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► To cite this version:

Estelle Geffard, Alexandre Walencik, Federico Garnier, Anne Cesbron, Nicolas Vince, et al.. Easy-HLA : an online software suite to reveal the full details of HLA typing for genetic analyses. Assises de génétique humaine et médicale 2018, Jan 2018, Nantes, France. [inserm-02161790](#)

HAL Id: [inserm-02161790](#)

<https://inserm.hal.science/inserm-02161790>

Submitted on 21 Jun 2019

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Easy-HLA : an online software suite to reveal the full details of HLA typing for genetic analyses.

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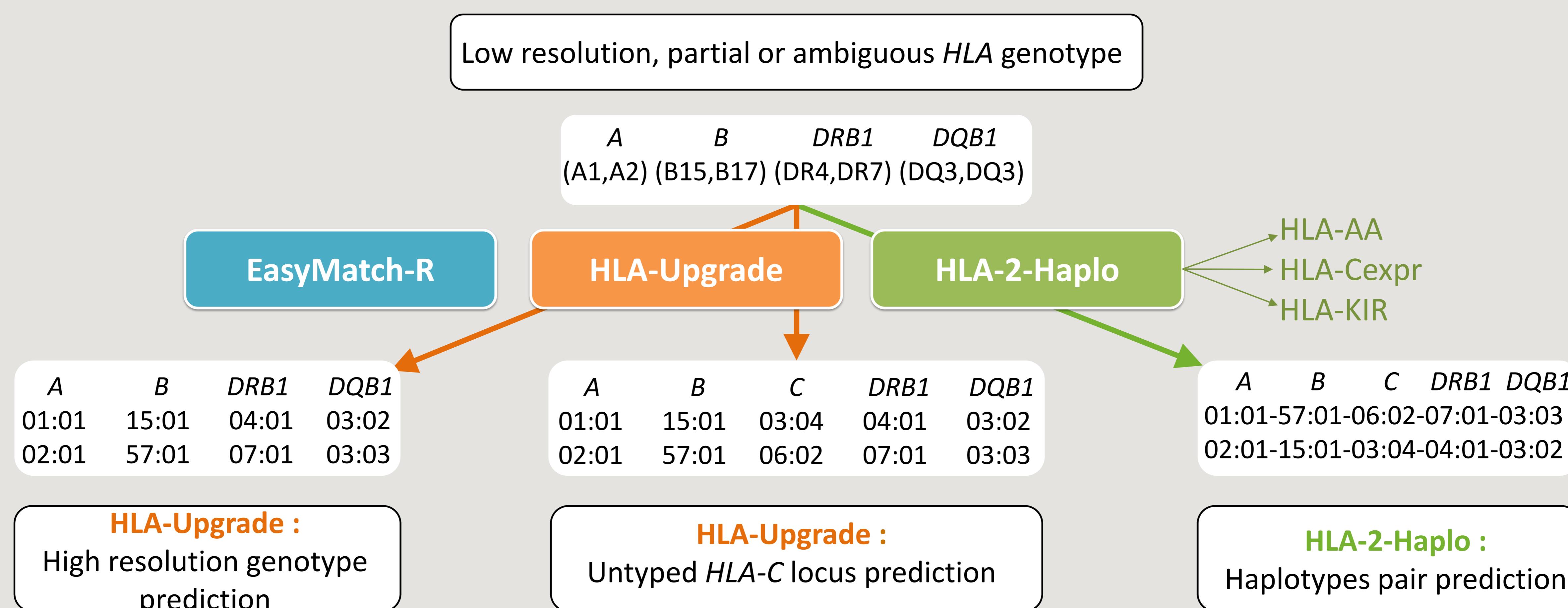
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Easy-HLA presentation

