New Associations with HIV Predisposing and Protective Alleles of the HLA System in a Peruvian Population

Supplementary Table S1. Complete allele frequencies detected in study population for each locus.

HLA-A	Freq	HLA-B	Freq	HLA-C	Freq	HLA-DPB1	Freq	HLA-DQA1	Freq	HLA-DQB1	Freq	HLA-DRB1	Freq
A*01:01	0.020	B*07:02	0.050	C*01:02	0.121	DPB1*02:01	0.070	DQA1*01:01	0.051	DQB1*02:01	0.060	DRB1*01:01	0.010
A*01:02	0.005	B*08:01	0.020	C*01:17	0.005	DPB1*02:02	0.005	DQA1*01:02	0.082	DQB1*02:02	0.005	DRB1*01:02	0.020
A*02:01	0.355	B*13:02	0.005	C*02:02	0.030	DPB1*03:01	0.040	DQA1*01:03	0.010	DQB1*02:188	0.005	DRB1*01:03	0.010
A*02:02	0.005	B*13:03	0.005	C*03:02	0.015	DPB1*04:01	0.160	DQA1*01:04	0.010	DQB1*02:197	0.010	DRB1*03:01	0.030
A*02:03	0.010	B*14:01	0.005	C*03:03	0.025	DPB1*04:02	0.295	DQA1*01:05	0.026	DQB1*02:59	0.005	DRB1*04:01	0.005
A*02:04	0.005	B*14:02	0.030	C*03:04	0.071	DPB1*05:01	0.040	DQA1*01:06	0.005	DQB1*03:02	0.210	DRB1*04:02	0.010
A*02:05	0.005	B*15:01	0.020	C*04:01	0.227	DPB1*09:01	0.005	DQA1*01:48	0.005	DQB1*03:03	0.050	DRB1*04:03	0.025
A*02:06	0.005	B*15:02	0.005	C*04:03	0.005	DPB1*104:01	0.015	DQA1*02:01	0.046	DQB1*03:22	0.015	DRB1*04:04	0.065
A*02:10	0.005	B*15:04	0.060	C*05:01	0.020	DPB1*105:01	0.005	DQA1*02:17	0.010	DQB1*03:229	0.005	DRB1*04:07	0.130
A*02:11	0.100	B*15:10	0.005	C*06:02	0.015	DPB1*107:01	0.045	DQA1*03:01	0.225	DQB1*03:251	0.015	DRB1*04:10	0.020
A*02:13	0.020	B*15:17	0.005	C*07:01	0.076	DPB1*1082:01	0.005	DQA1*03:02	0.107	DQB1*03:419	0.280	DRB1*04:11	0.015
A*02:22	0.045	B*15:39	0.010	C*07:02	0.187	DPB1*1083:01	0.005	DQA1*03:03	0.077	DQB1*03:49	0.005	DRB1*07:01	0.030
A*02:33	0.005	B*15:42	0.010	C*07:05	0.005	DPB1*10:01	0.010	DQA1*03:15	0.005	DQB1*03:95N	0.010	DRB1*08:02	0.110
A*02:58	0.005	B*18:01	0.015	C*07:18	0.005	DPB1*11:01	0.020	DQA1*04:01	0.112	DQB1*03:96	0.100	DRB1*08:03	0.010
A*02:60	0.005	B*27:05	0.005	C*08:01	0.040	DPB1*1243:01	0.005	DQA1*05:01	0.026	DQB1*03:99Q	0.015	DRB1*08:04	0.015
A*03:01	0.045	B*35:01	0.115	C*08:02	0.015	DPB1*126:01	0.010	DQA1*05:03	0.117	DQB1*04:02	0.040	DRB1*08:18	0.015
A*03:05	0.005	B*35:02	0.020	C*08:03	0.046	DPB1*1317:01Q	0.005	DQA1*05:05	0.061	DQB1*04:52	0.005	DRB1*09:01	0.145
A*11:01	0.020	B*35:04	0.015	C*08:27	0.005	DPB1*133:01	0.010	DQA1*05:48	0.020	DQB1*05:01	0.045	DRB1*09:21	0.025
A*23:01	0.005	B*35:05	0.040	C*12:02	0.010	DPB1*135:01	0.005	DQA1*06:01	0.005	DQB1*05:03	0.020	DRB1*10:01	0.015
A*24:02	0.110	B*35:09	0.010	C*12:03	0.020	DPB1*13:01	0.010			DQB1*05:226	0.005	DRB1*11:01	0.015
A*24:03	0.010	B*35:14	0.010	C*14:02	0.005	DPB1*14:01	0.135			DQB1*05:296	0.005	DRB1*11:02	0.010
A*25:01	0.015	B*35:20	0.005	C*15:02	0.030	DPB1*17:01	0.005			DQB1*06:01	0.005	DRB1*11:04	0.020
A*26:01	0.015	B*35:22	0.005	C*15:05	0.005	DPB1*184:01	0.005			DQB1*06:02	0.040	DRB1*12:01	0.005
A*30:01	0.010	B*35:25	0.005	C*16:02	0.005	DPB1*18:01	0.005			DQB1*06:03	0.005	DRB1*12:02	0.005
A*30:02	0.015	B*35:31	0.010	C*17:01	0.010	DPB1*21:01	0.005			DQB1*06:04	0.015	DRB1*13:02	0.030
A*30:04	0.005	B*35:43	0.010			DPB1*23:01	0.005			DQB1*06:09	0.010	DRB1*13:03	0.010
A*31:01	0.035	B*38:01	0.050			DPB1*352:01	0.005			DQB1*06:112N	0.005	DRB1*14:02	0.090
A*31:02	0.005	B*39:01	0.040			DPB1*40:01	0.005			DQB1*06:118	0.005	DRB1*14:06	0.005
A*31:04	0.005	B*39:05	0.020			DPB1*45:01	0.005			DQB1*06:44	0.005	DRB1*14:54	0.020

