



Figure S7: Phylogenetic tree for HLA-DRB CDS region.

Phylogenetic Tree for C4 CDS seq

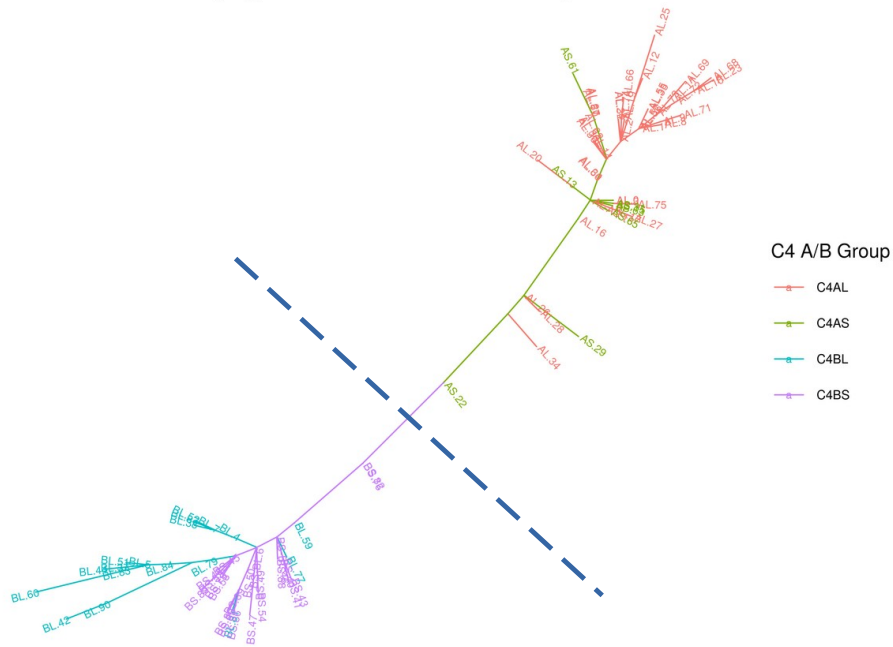
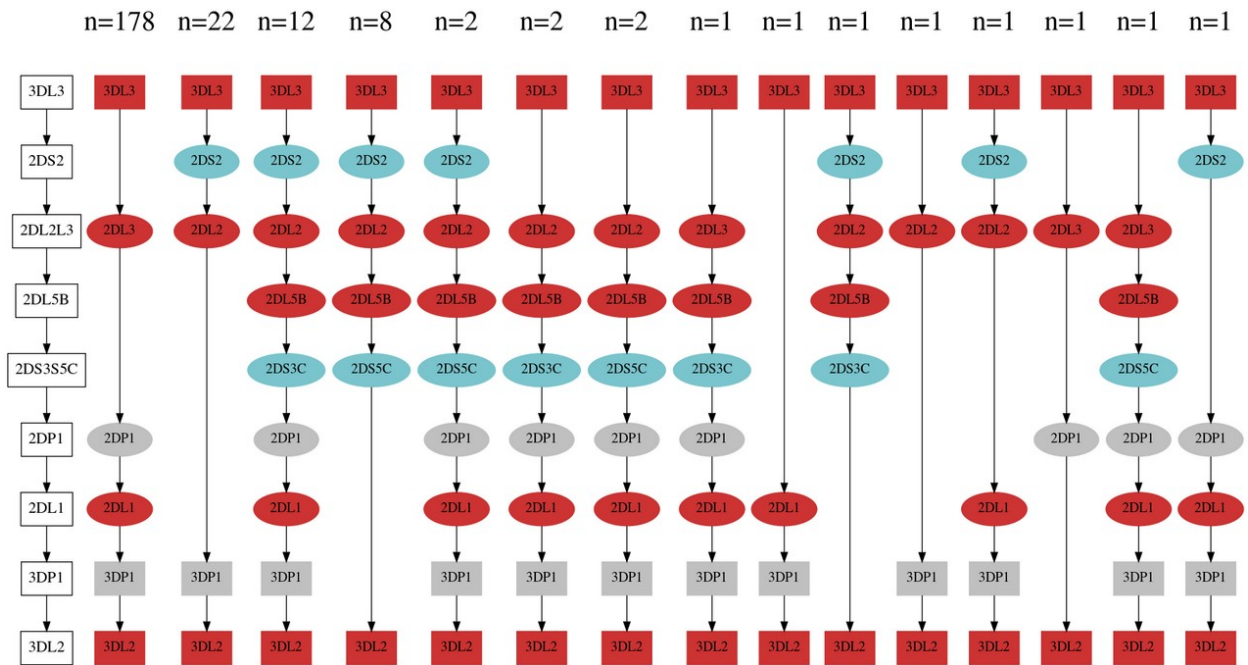


Figure S8: Phylogenetic tree for C4 CDS region.

