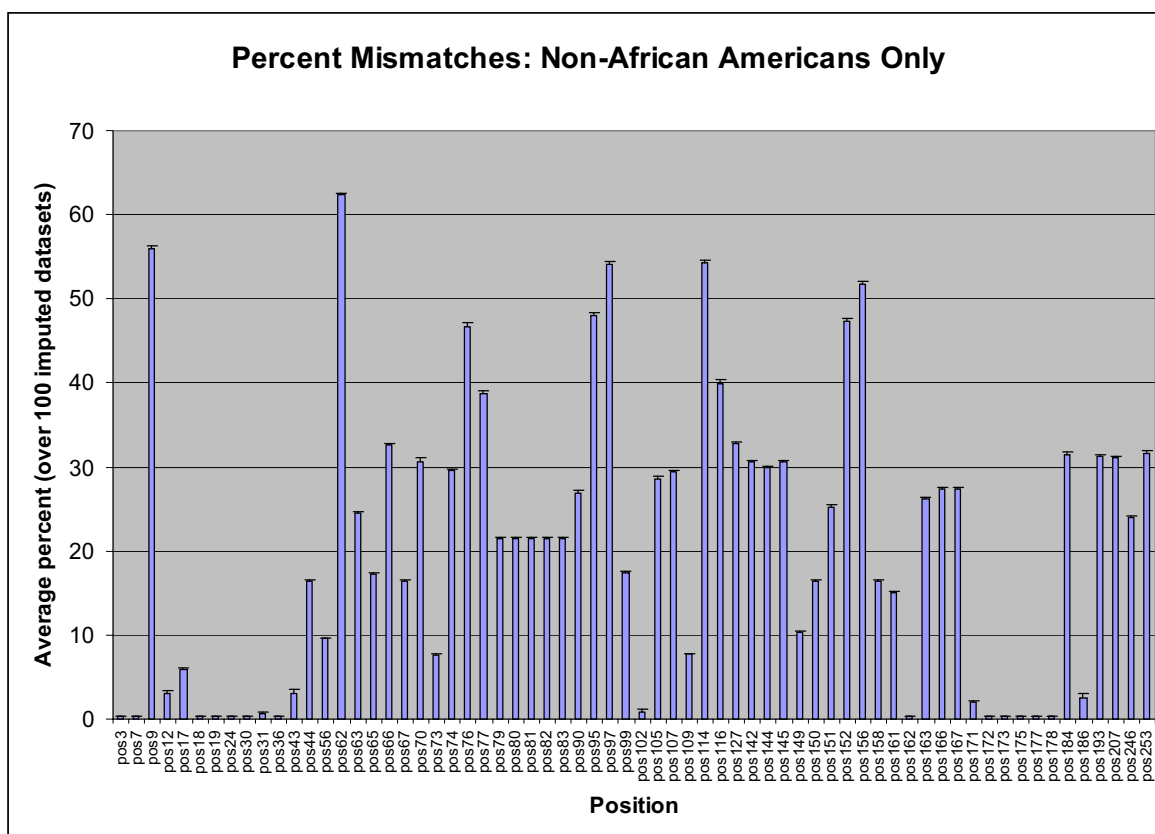


# Supporting Information

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**Fig. S1.** This figure shows the mismatches at 66 variable amino acid sites covering the  $\alpha 1$ ,  $\alpha 2$ , and  $\alpha 3$  domains of the HLA-A molecule, expressed as an average percent over the 100 imputed dataset. Error bars indicate standard deviation.





**Table S1. Recipient and Donor Characteristics**

	Overall % <i>n</i> = 705	Non-AA % <i>n</i> = 498	AA % <i>n</i> = 207	<i>P</i> -value*
Age				0.1845
<40	27.38	28.93	23.59	
40–50	24.11	23.90	24.62	
50–60	27.68	27.04	29.23	
60+	20.83	20.13	22.56	
Gender				0.9713
Male	60.28	60.24	60.39	
Female	39.72	39.76	39.61	
Delayed Graft Function				<.0001
Yes	38.39	32.37	47.00	
No	61.61	67.63	53.00	
Previous Transplant				0.341
Yes	13.03	13.81	11.11	
No	86.97	86.19	88.89	
ESRD Etiology				<.0001
Glomerulonephritis	21.36	24.10	14.98	
Hypertension	19.80	12.25	38.16	
Other	16.97	18.07	13.53	
Polycystic Kidneys	10.89	13.65	4.35	
Diabetes	30.98	31.93	28.99	
Most Recent PRA				0.4187
0	78.92	77.99	81.08	
0–20	9.64	10.07	8.65	
20+	11.44	11.94	10.27	
Donor Race				<.0001
African-American	10.30	7.11	17.44	
Non-African American	89.70	92.89	82.56	
Donor Cause of Death				<.0001
Cardiovascular	15.83	12.41	23.44	
Intercranial	34.25	33.02	36.98	
Trauma	39.10	44.96	26.04	
Other	10.82	9.60	13.54	

\**P* value represents a comparison between Non-AA and AA recipients  
ESRD, end stage renal disease; PRA, panel reactive antibodies.

**Table S2. Correlation matrix between amino acid mismatched sites associated with delayed graft function in Caucasians recipients**

Variable	MIS62	MIS90	MIS95	MIS105	MIS149	MIS163	MIS184	MIS193
MIS62								
MIS90	0.23							
MIS95	0.72	0.19						
MIS105	0.24	0.81	0.23					
MIS149	0.23	0.35	0.01	0.27				
MIS163	0.23	0.96	0.19	0.80	0.34			
MIS184	0.50	0.11	0.39	0.11	0.08	0.13		
MIS193	0.45	0.15	0.35	0.16	0.05	0.16	0.83	
MIS246	0.25	0.13	0.04	0.21	0.46	0.14	0.14	0.20

MIS: designates a mismatch at an individual amino acid site. The numbers in the Table indicate the pair-wise correlation coefficient value between amino acid mismatched sites associated with DGF.

**Table S3. HLA-A Family-Specific Mismatched Sites**

	Position	127	149	184	193	246
	Potential Contact**†	$\alpha 2$ Other	$\alpha 2$ T	$\alpha 3$	$\alpha 3$	$\alpha 3$
	Mean % mm†*	0.33	0.10	0.31	0.31	0.24
HLA-A families	HLA-A Specificity					
A3	A1	N	A	P	P	A
	A36	N	A	P	P	A
	A11	N	A	P	P	A
	A3	N	A	P	P	A
	A30	N	A	P	P	A
A9	A23	K	A	P	P	A
	A24	K	A	P	P	A
A2	A2	K	A/T	A	A	A
	A68	K	A	A	A	A
	A69	K	A	A	A	A
A10	A25	N	T	A	A	S
	A26	N	T	A	A	S
	A43	N	T	A	A	S
	A34	N	T	A	A	S
	A66	N	T	A	A	S
A19	A29	N	A	A	A	S
	A32	N	A	A	A	S
	A74	N	A	A	A	S
	A31	N	A	P	A	S
	A33	N	A	P	A	S
	A80	N	A	P	P	A

\*Amino acid sites are displayed based on the  $\alpha 1$ ,  $\alpha 2$ , and  $\alpha 2$  domains of the HLA-A molecule. T indicates a TCR contact site.

†Mean % mm indicates mean percent mismatches in this cohort of non-African American recipients.