Supplementary Table 3. Unadjusted amino acid omnibus test

Gene	Amino acid posit	deltaDeviance	deltaDF	P	Residues
HLA-A	-22	7.687	1	-2.255	V,x
HLA-A	-20	7.687	1	-2.255	A,x
HLA-A	-15	65.055	2	-14.126	V,L,x
HLA-A	-11	84.832	2	-18.421	S,L,x
HLA-A	-2	7.687	1	-2.255	W,x
HLA-A	9	191.951	3	-40.636	F,S,Y,T
HLA-A	12	14.677	1	-3.894	V,M
HLA-A	17	28.501	1	-7.028	R,S
HLA-A	19	NA	NA	NA	E
HLA-A	31	NA	NA	NA	T
HLA-A	35	NA	NA	NA	R
HLA-A	43	30.825	1	-7.549	Q,R
HLA-A	44	26.355	1	-6.546	R,K
HLA-A	56	3.993	1	-1.340	G,R
HLA-A	62	171.202	4	-35.239	G,Q,E,R,L
HLA-A	63	77.957	2	-16.928	E,N,Q
HLA-A	65	48.385	1	-11.456	R,G
HLA-A	66	135.241	1	-30.534	K,N
HLA-A	67	26.507	1	-6.581	V,M
HLA-A	70	187.156	1	-41.877	H,Q
HLA-A	73	10.942	1	-3.027	T,I
HLA-A	74	60.232	1	-14.074	H,D
HLA-A	76	24.772	2	-5.379	V,A,E
HLA-A	77	122.032	2	-26.499	D,N,S
HLA-A	79	0.755	1	-0.415	G,R
HLA-A	80	0.755	1	-0.415	T,I
HLA-A	81	0.755	1	-0.415	L,A
HLA-A	82	0.755	1	-0.415	R,L
HLA-A	83	0.755	1	-0.415	G,R
HLA-A	90	13.391	1	-3.597	A,D
HLA-A	95	150.706	2	-32.725	V,I,L
HLA-A	97	16.240	2	-3.526	R,I,M
HLA-A	99	48.385	1	-11.456	Y,F
HLA-A	102	0.887	1	-0.461	D,H
HLA-A	105	47.513	1	-11.262	S,P
HLA-A	107	60.143	1	-14.055	W,G
HLA-A	109	52.441	1	-12.353	F,L
HLA-A	114	222.727	3	-47.287	H,R,Q,E
HLA-A	116	171.822	2	-37.311	Y,D,H
HLA-A	127	107.455	1	-24.451	K,N

HLA-A	142	40.099	1	-9.617	T,I
HLA-A	144	101.371	1	-23.118	K,Q
HLA-A	145	40.099	1	-9.617	H,R
HLA-A	149	46.158	1	-10.962	A,T
HLA-A	150	26.507	1	-6.581	A,V
HLA-A	151	52.266	1	-12.315	H,R
HLA-A	152	187.731	4	-38.788	V,A,E,W,R
HLA-A	156	48.639	3	-9.808	L,R,W,Q
HLA-A	158	26.507	1	-6.581	A,V
HLA-A	161	27.010	1	-6.694	E,D
HLA-A	163	14.667	1	-3.892	T,R
HLA-A	166	83.370	1	-19.167	E,D
HLA-A	167	83.370	1	-19.167	W,G
HLA-A	171	0.767	1	-0.419	Y,H
HLA-A	184	0.471	1	-0.308	A,P
HLA-A	186	0.767	1	-0.419	K,R
HLA-A	193	3.364	1	-1.176	A,P
HLA-A	194	3.364	1	-1.176	V,I
HLA-A	207	3.364	1	-1.176	S,G
HLA-A	245	10.464	1	-2.915	A,V
HLA-A	246	130.641	1	-29.528	A,S
HLA-A	253	3.364	1	-1.176	Q,E
HLA-A	255	NA	NA	NA	Q
HLA-A	268	NA	NA	NA	K
HLA-A	276	13.645	2	-2.963	P,L,x
HLA-A	282	56.807	2	-12.336	I,V,x
HLA-A	283	57.739	2	-12.538	P,H,x
HLA-A	288	7.687	1	-2.255	I,x
HLA-A	294	11.371	2	-2.469	F,L,x
HLA-A	297	59.923	2	-13.012	V,M,x
HLA-A	298	84.212	2	-18.286	I,F,x
HLA-A	299	137.618	2	-29.883	T,A,x
HLA-A	307	84.212	2	-18.286	M,R,x
HLA-A	310	7.687	1	-2.255	R,x
HLA-A	311	56.807	2	-12.336	K,N,x
HLA-A	314	7.687	1	-2.255	D,x
HLA-A	321	13.645	2	-2.963	S,T,x
HLA-A	334	137.618	2	-29.883	V,M,x
HLA-B	-23	57.366	1	-13.442	L,R
HLA-B	-21	57.366	1	-13.442	M,T
HLA-B	-16	111.776	1	-25.398	V,L
HLA-B	-11	515.372	1	-113.367	S,W
HLA-B	-10	139.990	1	-31.572	A,G

HLA-B	-8	463.904	1	-102.168	L,V
HLA-B	4	0.646	1	-0.375	S,F
HLA-B	9	837.074	2	-181.768	D,Y,H
HLA-B	11	60.289	1	-14.087	A,S
HLA-B	12	105.243	1	-23.966	M,V
HLA-B	24	156.174	2	-33.913	S,T,A
HLA-B	30	177.265	1	-39.717	D,G
HLA-B	32	70.759	1	-16.394	Q,L
HLA-B	41	69.739	1	-16.169	A,T
HLA-B	45	91.320	3	-18.943	E,K,M,T
HLA-B	46	32.592	1	-7.944	E,A
HLA-B	52	NA	NA	NA	I
HLA-B	59	0.986	1	-0.494	Y,H
HLA-B	62	308.900	1	-68.421	R,G
HLA-B	63	36.432	1	-8.801	N,E
HLA-B	65	291.294	1	-64.585	Q,R
HLA-B	66	291.294	1	-64.585	I,N
HLA-B	67	808.622	4	-172.982	F,Y,S,C,M
HLA-B	69	656.023	1	-143.961	T,A
HLA-B	70	774.055	3	-166.737	N,Q,S,K
HLA-B	71	656.023	1	-143.961	T,A
HLA-B	74	29.030	1	-7.147	D,Y
HLA-B	76	NA	NA	NA	E
HLA-B	77	557.867	2	-121.139	S,N,D
HLA-B	80	550.155	2	-119.465	N,T,I
HLA-B	81	496.960	1	-109.361	L,A
HLA-B	82	541.380	1	-119.025	R,L
HLA-B	83	541.380	1	-119.025	G,R
HLA-B	90	NA	NA	NA	A
HLA-B	94	605.998	1	-133.081	T,I
HLA-B	95	679.536	2	-147.559	L,I,W
HLA-B	97	519.869	5	-109.387	S,R,T,W,V,N
HLA-B	99	47.202	2	-10.250	Y,S,F
HLA-B	103	74.346	1	-17.183	V,L
HLA-B	109	24.928	1	-6.225	L,F
HLA-B	113	298.490	1	-66.153	H,Y
HLA-B	114	287.098	2	-62.343	N,D,H
HLA-B	116	263.221	4	-55.035	Y,D,F,L,S
HLA-B	131	90.287	1	-20.686	R,S
HLA-B	143	54.079	1	-12.715	T,S
HLA-B	145	12.880	1	-3.479	R,L
HLA-B	147	54.079	1	-12.715	W,L
HLA-B	152	58.665	1	-13.728	V,E

HLA-B	156	841.916	3	-181.455	D,R,L,W
HLA-B	158	107.975	1	-24.565	A,T
HLA-B	162	NA	NA	NA	G
HLA-B	163	576.050	2	-125.088	T,E,L
HLA-B	166	NA	NA	NA	E
HLA-B	167	230.458	1	-51.325	W,S
HLA-B	171	0.023	1	-0.055	Y,H
HLA-B	177	113.348	1	-25.742	D,E
HLA-B	178	126.088	1	-28.532	T,K
HLA-B	180	113.348	1	-25.742	E,Q
HLA-B	194	133.368	1	-30.124	I,V
HLA-B	199	217.041	1	-48.398	A,V
HLA-B	211	NA	NA	NA	A
HLA-B	239	NA	NA	NA	R
HLA-B	245	NA	NA	NA	A
HLA-B	253	NA	NA	NA	E
HLA-B	267	NA	NA	NA	P
HLA-B	268	NA	NA	NA	K
HLA-B	270	NA	NA	NA	L
HLA-B	275	NA	NA	NA	E
HLA-B	282	82.794	1	-19.041	V,I
HLA-B	295	NA	NA	NA	A
HLA-B	296	NA	NA	NA	V
HLA-B	298	NA	NA	NA	V
HLA-B	299	NA	NA	NA	I
HLA-B	300	NA	NA	NA	G
HLA-B	305	77.196	1	-17.810	A,T
HLA-B	307	5.552	1	-1.734	M,V
HLA-B	325	75.950	2	-16.492	C,S,x
HLA-C	-18	6.897	1	-2.064	R,Q
HLA-C	-17	115.733	1	-26.265	A,T
HLA-C	-15	83.049	1	-19.097	L,I
HLA-C	-9	125.225	1	-28.343	G,A
HLA-C	-5	6.897	1	-2.064	T,I
HLA-C	1	50.491	1	-11.922	C,G
HLA-C	6	37.710	1	-9.086	R,K
HLA-C	9	237.062	3	-50.386	D,S,Y,F
HLA-C	11	233.821	1	-52.058	A,S
HLA-C	14	172.993	1	-38.784	R,W
HLA-C	16	20.079	1	-5.129	G,S
HLA-C	21	201.297	1	-44.963	R,H
HLA-C	24	4.388	1	-1.441	S,A
HLA-C	35	0.426	1	-0.289	R,Q

HLA-C	49	172.993	1	-38.784	A,E
HLA-C	66	514.863	1	-113.256	N,K
HLA-C	73	20.175	1	-5.151	A,T
HLA-C	77	166.464	1	-37.359	S,N
HLA-C	80	166.464	1	-37.359	N,K
HLA-C	90	6.868	1	-2.057	D,A
HLA-C	91	7.407	1	-2.187	G,R
HLA-C	94	299.686	1	-66.414	T,I
HLA-C	95	292.447	2	-63.504	L,I,F
HLA-C	97	358.951	1	-79.322	R,W
HLA-C	99	412.190	3	-88.295	Y,S,F,C
HLA-C	103	309.656	1	-68.586	L,V
HLA-C	113	1.141	1	-0.544	Y,H
HLA-C	114	83.387	1	-19.171	D,N
HLA-C	116	237.434	3	-50.467	S,F,Y,L
HLA-C	138	0.456	1	-0.301	T,K
HLA-C	143	6.897	1	-2.064	T,S
HLA-C	147	115.872	1	-26.295	L,W
HLA-C	152	45.237	1	-10.758	A,E
HLA-C	156	684.429	4	-146.086	L,R,W,D,Q
HLA-C	163	321.856	2	-69.890	T,L,E
HLA-C	170	6.897	1	-2.064	R,G
HLA-C	173	309.656	1	-68.586	E,K
HLA-C	177	2.743	1	-1.010	E,K
HLA-C	184	129.050	2	-28.023	P,H,R
HLA-C	193	141.891	1	-31.988	P,L
HLA-C	194	125.124	1	-28.320	L,V
HLA-C	211	20.079	1	-5.129	A,T
HLA-C	219	17.797	1	-4.610	R,W
HLA-C	248	37.710	1	-9.086	V,M
HLA-C	253	115.872	1	-26.295	Q,E
HLA-C	261	125.124	1	-28.320	M,V
HLA-C	267	115.872	1	-26.295	Q,P
HLA-C	270	6.897	1	-2.064	L,C
HLA-C	273	125.124	1	-28.320	S,R
HLA-C	275	185.938	2	-40.376	E,K,G
HLA-C	284	6.897	1	-2.064	I,N
HLA-C	285	129.333	2	-28.084	M,V,L
HLA-C	289	6.897	1	-2.064	A,S
HLA-C	291	6.897	1	-2.064	L,P
HLA-C	295	125.269	1	-28.352	V,A
HLA-C	303	172.993	1	-38.784	V,M
HLA-C	304	86.706	1	-19.900	V,M

HLA-C	305	125.269	1	-28.352	T,A
HLA-C	306	116.010	1	-26.325	A,V
HLA-C	307	125.127	1	-28.321	M,V
HLA-C	308	6.897	1	-2.064	M,I
HLA-C	309	6.897	1	-2.064	C,H
HLA-C	326	125.349	1	-28.370	C,S
HLA-C	339	125.349	1	-28.370	T,A
HLA-DPA1	11	80.202	1	-18.471	A,M
HLA-DPA1	18	NA	NA	NA	P
HLA-DPA1	28	15.792	1	-4.151	E,D
HLA-DPA1	31	17.311	1	-4.499	M,Q
HLA-DPA1	50	17.311	1	-4.499	Q,R
HLA-DPA1	66	NA	NA	NA	L
HLA-DPA1	72	NA	NA	NA	T
HLA-DPA1	73	NA	NA	NA	L
HLA-DPA1	83	18.612	1	-4.795	T,A
HLA-DPA1	96	3.086	1	-1.103	P,x
HLA-DPA1	111	20.595	2	-4.472	K,R,x
HLA-DPA1	127	20.595	2	-4.472	L,P,x
HLA-DPA1	160	20.595	2	-4.472	F,V,x
HLA-DPA1	190	3.086	1	-1.103	T,x
HLA-DPA1	228	20.595	2	-4.472	T,P,x
HLA-DPB1	8	111.998	1	-25.447	L,V
HLA-DPB1	9	188.607	2	-40.955	F,Y,H
HLA-DPB1	11	36.877	1	-8.900	G,L
HLA-DPB1	33	7.044	1	-2.099	E,Q
HLA-DPB1	35	31.807	2	-6.907	F,Y,L
HLA-DPB1	36	0.895	1	-0.463	A,V
HLA-DPB1	55	10.642	2	-2.311	A,D,E
HLA-DPB1	56	0.081	1	-0.110	A,E
HLA-DPB1	57	124.901	1	-28.272	E,D
HLA-DPB1	65	112.802	1	-25.623	I,L
HLA-DPB1	69	31.303	2	-6.797	K,E,R
HLA-DPB1	72	NA	NA	NA	V
HLA-DPB1	76	150.887	2	-32.765	M,V,I
HLA-DPB1	84	87.175	2	-18.930	G,D,V
HLA-DPB1	85	55.790	1	-13.094	G,E
HLA-DPB1	86	55.790	1	-13.094	P,A
HLA-DPB1	87	55.790	1	-13.094	M,V
HLA-DPB1	91	NA	NA	NA	R
HLA-DPB1	96	82.300	1	-18.932	R,K
HLA-DPB1	170	82.300	1	-18.932	T,I
HLA-DPB1	178	319.319	1	-70.691	L,M

