

Supplementary Materials for

HLA class II genes modulate vaccine-induced antibody responses to affect HIV-1 acquisition

Heather A. Prentice, Georgia D. Tomaras, Daniel E. Geraghty, Richard Apps, Youyi Fong, Philip K. Ehrenberg, Morgane Rolland, Gustavo H. Kijak, Shelly J. Krebs, Wyatt Nelson, Allan DeCamp, Xiaoying Shen, Nicole L. Yates, Susan Zolla-Pazner, Sorachai Nitayaphan, Supachai Rerks-Ngarm, Jaranit Kaewkungwal, Punnee Pitisuttithum, Guido Ferrari, M. Juliana McElrath, David C. Montefiori, Robert T. Bailer, Richard A. Koup, Robert J. O'Connell, Merlin L. Robb, Nelson L. Michael, Peter B. Gilbert, Jerome H. Kim, Rasmi Thomas*

*Corresponding author. E-mail: rthomas@hivresearch.org

Published 15 July 2015, *Sci. Transl. Med.* **7**, 296ra112 (2015)

DOI: 10.1126/scitranslmed.aab4005

The PDF file includes:

Fig. S1. Multiple alignment of different Env (120–204) and partial V2 sequences (160–183).

Fig. S2. Cocystal structure of HIV-1 gp120 (red) binding to CD4 (green) and the Fab of mAb 17b (blue) (23).

Table S1. Odds ratios for two-way interaction analysis of HLA class II alleles with Env-specific IgA and Env (120–204)–specific IgG.

Table S2. Association between Env-specific IgA or Env (120–204)–specific IgG and HLA class II alleles present in more than 5% of the study population.

Table S3. High IgG binding to multiple Env (120–204) antigens correlates with presence of DPB1*13 and is associated with decreased HIV-1 acquisition across multiple subtypes.

Table S4. IgG responses to five overlapping peptides spanning Env (120–204) were significantly associated with presence of DPB1*13.

Table S5. Comparison of frequency of amino acid (AA) sites in Env-gp70 in RV144 breakthrough infections stratified by DPB1*13.

Table S6. Odds ratios for IgA binding to different recombinant Env proteins on HIV-1 acquisition after stratification by absence or presence of HLA-DQB1*06.

Table S7. Odds ratios for HIV-1 acquisition in univariate analyses of all HLA class II alleles present in the placebo controls.

Table S8. Odds ratios for HIV-1 acquisition in univariate analyses of all HLA class II alleles present in the vaccinated volunteers.

```

120
gp70_BCaseA_V1_V2      VKLTPLCVTLNCIDLRNATNATSNSTNTNTTSSSGGLMMEQGEIKNCFSNITTSIR
gp70_A_GN              VKLTPLCVTLDCNATAS-----NVTNEMRNCFSNITTELK
gp70_C_GN              VKLTPLCVTLHCTNATFKNNVTND-----MNKEIRNCFSNITTEIR
AEA244V1V2Tags293F    VKLTPPCVTLHCTNANLTKANLTVN--NRTNVSNIIGNITDEVRCFSNMTTELR
BioRV144_V2_AE        -----KKKTELR
BioRV144_V2_C         -----KKKTEIR
BioRV144_V2_B         -----KKKTSIR
                        : .*.::

204
gp70_BCaseA_V1_V2      DKVQKEYALFYKLDIVPIDNPK---NSTNYRLISCNTSVITQA
gp70_A_GN              DKKQOVYSLFYKLDVVQINEKN--ETDKYRLINCNTSAITQA
gp70_C_GN              DKKQQGYALFYRPDIVLLKENRNSNNSNNEYILINCNASTITQA
AEA244V1V2Tags293F    DKKQKVHALFYKLDIVPIEDNN--DSSEYRLINCNTSVIKQP
BioRV144_V2_AE        DKKQKVYALFYKLDIVQ-----
BioRV144_V2_C         DKKQKVYALFYRLDIVP-----
BioRV144_V2_B         DKVQKEYALFYKLDVVP-----
** *: :.***: *.*

```

Fig. S1. Multiple alignment of different Env (120–204) and partial V2 sequences (160–183). HIV-1 Env amino acid sequences corresponding to either positions 120–204 or 160–183, relative to the HXB2 sequence reference from different viral subtypes (see table S3) were aligned using Clustal Omega. Sequences matching DPB1*13 specific epitope 120-133 are shown in bold.