A



B

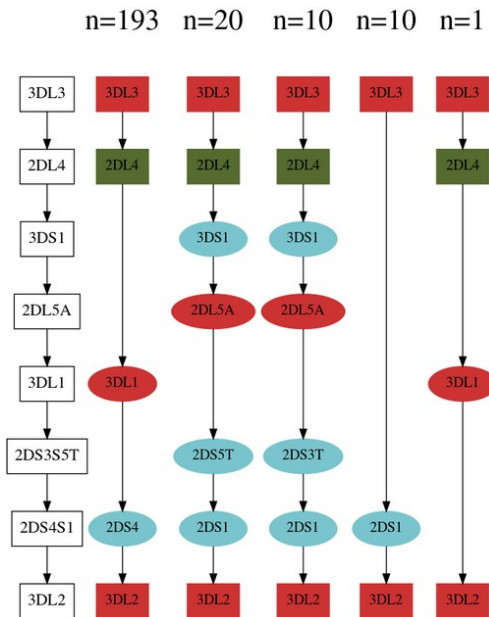


Figure S9: KIR haplotypes in centromere region (A) and telomere region (B).

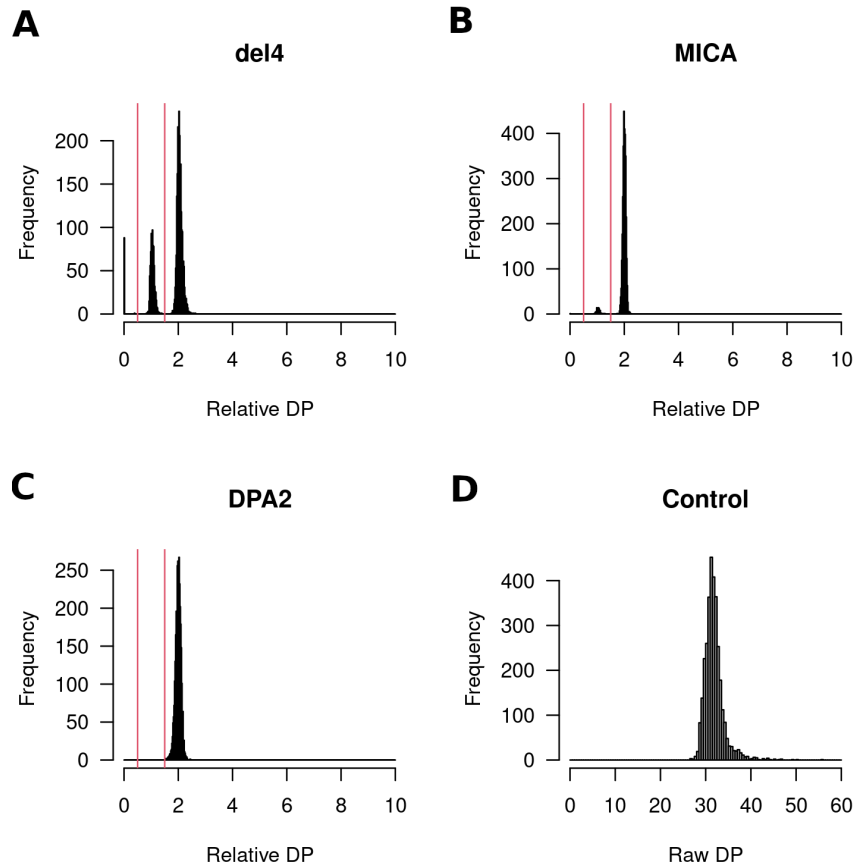


Figure S10: Normalized reads coverage enrichment for A) HLA-H/T/K/U, B) MICA, and C) DPA2 region. Raw reads coverage distribution is D). Peaks reveal copy number changes.