HLA-DPB1	194	57.774	2	-12.545	R,Q,x
HLA-DPB1	205	69.012	2	-14.986	V,x,M
HLA-DPB1	215	34.560	2	-7.505	I,x,T
HLA-DQA1	-16	2323.579	1	-506.340	M,L
HLA-DQA1	11	2467.039	1	-537.505	Y,C
HLA-DQA1	18	2467.039	1	-537.505	S,F
HLA-DQA1	25	1604.701	1	-350.157	Y,F
HLA-DQA1	26	2035.607	1	-443.779	T,S
HLA-DQA1	34	194.752	1	-43.535	Q,E
HLA-DQA1	40	472.137	1	-103.959	G,E
HLA-DQA1	41	493.293	1	-108.563	R,K
HLA-DQA1	45	2467.039	1	-537.505	V,A
HLA-DQA1	47	4453.846	3	-965.414	C,R,Q,K
HLA-DQA1	48	2467.039	1	-537.505	L,W
HLA-DQA1	50	2469.126	2	-536.164	V,E,L
HLA-DQA1	51	472.137	1	-103.959	L,F
HLA-DQA1	52	4252.376	2	-923.392	R,S,H
HLA-DQA1	53	2469.126	2	-536.164	Q,K,R
HLA-DQA1	54	1002.782	1	-219.350	F,L
HLA-DQA1	55	2467.039	1	-537.505	R,G
HLA-DQA1	56	3221.756	2	-699.595	x,G,R
HLA-DQA1	61	2467.039	1	-537.505	F,G
HLA-DQA1	64	2467.039	1	-537.505	T,R
HLA-DQA1	66	2467.039	1	-537.505	I,M
HLA-DQA1	69	2486.066	2	-539.842	L,A,T
HLA-DQA1	75	488.565	1	-107.534	S,I
HLA-DQA1	76	3221.756	2	-699.595	L,M,V
HLA-DQA1	80	2467.039	1	-537.505	S,Y
HLA-DQA1	107	488.565	1	-107.534	I,T
HLA-DQA1	129	1813.514	1	-395.527	H,Q
HLA-DQA1	130	493.293	1	-108.563	S,A
HLA-DQA1	156	488.565	1	-107.534	L,F
HLA-DQA1	161	488.565	1	-107.534	E,D
HLA-DQA1	163	488.565	1	-107.534	S,I
HLA-DQA1	175	2476.214	2	-537.703	K,Q,E
HLA-DQA1	187	2035.607	1	-443.779	A,T
HLA-DQA1	207	1798.442	1	-392.252	V,M
HLA-DQA1	215	564.872	1	-124.135	F,L
HLA-DQA1	218	2467.039	1	-537.505	R,Q
HLA-DQB1	-27	218.161	2	-47.373	A,S,x
HLA-DQB1	-21	2601.661	2	-564.943	G,D,x
HLA-DQB1	-18	0.843	2	-0.183	A,V,x
HLA-DQB1	-17	49.780	2	-10.810	A,x,P

HLA-DQB1	-10	678.904	2	-147.422	S,A,x
HLA-DQB1	-9	218.161	2	-47.373	M,I,x
HLA-DQB1	-6	2601.661	2	-564.943	T,S,x
HLA-DQB1	-5	3628.641	3	-786.267	P,L,S,x
HLA-DQB1	-4	2601.661	2	-564.943	V,L,x
HLA-DQB1	3	49.577	1	-11.720	S,P
HLA-DQB1	9	1820.906	2	-395.405	Y,F,L
HLA-DQB1	13	1204.367	1	-263.164	G,A
HLA-DQB1	14	216.276	1	-48.231	M,L
HLA-DQB1	23	NA	NA	NA	R
HLA-DQB1	26	1567.122	2	-340.296	L,Y,G
HLA-DQB1	28	670.975	1	-147.212	S,T
HLA-DQB1	30	894.423	2	-194.222	S,Y,H
HLA-DQB1	37	709.166	2	-153.993	I,Y,D
HLA-DQB1	38	184.131	1	-41.216	V,A
HLA-DQB1	45	1151.937	1	-251.769	G,E
HLA-DQB1	46	670.975	1	-147.212	E,V
HLA-DQB1	47	670.975	1	-147.212	F,Y
HLA-DQB1	52	671.616	1	-147.352	L,P
HLA-DQB1	53	2464.611	1	-536.978	L,Q
HLA-DQB1	55	2334.797	2	-506.995	L,R,P
HLA-DQB1	56	1.151	1	-0.548	P,L
HLA-DQB1	57	6249.235	3	-1355.204	A,D,V,S
HLA-DQB1	66	624.002	1	-136.997	D,E
HLA-DQB1	67	624.002	1	-136.997	I,V
HLA-DQB1	70	2453.104	2	-532.685	R,G,E
HLA-DQB1	71	750.696	3	-161.671	K,T,A,D
HLA-DQB1	74	710.298	2	-154.239	A,E,S
HLA-DQB1	75	211.132	1	-47.109	V,L
HLA-DQB1	77	204.355	1	-45.630	R,T
HLA-DQB1	84	2464.611	1	-536.978	Q,E
HLA-DQB1	85	2464.611	1	-536.978	L,V
HLA-DQB1	86	2610.413	2	-566.844	E,A,G
HLA-DQB1	87	3645.367	2	-791.581	L,F,Y
HLA-DQB1	89	2464.611	1	-536.978	T,G
HLA-DQB1	90	2464.611	1	-536.978	T,I
HLA-DQB1	116	216.276	1	-48.231	V,I
HLA-DQB1	125	3012.659	2	-654.191	A,G,S
HLA-DQB1	126	3.161	1	-1.123	Q,H
HLA-DQB1	130	23.104	1	-5.814	R,Q
HLA-DQB1	135	472.551	1	-104.049	D,G
HLA-DQB1	140	393.983	1	-86.949	A,T
HLA-DQB1	167	1205.946	1	-263.507	R,H

HLA-DQB1	182	393.771	1	-86.903	S,N
HLA-DQB1	185	2158.008	1	-470.371	T,I
HLA-DQB1	197	49.577	1	-11.720	S,N
HLA-DQB1	203	2407.217	2	-522.721	I,V,x
HLA-DQB1	220	2470.906	2	-536.550	H,R,x
HLA-DQB1	221	2470.906	2	-536.550	H,Q,x
HLA-DQB1	224	223.680	2	-48.571	Q,R,x
HLA-DRB1	-25	80.191	2	-17.413	R,K,x
HLA-DRB1	-24	2057.637	2	-446.810	L,F,x
HLA-DRB1	-17	1573.095	2	-341.593	A,T,x
HLA-DRB1	-16	80.191	2	-17.413	V,A,x
HLA-DRB1	-1	2730.308	2	-592.879	A,S,x
HLA-DRB1	4	855.614	1	-187.359	R,Q
HLA-DRB1	9	2965.803	2	-644.016	E,W,K
HLA-DRB1	10	113.318	2	-24.607	Y,Q,E
HLA-DRB1	11	4598.456	5	-993.623	S,P,V,L,G,D
HLA-DRB1	12	62.793	1	-14.639	T,K
HLA-DRB1	13	4732.895	5	-1022.797	S,R,H,F,G,Y
HLA-DRB1	14	1002.102	1	-219.203	E,K
HLA-DRB1	16	26.813	1	-6.650	H,Y
HLA-DRB1	25	1002.102	1	-219.203	R,Q
HLA-DRB1	26	1669.514	2	-362.530	Y,F,L
HLA-DRB1	28	1025.631	2	-222.713	D,E,H
HLA-DRB1	30	1340.255	5	-286.916	Y,C,L,R,G,H
HLA-DRB1	31	113.035	2	-24.545	F,I,V
HLA-DRB1	32	401.529	1	-88.592	H,Y
HLA-DRB1	33	2055.925	1	-448.193	N,H
HLA-DRB1	37	3636.529	4	-786.402	N,S,Y,F,L
HLA-DRB1	38	152.698	2	-33.158	V,A,L
HLA-DRB1	40	55.843	1	-13.105	F,Y
HLA-DRB1	47	135.982	1	-30.696	F,Y
HLA-DRB1	57	1443.401	3	-311.949	D,S,V,A
HLA-DRB1	58	762.817	1	-167.183	A,E
HLA-DRB1	60	1436.473	2	-311.926	Y,S,H
HLA-DRB1	67	4948.109	2	-1074.468	L,I,F
HLA-DRB1	70	2524.408	2	-548.168	Q,D,R
HLA-DRB1	71	5836.723	3	-1265.643	K,A,E,R
HLA-DRB1	73	303.131	1	-67.164	G,A
HLA-DRB1	74	2511.514	4	-542.269	R,A,L,Q,E
HLA-DRB1	77	1700.917	1	-371.063	N,T
HLA-DRB1	78	855.853	1	-187.411	Y,V
HLA-DRB1	85	101.480	1	-23.142	V,A
HLA-DRB1	86	0.371	1	-0.266	V,G

HLA-DRB1	96	3818.584	3	-827.502	H,Q,Y,E
HLA-DRB1	98	554.070	1	-121.785	K,E
HLA-DRB1	104	554.070	1	-121.785	S,A
HLA-DRB1	112	414.389	1	-91.391	H,Y
HLA-DRB1	120	1949.075	1	-424.979	S,N
HLA-DRB1	133	2389.548	1	-520.671	R,L
HLA-DRB1	140	2837.924	1	-618.072	T,A
HLA-DRB1	142	2389.548	1	-520.671	V,M
HLA-DRB1	149	63.877	1	-14.878	H,Q
HLA-DRB1	166	55.843	1	-13.105	R,Q
HLA-DRB1	180	2091.410	2	-454.144	V,L,x
HLA-DRB1	181	914.644	2	-198.612	T,x,M
HLA-DRB1	189	47.198	2	-10.249	R,x,S
HLA-DRB1	231	66.198	2	-14.375	Q,x,P
HLA-DRB1	233	95.363	2	-20.708	R,T,x

Supplementary Table 4A. Independent amino acid associations in HLA-DRB1-DQA1-DQB1

					Unadjusted				***Adjusted***				
Gene	**mino acid positi**	**Residue**	**Case frequenc**	**ontrol frequen**	**OR (univariate**	**95% CI lower**	**95% CI upper**	**log10(p)**	**OR (univariate)**	**95% CI lower**	**95% CI upper**	**log10(p)**	**Adjusted for**
HLA-DQB1	***#57***							-1355.200					--
		Asp	0.123	0.472	0.159	0.150	0.169	-1062.406					
		Ala	0.747	0.359	5.171	4.906	5.452	-1090.529					
		Val	0.123	0.160	0.723	0.680	0.769	-24.482					
		Ser	0.007	0.009	0.802	0.633	1.015	-1.193					
HLA-DRB1	***#13***							-1022.797				-721.900	*DQB1#57*
		Ser	0.389	0.336	1.277	1.220	1.336	-25.438	0.916	0.866	0.969	-2.681	
		His	0.415	0.195	3.644	3.447	3.852	-519.296	2.992	2.803	3.193	-251.699	
		Arg	0.013	0.149	0.078	0.067	0.090	-508.267	0.120	0.097	0.149	-139.386	
		Tyr	0.045	0.144	0.281	0.258	0.306	-219.236	0.155	0.140	0.172	-353.000	
		Phe	0.107	0.136	0.747	0.700	0.798	-17.647	1.654	1.469	1.862	-16.116	
		Gly	0.030	0.040	0.716	0.636	0.805	-7.751	3.094	2.694	3.553	-54.478	
HLA-DRB1	***#71***							-1265.643				-95.900	*DQB1#57,DRB1#13*
		Arg	0.305	0.465	0.486	0.464	0.509	-218.785	0.475	0.436	0.517	-67.344	
		Lys	0.620	0.273	4.704	4.463	4.958	-935.523	2.027	1.868	2.199	-64.651	
		Ala	0.006	0.141	0.038	0.031	0.047	-574.311	0.436	0.143	1.329	-0.873	
		Glu	0.069	0.120	0.530	0.491	0.573	-61.221	1.006	0.894	1.133	-0.037	

Supplementary Table 4B. All amino acid position associations in HLA-DRB1-DQA1-DQB1