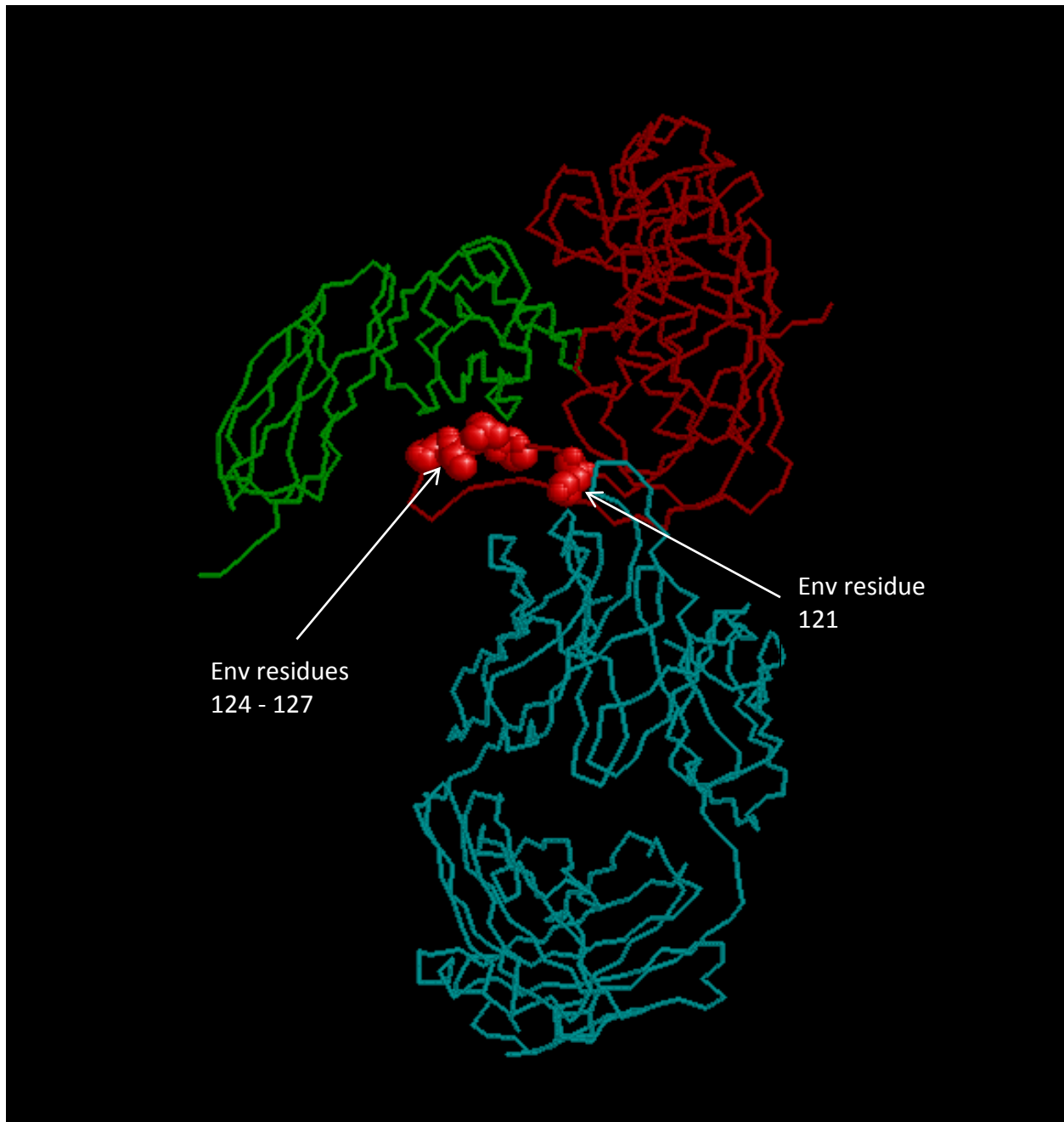


Fig. S2. Cocrystal structure of HIV-1 gp120 (red) binding to CD4 (green) and the Fab of mAb 17b (blue) (23). The IgG response identified, which was found to associate with both presence of DPB1*13 and also reduced risk of HIV-1 acquisition, was directed to the Env residues with atoms highlighted in red spheres (residues 124P, 125L, 126C, 127V). IgG binding to this region of Env would be expected to disrupt interaction with CD4. Also highlighted in red is Env residue 121K, binding site of the well-characterized neutralizing mAb 17b.