A*32:01 0.010	B*39:06 0.025		DPB1*585:01 0.005			DRB1*15:01 0.025
A*33:01 0.020	B*39:09 0.030		DPB1*651:01 0.035			DRB1*15:03 0.015
A*33:03 0.005	B*39:13 0.020		DPB1*835:01 0.005			DRB1*16:01 0.005
A*34:02 0.005	B*40:01 0.005		DPB1*882:01 0.005			DRB1*16:02 0.040
A*68:01 0.040	B*40:02 0.040		DPB1*954:01 0.005			
A*68:02 0.010	B*40:04 0.045		DPB1*968:01 0.005			
A*69:01 0.005	B*40:08 0.005					
A*80:01 0.010	B*40:09 0.005					
	B*41:01 0.005					
	B*44:02 0.010					
	B*44:03 0.010					
	B*46:01 0.005					
	B*48:01 0.065					
	B*48:04 0.005					
	B*49:01 0.020					
	B*51:01 0.040					
	B*51:08 0.005					
	B*51:13 0.005					
	B*52:01 0.010					
	B*53:01 0.020					
	B*54:01 0.005					
	B*55:01 0.005					
	B*57:03 0.005					

Supplementary Table S2. Allele frequency distribution of HLA class I and II systems and his association between PLHIV (cases) and HIV-uninfected (controls) in Peru.

HLA alleles	Allele frequency		Allele effect			
	PLHIV	HIV-uninfected	OR	CI	*p*	*p* adj
A*02:01	0.339	0.375	0.866	0.4302-1.7441	0.687	0.687
A*02:11	0.134	0.057	2.273	0.6852-7.5384	0.180	0.453
A*24:02	0.107	0.114	1.768	0.5995-5.2154	0.302	0.453
B*15:04	0.054	0.068	0.880	0.1826-4.2383	0.873	0.873
B*35:01	0.116	0.114	0.884	0.2826-2.7639	0.832	0.873
B*48:01	0.054	0.080	0.723	0.1929-2.7057	0.630	0.873
C*01:02	0.091	0.159	1.015	0.3582-2.8781	0.977	0.977
C*03:04	0.082	0.057	0.549	0.1301-2.3179	0.415	0.691
C*04:01	0.236	0.216	1.192	0.52-2.7332	0.678	0.848
C*07:01	0.118	0.023	10.222	1.4014-74.5521	**0.022**	0.109
C*07:02	0.182	0.193	1.555	0.5866-4.1221	0.375	0.691
DPB1*02:01	0.080	0.057	0.556	0.0844-3.6697	0.542	0.542
DPB1*04:01	0.188	0.125	1.835	0.689-4.8881	0.225	0.449
DPB1*04:02	0.277	0.318	1.395	0.6514-2.9863	0.392	0.522
DPB1*14:01	0.098	0.182	0.517	0.1862-1.4331	0.205	0.449
DQA1*01:01	0.056	0.046	0.843	0.1452-4.8932	0.849	0.849
DQA1*01:02	0.120	0.034	1.959	0.4673-8.2107	0.358	0.568
DQA1*03:01	0.232	0.216	1.170	0.5031-2.7201	0.716	0.818
DQA1*03:02	0.148	0.057	5.297	1.4752-19.0213	**0.011**	0.085
DQA1*03:03	0.056	0.102	0.351	0.074-1.668	0.188	0.376
DQA1*04:01	0.074	0.159	0.352	0.0893-1.3855	0.135	0.376
DQA1*05:03	0.093	0.148	0.629	0.2015-1.9664	0.426	0.568
DQA1*05:05	0.037	0.091	0.317	0.0577-1.7399	0.186	0.376
DQB1*02:01	0.080	0.034	2.700	0.4822-15.1198	0.258	0.258
DQB1*03:02	0.241	0.171	2.128	0.77-5.8808	0.145	0.258
DQB1*03:419	0.223	0.352	0.327	0.112-0.9563	**0.041**	0.165
DQB1*03:96	0.071	0.136	0.454	0.1243-1.6603	0.233	0.258
DRB1*04:04	0.063	0.068	3.059	0.5937-15.7629	0.181	0.302
DRB1*04:07	0.125	0.136	1.015	0.3323-3.0992	0.979	0.979
DRB1*08:02	0.071	0.159	0.347	0.087-1.384	0.134	0.302
DRB1*09:01	0.170	0.114	4.788	1.3941-16.4434	**0.013**	0.064
DRB1*14:02	0.063	0.125	0.625	0.1837-2.1229	0.451	0.563

OR: odds ratio; CI: confidence interval. P-values were calculated using a logistic regression model. The adjusted p-values (P adj) were calculated using 10,000 permutation results and by imposing a false discovery rate (FDR) of 0.05. A p-value < 0.05 was considered statistically significant (highlighted in bold).