			Unadjusted			Adj. DQb1#57			Adj. DQb1#57,DRb1#13			Adj. DQb1#57,DRb1#13,DRb1#71		
Gene	Amino acid positior	Residues	Deviance	df	log10(p)	Deviance	df	log10(p)	Deviance	df	log10(p)	Deviance	df	log10(p)
HLA-DQA1	-16	M,L	2323.579	1	-506.340	155.034	3	-32.665	74.152	10	-11.158	104.717	12	-16.181
HLA-DQA1	11	Y,C	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	18	S,F	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	25	Y,F	1604.701	1	-350.157	1928.957	2	-418.868	87.570	8	-14.840	71.787	11	-10.253
HLA-DQA1	26	T,S	2035.607	1	-443.779	1226.851	3	-264.961	61.588	9	-9.179	22.708	12	-1.518
HLA-DQA1	34	Q,E	194.752	1	-43.535	202.977	4	-42.065	109.797	11	-17.697	58.985	15	-6.424
HLA-DQA1	40	G,E	472.137	1	-103.959	96.458	2	-20.946	66.117	11	-9.178	61.183	15	-6.802
HLA-DQA1	41	R,K	493.293	1	-108.563	2.488	1	-0.940	42.558	3	-8.515	25.211	5	-3.897
HLA-DQA1	45	V,A	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	47	C,R,Q,K	4453.846	3	-965.414	2996.286	7	-643.217	83.494	20	-9.003	77.929	26	-6.361
HLA-DQA1	48	L,W	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	50	V,E,L	2469.126	2	-536.164	705.540	5	-149.507	74.390	16	-8.775	68.764	21	-6.257
HLA-DQA1	51	L,F	472.137	1	-103.959	96.458	2	-20.946	66.117	11	-9.178	61.183	15	-6.802
HLA-DQA1	52	R,S,H	4252.376	2	-923.392	2782.960	5	-599.720	26.244	12	-2.004	57.739	15	-6.211
HLA-DQA1	53	Q,K,R	2469.126	2	-536.164	705.540	5	-149.507	74.390	16	-8.775	68.764	21	-6.257
HLA-DQA1	54	F,L	1002.782	1	-219.350	1987.053	2	-431.483	17.463	4	-2.804	19.038	5	-2.723
HLA-DQA1	55	R,G	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	56	x,G,R	3221.756	2	-699.595	1512.624	5	-324.267	67.062	17	-7.163	59.875	22	-4.632
HLA-DQA1	61	F,G	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	64	T,R	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	66	I,M	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	69	L,A,T	2486.066	2	-539.842	860.315	5	-182.987	82.580	13	-11.444	114.055	16	-16.121
HLA-DQA1	75	S,I	488.565	1	-107.534	53.544	2	-11.627	132.398	10	-22.820	126.377	14	-19.453
HLA-DQA1	76	L,M,V	3221.756	2	-699.595	1512.624	5	-324.267	67.062	17	-7.163	59.875	22	-4.632
HLA-DQA1	80	S,Y	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQA1	107	I,T	488.565	1	-107.534	53.544	2	-11.627	132.398	10	-22.820	126.377	14	-19.453
HLA-DQA1	129	H,Q	1813.514	1	-395.527	832.670	3	-179.449	73.843	7	-12.609	53.687	9	-7.664
HLA-DQA1	130	S,A	493.293	1	-108.563	2.488	1	-0.940	42.558	3	-8.515	25.211	5	-3.897
HLA-DQA1	156	L,F	488.565	1	-107.534	53.544	2	-11.627	132.398	10	-22.820	126.377	14	-19.453
HLA-DQA1	161	E,D	488.565	1	-107.534	53.544	2	-11.627	132.398	10	-22.820	126.377	14	-19.453
HLA-DQA1	163	S,I	488.565	1	-107.534	53.544	2	-11.627	132.398	10	-22.820	126.377	14	-19.453
HLA-DQA1	175	K,Q,E	2476.214	2	-537.703	911.506	5	-194.065	147.624	17	-22.147	142.262	23	-18.453
HLA-DQA1	187	A,T	2035.607	1	-443.779	1226.851	3	-264.961	61.588	9	-9.179	22.708	12	-1.518
HLA-DQA1	207	V,M	1798.442	1	-392.252	693.035	4	-147.950	25.496	7	-3.208	22.899	9	-2.192
HLA-DQA1	215	F,L	564.872	1	-124.135	312.177	3	-66.638	66.319	8	-10.577	28.975	11	-2.640
HLA-DQA1	218	R,Q	2467.039	1	-537.505	663.868	3	-142.844	7.906	8	-0.354	37.809	10	-4.388
HLA-DQB1	-27	A,S,x	218.161	2	-47.373	158.003	4	-32.407	136.424	10	-23.643	112.270	12	-17.672
HLA-DQB1	-21	G,D,x	2601.661	2	-564.943	666.581	3	-143.432	99.321	10	-16.128	129.614	14	-20.091
HLA-DQB1	-18	A,V,x	0.843	2	-0.183	781.918	4	-167.198	252.162	14	-44.989	252.706	21	-40.930
HLA-DQB1	-17	A,x,P	49.780	2	-10.810	17.140	3	-3.179	93.842	5	-17.980	91.139	6	-16.755
HLA-DQB1	-10	S,A,x	678.904	2	-147.422	681.787	3	-146.729	78.182	8	-12.945	84.819	12	-12.307
HLA-DQB1	-9	M,I,x	218.161	2	-47.373	158.003	4	-32.407	136.424	10	-23.643	112.270	12	-17.672
HLA-DQB1	-6	T,S,x	2601.661	2	-564.943	666.581	3	-143.432	99.321	10	-16.128	129.614	14	-20.091
HLA-DQB1	-5	P,L,S,x	3628.641	3	-786.267	730.234	5	-154.847	169.619	15	-27.535	144.642	20	-20.178
HLA-DQB1	-4	V,L,x	2601.661	2	-564.943	666.581	3	-143.432	99.321	10	-16.128	129.614	14	-20.091
HLA-DQB1	3	S,P	49.577	1	-11.720	1.867	1	-0.765	18.433	1	-4.754	18.450	1	-4.758
HLA-DQB1	9	Y,F,L	1820.906	2	-395.405	73.969	2	-16.062	134.167	7	-25.073	137.548	9	-24.480
HLA-DQB1	13	G,A	1204.367	1	-263.164	101.560	2	-22.053	174.782	8	-32.892	167.581	11	-29.430
HLA-DQB1	14	M,L	216.276	1	-48.231	87.625	2	-19.027	64.633	7	-10.749	39.416	9	-5.014
HLA-DQB1	23	R	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
HLA-DQB1	26	L,Y,G	1567.122	2	-340.296	411.846	4	-87.115	258.313	17	-44.380	192.094	23	-27.922
HLA-DQB1	28	S,T	670.975	1	-147.212	667.972	1	-146.559	2.332	4	-0.171	13.725	7	-1.250
HLA-DQB1	30	S,Y,H	894.423	2	-194.222	761.821	3	-164.084	89.464	11	-13.673	133.157	17	-19.336
HLA-DQB1	37	I,Y,D	709.166	2	-153.993	669.822	2	-145.450	20.766	5	-3.047	32.181	8	-4.063
HLA-DQB1	38	V,A	184.131	1	-41.216	747.056	3	-160.882	84.806	11	-12.764	71.001	16	-8.176
HLA-DQB1	45	G,E	1151.937	1	-251.769	107.062	2	-23.248	156.944	8	-29.157	149.720	11	-25.769
HLA-DQB1	46	E,V	670.975	1	-147.212	667.972	1	-146.559	2.332	4	-0.171	13.725	7	-1.250
HLA-DQB1	47	F,Y	670.975	1	-147.212	667.972	1	-146.559	2.332	4	-0.171	13.725	7	-1.250
HLA-DQB1	52	L,P	671.616	1	-147.352	667.391	1	-146.433	2.566	4	-0.199	15.708	7	-1.554
HLA-DQB1	53	L,Q	2464.611	1	-536.978	655.554	1	-143.859	5.924	6	-0.365	38.867	9	-4.915
HLA-DQB1	55	L,R,P	2334.797	2	-506.995	810.378	2	-175.971	105.400	10	-17.347	153.626	16	-23.823
HLA-DQB1	56	P,L	1.151	1	-0.548	404.837	1	-89.312	110.071	5	-21.403	112.327	6	-21.178
HLA-DQB1	57	A,D,V,S	6249.235	3	-1355.204	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-DQB1	66	D,E	624.002	1	-136.997	1024.838	2	-222.541	127.532	9	-22.419	142.940	13	-23.266
HLA-DQB1	67	I,V	624.002	1	-136.997	1024.838	2	-222.541	127.532	9	-22.419	142.940	13	-23.266
HLA-DQB1	70	R,G,E	2453.104	2	-532.685	871.221	3	-187.811	141.173	15	-21.870	173.089	20	-25.663
HLA-DQB1	71	K,T,A,D	750.696	3	-161.671	1140.627	4	-244.927	177.400	16	-28.554	167.553	22	-23.658
HLA-DQB1	74	A,E,S	710.298	2	-154.239	829.745	3	-178.815	175.533	13	-29.860	165.781	19	-24.722
HLA-DQB1	75	V,L	211.132	1	-47.109	828.857	3	-178.622	175.991	13	-29.953	165.129	19	-24.595
HLA-DQB1	77	R,T	204.355	1	-45.630	754.993	3	-162.603	67.199	11	-9.382	55.122	16	-5.469
HLA-DQB1	84	Q,E	2464.611	1	-536.978	655.554	1	-143.859	5.924	6	-0.365	38.867	9	-4.915
HLA-DQB1	85	L,V	2464.611	1	-536.978	655.554	1	-143.859	5.924	6	-0.365	38.867	9	-4.915
HLA-DQB1	86	E,A,G	2610.413	2	-566.844	655.555	2	-142.352	16.661	10	-1.085	46.211	14	-4.587
HLA-DQB1	87	L,F,Y	3645.367	2	-791.581	664.615	2	-144.319	68.864	8	-11.082	46.157	12	-5.186
HLA-DQB1	89	T,G	2464.611	1	-536.978	655.554	1	-143.859	5.924	6	-0.365	38.867	9	-4.915
HLA-DQB1	90	T,I	2464.611	1	-536.978	655.554	1	-143.859	5.924	6	-0.365	38.867	9	-4.915
HLA-DQB1	116	V,I	216.276	1	-48.231	87.625	2	-19.027	64.633	7	-10.749	39.416	9	-5.014
HLA-DQB1	125	A,G,S	3012.659	2	-654.191	667.261	4	-142.369	80.767	13	-11.102	51.555	17	-4.617
HLA-DQB1	126	Q,H	3.161	1	-1.123	0.142	1	-0.151	0.148	1	-0.155	0.283	1	-0.226
HLA-DQB1	130	R,Q	23.104	1	-5.814	0.002	1	-0.016	10.736	4	-1.527	7.343	5	-0.707
HLA-DQB1	135	D,G	472.551	1	-104.049	1850.039	1	-403.463	8.640	3	-1.462	8.701	3	-1.474
HLA-DQB1	140	A,T	393.983	1	-86.949	1325.916	2	-287.919	9.510	10	-0.315	52.350	15	-5.306
HLA-DQB1	167	R,H	1205.946	1	-263.507	101.343	2	-22.006	173.887	7	-33.420	166.693	10	-29.872
HLA-DQB1	182	S,N	393.771	1	-86.903	1325.736	2	-287.880	9.211	10	-0.291	52.264	15	-5.292
HLA-DQB1	185	T,I	2158.008	1	-470.371	930.713	2	-202.102	169.475	10	-30.448	144.799	16	-22.083
HLA-DQB1	197	S,N	49.577	1	-11.720	1.867	1	-0.765	18.433	1	-4.754	18.450	1	-4.758