Table S1. Odds ratios for two-way interaction analysis of HLA class II alleles with Env-specific IgA and Env (120–204)–specific IgG.

Allele	G grouping†	Env-Specific IgA-Allele Interaction*						Env (120–204)–Specific IgG-Allele Interaction*			
		Infected	Uninfected	OR!!	95% CI	P	q	OR!!	95% CI	P	q
		N=41 (%)	N=202‡ (%)								
DRB1*03	DRB1*03:01:01G	2 (4.9)	25 (12.4)	0.76	0.11-5.36	0.78	0.93	1.13	0.23-5.57	0.88	0.93
DRB1*04		5 (12.2)	34 (16.8)	0.79	0.32-1.97	0.62	0.93	1.15	0.40-3.31	0.80	0.93
DRB1*07		11 (26.8)	31 (15.3)	0.94	0.44-1.99	0.87	0.93	1.89	0.74-4.80	0.18	0.74
DRB1*09	DRB1*09:01:02G	8 (19.5)	37 (18.3)	1.17	0.51-2.67	0.71	0.93	1.09	0.44-2.71	0.85	0.93
DRB1*11		3 (7.3)	27 (13.4)	0.60	0.14-2.59	0.50	0.93	0.24	0.02-3.21	0.28	0.88
DRB1*12		12 (29.3)	63 (31.2)	0.66	0.29-1.49	0.32	0.88	1.05	0.47-2.38	0.90	0.93
DRB1*14		8 (19.5)	36 (17.8)	0.65	0.27-1.57	0.34	0.88	1.07	0.42-2.76	0.89	0.93
DRB1*15		15 (36.6)	85 (42.1)	1.77	0.88-3.55	0.11	0.64	0.84	0.38-1.84	0.66	0.93
DRB1*04:05		2 (4.9)	24 (11.9)	0.97	0.24-3.98	0.97	0.97	1.70	0.43-6.65	0.45	0.93
DRB1*07:01	DRB1*07:01:01G	10 (24.4)	31 (15.3)	1.08	0.50-2.31	0.85	0.93	2.48	0.93-6.61	0.07	0.52
DRB1*12:02		12 (29.3)	58 (28.7)	0.70	0.31-1.60	0.40	0.93	1.11	0.49-2.50	0.81	0.93
DRB1*15:01	DRB1*15:01:01G	7 (17.1)	27 (13.4)	4.86	1.26-18.79	0.02	0.32	1.56	0.61-4.02	0.35	0.88
DRB1*15:02		9 (22.0)	60 (29.7)	1.09	0.49-2.42	0.83	0.93	0.49	0.18-1.35	0.17	0.74
DQB1*02		12 (29.3)	45 (22.3)	1.05	0.50-2.21	0.90	0.93	1.52	0.66-3.53	0.33	0.88
DQB1*03		23 (56.1)	114 (56.4)	0.89	0.46-1.72	0.73	0.93	1.03	0.49-2.19	0.93	0.94
DQB1*04		0 (0.0)	21 (10.4)	-	-	-	-	-	-	-	-
DQB1*05		23 (56.1)	122 (60.4)	0.85	0.43-1.67	0.63	0.93	0.78	0.36-1.71	0.53	0.93
DQB1*06		10 (24.4)	39 (19.3)	7.57	2.11-27.20	0.002	0.11	0.93	0.35-2.42	0.88	0.93
DQB1*03:01	DQB1*03:01:01G	15 (36.6)	72 (35.6)	0.71	0.34-1.46	0.35	0.88	0.94	0.42-2.13	0.89	0.93
DQB1*03:03	DQB1*03:03:02G	9 (22.0)	43 (21.3)	1.09	0.50-2.38	0.83	0.93	1.19	0.49-2.91	0.70	0.93
DQB1*05:01	DQB1*05:01:01G	8 (19.5)	49 (24.3)	0.90	0.39-2.09	0.80	0.93	0.61	0.23-1.63	0.33	0.88