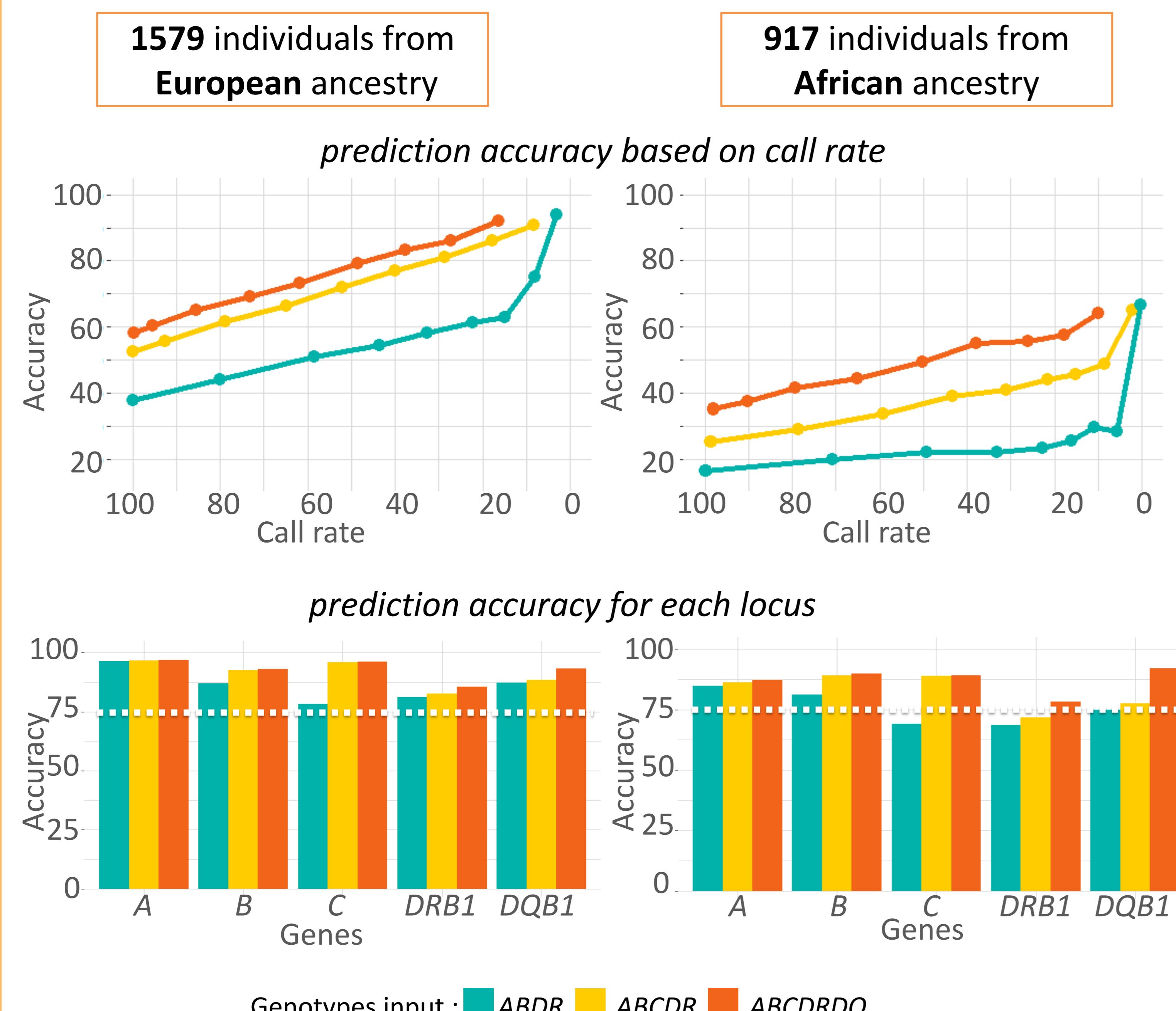
The *HLA* has a pivotal role between clinic and research. The determination of *HLA* alleles of an individual is required in transplantation. Moreover the *HLA* is described as associated with countless immune pathologies described by association studies. As the *HLA* system is the most polymorphic one, both nomenclature and methods constantly refined since the discovery of *HLA* antigens, leading to difficulties to use old archived typings. We developed a web application called Easy-HLA to facilitate the comprehension of *HLA* typing. Easy-HLA is based on validated and published *HLA* haplotypes frequencies. *HLA* haplotypes frequencies are used to solve typing ambiguities, predict *HLA* typing of loci (*HLA*-Upgrade) as well as haplotypes pairs (*HLA*-2-Haplo) or search for matched HSCT donors (EasyMatch-R). It provides new functional immunogenomics parameters: *HLA*-Cexpr imputes *HLA*-C expression, *HLA*-AA provides amino acid equivalence of *HLA* alleles and *HLA*-KIRlig gives KIR ligand classification of *HLA* alleles.