HLA-DQB1	203	I,V,x	2407.217	2	-522.721	657.188	3	-141.395	24.867	8	-2.786	55.494	10	-7.593
HLA-DQB1	220	H,R,x	2470.906	2	-536.550	661.426	3	-142.314	6.889	8	-0.261	37.480	10	-4.330
HLA-DQB1	221	H,Q,x	2470.906	2	-536.550	661.426	3	-142.314	6.889	8	-0.261	37.480	10	-4.330
HLA-DQB1	224	Q,R,x	223.680	2	-48.571	88.310	3	-18.297	64.876	8	-10.292	40.342	10	-4.831
HLA-DRB1	-25	R,K,x	80.191	2	-17.413	352.258	7	-71.393	140.229	7	-26.342	146.222	11	-25.055
HLA-DRB1	-24	L,F,x	2057.637	2	-446.810	1427.950	6	-304.668	101.895	5	-19.676	105.831	8	-18.564
HLA-DRB1	-17	A,T,x	1573.095	2	-341.593	849.680	7	-178.454	176.767	6	-34.783	141.049	9	-25.203
HLA-DRB1	-16	V,A,x	80.191	2	-17.413	352.258	7	-71.393	140.229	7	-26.342	146.222	11	-25.055
HLA-DRB1	-1	A,S,x	2730.308	2	-592.879	854.490	7	-179.492	97.025	4	-19.374	100.370	6	-18.678
HLA-DRB1	4	R,Q	855.614	1	-187.359	1851.267	2	-401.998	43.580	4	-8.106	1.898	4	-0.122
HLA-DRB1	9	E,W,K	2965.803	2	-644.016	2862.273	6	-615.524	80.877	5	-15.260	41.516	5	-7.132
HLA-DRB1	10	Y,Q,E	113.318	2	-24.607	84.544	5	-16.028	42.231	3	-8.446	45.092	3	-9.053
HLA-DRB1	11	S,P,V,L,G,D	4598.456	5	-993.623	3155.592	15	-667.711	84.746	5	-16.070	46.192	5	-8.081
HLA-DRB1	12	T,K	62.793	1	-14.639	47.328	4	-8.885	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	13	S,R,H,F,G,Y	4732.895	5	-1022.797	3411.777	16	-721.935	NA	NA	NA	NA	NA	NA
HLA-DRB1	14	E,K	1002.102	1	-219.203	1970.177	2	-427.818	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	16	H,Y	26.813	1	-6.650	322.145	3	-68.796	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	25	R,Q	1002.102	1	-219.203	1970.177	2	-427.818	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	26	Y,F,L	1669.514	2	-362.530	256.313	7	-50.901	118.916	6	-22.560	69.425	6	-12.270
HLA-DRB1	28	D,E,H	1025.631	2	-222.713	2115.907	6	-453.715	109.913	3	-22.941	68.610	3	-14.072
HLA-DRB1	30	Y,C,L,R,G,H	1340.255	5	-286.916	2228.429	10	-473.088	147.194	4	-30.090	108.212	4	-21.757
HLA-DRB1	31	F,I,V	113.035	2	-24.545	225.070	5	-45.914	37.303	1	-8.995	39.616	1	-9.510
HLA-DRB1	32	H,Y	401.529	1	-88.592	50.121	4	-9.468	105.732	5	-20.486	141.195	9	-25.233
HLA-DRB1	33	N,H	2055.925	1	-448.193	965.814	3	-208.329	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	37	N,S,Y,F,L	3636.529	4	-786.402	3074.812	12	-653.831	213.762	11	-38.988	145.130	12	-24.260
HLA-DRB1	38	V,A,L	152.698	2	-33.158	41.382	2	-8.986	104.686	2	-22.732	107.122	2	-23.261
HLA-DRB1	40	F,Y	55.843	1	-13.105	36.724	1	-8.866	37.303	1	-8.995	39.616	1	-9.510
HLA-DRB1	47	F,Y	135.982	1	-30.696	592.090	4	-126.098	116.243	7	-21.334	100.351	7	-18.040
HLA-DRB1	57	D,S,V,A	1443.401	3	-311.949	2257.855	9	-480.667	186.736	12	-32.754	202.151	12	-35.931
HLA-DRB1	58	A,E	762.817	1	-167.183	38.847	3	-7.728	0.323	3	-0.020	33.246	5	-5.473
HLA-DRB1	60	Y,S,H	1436.473	2	-311.926	1944.029	6	-416.465	162.384	7	-30.996	97.773	6	-18.136
HLA-DRB1	67	L,I,F	4948.109	2	-1074.468	2283.776	8	-487.520	216.586	13	-38.278	130.546	10	-22.442
HLA-DRB1	70	Q,D,R	2524.408	2	-548.168	1652.477	8	-350.856	154.839	14	-25.113	77.102	10	-11.732
HLA-DRB1	71	K,A,E,R	5836.723	3	-1265.643	1987.409	10	-420.950	487.513	12	-95.998	NA	NA	NA
HLA-DRB1	73	G,A	303.131	1	-67.164	791.727	3	-170.569	9.275	3	-1.588	0.774	2	-0.168
HLA-DRB1	74	R,A,L,Q,E	2511.514	4	-542.269	2519.326	12	-533.641	301.357	12	-56.613	121.267	10	-20.553
HLA-DRB1	77	N,T	1700.917	1	-371.063	35.630	3	-7.047	9.275	3	-1.588	0.774	2	-0.168
HLA-DRB1	78	Y,V	855.853	1	-187.411	1850.299	2	-401.787	42.526	2	-9.234	1.097	2	-0.238
HLA-DRB1	85	V,A	101.480	1	-23.142	7.844	2	-1.703	70.807	2	-15.376	72.061	2	-15.648
HLA-DRB1	86	V,G	0.371	1	-0.266	583.286	4	-124.193	463.615	10	-92.585	210.566	13	-37.037
HLA-DRB1	96	H,Q,Y,E	3818.584	3	-827.502	1515.611	11	-317.869	80.941	7	-14.053	49.030	8	-7.202
HLA-DRB1	98	K,E	554.070	1	-121.785	311.415	3	-66.473	43.646	6	-7.061	9.417	7	-0.650
HLA-DRB1	104	S,A	554.070	1	-121.785	311.415	3	-66.473	43.646	6	-7.061	9.417	7	-0.650
HLA-DRB1	112	H,Y	414.389	1	-91.391	92.716	4	-18.458	52.450	4	-9.954	29.149	3	-5.681
HLA-DRB1	120	S,N	1949.075	1	-424.979	998.089	3	-215.330	38.590	5	-6.542	48.205	7	-7.488
HLA-DRB1	133	R,L	2389.548	1	-520.671	689.439	4	-147.171	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	140	T,A	2837.924	1	-618.072	2252.078	4	-485.981	37.303	1	-8.995	39.616	1	-9.510
HLA-DRB1	142	V,M	2389.548	1	-520.671	689.439	4	-147.171	0.000	0	0.000	0.000	0	0.000
HLA-DRB1	149	H,Q	63.877	1	-14.878	48.171	4	-9.061	1.289	4	-0.064	8.593	6	-0.704
HLA-DRB1	166	R,Q	55.843	1	-13.105	36.724	1	-8.866	37.303	1	-8.995	39.616	1	-9.510
HLA-DRB1	180	V,L,x	2091.410	2	-454.144	1532.350	5	-328.542	99.957	5	-19.268	107.402	7	-19.498
HLA-DRB1	181	T,x,M	914.644	2	-198.612	2315.214	5	-498.270	178.454	4	-36.796	139.500	4	-28.442
HLA-DRB1	189	R,x,S	47.198	2	-10.249	307.258	4	-64.531	108.054	4	-21.723	106.781	4	-21.452
HLA-DRB1	231	Q,x,P	66.198	2	-14.375	338.662	4	-71.308	135.734	4	-27.636	136.789	4	-27.862
HLA-DRB1	233	R,T,x	95.363	2	-20.708	347.994	7	-70.480	109.343	8	-19.284	115.406	10	-19.365

Supplementary Table 4C. All classical allele associations in HLA-DRB1-DQA1-DQB1

	Unadjusted		**Adj. DQb1#57**		**Adj.DQb1#57,DRb1#13**		**Adj.DQb1#57,DRb1#13,DRb1#71**	
Classical allele	**Deviance**	**log10(p)**	**Deviance**	**log10(p)**	**Deviance**	**log10(p)**	**Deviance**	**log10(p)**
HLA-DQA1*01	2465.944	-537.267	657.692	-144.324	0.007	-0.029	28.463	-7.020
HLA-DQA1*0101	211.449	-47.178	13.516	-3.626	56.131	-13.169	31.273	-7.650
HLA-DQA1*0102	1798.442	-392.252	324.950	-71.917	8.493	-2.448	16.270	-4.260
HLA-DQA1*0103	493.293	-108.563	2.488	-0.940	32.625	-7.952	0.011	-0.039
HLA-DQA1*02	1002.782	-219.350	1983.310	-432.417	12.415	-3.371	10.591	-2.944
HLA-DQA1*0201	1002.782	-219.350	1983.310	-432.417	12.415	-3.371	10.591	-2.944
HLA-DQA1*03	2035.607	-443.779	1174.533	-256.680	43.688	-10.414	4.842	-1.556
HLA-DQA1*0301	2035.607	-443.779	1174.533	-256.680	43.688	-10.414	4.842	-1.556
HLA-DQA1*04	2.444	-0.928	413.684	-91.238	102.087	-23.275	103.866	-23.665
HLA-DQA1*0401	2.444	-0.928	413.684	-91.238	102.087	-23.275	103.866	-23.665
HLA-DQA1*05	488.565	-107.534	6.459	-1.957	47.089	-11.169	6.069	-1.861
HLA-DQA1*0501	488.565	-107.534	6.459	-1.957	47.089	-11.169	6.069	-1.861
HLA-DQA1*06	37.119	-8.954	6.934	-2.073	27.556	-6.816	27.545	-6.814
HLA-DQA1*0601	37.119	-8.954	6.934	-2.073	27.556	-6.816	27.545	-6.814
HLA-DQB1*02	671.616	-147.352	667.391	-146.433	1.246	-0.578	4.017	-1.346
HLA-DQB1*0201	1744.674	-380.570	28.885	-7.115	2.331	-0.897	5.700	-1.770
HLA-DQB1*0202	472.551	-104.049	1850.039	-403.463	1.808	-0.748	1.822	-0.752
HLA-DQB1*03	387.451	-85.527	800.644	-175.408	42.328	-10.112	20.559	-5.238
HLA-DQB1*0301	1183.774	-258.688	106.163	-24.168	61.065	-14.258	14.874	-3.940
HLA-DQB1*0302	3407.438	-741.780	664.536	-145.812	0.367	-0.264	4.724	-1.527
HLA-DQB1*0303	357.122	-78.924	6.215	-1.897	26.234	-6.519	2.536	-0.954
HLA-DQB1*0304	8.413	-2.429	0.684	-0.389	0.245	-0.207	0.920	-0.472
HLA-DQB1*04	1.151	-0.548	404.837	-89.312	94.502	-21.611	106.156	-24.167
HLA-DQB1*0402	1.151	-0.548	404.837	-89.312	94.502	-21.611	106.156	-24.167
HLA-DQB1*05	216.276	-48.231	14.433	-3.838	51.322	-12.106	26.759	-6.637
HLA-DQB1*0501	77.120	-17.794	0.002	-0.016	3.974	-1.335	1.003	-0.499
HLA-DQB1*0502	3.350	-1.173	0.000	0.000	0.000	0.000	0.000	0.000
HLA-DQB1*0503	410.562	-90.558	87.623	-20.101	47.926	-11.354	26.334	-6.542
HLA-DQB1*06	2504.339	-545.608	300.830	-66.663	22.240	-5.619	4.273	-1.412
HLA-DQB1*0601	49.577	-11.720	1.867	-0.765	18.433	-4.754	18.450	-4.758
HLA-DQB1*0602	2661.709	-579.794	702.755	-154.123	34.436	-8.356	35.058	-8.495
HLA-DQB1*0603	467.056	-102.853	1.760	-0.734	29.722	-7.302	0.338	-0.251
HLA-DQB1*0604	0.902	-0.466	14.591	-3.874	73.846	-17.073	70.727	-16.387
HLA-DQB1*0609	90.902	-20.821	60.527	-14.139	67.605	-15.699	69.233	-16.058
HLA-DRB1*01	67.228	-15.616	3.868	-1.308	0.427	-0.290	34.231	-8.310
HLA-DRB1*0101	22.747	-5.733	20.158	-5.147	37.136	-8.958	27.329	-6.765
HLA-DRB1*0102	15.748	-4.140	3.188	-1.130	3.414	-1.190	4.545	-1.481
HLA-DRB1*0103	60.231	-14.074	11.226	-3.093	32.173	-7.851	0.000	0.000
HLA-DRB1*03	1699.865	-370.834	27.555	-6.816	0.351	-0.257	0.113	-0.132
HLA-DRB1*0301	1699.865	-370.834	27.555	-6.816	0.351	-0.257	0.113	-0.132
HLA-DRB1*04	2055.983	-448.206	959.568	-209.957	1.095	-0.530	1.163	-0.552
HLA-DRB1*0401	1630.963	-355.864	1263.904	-276.102	354.408	-78.333	1.389	-0.622
HLA-DRB1*0402	92.900	-21.260	10.575	-2.941	0.738	-0.408	2.844	-1.038
HLA-DRB1*0403	0.096	-0.121	13.537	-3.631	38.627	-9.290	12.598	-3.413
HLA-DRB1*0404	159.037	-35.736	20.669	-5.263	323.673	-71.639	59.925	-14.006
HLA-DRB1*0405	247.382	-55.015	75.379	-17.411	15.271	-4.031	96.831	-22.122
HLA-DRB1*0407	174.840	-39.188	25.707	-6.401	91.063	-20.856	9.961	-2.796
HLA-DRB1*0408	0.354	-0.258	3.070	-1.098	2.808	-1.028	13.839	-3.701
HLA-DRB1*07	1002.102	-219.203	1964.008	-428.224	0.000	0.000	0.000	0.000
HLA-DRB1*0701	1002.102	-219.203	1964.008	-428.224	0.000	0.000	0.000	0.000
HLA-DRB1*08	0.137	-0.148	376.731	-83.193	67.397	-15.654	67.521	-15.681
HLA-DRB1*0801	4.009	-1.344	410.376	-90.518	98.673	-22.526	98.821	-22.558
HLA-DRB1*0803	37.119	-8.954	6.934	-2.073	27.556	-6.816	27.545	-6.814
HLA-DRB1*0804	2.576	-0.964	2.697	-0.998	0.736	-0.408	0.738	-0.409
HLA-DRB1*09	1.049	-0.515	201.602	-45.030	42.273	-10.100	0.965	-0.487
HLA-DRB1*0901	1.049	-0.515	201.602	-45.030	42.273	-10.100	0.965	-0.487
HLA-DRB1*10	55.843	-13.105	36.724	-8.866	37.303	-8.995	39.616	-9.510
HLA-DRB1*1001	55.843	-13.105	36.724	-8.866	37.303	-8.995	39.616	-9.510
HLA-DRB1*11	762.817	-167.183	35.802	-8.661	0.011	-0.037	25.351	-6.321
HLA-DRB1*1101	496.474	-109.255	32.287	-7.876	1.890	-0.772	11.120	-3.069

HLA-DRB1*1102	9.240	-2.626	1.704	-0.717	6.174	-1.887	2.636	-0.981
HLA-DRB1*1103	31.340	-7.664	1.061	-0.519	7.782	-2.278	1.424	-0.633
HLA-DRB1*1104	229.586	-51.134	16.207	-4.246	1.550	-0.671	1.291	-0.592
HLA-DRB1*12	95.974	-21.934	4.657	-1.510	67.397	-15.654	67.521	-15.681
HLA-DRB1*1201	95.974	-21.934	4.657	-1.510	67.397	-15.654	67.521	-15.681
HLA-DRB1*13	408.176	-90.039	2.467	-0.935	17.657	-4.577	4.020	-1.347
HLA-DRB1*1301	432.870	-95.414	1.496	-0.655	22.189	-5.607	3.852	-1.304
HLA-DRB1*1302	23.487	-5.900	0.000	-0.005	2.573	-0.964	0.108	-0.130
HLA-DRB1*1303	120.741	-27.361	10.708	-2.972	1.873	-0.767	0.493	-0.316
HLA-DRB1*14	414.389	-91.391	91.839	-21.027	51.940	-12.242	28.904	-7.119
HLA-DRB1*1401	414.389	-91.391	91.839	-21.027	51.940	-12.242	28.904	-7.119
HLA-DRB1*15	2691.402	-586.244	672.651	-147.577	0.043	-0.078	0.000	0.000
HLA-DRB1*1501	2648.407	-576.904	683.413	-149.917	11.827	-3.234	18.281	-4.720
HLA-DRB1*1502	50.208	-11.859	1.961	-0.792	18.260	-4.715	18.281	-4.720
HLA-DRB1*16	2.425	-0.923	0.544	-0.336	0.043	-0.078	0.000	0.000
HLA-DRB1*1601	2.425	-0.923	0.544	-0.336	0.043	-0.078	0.000	0.000

