

Table S1 Results obtained from the phylogenetic correction analysis

DEPENDENT MODEL					INDEPENDENT MODEL						
Trial	Likelihood Harmonic Mean	Acceptance rate	Likelihood Harmonic Mean	Acceptance rate	Best model or LR	Trial	Likelihood Harmonic Mean	Acceptance rate	Likelihood Harmonic Mean	Acceptance rate	Best model or LR
P30_A24						P12_B49					
1	-79,909	-0,27	-80,979	-0,283333	2,141052	1	-43,936	-0,303333	-44,618	-0,23	1,36343
2	-80,063	-0,246667	-82,588	-0,303333	5,048832	2	-47,563	-0,383333	-43,912	-0,326667	Independent
3	-79,745	-0,256667	-80,998	-0,303333	2,505056	3	-50,098	-0,273333	-43,184	-0,333333	Independent
4	-79,869	-0,28	-80,949	-0,326667	2,160222	4	-43,231	-0,33	-43,937	-0,29	1,411416
5	-80,034	-0,323333	-81,155	-0,316667	2,241514	5	-43,256	-0,396667	-43,839	-0,356667	1,16582
P83_A02						P55_A03					
1	-74,160	-0,33	-73,432	-0,263333	Independent	1	-58,711	-0,303333	-63,039	-0,32	8,656066
2	-74,577	-0,366667	-73,703	-0,336667	Independent	2	-58,725	-0,223333	-62,976	-0,386667	8,501514
3	-73,972	-0,363333	-73,675	-0,393333	Independent	3	-59,391	-0,28	-63,239	-0,373333	7,697352
4	-74,563	-0,24	-74,271	-0,33	Independent	4	-58,636	-0,243333	-63,069	-0,39	8,8667
5	-74,161	-0,313333	-73,699	-0,346667	Independent	5	-59,079	-0,363333	-63,151	-0,376667	8,144018
P125_A01						P90_B40					
1	-69,711	-0,253333	-68,555	-0,216667	Independent	1	-62,562	-0,26	-60,692	-0,283333	Independent
2	-69,651	-0,336667	-68,832	-0,25	Independent	2	-62,627	-0,26	-60,742	-0,27	Independent
3	-69,192	-0,233333	-69,167	-0,263333	Independent	3	-61,816	-0,253333	-59,865	-0,303333	Independent
4	-70,543	-0,333333	-68,962	-0,246667	Independent	4	-62,132	-0,27	-60,111	-0,316667	Independent
5	-69,216	-0,29	-69,495	-0,25	0,559012	5	-61,616	-0,293333	-60,263	-0,27	Independent
P28_A03						P146_A02					
1	-68,414	-0,313333	-77,153	-0,263333	17,477414	1	-95,943	-0,26	-96,498	-0,353333	1,10969
2	-68,686	-0,263333	-78,305	-0,26	19,23724	2	-96,319	-0,286667	-96,548	-0,35	0,458024
3	-68,630	-0,27	-77,913	-0,313333	18,564472	3	-96,687	-0,253333	-96,542	-0,366667	Independent
4	-69,576	-0,296667	-77,007	-0,226667	14,863502	4	-95,949	-0,25	-96,378	-0,313333	0,856946
5	-69,609	-0,313333	-77,644	-0,26	16,071304	5	-95,916	-0,263333	-96,524	-0,346667	1,216658
P46_A24						P215_A01					
1	-74,510	-0,236667	-76,025	-0,27	3,0299	1	-71,102	-0,31	-68,838	-0,366667	Independent
2	-74,646	-0,236667	-75,389	-0,27	1,48498	2	-69,856	-0,263333	-68,598	-0,293333	Independent
3	-74,692	-0,296667	-75,389	-0,273333	1,394476	3	-69,876	-0,293333	-68,181	-0,286667	Independent
4	-75,268	-0,37	-75,934	-0,24	1,331736	4	-69,459	-0,32	-68,119	-0,34	Independent
5	-74,473	-0,253333	-75,473	-0,323333	1,99874	5	-69,365	-0,223333	-68,609	-0,343333	Independent
P81_B40						P339_A01					
1	-50,939	-0,256667	-51,632	-0,33	1,38668	1	-61,280	-0,386667	-60,927	-0,39	Independent
2	-50,381	-0,253333	-51,254	-0,343333	1,744834	2	-61,818	-0,38	-60,804	-0,353333	Independent