DQB1*05:02	DQB1*05:02:01G	14 (34.1)	73 (36.1)	0.80	0.40-1.60	0.53	0.93	1.32	0.60-2.87	0.49	0.93
DQB1*05:03	DQB1*05:03:01G	5 (12.2)	19 (9.4)	0.45	0.14-1.47	0.19	0.74	1.44	0.48-4.32	0.52	0.93
DQB1*06:01	DQB1*06:01:01G	7 (17.1)	32 (15.8)	6.79	1.53-30.16	0.01	0.26	0.84	0.27-2.61	0.77	0.93
DPB1*02		15 (36.6)	58 (28.9)	0.75	0.37-1.54	0.43	0.93	1.66	0.76-3.66	0.21	0.78
DPB1*04		14 (34.1)	57 (28.4)	1.74	0.85-3.56	0.13	0.72	1.26	0.57-2.82	0.57	0.93
DPB1*05		11 (26.8)	74 (36.8)	0.41	0.18-0.91	0.03	0.32	0.59	0.25-1.39	0.23	0.81
DPB1*13		11 (26.8)	66 (32.8)	0.44	0.20-0.95	0.04	0.32	0.27	0.10-0.76	0.01	0.26
DPB1*02:01		9 (22.0)	33 (16.4)	0.73	0.32-1.68	0.46	0.93	2.09	0.89-4.93	0.09	0.60
DPB1*02:02		7 (17.1)	28 (13.9)	1.10	0.39-3.05	0.86	0.93	0.62	0.18-2.18	0.46	0.93
DPB1*04:01		9 (22.0)	45 (22.4)	2.68	1.09-6.59	0.03	0.32	1.83	0.76-4.40	0.18	0.74

* Previously reported values for Env-specific IgA and Env (120–204)–specific IgG (3). Sex, baseline behavioral risk score, and one significant principal component axis were included as covariates for all models.

† Nomenclature used for alleles that were ambiguous for exon 2 by 4-digit HLA typing.

‡ 201 HIV-1 uninfected individuals with complete DPB1 genotyping.

!! Estimated odds ratios and 95% CIs reflect the results from logistic regression analysis including a two-way interaction term for Env-specific IgA or Env (120–204)–specific IgG and presence of the given allele.

Table S2. Association between Env-specific IgA or Env (120–204)–specific IgG and HLA class II alleles present in more than 5% of the study population.

Allele	n (%)†	Env-Specific IgA*			Env (120–204)–Specific IgG*		
		$\beta \pm SE$	P	q	$\beta \pm SE$	P	q
DRB1*03	27 (11.1)	-0.28 ± 0.20	0.17	0.52	-0.04 ± 0.20	0.83	0.94
DRB1*04	39 (16.0)	0.03 ± 0.18	0.85	0.94	0.09 ± 0.18	0.60	0.85
DRB1*07	42 (17.3)	-0.10 ± 0.17	0.56	0.85	-0.35 ± 0.17	0.04	0.36
DRB1*09	45 (18.5)	0.34 ± 0.16	0.04	0.36	0.20 ± 0.17	0.23	0.58
DRB1*11	30 (12.3)	0.10 ± 0.20	0.61	0.85	-0.24 ± 0.19	0.22	0.58
DRB1*12	75 (30.9)	-0.28 ± 0.14	0.05	0.36	0.21 ± 0.14	0.13	0.52
DRB1*14	44 (18.1)	-0.08 ± 0.17	0.64	0.85	-0.01 ± 0.17	0.97	0.97
DRB1*15	100 (41.2)	-0.01 ± 0.13	0.96	0.97	0.07 ± 0.13	0.60	0.85
DRB1*04:05	26 (10.7)	0.29 ± 0.21	0.17	0.52	0.35 ± 0.21	0.09	0.50
DRB1*07:01	41 (16.9)	-0.07 ± 0.17	0.68	0.87	-0.31 ± 0.17	0.07	0.48
DRB1*12:02	70 (28.8)	-0.30 ± 0.14	0.04	0.36	0.15 ± 0.14	0.28	0.65
DRB1*15:01	34 (14.0)	0.20 ± 0.19	0.29	0.65	-0.10 ± 0.19	0.59	0.85
DRB1*15:02	69 (28.4)	-0.16 ± 0.14	0.25	0.63	0.20 ± 0.14	0.15	0.52
DQB1*02	57 (23.5)	-0.16 ± 0.15	0.30	0.65	-0.30 ± 0.15	0.05	0.36
DQB1*03	137 (56.4)	0.13 ± 0.13	0.33	0.68	0.03 ± 0.13	0.76	0.89
DQB1*04	21 (8.6)	0.11 ± 0.23	0.63	0.85	0.08 ± 0.23	0.72	0.88
DQB1*05	145 (59.7)	-0.17 ± 0.13	0.19	0.55	-0.02 ± 0.13	0.88	0.94
DQB1*06	49 (20.2)	0.12 ± 0.16	0.46	0.81	-0.14 ± 0.16	0.40	0.77
DQB1*03:01	87 (35.8)	0.08 ± 0.13	0.54	0.85	0.02 ± 0.13	0.88	0.94
DQB1*03:03	52 (21.4)	0.25 ± 0.16	0.10	0.50	0.16 ± 0.16	0.31	0.67
DQB1*05:01	57 (23.5)	-0.02 ± 0.15	0.90	0.95	0.39 ± 0.15	0.01	0.30
DQB1*05:02	87 (35.8)	-0.10 ± 0.13	0.46	0.81	-0.12 ± 0.13	0.38	0.75
DQB1*05:03	24 (9.9)	-0.09 ± 0.22	0.68	0.87	-0.15 ± 0.22	0.50	0.85
DQB1*06:01	39 (16.0)	0.08 ± 0.18	0.64	0.85	0.03 ± 0.18	0.87	0.94
DPB1*02	73 (30.2)	0.08 ± 0.14	0.53	0.85	-0.09 ± 0.14	0.50	0.85
DPB1*04	71 (29.3)	-0.20 ± 0.17	0.17	0.52	-0.30 ± 0.14	0.03	0.36
DPB1*05	85 (35.1)	-0.04 ± 0.14	0.75	0.89	0.05 ± 0.14	0.71	0.88
DPB1*13	77 (31.8)	0.18 ± 0.14	0.20	0.55	0.44 ± 0.14	0.002	0.09
DPB1*02:01	42 (17.4)	0.30 ± 0.17	0.08	0.50	-0.02 ± 0.17	0.92	0.95
DPB1*02:02	35 (14.5)	-0.14 ± 0.18	0.44	0.81	-0.27 ± 0.18	0.14	0.52
DPB1*04:01	54 (22.3)	-0.22 ± 0.15	0.15	0.52	-0.25 ± 0.15	0.10	0.50