Supplementary Table 5A. HLA-B associations

				Unadjusted			Adj.DRB1,DQA1,DQB1			Adj.DRB1,DQA1,DQB1,HLA-B*3906		
Gene	**Amino acid position**	**Residues**	**Classical alle**	**deviance**	**df**	**log10(p)**	**deviance**	**df**	**log10(p)**	**deviance**	**df**	**log10(p)**
HLA-B	-10	A,G	--	139.990	1	-31.572	12.629	1	-3.420	0.050	1	-0.084
HLA-B	-11	S,W	--	515.372	1	-113.367	6.984	1	-2.085	0.027	1	-0.061
HLA-B	-16	V,L	--	111.776	1	-25.398	0.781	1	-0.424	7.452	1	-2.198
HLA-B	-21	M,T	--	57.366	1	-13.442	2.397	1	-0.915	9.199	1	-2.616
HLA-B	-23	L,R	--	57.366	1	-13.442	2.397	1	-0.915	9.199	1	-2.616
HLA-B	-8	L,V	--	463.904	1	-102.168	6.758	1	-2.030	0.006	1	-0.028
HLA-B	103	V,L	--	74.346	1	-17.183	2.091	1	-0.829	7.734	1	-2.266
HLA-B	109	L,F	--	24.928	1	-6.225	0.492	1	-0.316	0.588	1	-0.353
HLA-B	11	A,S	--	60.289	1	-14.087	81.193	1	-18.689	25.653	1	-6.389
HLA-B	113	H,Y	--	298.490	1	-66.153	23.452	1	-5.892	10.166	1	-2.845
HLA-B	114	N,D,H	--	287.098	2	-62.343	28.810	2	-6.256	17.776	2	-3.860
HLA-B	116	Y,D,F,L,S	--	263.221	4	-55.035	127.112	4	-25.792	53.563	4	-10.187
HLA-B	12	M,V	--	105.243	1	-23.966	68.491	1	-15.895	19.783	1	-5.062
HLA-B	131	R,S	--	90.287	1	-20.686	18.324	1	-4.730	5.694	1	-1.769
HLA-B	143	T,S	--	54.079	1	-12.715	0.819	1	-0.437	4.965	1	-1.587
HLA-B	145	R,L	--	12.880	1	-3.479	19.762	1	-5.057	21.516	1	-5.455
HLA-B	147	W,L	--	54.079	1	-12.715	0.819	1	-0.437	4.965	1	-1.587
HLA-B	152	V,E	--	58.665	1	-13.728	0.187	1	-0.177	4.924	1	-1.577
HLA-B	156	D,R,L,W	--	841.916	3	-181.455	35.965	3	-7.118	20.525	3	-3.879
HLA-B	158	A,T	--	107.975	1	-24.565	216.964	1	-48.381	12.316	1	-3.348
HLA-B	162	G	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	163	T,E,L	--	576.050	2	-125.088	44.058	2	-9.567	6.907	2	-1.500
HLA-B	166	E	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	167	W,S	--	230.458	1	-51.325	12.271	1	-3.337	5.835	1	-1.804
HLA-B	171	Y,H	--	0.023	1	-0.055	25.644	1	-6.387	35.788	1	-8.658
HLA-B	177	D,E	--	113.348	1	-25.742	13.267	1	-3.569	3.225	1	-1.139
HLA-B	178	T,K	--	126.088	1	-28.532	3.070	1	-1.098	12.287	1	-3.341
HLA-B	180	E,Q	--	113.348	1	-25.742	13.267	1	-3.569	3.225	1	-1.139
HLA-B	194	I,V	--	133.368	1	-30.124	12.077	1	-3.292	3.643	1	-1.249
HLA-B	199	A,V	--	217.041	1	-48.398	10.213	1	-2.856	4.549	1	-1.482
HLA-B	211	A	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	239	R	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	24	S,T,A	--	156.174	2	-33.913	52.964	2	-11.501	13.167	2	-2.859
HLA-B	245	A	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	253	E	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	267	P	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	268	K	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	270	L	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	275	E	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	282	V,I	--	82.794	1	-19.041	10.852	1	-3.006	29.247	1	-7.196
HLA-B	295	A	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	296	V	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	298	V	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	299	I	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	30	D,G	--	177.265	1	-39.717	99.292	1	-22.662	107.567	1	-24.476
HLA-B	300	G	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	305	A,T	--	77.196	1	-17.810	10.114	1	-2.832	27.982	1	-6.912
HLA-B	307	M,V	--	5.552	1	-1.734	0.817	1	-0.436	0.909	1	-0.468
HLA-B	32	Q,L	--	70.759	1	-16.394	10.540	1	-2.932	1.030	1	-0.508
HLA-B	325	C,S,x	--	75.950	2	-16.492	69.397	2	-15.069	28.970	2	-6.291
HLA-B	4	S,F	--	0.646	1	-0.375	1.592	1	-0.684	1.621	1	-0.693
HLA-B	41	A,T	--	69.739	1	-16.169	0.530	1	-0.331	7.258	1	-2.151
HLA-B	45	E,K,M,T	--	91.320	3	-18.943	10.326	3	-1.796	30.848	3	-6.039
HLA-B	46	E,A	--	32.592	1	-7.944	1.929	1	-0.783	0.281	1	-0.225
HLA-B	52	I	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	59	Y,H	--	0.986	1	-0.494	0.502	1	-0.320	0.507	1	-0.322
HLA-B	62	R,G	--	308.900	1	-68.421	20.281	1	-5.175	17.777	1	-4.605
HLA-B	63	N,E	--	36.432	1	-8.801	18.762	1	-4.830	2.000	1	-0.803
HLA-B	65	Q,R	--	291.294	1	-64.585	17.950	1	-4.644	15.647	1	-4.117
HLA-B	66	I,N	--	291.294	1	-64.585	17.950	1	-4.644	15.647	1	-4.117
HLA-B	67	F,Y,S,C,M	--	808.622	4	-172.982	97.390	4	-19.452	85.253	4	-16.873
HLA-B	69	T,A	--	656.023	1	-143.961	13.440	1	-3.609	4.444	1	-1.456
HLA-B	70	N,Q,S,K	--	774.055	3	-166.737	47.828	3	-9.635	38.854	3	-7.730
HLA-B	71	T,A	--	656.023	1	-143.961	13.440	1	-3.609	4.444	1	-1.456
HLA-B	74	D,Y	--	29.030	1	-7.147	0.773	1	-0.421	22.235	1	-5.618
HLA-B	76	E	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	77	S,N,D	--	557.867	2	-121.139	44.473	2	-9.657	22.582	2	-4.904
HLA-B	80	N,T,I	--	550.155	2	-119.465	39.484	2	-8.574	18.907	2	-4.106
HLA-B	81	L,A	--	496.960	1	-109.361	14.755	1	-3.912	5.177	1	-1.640
HLA-B	82	R,L	--	541.380	1	-119.025	37.816	1	-9.109	17.196	1	-4.472
HLA-B	83	G,R	--	541.380	1	-119.025	37.816	1	-9.109	17.196	1	-4.472
HLA-B	9	D,Y,H	--	837.074	2	-181.768	55.080	2	-11.961	59.813	2	-12.988
HLA-B	90	A	--	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-B	94	T,I	--	605.998	1	-133.081	39.389	1	-9.459	20.836	1	-5.301
HLA-B	95	L,I,W	--	679.536	2	-147.559	143.187	2	-31.093	38.427	2	-8.344
HLA-B	97	S,R,T,W,V,N	--	519.869	5	-109.387	184.214	5	-37.172	88.786	5	-16.918

HLA-B	99	Y,S,F	--	47.202	2	-10.250	2.180	2	-0.473	1.400	2	-0.304
HLA-B	--	--	HLA-B*07	379.502	1	-83.797	1.602	1	-0.687	5.088	1	-1.618
HLA-B	--	--	HLA-B*0702	406.312	1	-89.633	1.149	1	-0.547	4.266	1	-1.410
HLA-B	--	--	HLA-B*0705	10.866	1	-3.009	1.730	1	-0.725	1.858	1	-0.762
HLA-B	--	--	HLA-B*08	605.271	1	-132.923	50.532	1	-11.931	42.215	1	-10.087
HLA-B	--	--	HLA-B*0801	605.271	1	-132.923	50.532	1	-11.931	42.215	1	-10.087
HLA-B	--	--	HLA-B*13	12.880	1	-3.479	19.331	1	-4.959	21.058	1	-5.351
HLA-B	--	--	HLA-B*1302	12.880	1	-3.479	19.331	1	-4.959	21.058	1	-5.351
HLA-B	--	--	HLA-B*14	126.825	1	-28.693	9.428	1	-2.670	8.061	1	-2.345
HLA-B	--	--	HLA-B*1401	57.334	1	-13.435	6.551	1	-1.980	5.898	1	-1.819
HLA-B	--	--	HLA-B*1402	71.975	1	-16.662	3.632	1	-1.247	2.944	1	-1.064
HLA-B	--	--	HLA-B*15	320.159	1	-70.874	3.511	1	-1.215	1.169	1	-0.554
HLA-B	--	--	HLA-B*1501	339.432	1	-75.072	4.086	1	-1.364	1.545	1	-0.670
HLA-B	--	--	HLA-B*1503	1.995	1	-0.802	0.153	1	-0.157	0.119	1	-0.136
HLA-B	--	--	HLA-B*1516	0.646	1	-0.375	1.403	1	-0.627	1.434	1	-0.636
HLA-B	--	--	HLA-B*1517	1.261	1	-0.582	0.635	1	-0.371	0.581	1	-0.351
HLA-B	--	--	HLA-B*1518	2.429	1	-0.924	0.515	1	-0.325	0.744	1	-0.411
HLA-B	--	--	HLA-B*18	175.373	1	-39.304	94.552	1	-21.622	102.625	1	-23.393
HLA-B	--	--	HLA-B*1801	175.373	1	-39.304	94.552	1	-21.622	102.625	1	-23.393
HLA-B	--	--	HLA-B*27	9.447	1	-2.675	29.836	1	-7.328	20.405	1	-5.203
HLA-B	--	--	HLA-B*2702	7.016	1	-2.093	3.997	1	-1.341	3.276	1	-1.153
HLA-B	--	--	HLA-B*2705	7.164	1	-2.129	27.236	1	-6.745	18.440	1	-4.756
HLA-B	--	--	HLA-B*35	91.606	1	-20.976	12.342	1	-3.354	5.164	1	-1.637
HLA-B	--	--	HLA-B*3501	73.127	1	-16.915	16.067	1	-4.214	8.396	1	-2.425
HLA-B	--	--	HLA-B*3502	24.928	1	-6.225	0.519	1	-0.327	0.618	1	-0.365
HLA-B	--	--	HLA-B*3503	4.331	1	-1.427	0.315	1	-0.241	0.000	1	-0.007
HLA-B	--	--	HLA-B*3508	0.419	1	-0.286	0.109	1	-0.130	0.182	1	-0.174
HLA-B	--	--	HLA-B*37	41.849	1	-10.006	1.587	1	-0.682	0.623	1	-0.366
HLA-B	--	--	HLA-B*3701	41.849	1	-10.006	1.587	1	-0.682	0.623	1	-0.366
HLA-B	--	--	HLA-B*38	5.636	1	-1.755	0.122	1	-0.139	0.307	1	-0.237
HLA-B	--	--	HLA-B*3801	5.636	1	-1.755	0.122	1	-0.139	0.307	1	-0.237
HLA-B	--	--	HLA-B*39	190.172	1	-42.535	300.959	1	-66.691	26.170	1	-6.505
HLA-B	--	--	HLA-B*3901	2.407	1	-0.918	18.447	1	-4.758	26.170	1	-6.505
HLA-B	--	--	HLA-B*3906	273.147	1	-60.631	340.953	1	-75.403	NA	1	NA
HLA-B	--	--	HLA-B*40	23.614	1	-5.929	0.084	1	-0.113	1.148	1	-0.547
HLA-B	--	--	HLA-B*4001	54.079	1	-12.715	0.641	1	-0.373	4.514	1	-1.474
HLA-B	--	--	HLA-B*4002	34.494	1	-8.369	9.756	1	-2.748	7.993	1	-2.328
HLA-B	--	--	HLA-B*4006	0.329	1	-0.247	0.015	1	-0.044	0.000	1	-0.005
HLA-B	--	--	HLA-B*41	4.395	1	-1.443	0.061	1	-0.094	0.188	1	-0.177
HLA-B	--	--	HLA-B*4101	7.354	1	-2.175	4.537	1	-1.479	5.094	1	-1.620
HLA-B	--	--	HLA-B*4102	38.744	1	-9.316	4.600	1	-1.495	4.047	1	-1.354
HLA-B	--	--	HLA-B*44	216.012	1	-48.174	7.291	1	-2.159	2.703	1	-0.999
HLA-B	--	--	HLA-B*4402	46.772	1	-11.098	0.721	1	-0.402	3.586	1	-1.235
HLA-B	--	--	HLA-B*4403	252.460	1	-56.122	46.733	1	-11.090	43.228	1	-10.312
HLA-B	--	--	HLA-B*4405	0.034	1	-0.068	3.025	1	-1.086	3.876	1	-1.310
HLA-B	--	--	HLA-B*45	10.274	1	-2.870	2.132	1	-0.841	1.680	1	-0.710
HLA-B	--	--	HLA-B*4501	10.274	1	-2.870	2.132	1	-0.841	1.680	1	-0.710
HLA-B	--	--	HLA-B*47	5.552	1	-1.734	0.803	1	-0.432	0.896	1	-0.464
HLA-B	--	--	HLA-B*4701	5.552	1	-1.734	0.803	1	-0.432	0.896	1	-0.464
HLA-B	--	--	HLA-B*49	9.184	1	-2.612	1.201	1	-0.564	0.871	1	-0.455
HLA-B	--	--	HLA-B*4901	9.184	1	-2.612	1.201	1	-0.564	0.871	1	-0.455
HLA-B	--	--	HLA-B*50	21.799	1	-5.519	70.981	1	-16.443	73.329	1	-16.960
HLA-B	--	--	HLA-B*5001	21.799	1	-5.519	70.981	1	-16.443	73.329	1	-16.960
HLA-B	--	--	HLA-B*51	18.807	1	-4.840	1.274	1	-0.587	0.080	1	-0.109
HLA-B	--	--	HLA-B*5101	18.807	1	-4.840	1.274	1	-0.587	0.080	1	-0.109
HLA-B	--	--	HLA-B*52	25.876	1	-6.439	0.811	1	-0.434	1.205	1	-0.565
HLA-B	--	--	HLA-B*5201	25.876	1	-6.439	0.811	1	-0.434	1.205	1	-0.565
HLA-B	--	--	HLA-B*53	2.175	1	-0.853	1.814	1	-0.750	1.636	1	-0.697
HLA-B	--	--	HLA-B*5301	2.175	1	-0.853	1.814	1	-0.750	1.636	1	-0.697
HLA-B	--	--	HLA-B*55	31.817	1	-7.771	0.403	1	-0.279	0.113	1	-0.133
HLA-B	--	--	HLA-B*5501	31.817	1	-7.771	0.403	1	-0.279	0.113	1	-0.133
HLA-B	--	--	HLA-B*56	0.368	1	-0.264	0.021	1	-0.053	0.323	1	-0.244
HLA-B	--	--	HLA-B*5601	0.368	1	-0.264	0.021	1	-0.053	0.323	1	-0.244
HLA-B	--	--	HLA-B*57	356.914	1	-78.878	28.796	1	-7.095	25.807	1	-6.423
HLA-B	--	--	HLA-B*5701	356.914	1	-78.878	28.796	1	-7.095	25.807	1	-6.423
HLA-B	--	--	HLA-B*58	2.140	1	-0.843	0.047	1	-0.082	0.091	1	-0.117
HLA-B	--	--	HLA-B*5801	2.140	1	-0.843	0.047	1	-0.082	0.091	1	-0.117

