

Table S4: Soft- and hardware environment of the HMA implementations used for this experiment ordered by affiliation superscript. This order does not correspond with the arbitrary numbering of the participants used in the publication.

	ZKRD	NMDP	ANRI	CSCR	DKMS	FGM	BMDW
<b>Program name</b>	OptiMatch <sup>®</sup>	HapLogic <sup>™</sup>	Genius	Prometheus	Hap-E Search <sup>®</sup>	Syrenad match	BMDWmatch
<b>Operating system, etc.</b>	Linux	Linux	MS Windows <sup>®</sup>	MS Windows <sup>®</sup>	Linux, Oracle <sup>®</sup>	Linux	MS Windows <sup>®</sup>
<b>Architecture</b>	x86_64	x86_64	x86	x86	x86_64	x86_64	x86
<b>Languages</b>	Object Pascal, BASM	Java	T-SQL, C#	Object Pascal	SQL, PL/SQL	PL/SQL	Object Pascal
<b>Speed optimizations</b>	memory persistent HLA reference data, HF data; software caching; hand-optimized inline assembler code; etc.	memory persistent HLA reference data, HF data; donor registry data; trimming	indexed lookup table for HF data; distinct donor phenotype list to prevent repeated genotype lookups; multithreading	special indices for haplotypes; maximum of data in RAM; HLA nomenclature filtering based on frequency data	indexing system for HLA nomenclature; preassembling of HF data in tree-like structure	indexing system for donor HLA	in-memory lookup tables
<b>Trimming of set of diplotypes</b>	No	Yes	No	No	No	n/a	n/a
<b>Loading of DNA-to-serology mappings</b>	Yes	Yes	Yes	Yes	Yes	No	No
<b>Loading of haplotype frequencies</b>	Yes	Yes	Yes	Yes	Yes	n/a	n/a