* Previously reported values (3).

† 201 HIV-1 uninfected individuals with complete DPB1 genotyping.

Table S3. High IgG binding to multiple Env (120–204) antigens correlates with presence of DPB1*13 and is associated with decreased HIV-1 acquisition across multiple subtypes.

Antigen (HIV-1 subtype)*	Alias	DPB1*13 Association		Antigen-DPB1*13 Interaction†		
		$\beta \pm SD$	P	DPB1*13	Odds Ratio (95% CI)	P
Env 120–204–specific IgG (CRF01_AE)‡	AEA244V1V2Tags293F	0.38 ± 0.14	0.006	Present	0.07 (0.01-0.41)	0.003
				Absent	0.93 (0.64-1.36)	0.71
				Interaction	-	0.009
Env 120–204–specific IgG (B)‡	gp70_BCaseA_V1_V2	0.45 ± 0.14	0.001	Present	0.26 (0.10-0.67)	0.005
				Absent	1.03 (0.68-1.56)	0.90
				Interaction	-	0.01
Env 120–204–specific IgG (A)‡	gp70_A_GN	0.55 ± 0.13	<0.001	Present	0.31 (0.12-0.85)	0.02
				Absent	1.14 (0.73-1.78)	0.55
				Interaction	-	0.02
Env 120–204–specific IgG (C)‡	gp70_C_GN	0.42 ± 0.14	0.002	Present	0.19 (0.07-0.52)	0.001
				Absent	0.98 (0.64-1.50)	0.93
				Interaction	-	0.006
Env 160–183–specific IgG (CRF01_AE)	BioRV144_V2_AE	0.35 ± 0.14	0.01	Present	0.64 (0.27-1.50)	0.30
				Absent	0.83 (0.55-1.27)	0.40
				Interaction	-	0.71
Env 160–183–specific IgG (B)	BioRV144_V2_B	0.19 ± 0.14	0.18	Present	0.77 (0.37-1.61)	0.49
				Absent	0.90 (0.60-1.36)	0.63

				Interaction	-	0.90
Env 160–183–specific IgG (C)	BioRV144_V2_C	0.33 ± 0.14	0.02	Present	0.80 (0.36-1.76)	0.58
				Absent	0.95 (0.63-1.44)	0.81
				Interaction	-	0.70

* Env sequences from different viral subtypes and their amino acid positions relative to HXB2 sequence.

† The odds ratio is reported per 1-SD increase; sex, baseline behavioral risk score, and one significant principal component axis were included as covariates.

‡ Antigen reported in Zolla-Pazner et al. 2014 (43).

Table S4. IgG responses to five overlapping peptides spanning Env (120–204) were significantly associated with presence of DPB1*13.

