Table S1: Characterstics of the matching validation tasks and associated data sets with 1,000 patients and 10,000 donors each

	MVT/MVS 1	MVT/MVS 2	MVT/MVS 3
Basic parameters			
HLA loci considered for matching	A, B, DRB1	A, B, DRB1	A, C, B, DRB1, DQB1
IPD-IMGT/HLA Database version	2.16.0	2.16.0	3.4.0
Patient data			
serologic designations	0.0%	10.4%	0.0%
1st-field allele designations (XX codes)	12.0%	0.0%	14.0%
multiple allele codes (no ARD groups)	39.3%	38.4%	15.4%
2 field allele designations or ARD groups	48.7%	51.2%	70.6%
Donor data			
serologic designations	0.0%	61.8%	0.0%
1st-field allele designations (XX codes)	61.1%	0.0%	60.8%
multiple allele codes (no ARD groups)	23.9%	23.5%	32.9%
2 field allele designations or ARD groups	15.0%	14.7%	6.3%
without HLA-C	n/a	n/a	80%
without HLA-DRB1	0%	0%	10%
without HLA-DQB1	n/a	n/a	90%
HLA matching			
allele level matching	✓	✓	✓
antigen level matching		✓	
probabilistic matching			✓

Table S2: Types of HLA assignments used and their resolution

Assignment	**Resolution**	**Example**
Serological / Antigen	low	DR14
XX-code	low	DRB1*14:XX
Multiple allele code	non-high	DRB1*14:MAC
ARD group (two fields)	high	DRB1*14:01g
Allele	high	DRB1*14:01
WMDA extension	n/a	UUUU (untested)

Table S3: Counting mismatches for 2 by 2 comparisons of patient and donor alleles. A, B, C, D stand for pairwise mismatched expressed alleles, N codes a null allele. The column #GvH gives the number of mismatches in Graft vs. Host direction, #HvG the number of mismatches in Host vs. Graft direction. The column #Max gives the maximum of the columns #GvH and #HvG. The application of this counting schema to allelic ambiguities is described in section *"Matching with allelic ambiguities"* of the WMDA HLA matching framework (18). Alterations to the original table given in this publication are shown in red.

Patient	Donor	#GvH	#HvG	#Max
AB	AB	0	0	0
AA	AA	0	0	0
AA	NA	0	0	0
NA	AA	0	0	0
NA	NA	0	0	0
NN	NN	0	0	0
AA	AB	0	1	1
NA	AB	0	1	1
NN	NA	0	1	1
AB	AA	1	0	1
AB	NA	1	0	1
NA	NN	1	0	1
AB	AC	1	1	1
NA	NB	1	1	1
NN	AA	0	**2**	**2**
NN	AB	0	2	2
AA	NN	**2**	0	**2**
AB	NN	2	0	2
AA	BB	**2**	**2**	**2**
AA	NB	**2**	**2**	**2**
NA	BB	**2**	**2**	**2**
AA	BC	**2**	2	2
NA	BC	**2**	2	2
AB	CC	2	**2**	2
AB	NC	2	**2**	2
AB	CD	2	2	2

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**
Program name	OptiMatch®	HapLogic™	Genius	Prometheus	Hap-E Search®	Syrenad match	BMDWmatch
Operating system, etc.	Linux	Linux	MS Windows®	MS Windows®	Linux, Oracle®	Linux	MS Windows®
Architecture	x86_64	x86_64	x86	x86	x86_64	x86_64	x86
Languages	Object Pascal, BASM	Java	T-SQL, C#	Object Pascal	SQL, PL/SQL	PL/SQL	Object Pascal
Speed optimizations	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
Trimming of set of diplotypes	No	Yes	No	No	No	n/a	n/a
Loading of DNA-to-serology mappings	Yes	Yes	Yes	Yes	Yes	No	No
Loading of haplotype frequencies	Yes	Yes	Yes	Yes	Yes	n/a	n/a