Supplementary Table 5B. HLA-DPB1 associations

				Unadjusted			Adj.DRB1,DQA1,DQB1			Adj.DRB1,DQA1,DQB1,B			Adj.DRB1,DQA1,DQB1,B,DPB1*0402		
Gene	Amino acid position	Residues	Classical alle	deviance	df	log10(p)	deviance	df	log10(p)	deviance	df	log10(p)	deviance	df	log10(p)
HLA-DPB1	11	G,L	--	36.8773691	1	-8.900327297	67.13305865	1	-15.59553091	56.57480927	1	-13.26679883	23.5046864	1	-5.9044476
HLA-DPB1	170	T,I	--	82.3000339	1	-18.93211076	12.07256236	1	-3.290990318	15.525023	1	-4.089267319	0.27596924	1	-0.2223156
HLA-DPB1	178	L,M	--	319.31925	1	-70.69081611	246.1438685	1	-54.7448632	246.2546442	1	-54.76901476	0.59530998	1	-0.3561792
HLA-DPB1	194	R,Q,x	--	57.7737476	2	-12.54540988	49.64503895	2	-10.78028323	32.87468285	2	-7.138646679	47.6097306	2	-10.338322
HLA-DPB1	205	V,x,M	--	69.0116355	2	-14.98568624	5.821696297	2	-1.264165289	5.739014124	2	-1.246211083	6.32569139	2	-1.3736064
HLA-DPB1	215	I,x,T	--	34.5601854	2	-7.504648897	26.5020635	2	-5.754849968	29.65155477	2	-6.438753307	21.2424169	2	-4.6127322
HLA-DPB1	33	E,Q	--	7.04375657	1	-2.099403355	8.639210964	1	-2.482798966	19.97362241	1	-5.105031455	13.1172192	1	-3.5337346
HLA-DPB1	35	F,Y,L	--	31.8067619	2	-6.906750587	18.97958767	2	-4.121365097	3.968424974	2	-0.861732534	14.8292314	2	-3.2201267
HLA-DPB1	36	A,V	--	0.89524249	1	-0.463365077	1.636166388	1	-0.697123261	0.32337294	1	-0.244439438	24.7008665	1	-6.174223
HLA-DPB1	55	A,D,E	--	10.6424251	2	-2.310973245	7.115041574	2	-1.545011647	0.512167032	2	-0.111215658	27.2472378	2	-5.9166625
HLA-DPB1	56	A,E	--	0.08050192	1	-0.109792338	0.050098849	1	-0.084657498	0.507616031	1	-0.322235523	27.209428	1	-6.7385795
HLA-DPB1	57	E,D	--	124.901217	1	-28.27170802	82.61619415	1	-19.00157761	60.41695812	1	-14.11492776	30.2220035	1	-7.4141861
HLA-DPB1	65	I,L	--	112.801969	1	-25.62262282	98.77541427	1	-22.54848374	89.24954362	1	-20.45839184	50.463244	1	-11.915718
HLA-DPB1	69	K,E,R	--	31.3034255	2	-6.797452489	36.74347329	2	-7.978743847	39.39506929	2	-8.554530603	15.880234	2	-3.448349
HLA-DPB1	72	V	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-DPB1	76	M,V,I	--	150.887175	2	-32.76473367	9.307451854	2	-2.02108749	7.729575607	2	-1.678456017	0.5461958	2	-0.1186049
HLA-DPB1	8	L,V	--	111.998303	1	-25.44658296	20.78733633	1	-5.289703218	22.59741274	1	-5.699505762	2.15198539	1	-0.8465337
HLA-DPB1	84	G,D,V	--	87.1754164	2	-18.92990115	36.47156212	2	-7.919699087	39.24816045	2	-8.522629753	21.139563	2	-4.5903978
HLA-DPB1	85	G,E	--	55.7904861	1	-13.09355313	8.379058447	1	-2.420709252	10.09411821	1	-2.827562531	0.05817017	1	-0.0918305
HLA-DPB1	86	P,A	--	55.7904861	1	-13.09355313	8.379058447	1	-2.420709252	10.09411821	1	-2.827562531	0.05817017	1	-0.0918305
HLA-DPB1	87	M,V	--	55.7904861	1	-13.09355313	8.379058447	1	-2.420709252	10.09411821	1	-2.827562531	0.05817017	1	-0.0918305
HLA-DPB1	9	F,Y,H	--	188.606655	2	-40.95541472	27.49905311	2	-5.971343511	31.53955921	2	-6.848728264	11.9953143	2	-2.6047494
HLA-DPB1	91	R	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-DPB1	96	R,K	--	82.3000339	1	-18.93211076	12.07256236	1	-3.290990318	15.525023	1	-4.089267319	0.27596924	1	-0.2223156
HLA-DPB1	--	--	HLA-DPB1*0	51.8180309	1	-12.2154536	49.35291231	1	-11.66995818	31.39033037	1	-7.675657289	47.3904831	1	-11.235343
HLA-DPB1	--	--	HLA-DPB1*0	51.8180309	1	-12.2154536	49.35291231	1	-11.66995818	31.39033037	1	-7.675657289	47.3904831	1	-11.235343
HLA-DPB1	--	--	HLA-DPB1*0	51.7929791	1	-12.20991236	28.8543066	1	-7.107726123	17.15289289	1	-4.462327259	4.73254845	1	-1.5287523
HLA-DPB1	--	--	HLA-DPB1*0	6.29083769	1	-1.915911267	11.29915982	1	-3.110462036	12.32214597	1	-3.349094591	2.60962529	1	-0.9738066
HLA-DPB1	--	--	HLA-DPB1*0	174.218334	1	-39.05209551	32.66814045	1	-7.961322623	5.105155024	1	-1.622423361	3.20523287	1	-1.1342858
HLA-DPB1	--	--	HLA-DPB1*0	143.494179	1	-32.33881776	90.23930433	1	-20.6756599	64.97910765	1	-15.12092485	39.0193275	1	-9.3771329
HLA-DPB1	--	--	HLA-DPB1*0	143.494179	1	-32.33881776	90.23930433	1	-20.6756599	64.97910765	1	-15.12092485	39.0193275	1	-9.3771329
HLA-DPB1	--	--	HLA-DPB1*0	169.097794	1	-37.93377981	55.62869974	1	-13.0578119	47.81009565	1	-11.32830169	4.9089091	1	-1.5731878
HLA-DPB1	--	--	HLA-DPB1*0	9.89639988	1	-2.780933303	2.326959845	1	-0.895683675	4.34042493	1	-1.429251244	4.93160492	1	-1.5788929
HLA-DPB1	--	--	HLA-DPB1*0	321.715081	1	-71.21267741	247.8020436	1	-55.10637769	249.4723402	1	-55.47052526	NA	NA	NA
HLA-DPB1	--	--	HLA-DPB1*0	57.212063	1	-13.40753014	8.48867614	1	-2.446889503	6.025059862	1	-1.850652978	9.13083972	1	-2.5997447
HLA-DPB1	--	--	HLA-DPB1*0	57.212063	1	-13.40753014	8.48867614	1	-2.446889503	6.025059862	1	-1.850652978	9.13083972	1	-2.5997447
HLA-DPB1	--	--	HLA-DPB1*0	24.8681893	1	-6.211923061	0.117106575	1	-0.135373787	0.486629403	1	-0.313869169	0.01184067	1	-0.0393631
HLA-DPB1	--	--	HLA-DPB1*0	24.8681893	1	-6.211923061	0.117106575	1	-0.135373787	0.486629403	1	-0.313869169	0.01184067	1	-0.0393631
HLA-DPB1	--	--	HLA-DPB1*0	0.34957485	1	-0.256212897	1.314823415	1	-0.599421945	0.970637257	1	-0.488756793	2.21931791	1	-0.8655256
HLA-DPB1	--	--	HLA-DPB1*0	0.34957485	1	-0.256212897	1.314823415	1	-0.599421945	0.970637257	1	-0.488756793	2.21931791	1	-0.8655256
HLA-DPB1	--	--	HLA-DPB1*1	19.7551097	1	-5.05538886	2.470568166	1	-0.935557033	2.508005891	1	-0.945888249	5.52262195	1	-1.7264871
HLA-DPB1	--	--	HLA-DPB1*1	19.7551097	1	-5.05538886	2.470568166	1	-0.935557033	2.508005891	1	-0.945888249	5.52262195	1	-1.7264871
HLA-DPB1	--	--	HLA-DPB1*1	47.2454213	1	-11.2032029	0.011096225	1	-0.038053741	2.542257245	1	-0.955318244	0.86501981	1	-0.4530408
HLA-DPB1	--	--	HLA-DPB1*1	47.2454213	1	-11.2032029	0.011096225	1	-0.038053741	2.542257245	1	-0.955318244	0.86501981	1	-0.4530408
HLA-DPB1	--	--	HLA-DPB1*1	5.05071273	1	-1.608785855	0.993194497	1	-0.496259879	1.128273106	1	-0.540390437	0.26693744	1	-0.2179622
HLA-DPB1	--	--	HLA-DPB1*1	5.05071273	1	-1.608785855	0.993194497	1	-0.496259879	1.128273106	1	-0.540390437	0.26693744	1	-0.2179622
HLA-DPB1	--	--	HLA-DPB1*1	1.82702628	1	-0.753306496	1.57109769	1	-0.677682123	1.283440344	1	-0.58962716	2.93918806	1	-1.063214
HLA-DPB1	--	--	HLA-DPB1*1	1.82702628	1	-0.753306496	1.57109769	1	-0.677682123	1.283440344	1	-0.58962716	2.93918806	1	-1.063214
HLA-DPB1	--	--	HLA-DPB1*1	25.686255	1	-6.396122181	25.3803302	1	-6.327262138	27.00511304	1	-6.69267945	21.9003626	1	-5.5418463
HLA-DPB1	--	--	HLA-DPB1*1	25.686255	1	-6.396122181	25.3803302	1	-6.327262138	27.00511304	1	-6.69267945	21.9003626	1	-5.5418463
HLA-DPB1	--	--	HLA-DPB1*1	3.86945369	1	-1.308277492	0.65450122	1	-0.378296279	0.530121085	1	-0.331096261	0.09603359	1	-0.1211093
HLA-DPB1	--	--	HLA-DPB1*1	3.86945369	1	-1.308277492	0.65450122	1	-0.378296279	0.530121085	1	-0.331096261	0.09603359	1	-0.1211093
HLA-DPB1	--	--	HLA-DPB1*1	7.61747663	1	-2.238032219	4.197422848	1	-1.392700899	1.685187051	1	-0.711668846	0.71339548	1	-0.3997691
HLA-DPB1	--	--	HLA-DPB1*1	7.61747663	1	-2.238032219	4.197422848	1	-1.392700899	1.685187051	1	-0.711668846	0.71339548	1	-0.3997691
HLA-DPB1	--	--	HLA-DPB1*1	3.4621886	1	-1.20212918	1.102051942	1	-0.531924219	1.322419302	1	-0.601785043	0.74151217	1	-0.4098529
HLA-DPB1	--	--	HLA-DPB1*1	3.4621886	1	-1.20212918	1.102051942	1	-0.531924219	1.322419302	1	-0.601785043	0.74151217	1	-0.4098529
HLA-DPB1	--	--	HLA-DPB1*2	1.30400715	1	-0.596051902	3.251671056	1	-1.146601879	4.309144223	1	-1.42126882	3.56732554	1	-1.2296846
HLA-DPB1	--	--	HLA-DPB1*2	1.30400715	1	-0.596051902	3.251671056	1	-1.146601879	4.309144223	1	-1.42126882	3.56732554	1	-1.2296846
HLA-DPB1	--	--	HLA-DPB1*2	0.1971143	1	-0.182394805	1.733579078	1	-0.725947362	1.912253303	1	-0.778030083	1.59560778	1	-0.6850237
HLA-DPB1	--	--	HLA-DPB1*2	0.1971143	1	-0.182394805	1.733579078	1	-0.725947362	1.912253303	1	-0.778030083	1.59560778	1	-0.6850237