Peptide (Start-end)*	Peptide Sequence	DPB1*13+,	DPB1*13+,	DPB1*13-,	DPB1*13-,	Fisher's P
		Yes %	No %	Yes %	No %	
116-130	LKPCVKLTPLCVTLN	9.1	90.9	2.4	97.6	0.04
119-133	CVKLTPLCVTLNCTD	37.7	62.3	21.8	78.2	0.01
163-177	TEIRDKKQKVYALFY	63.6	36.4	47.3	52.7	0.02
166-180	RDKKQKVYSLFYRLD	40.3	59.7	26.7	73.3	0.04
169-183	KKQVYALFYKLDVVP	15.6	84.4	4.8	95.2	0.01

* Env amino acid positions relative to the HXB2 reference.

Table S5. Comparison of frequency of amino acid (AA) sites in Env-gp70 in RV144 breakthrough infections* stratified by DPB1*13.

HXB2 position	Consensus AA	Vaccinated					Placebo					Vaccinated	Placebo	DPB1*13+	DPB1*13-
		DPB1*13+		DPB1*13-			DPB1*13+		DPB1*13-			DPB1*13+	DPB1*13+	Vax vs	Vax vs
		Yes	No	Yes	No	Total	Yes	No	Yes	No	Total	vs DPB1*13-	vs DPB1*13-	Placebo	Placebo
120	V	7	1	34	2	44	18	0	47	1	66				
124	P	8	0	33	3	44	17	1	44	4	66				
160	N	8	0	36	0	44	17	1	48	0	66				
165	L	5	3	23	13	44	14	4	28	20	66				
166	R	4	4	25	11	44	8	10	29	19	66				
168	K	0	8	5	31	44	2	16	6	42	66				
169	K	4	4	26	10	44	13	5	44	4	66				
170	Q	5	3	28	8	44	11	7	37	11	66				
171	K	4	4	24	12	44	14	4	33	15	66				
172	V	6	2	29	7	44	13	5	37	11	66				
173	H	8	0	15	21	44	9	9	19	29	66	0.004	0.58	0.02	1.00
178	K	5	3	28	8	44	9	9	34	14	66				
179	L	8	0	33	3	44	18	0	44	4	66				
181	I	8	0	32	4	44	14	4	35	13	66				
197	N	8	0	34	2	44	17	1	48	0	66				

* Virus sequences previously published in Rolland et al. 2012 (7)

Table S6. Odds ratios for IgA binding to different recombinant Env proteins on HIV-1 acquisition after stratification by absence or presence of HLA-DQB1*06.

Variable of Interest	Interacting Variable	Infected N=41 (%)	Uninfected N=202 (%)	OR	(95% CI)	P
A.conenv03	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	4.36	(1.7-11.5)	0.003
Subtype A	Absent	31 (75.6)	163 (80.7)	1.29	(0.9-1.9)	0.17
	Interaction			-	-	0.02
IgA A.00MSA	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	4.41	(1.7-11.7)	0.003
Subtype A	Absent	31 (75.6)	163 (80.7)	1.04	(0.7-1.5)	0.83
	Interaction			-	-	0.01
US1SIV_{cpz}	DQB1*06					
gp140	Present	10 (24.4)	39 (19.3)	2.09	(1.0-4.2)	0.04
Chimp ancestral	Absent	31 (75.6)	163 (80.7)	1.15	(0.8-1.6)	0.42
	Interaction			-	-	0.24
G.DRCBL	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	2.01	(1.0-4.1)	0.06
Subtype G	Absent	31 (75.6)	163 (80.7)	1.27	(0.9-1.8)	0.21
	Interaction			-	-	0.28
E.97CNGX2F	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	4.94	(1.9-12.8)	0.001
Subtype CRF01_AE	Absent	31 (75.6)	163 (80.7)	0.96	(0.6-1.4)	0.84
	Interaction			-	-	0.002
B.conenv03	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	28.66	(0.8-982.7)	0.06
Subtype B	Absent	31 (75.6)	163 (80.7)	1.07	(0.7-1.6)	0.74
	Interaction			-	-	0.05
C.conenv03	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	3.61	(0.9-14.1)	0.06
Subtype C	Absent	31 (75.6)	163 (80.7)	1.08	(0.7-1.6)	0.72
	Interaction			-	-	0.10
CON6 gp120	DQB1*06					
Subtype B	Present	10 (24.4)	39 (19.3)	2.82	(0.8-10.0)	0.11
	Absent	31 (75.6)	163 (80.7)	0.94	(0.6-1.4)	0.74
	Interaction			-	-	0.14
CON-S	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	93.53	(1.6->999.9)	0.03
Subtype M	Absent	31 (75.6)	163 (80.7)	1.03	(0.7-1.5)	0.88
	Interaction			-	-	0.03
G.conenv03	DQB1*06					
gp140CF	Present	10 (24.4)	39 (19.3)	2.13	(1.1-4.2)	0.03
Subtype G	Absent	31 (75.6)	163 (80.7)	1.14	(0.8-1.7)	0.51
	Interaction			-	-	0.13

