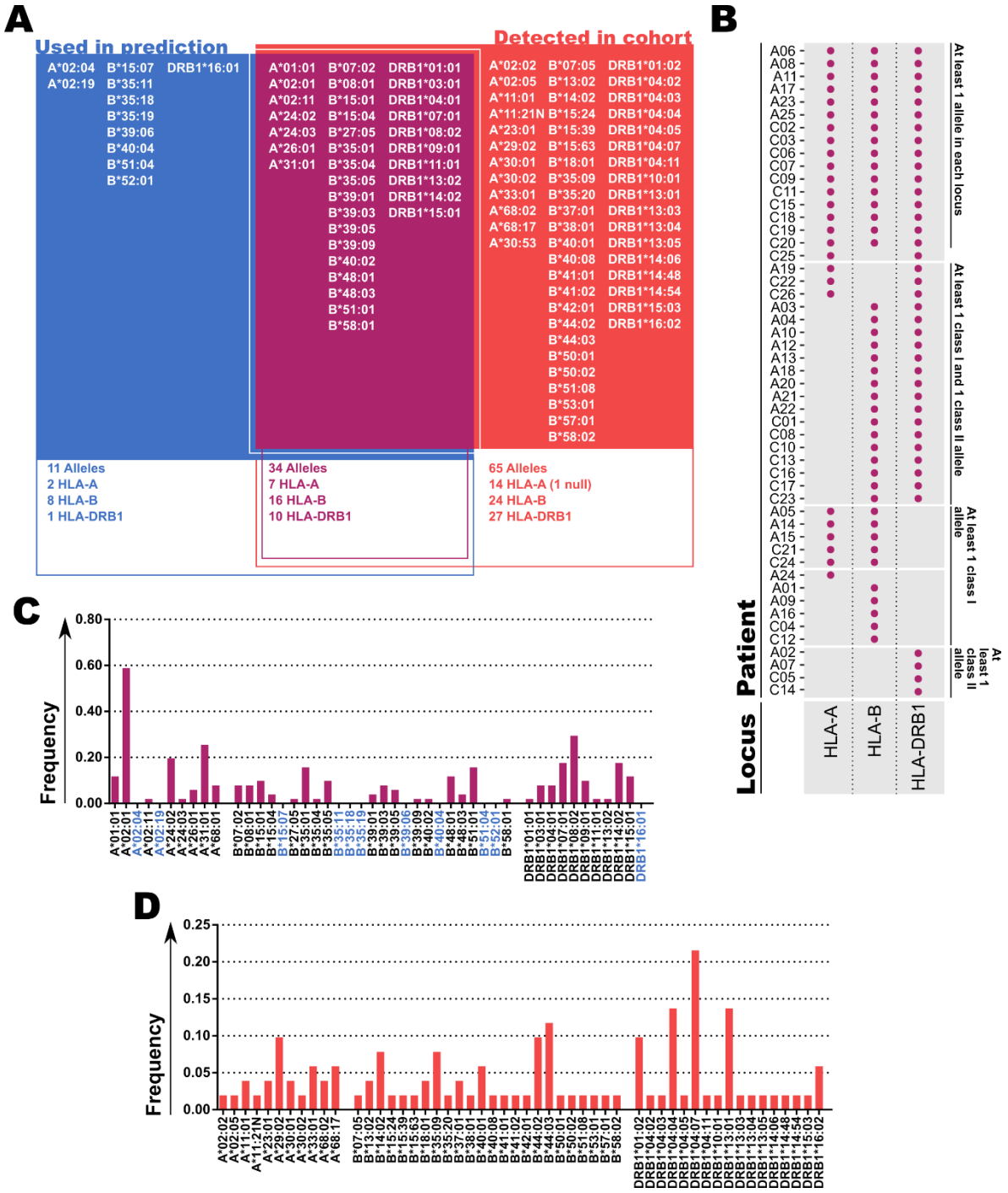
Supplementary Figure 1. **Comparison between the alleles used for bioinformatic prediction of epitopes and those found in the cohort after HLA sequencing.**




**A.** List of alleles used for prediction (blue and purple) and sequenced in the population sample (red and purple). **B.** Rain plot showing all patients had at least one class I and one class II allele represented in the lists used for bioinformatic prediction. **C.** Frequency of the alleles used for prediction as detected in the cohort. Alleles with a frequency of 0 are highlighted in blue. **D.** Frequency of the alleles found in the cohort which were not used for epitope prediction.

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