Supplementary Table 5C. HLA-A associations

				Unadjusted			Adj.DRB1,DQA1,DQB1			Adj.DRB1,DQA1,DQB1,B			Adj.DRB1,DQA1,DQB1,B,DPB1			Adj.DRB1,DQA1,DQB1,B,DPB1,A#62		
Gene	Amino acid position	Residues	Classical alle	deviance	df	log10(p)	deviance	df	log10(p)	deviance	df	log10(p)	deviance	df	log10(p)	deviance	df	log10(p)
HLA-A	-11	S,L,x	--	84.8322337	2	-18.4210855	36.58215212	2	-7.9437134	12.38167225	2	-2.688645967	12.2696524	2	-2.6643212	25.146168	4	-4.3277425
HLA-A	-15	V,L,x	--	65.0546264	2	-14.12643264	148.7159772	2	-32.29326414	82.19405624	2	-17.84821254	84.0576904	2	-18.252896	1.44906868	3	-0.1585941
HLA-A	-2	W,x	--	7.68681175	1	-2.254723662	3.55021607	1	-1.22520797	1.232323583	1	-0.573560913	1.02035729	1	-0.5052413	0.65142846	1	-0.377162
HLA-A	-20	A,x	--	7.68681175	1	-2.254723662	3.55021607	1	-1.22520797	1.232323583	1	-0.573560913	1.02035729	1	-0.5052413	0.65142846	1	-0.377162
HLA-A	-22	V,x	--	7.68681175	1	-2.254723662	3.55021607	1	-1.22520797	1.232323583	1	-0.573560913	1.02035729	1	-0.5052413	0.65142846	1	-0.377162
HLA-A	102	D,H	--	0.88711454	1	-0.460597122	6.17634586	1	-1.887832905	5.139526612	1	-1.631025029	5.62298251	1	-1.751378	1.49252665	1	-0.6539898
HLA-A	105	S,P	--	47.512969	1	-11.26247936	272.5386977	1	-60.49837943	188.3509137	1	-42.13770099	189.274121	1	-42.339224	51.3187774	2	-11.143731
HLA-A	107	W,G	--	60.1434708	1	-14.05458582	48.44651866	1	-11.46926214	42.1806441	1	-10.07977423	40.3471359	1	-9.6724022	1.28912002	2	-0.2799289
HLA-A	109	F,L	--	52.4411289	1	-12.35326198	28.04268941	1	-6.925664347	22.88541394	1	-5.764593372	22.4890388	1	-5.6750056	5.39262161	1	-1.6941744
HLA-A	114	H,R,Q,E	--	222.727025	3	-47.28679547	255.0415471	3	-54.27462981	174.1366337	3	-36.78843158	168.561345	3	-35.584758	30.1745582	5	-4.8656174
HLA-A	116	Y,D,H	--	171.821873	2	-37.31064566	230.872441	2	-50.13331357	134.4806908	2	-29.20211097	132.857592	2	-28.84966	2.53654367	3	-0.3290837
HLA-A	12	V,M	--	14.6766244	1	-3.894083929	0.256747763	1	-0.212990816	0.184318561	1	-0.175426489	0.19963241	1	-0.183747	1.39078415	1	-0.6229257
HLA-A	127	K,N	--	107.454732	1	-24.45112302	188.892541	1	-42.25593095	120.1441832	1	-27.23043169	119.052743	1	-26.991479	2.92504045	1	-1.0594086
HLA-A	142	T,I	--	40.0988047	1	-9.617196772	37.44925771	1	-9.02769347	32.62093659	1	-7.950775255	31.4056776	1	-7.6790902	3.42112894	3	-0.4799931
HLA-A	144	K,Q	--	101.371408	1	-23.11772255	39.40372898	1	-9.46263659	47.74525007	1	-11.31393714	46.6463283	1	-11.070448	47.5741818	4	-8.9363767
HLA-A	145	H,R	--	40.0988047	1	-9.617196772	37.44925771	1	-9.02769347	32.62093659	1	-7.950775255	31.4056776	1	-7.6790902	3.42112894	3	-0.4799931
HLA-A	149	A,T	--	46.1577631	1	-10.96215991	16.56024299	1	-4.326714245	21.71843623	1	-5.500667329	18.5255366	1	-4.7756144	5.22401871	3	-0.806571
HLA-A	150	A,V	--	26.5065229	1	-6.58062302	129.0876456	1	-29.1878299	71.14113778	1	-16.47812584	72.7694299	1	-16.836491	13.0570699	1	-3.5197893
HLA-A	151	H,R	--	52.2662897	1	-12.31459633	21.66453056	1	-5.488463283	23.73860431	1	-5.957240268	25.24303	1	-6.2963485	44.7463743	3	-8.9798333
HLA-A	152	V,A,E,W,R	--	187.730943	4	-38.7881482	209.5547418	4	-43.47984124	141.5456679	4	-28.88029117	142.839817	4	-29.157414	104.717895	7	-18.942472
HLA-A	156	L,R,W,Q	--	48.6392399	3	-9.807774766	171.907925	3	-36.30723895	99.85667322	3	-20.77768682	98.5545111	3	-20.49772	62.2255343	9	-9.3024786
HLA-A	158	A,V	--	26.5065229	1	-6.58062302	129.0876456	1	-29.1878299	71.14113778	1	-16.47812584	72.7694299	1	-16.836491	13.0570699	1	-3.5197893
HLA-A	161	E,D	--	27.0099339	1	-6.69376259	7.754217263	1	-2.270938439	9.002816735	1	-2.569338397	10.7131811	1	-2.9731605	91.1146417	1	-20.867789
HLA-A	163	T,R	--	14.6671557	1	-3.891902333	224.7660211	1	-50.08315779	154.7841047	1	-34.80662626	156.445421	1	-35.169666	39.8650402	4	-7.335762
HLA-A	166	E,D	--	83.3695589	1	-19.16709498	0.666407684	1	-0.382677873	0.068004976	1	-0.100035126	0.07645153	1	-0.1067016	15.2783402	3	-2.7976221
HLA-A	167	W,G	--	83.3695589	1	-19.16709498	0.666407684	1	-0.382677873	0.068004976	1	-0.100035126	0.07645153	1	-0.1067016	15.2783402	3	-2.7976221
HLA-A	17	R,S	--	28.5007956	1	-7.028445867	9.824865504	1	-2.764046834	3.941404773	1	-1.326873797	5.31570753	1	-1.6750181	1.31382788	2	-0.2852941
HLA-A	171	Y,H	--	0.76745792	1	-0.419069764	0.001578847	1	-0.013987993	0.855115441	1	-0.449638051	0.51259389	1	-0.324205	3.96358619	1	-1.3325979
HLA-A	184	A,P	--	0.47090752	1	-0.307532075	9.077413175	1	-2.587059468	15.70234595	1	-4.129993296	15.3470238	1	-4.0483627	8.07735492	4	-1.0516588
HLA-A	186	K,R	--	0.76745792	1	-0.419069764	0.001578847	1	-0.013987993	0.855115441	1	-0.449638051	0.51259389	1	-0.324205	3.96358619	1	-1.3325979
HLA-A	19	E	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-A	193	A,P	--	3.36421934	1	-1.176348729	0.465914694	1	-0.305506567	2.376567138	1	-0.909502319	2.47692834	1	-0.937314	25.21196	4	-4.3409777
HLA-A	194	V,I	--	3.36421934	1	-1.176348729	0.465914694	1	-0.305506567	2.376567138	1	-0.909502319	2.47692834	1	-0.937314	25.21196	4	-4.3409777
HLA-A	207	S,G	--	3.36421934	1	-1.176348729	0.465914694	1	-0.305506567	2.376567138	1	-0.909502319	2.47692834	1	-0.937314	25.21196	4	-4.3409777
HLA-A	245	A,V	--	10.4636811	1	-2.914550882	2.740211658	1	-1.009431157	2.483726775	1	-0.939191136	2.22138651	1	-0.8661075	4.60290483	2	-0.9995081
HLA-A	246	A,S	--	130.640952	1	-29.52768494	53.02688597	1	-12.48278571	30.64893186	1	-7.509765052	28.6821467	1	-7.0691203	27.1969711	4	-4.7414394
HLA-A	253	Q,E	--	3.36421934	1	-1.176348729	0.465914694	1	-0.305506567	2.376567138	1	-0.909502319	2.47692834	1	-0.937314	25.21196	4	-4.3409777
HLA-A	255	Q	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-A	268	K	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-A	276	P,L,x	--	13.6447467	2	-2.962919105	80.97196321	2	-17.58283841	55.22040611	2	-11.99095883	56.6450146	2	-12.300309	23.7122626	3	-4.5423497
HLA-A	282	I,V,x	--	56.8074938	2	-12.33559053	155.4620376	2	-33.75815253	72.48435608	2	-15.73977793	73.8088687	2	-16.027392	2.82583195	3	-0.3775112
HLA-A	283	P,H,x	--	57.7386637	2	-12.53779152	18.12028654	2	-3.934770227	10.90942105	2	-2.368950682	10.3005451	2	-2.236735	27.1579418	2	-5.8972721
HLA-A	288	I,x	--	7.68681175	1	-2.254723662	3.55021607	1	-1.22520797	1.232323583	1	-0.573560913	1.02035729	1	-0.5052413	0.65142846	1	-0.377162
HLA-A	294	F,L,x	--	11.3711069	2	-2.469204485	3.961004712	2	-0.860121245	3.539422646	2	-0.768575862	3.43297983	2	-0.7454621	25.8773053	5	-4.0256709
HLA-A	297	V,M,x	--	59.9229984	2	-13.01211378	31.52808481	2	-6.846236629	24.05923009	2	-5.224395434	23.4565343	2	-5.0935217	6.0416689	2	-1.3119317
HLA-A	298	I,F,x	--	84.2117654	2	-18.28635252	36.09949734	2	-7.838906246	12.08528556	2	-2.624286416	11.9706852	2	-2.5994013	23.7145901	3	-4.5428354
HLA-A	299	T,A,x	--	137.618095	2	-29.88338958	55.99552235	2	-12.15927318	31.69311511	2	-6.882072504	29.5386245	2	-6.4142308	27.8404192	5	-4.4077278
HLA-A	307	M,R,x	--	84.2117654	2	-18.28635252	36.09949734	2	-7.838906246	12.08528556	2	-2.624286416	11.9706852	2	-2.5994013	23.7145901	3	-4.5428354
HLA-A	31	T	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-A	310	R,x	--	7.68681175	1	-2.254723662	3.55021607	1	-1.22520797	1.232323583	1	-0.573560913	1.02035729	1	-0.5052413	0.65142846	1	-0.377162
HLA-A	311	K,N,x	--	56.8074938	2	-12.33559053	155.4620376	2	-33.75815253	72.48435608	2	-15.73977793	73.8088687	2	-16.027392	2.82583195	3	-0.3775112
HLA-A	314	D,x	--	7.68681175	1	-2.254723662	3.55021607	1	-1.22520797	1.232323583	1	-0.573560913	1.02035729	1	-0.5052413	0.65142846	1	-0.377162
HLA-A	321	S,T,x	--	13.6447467	2	-2.962919105	80.97196321	2	-17.58283841	55.22040611	2	-11.99095883	56.6450146	2	-12.300309	23.7122626	3	-4.5423497
HLA-A	334	V,M,x	--	137.618095	2	-29.88338958	55.99552235	2	-12.15927318	31.69311511	2	-6.882072504	29.5386245	2	-6.4142308	27.8404192	5	-4.4077278
HLA-A	35	R	--	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLA-A	43	Q,R	--	30.8251873	1	-7.549213327	35.42661134	1	-8.577010548	8.146972988	1	-2.365189327	8.24035725	1	-2.3875439	4.15522355	1	-1.381886
HLA-A	44	R,K	--	26.3546834	1	-6.546484276	129.239652	1	-29.22108942	71.26660337	1	-16.50574291	72.9062623	1	-16.866601	13.1229958	1	-3.5350736
HLA-A	56	G,R	--	3.99325805	1	-1.340248709	5.017327833	1	-1.600415098	40.31281452	1	-9.664772835	40.0213509	1	-9.5999768	10.2570936	1	-2.8659504
HLA-A	62	G,Q,E,R,L	--	171.202359	4	-35.23859606	275.8547558	4	-57.7583113	223.450915	4	-46.46972767	216.78049	4	-45.034307	NA	NA	NA
HLA-A	63	E,N,Q	--	77.9566292	2	-16.92806694	20.63336671	2	-4.480478652	56.70106361	2	-12.31247952	51.2719548	2	-11.133564	0	0	0
HLA-A	65	R,G	--	48.3852085	1	-11.45568416	150.3342873	1	-33.83410699	70.54828219	1	-16.34761972	71.7704147	1	-16.616634	0	0	0
HLA-A	66	K,N	--	135.240884	1	-30.53395261	208.3623873	1	-46.504847	133.7361382	1	-30.20480658	131.807315	1	-29.782859	0	0	0
HLA-A	67	V,M	--	26.5065229	1	-6.58062302	129.0876456	1	-29.1878299	71.14113778	1	-16.47812584	72.7694299	1	-16.836491	13.0570699	1	-3.5197893
HLA-A	70	H,Q	--	187.155672	1	-41.87678948	2.516369289	1	-0.948192752	0.002949511	1	-0.019229373	0.01743033	1	-0.0481938	41.9533873	2	-9.1100623
HLA-A	73	T,I	--	10.9421439	1	-3.026865971	39.1483245	1	-9.40582829	39.60490177	1	-9.50737654	36.8434706	1	-8.8927762	17.6526331	2	-3.8332206
HLA-A	74	H,D	--	60.2323649	1	-14.07419978	48.47702948	1	-11.47601906	42.21114332	1	-10.08654732	40.3775447	1	-9.6791617	1.16210037	1	-0.5512467
HLA-A	76	V,A,E	--	24.7716997	2	-5.379106239	142.7170832	2	-30.99062085	35.55376575	2	-7.720402139	37.1818963	2	-8.0739462	23.6930712	4	-4.036099
HLA-A	77	D,N,S	--	122.031838	2	-26.49887695	30.93230773	2	-6.71686528	39.75980732	2	-8.633732461	37.0285664	2	-8.040651	24.1295412	4	-4.1235615
HLA-A	79	G,R	--	0.75459491	1	-0.414510685	52.5823908	1	-12.38450038	11.48294439	1	-3.153429297	12.8801318	1	-3.4787457	9.93852246	2	-2.1581227
HLA-A	80	T,I	--	0.75459491	1	-0.414510685	52.5823908	1	-12.38450038	11.48294439	1	-3.153429297	12.8801318	1	-3.4787457	9.93852246	2	-2.1581227
HLA-A	81	L,A	--	0.75459491	1	-0.414510685	52.5823908	1	-12.38450038	11.48294439	1	-3.153429297	12.8801318	1	-3.4787457	9.93852246	2	-2.1581227
HLA-A	82	R,L	--	0.75459491	1	-0.414510685	52.5823908	1	-12.38450038	11.48294439	1	-3.153429297	12.8801318	1	-3.4787457	9.93852246	2	-2.1581227
HLA-A	83	G,R	--	0.75459491	1	-0.414510685	52.5823908	1	-12.38450038	11.48294439	1	-3.153429297	12.8801318	1	-3.4787457	9.93852246	2	-2.1581227
HLA-A	9	F,S,Y,T	--	191.951369	3	-40.63592934	175.0746298	3	-36.99096144	72.78477991	3	-14.96620533	71.58225	3	-14.708601	37.2488565	7	-5.375926