AE.conenv03140CF	DQB1*06					
Subtype CRF01_AE	Present	10 (24.4)	39 (19.3)	5.57	(1.6-19.0)	0.006
	Absent	31 (75.6)	163 (80.7)	0.87	(0.6-1.3)	0.48
	Interaction			-	-	0.01
B.JRFL gp140	DQB1*06					
Subtype B	Present	10 (24.4)	39 (19.3)	4.08	(1.2-14.5)	0.03
	Absent	31 (75.6)	163 (80.7)	0.93	(0.6-1.4)	0.70
	Interaction			-	-	0.04
E.92TH023 gD-	DQB1*06					
Subtype CRF01_AE	Present	10 (24.4)	39 (19.3)	4.77	(1.0-22.5)	0.05
	Absent	31 (75.6)	163 (80.7)	1.06	(0.7-1.6)	0.79
	Interaction			-	-	0.09
E.A244 gD-	DQB1*06					
Subtype CRF01_AE	Present	10 (24.4)	39 (19.3)	6.82	(2.1-22.5)	0.002
	Absent	31 (75.6)	163 (80.7)	0.96	(0.7-1.4)	0.85
	Interaction			-	-	0.002

Table S7. Odds ratios for HIV-1 acquisition in univariate analyses of all HLA class II alleles present in the placebo controls*.

Allele	Infected	Uninfected	OR	95% CI	P
	N=67 (%)	N=450 (%)			
DRB1*03	7 (10.4)	46 (10.2)	1.02	(0.44-2.37)	0.96
DRB1*04	7 (10.4)	73 (16.3)	0.60	(0.26-1.37)	0.22
DRB1*07	18 (26.9)	87 (19.4)	1.53	(0.85-2.75)	0.16
DRB1*09	14 (20.9)	86 (19.2)	1.12	(0.59-2.10)	0.74
DRB1*11	4 (6.0)	39 (8.7)	0.67	(0.23-1.93)	0.46
DRB1*12	25 (37.3)	145 (32.3)	1.25	(0.73-2.13)	0.42
DRB1*14	16 (23.9)	71 (15.8)	1.67	(0.90-3.09)	0.10
DRB1*15	18 (26.9)	184 (41.0)	0.53	(0.30-0.94)	0.03
DRB1*04:05	6 (9.0)	46 (10.2)	0.86	(0.35-2.10)	0.74
DRB1*07:01	18 (26.9)	87 (19.4)	1.53	(0.85-2.75)	0.16
DRB1*12:02	23 (34.3)	141 (31.4)	1.14	(0.66-1.96)	0.63
DRB1*15:01	6 (9.0)	74 (16.5)	0.50	(0.21-1.20)	0.12
DRB1*15:02	12 (17.9)	116 (25.8)	0.63	(0.32-1.21)	0.16
DQB1*02	22 (32.8)	120 (26.7)	1.34	(0.77-2.33)	0.30
DQB1*03	37 (55.2)	250 (55.7)	0.98	(0.59-1.65)	0.94
DQB1*04	5 (7.5)	42 (9.4)	0.78	(0.30-2.05)	0.62
DQB1*05	40 (59.7)	265 (59.0)	1.03	(0.61-1.74)	0.92
DQB1*06	10 (14.9)	89 (19.8)	0.71	(0.35-1.45)	0.34
DQB1*03:01	23 (34.3)	153 (34.1)	1.01	(0.59-1.74)	0.97
DQB1*03:03	17 (25.4)	103 (22.9)	1.14	(0.63-2.07)	0.66
DQB1*05:01	13 (19.4)	114 (25.4)	0.71	(0.37-1.34)	0.29
DQB1*05:02	23 (34.3)	136 (30.3)	1.20	(0.70-2.07)	0.50
DQB1*05:03	7 (10.4)	49 (10.9)	0.95	(0.41-2.20)	0.91
DQB1*06:01	7 (10.4)	68 (15.1)	0.65	(0.29-1.49)	0.31
DPB1*02	17 (25.4)	114 (25.4)	1.00	(0.55-1.80)	1.00
DPB1*04	20 (29.9)	125 (27.8)	1.10	(0.63-1.94)	0.73
DPB1*05	24 (35.8)	180 (40.1)	0.83	(0.49-1.42)	0.51
DPB1*13	18 (26.9)	142 (31.6)	0.79	(0.45-1.41)	0.43
DPB1*02:01	10 (14.9)	78 (17.4)	0.83	(0.41-1.71)	0.62
DPB1*02:02	8 (11.9)	42 (9.4)	1.31	(0.59-2.94)	0.51
DPB1*04:01	15 (22.4)	104 (23.2)	0.96	(0.52-1.77)	0.89