3	-50,726	-0,293333	-52,302	-0,336667	3,15293	3	-61,837	-0,4	-60,764	-0,39	Independent
4	-50,445	-0,233333	-51,213	-0,316667	1,536788	4	-61,902	-0,326667	-61,042	-0,376667	Independent
5	-50,879	-0,316667	-51,668	-0,326667	1,577856	5	-61,577	-0,39	-61,331	-0,343333	Independent
P118_A11						P312_B49					
1	-33,662	-0,32	-36,381	-0,323333	5,437886	1	-60,804	-0,263333	-61,359	-0,373333	1,111334
2	-34,337	-0,236667	-36,532	-0,29	4,39053	2	-62,973	-0,283333	-61,437	-0,276667	Independent
3	-33,420	-0,31	-36,155	-0,326667	5,471404	3	-60,716	-0,316667	-61,128	-0,256667	0,823558
4	-33,820	-0,253333	-36,029	-0,306667	4,418136	4	-60,553	-0,306667	-61,112	-0,216667	1,119274
5	-33,743	-0,246667	-36,257	-0,27	5,027364	5	-61,315	-0,333333	-60,714	-0,226667	Independent
P242_B57						P342_A24					
1	-44,783	-0,246667	-48,827	-0,39	8,087374	1	-56,254	-0,323333	-54,463	-0,29	Independent
2	-45,069	-0,36	-50,875	-0,373333	11,610946	2	-56,548	-0,316667	-54,907	-0,296667	Independent
3	-45,489	-0,303333	-49,088	-0,36	7,198572	3	-56,623	-0,256667	-54,746	-0,316667	Independent
4	-45,866	-0,296667	-49,073	-0,33	6,412982	4	-58,037	-0,316667	-54,228	-0,306667	Independent
5	-45,519	-0,356667	-49,089	-0,4	7,139418	5	-56,630	-0,21	-54,705	-0,28	Independent
P303_B08						P342_A31					
1	-47,024	-0,203333	-47,167	-0,223333	0,285048	1	-39,333	-0,326667	-38,603	-0,31	Independent
2	-47,315	-0,293333	-47,264	-0,303333	Independent	2	-39,717	-0,29	-39,587	-0,313333	Independent
3	-47,225	-0,243333	-47,288	-0,246667	0,125084	3	-40,592	-0,306667	-39,134	-0,27	Independent
4	-47,557	-0,22	-47,498	-0,2	Independent	4	-38,993	-0,253333	-38,455	-0,223333	Independent
5	-47,926	-0,29	-47,155	-0,286667	Independent	5	-39,465	-0,22	-38,684	-0,293333	Independent
P65_A02						P357_A11					
1	-78,613	-0,266667	-79,734	-0,336667	2,24172	1	-53,572	-0,22	-55,381	-0,326667	3,318628
2	-78,611	-0,253333	-80,122	-0,306667	3,021794	2	-52,822	-0,3	-54,681	-0,363333	3,71707
3	-78,806	-0,32	-79,944	-0,346667	2,274386	3	-53,117	-0,273333	-54,666	-0,333333	3,077676
4	-78,469	-0,303333	-79,920	-0,353333	2,901506	4	-53,645	-0,35	-56,699	-0,31	6,109122
5	-78,805	-0,343333	-79,850	-0,286667	2,090716	5	-53,122	-0,22	-56,591	-0,366667	6,938418
P357_B07						P372_A31					
1	-73,839	-0,31	-75,075	-0,373333	2,47302	1	-62,109	-0,256667	-59,910	-0,246667	Independent
2	-74,004	-0,3	-75,016	-0,353333	2,143562	2	-59,910	-0,286667	-59,792	-0,323333	Independent
3	-73,801	-0,313333	-75,054	-0,243333	2,505346	3	-59,895	-0,3	-59,211	-0,223333	Independent
4	-73,942	-0,3	-75,784	-0,276667	3,683128	4	-60,503	-0,273333	-59,253	-0,236667	Independent
5	-73,864	-0,283333	-74,894	-0,32	2,060035	5	-59,829	-0,28	-59,230	-0,316667	Independent

Details of the results obtained from the phylogenetic correction performed over the 22 positions where polymorphisms were significantly associated with an HLA allele (q -value<0.2). Five trials were performed per position. When the best model fitted to data is the independent model, this is shown on the sixth column.