In this example, a given *HLA* serological typing (*HLA*-A~B~DRB1~DQB1) is processed by Easy-HLA. *HLA*-Upgrade statistically predicts high resolution typing by leveling-up the *HLA* genotype and also predict an untyped locus such as *HLA*-C. *HLA*-2-Haplo imputes the corresponding haplotypes pair.

HLA-Upgrade validation

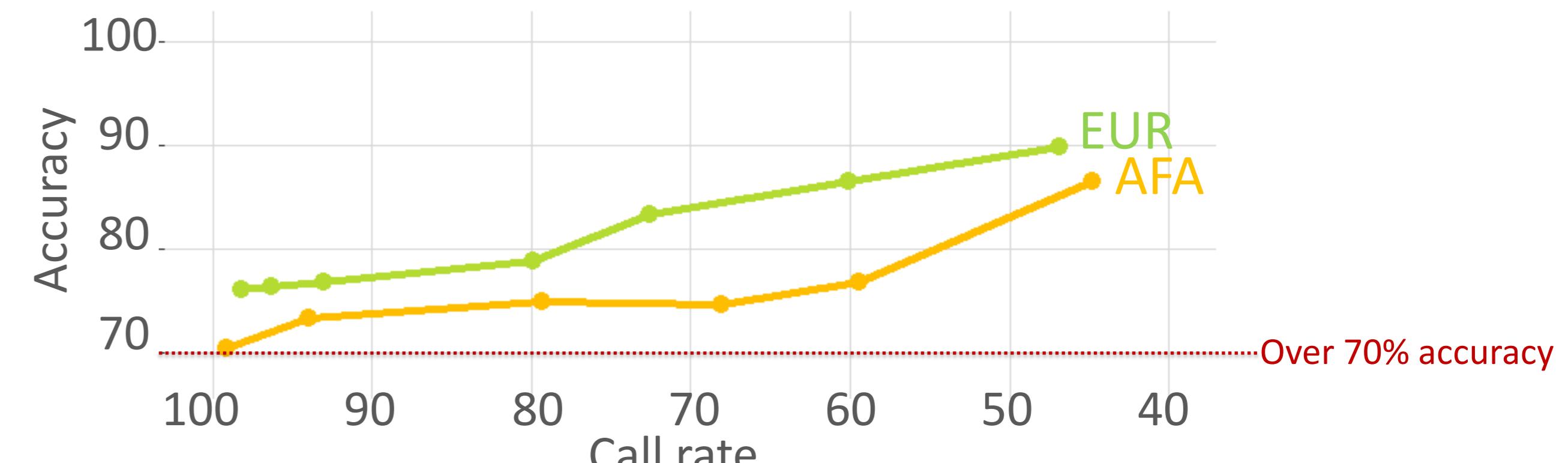
- 2 datasets with high-resolution *HLA* typing downgraded to low resolution



HLA-Upgrade can predict successfully *HLA*-A~B~C~DRB1~DQB1 high resolution typing in different populations from low resolution/partially known *HLA* typing. The accuracy of the most probable prediction increases as the call rate is reduced. The prediction accuracy by locus is on average 10% above for European compared to African-American.

HLA-2-Haplo validation

- Prediction compared to familial determined haplotypes
- 273 individuals from **European** ancestry and 116 from **African** ancestry



HLA-2-Haplo imputes haplotypes pairs with high confidence: >70% of haplotypes pairs correctly predicted. There is no significant difference of prediction accuracy between population.

HLA-2-Haplo accuracy relies on the number of haplotypes in the database, it performs haplotyping one sample at a time regardless of the input sample size.

Easy-HLA conclusion

Our results validate the haplotypes efficiency in predicting high resolution *HLA* typing and determining haplotypes pairs. Our tools can be used in multiple conditions both in clinic and research to: update cohorts, help HSCT donor matching search, bring new parameters for association studies. Both *HLA*-Upgrade and *HLA*-2-Haplo show good performance in term of accuracy.

Easy-HLA is tuned to deliver updated *HLA* information from all *HLA* typing resolution. These predictions are all done in silico and as such do not require additional typing in the laboratory. Our software will continue improving as we will update our database with additional *HLA* haplotypes.