* Alleles found to have population frequencies (2N) greater than 5%.

Table S8. Odds ratios for HIV-1 acquisition in univariate analyses of all HLA class II alleles present in the vaccinated volunteers*.

Allele	Infected N=41 (%)	Uninfected N=202† (%)	OR	95% CI	P
DRB1*03	2 (4.9)	25 (12.4)	0.32	0.07-1.42	0.14
DRB1*04	5 (12.2)	34 (16.8)	0.69	0.24-1.97	0.49
DRB1*07	11 (26.8)	31 (15.3)	2.11	0.94-4.72	0.07
DRB1*09	8 (19.5)	37 (18.3)	1.16	0.48-2.80	0.74
DRB1*11	3 (7.3)	27 (13.4)	0.50	0.14-1.76	0.28
DRB1*12	12 (29.3)	63 (31.2)	0.90	0.42-1.92	0.79
DRB1*14	8 (19.5)	36 (17.8)	1.11	0.47-2.63	0.81
DRB1*15	15 (36.6)	85 (42.1)	0.74	0.36-1.50	0.41
DRB1*04:05	2 (4.9)	24 (11.9)	0.37	0.08-1.69	0.20
DRB1*07:01	10 (24.4)	31 (15.3)	1.87	0.82-4.25	0.14
DRB1*12:02	12 (29.3)	58 (28.7)	0.99	0.46-2.12	0.99
DRB1*15:01	7 (17.1)	27 (13.4)	1.41	0.56-3.56	0.47
DRB1*15:02	9 (22.0)	60 (29.7)	0.58	0.25-1.31	0.19
DQB1*02	12 (29.3)	45 (22.3)	1.47	0.69-3.15	0.32
DQB1*03	23 (56.1)	114 (56.4)	0.94	0.47-1.86	0.85
DQB1*04	0 (0.0)	21 (10.4)	-	-	-
DQB1*05	23 (56.1)	122 (60.4)	0.75	0.37-1.51	0.42
DQB1*06	10 (24.4)	39 (19.3)	1.54	0.69-3.46	0.30
DQB1*03:01	15 (36.6)	72 (35.6)	1.02	0.50-2.08	0.96
DQB1*03:03	9 (22.0)	43 (21.3)	1.02	0.44-2.36	0.96
DQB1*05:01	8 (19.5)	49 (24.3)	0.58	0.24-1.39	0.22
DQB1*05:02	14 (34.1)	73 (36.1)	0.97	0.47-1.99	0.93
DQB1*05:03	5 (12.2)	19 (9.4)	1.36	0.46-3.96	0.58
DQB1*06:01	7 (17.1)	32 (15.8)	1.28	0.51-3.18	0.60
DPB1*02	15 (36.6)	58 (28.9)	1.51	0.74-3.09	0.26
DPB1*04	14 (34.1)	57 (28.4)	1.28	0.62-2.66	0.51
DPB1*05	11 (26.8)	74 (36.8)	0.64	0.30-1.38	0.26
DPB1*13	11 (26.8)	66 (32.8)	0.65	0.30-1.40	0.27
DPB1*02:01	9 (22.0)	33 (16.4)	1.58	0.68-3.69	0.29
DPB1*02:02	7 (17.1)	28 (13.9)	1.33	0.53-3.34	0.54
DPB1*04:01	9 (22.0)	45 (22.4)	0.94	0.41-2.13	0.88

* Alleles found to have population frequencies (2N) greater than 5% when cases and controls were combined.

† 201 HIV-1 uninfected individuals with complete DPB1 genotyping.