HLA-A	90	A,D	--	13.3914799	1	-3.597274685	220.3044902	1	-49.11003327	150.4498041	1	-33.85935579	151.209027	1	-34.025298	35.2494965	2	-7.6543309
HLA-A	95	V,I,L	--	150.706259	2	-32.72544835	275.628459	2	-59.85195939	153.2624914	2	-33.28052715	152.489757	2	-33.11273	5.43529762	3	-0.8460018
HLA-A	97	R,I,M	--	16.2396512	2	-3.526395457	75.90495609	2	-16.48255179	51.98197196	2	-11.28774179	53.2715659	2	-11.567774	35.6120821	5	-5.9448028
HLA-A	99	Y,F	--	48.3852085	1	-11.45568416	150.3342873	1	-33.83410699	70.54828219	1	-16.34761972	71.7704147	1	-16.616634	0	0	0
HLA-A			HLA-A*01	26.5065229	1	-6.58062302	130.2461776	1	-29.44131325	72.09115218	1	-16.68722408	73.7789756	1	-17.058626	14.2959535	1	-3.8063182
HLA-A			HLA-A*0101	26.5065229	1	-6.58062302	130.2461776	1	-29.44131325	72.09115218	1	-16.68722408	73.7789756	1	-17.058626	14.2959535	1	-3.8063182
HLA-A			HLA-A*02	60.2323649	1	-14.07419978	47.87462201	1	-11.34259515	41.73726432	1	-9.981299148	39.8682212	1	-9.5659299	0.01564634	1	-0.0455375
HLA-A			HLA-A*0201	37.247022	1	-8.982658583	30.93631314	1	-7.574081489	33.10862812	1	-8.059726975	31.8666104	1	-7.7821701	3.13055141	1	-1.1144254
HLA-A			HLA-A*0202	7.68681175	1	-2.254723662	3.578865186	1	-1.232702252	3.29946359	1	-1.15925103	3.07123446	1	-1.098602	2.21064918	1	-0.8630862
HLA-A			HLA-A*0205	25.0162225	1	-6.2452697	32.4957675	1	-7.922805124	7.087996296	1	-2.110127296	6.96042251	1	-2.0791864	3.37626703	1	-1.1795246
HLA-A			HLA-A*0206	13.5853598	1	-3.642148167	0.106298631	1	-0.128194747	0.167085939	1	-0.165760734	0.02513809	1	-0.0584769	0.16297753	1	-0.1634038
HLA-A			HLA-A*03	27.0099339	1	-6.69376259	8.103951521	1	-2.354883781	10.42645386	1	-2.905797883	12.5452361	1	-3.4009714	96.6609923	1	-22.084736
HLA-A			HLA-A*0301	27.6533832	1	-6.838278619	7.646096668	1	-2.244923634	9.751561391	1	-2.74673357	11.9759094	1	-3.2684696	92.90021	1	-21.259648
HLA-A			HLA-A*0302	0.01405504	1	-0.0430498	0.478082836	1	-0.310431886	0.749571205	1	-0.412724643	0.55287633	1	-0.3399462	2.23134477	1	-0.8689074
HLA-A			HLA-A*11	117.858753	1	-26.73005376	47.39774374	1	-11.23695144	36.85368245	1	-8.895051002	40.986998	1	-9.8146128	12.6127338	1	-3.4166564
HLA-A			HLA-A*1101	117.858753	1	-26.73005376	47.39774374	1	-11.23695144	36.85368245	1	-8.895051002	40.986998	1	-9.8146128	12.6127338	1	-3.4166564
HLA-A			HLA-A*23	50.1856545	1	-11.85428606	13.76811721	1	-3.684414817	9.623136397	1	-2.716379231	9.2301898	1	-2.6233191	27.9342182	1	-6.9013201
HLA-A			HLA-A*2301	50.1856545	1	-11.85428606	13.76811721	1	-3.684414817	9.623136397	1	-2.716379231	9.2301898	1	-2.6233191	27.9342182	1	-6.9013201
HLA-A			HLA-A*24	100.506133	1	-22.92800412	212.0417987	1	-47.30758678	104.8393105	1	-23.87793709	105.851349	1	-24.099747	29.1687855	1	-7.1782285
HLA-A			HLA-A*2402	100.506133	1	-22.92800412	212.0417987	1	-47.30758678	104.8393105	1	-23.87793709	105.851349	1	-24.099747	29.1687855	1	-7.1782285
HLA-A			HLA-A*25	19.4731579	1	-4.991300466	4.475937156	1	-1.463752926	15.78493641	1	-4.148954145	13.191083	1	-3.5508545	4.16014017	1	-1.3831468
HLA-A			HLA-A*2501	19.4731579	1	-4.991300466	4.475937156	1	-1.463752926	15.78493641	1	-4.148954145	13.191083	1	-3.5508545	4.16014017	1	-1.3831468
HLA-A			HLA-A*26	18.5948147	1	-4.791398306	6.50955519	1	-1.969415075	5.087041186	1	-1.617887725	4.00326807	1	-1.3428281	0.0162012	1	-0.0463777
HLA-A			HLA-A*2601	18.5948147	1	-4.791398306	6.50955519	1	-1.969415075	5.087041186	1	-1.617887725	4.00326807	1	-1.3428281	0.0162012	1	-0.0463777
HLA-A			HLA-A*29	18.1091841	1	-4.680700473	2.971573174	1	-1.071914556	33.81015305	1	-8.21637559	30.6658855	1	-7.5135598	0	0	0
HLA-A			HLA-A*2901	0.88711454	1	-0.460597122	6.183909791	1	-1.889689455	5.266788649	1	-1.662818867	5.55424789	1	-1.7343358	1.73978079	1	-0.7277716
HLA-A			HLA-A*2902	20.1497809	1	-5.145035725	1.664158455	1	-0.705439448	29.73698433	1	-7.30555509	26.6253094	1	-6.6073259	1.73978079	1	-0.7277716
HLA-A			HLA-A*30	28.5007956	1	-7.028445867	9.724403231	1	-2.740316901	3.40019644	1	-1.185827977	4.90752512	1	-1.5728398	0.00113223	1	-0.0118169
HLA-A			HLA-A*3001	15.8989153	1	-4.175113016	1.448765814	1	-0.640684292	15.45676917	1	-4.073585208	13.6579333	1	-3.6589361	4.84235669	1	-1.556441
HLA-A			HLA-A*3002	105.178684	1	-23.95232015	23.82597807	1	-5.97695485	0.43750399	1	-0.293854566	0.0017776	1	-0.0148566	2.42101948	1	-0.9218442
HLA-A			HLA-A*3004	1.10267399	1	-0.532125593	0.0000402	1	-0.002203011	0.030937117	1	-0.065309314	0.03649904	1	-0.071354	0.42478329	1	-0.2885641
HLA-A			HLA-A*31	8.26800773	1	-2.394159054	44.45786615	1	-10.58520936	45.66294355	1	-10.85246314	40.2585571	1	-9.6527115	16.6506194	1	-4.3474091
HLA-A			HLA-A*3101	8.26800773	1	-2.394159054	44.45786615	1	-10.58520936	45.66294355	1	-10.85246314	40.2585571	1	-9.6527115	16.6506194	1	-4.3474091
HLA-A			HLA-A*32	52.4411289	1	-12.35326198	28.74868355	1	-7.084041604	22.73723338	1	-5.73110867	22.4599444	1	-5.6684275	5.53191124	1	-1.7287929
HLA-A			HLA-A*3201	52.4411289	1	-12.35326198	28.74868355	1	-7.084041604	22.73723338	1	-5.73110867	22.4599444	1	-5.6684275	5.53191124	1	-1.7287929
HLA-A			HLA-A*33	2.56059931	1	-0.960359692	0.756323765	1	-0.415124614	0.367357059	1	-0.264043247	0.88467977	1	-0.4597668	0.22966009	1	-0.1994369
HLA-A			HLA-A*3301	0.76745792	1	-0.419069764	0.000150369	1	-0.004269984	0.795554328	1	-0.428960141	0.36978041	1	-0.265101	3.55987394	1	-1.2277353
HLA-A			HLA-A*3303	3.04869745	1	-1.092578301	3.130503937	1	-1.114412731	7.80435776	1	-2.282992368	8.84010062	1	-2.5306451	5.19206462	1	-1.6441608
HLA-A			HLA-A*34	5.23598072	1	-1.65512984	3.254531216	1	-1.147359609	4.569463375	1	-1.487492251	5.6908353	1	-1.7681805	7.50536575	1	-2.2110158
HLA-A			HLA-A*3402	5.23598072	1	-1.65512984	3.254531216	1	-1.147359609	4.569463375	1	-1.487492251	5.6908353	1	-1.7681805	7.50536575	1	-2.2110158
HLA-A			HLA-A*66	22.5983444	1	-5.699716371	9.507807294	1	-2.689095428	8.930024401	1	-2.552035243	9.04663942	1	-2.5797502	5.32308635	1	-1.6768571
HLA-A			HLA-A*6601	22.5983444	1	-5.699716371	9.507807294	1	-2.689095428	8.930024401	1	-2.552035243	9.04663942	1	-2.5797502	5.32308635	1	-1.6768571
HLA-A			HLA-A*68	10.4636811	1	-2.914550882	3.23680772	1	-1.142662667	3.365276523	1	-1.176627477	2.95353853	1	-1.0670711	2.18157333	1	-0.8548918
HLA-A			HLA-A*6801	3.61810008	1	-1.242952547	2.895652985	1	-1.051495199	3.692878063	1	-1.2624476	3.33659509	1	-1.1690607	1.32867293	1	-0.6037284
HLA-A			HLA-A*6802	14.6766244	1	-3.894083929	0.321765572	1	-0.243707411	0.007842991	1	-0.031782812	0.00014299	1	-0.0041633	0.65844162	1	-0.3797487

Supplementary Table 6A. Haplotypes defined by top three amino acid positions (with at least 4 counts in the datasets)

DQβ1#57	DRβ1#13	DRβ1#71	OR.regressio	OR.low	OR.high	CtrlFreq	CaseFreq	P
A	G	R	4.45506887	1.55E+00	1.28E+01	4.66E-05	5.56E-04	0.1566434
A	H	K	2.12696421	2.04E+00	2.22E+00	0.05043778	2.48E-01	6.5823E-73
A	H	E	1.32743553	1.18E+00	1.50E+00	0.00479695	1.55E-02	0.01952865
A	S	K	1	1.00E+00	1.00E+00	0.14539866	3.32E-01	NA
A	H	R	0.88520108	8.46E-01	9.26E-01	0.05374441	1.07E-01	0.00750154
A	S	R	0.65235867	3.70E-01	1.15E+00	0.00027943	4.32E-04	0.4510501
A	S	E	0.52732962	3.37E-01	8.24E-01	0.0005123	6.18E-04	0.1520597
D	F	R	0.48059572	4.37E-01	5.29E-01	0.01220194	1.38E-02	2.4498E-14
A	F	R	0.4592914	3.15E-01	6.69E-01	0.00074516	8.65E-04	0.03858478
S	R	A	0.4193292	2.45E-01	7.18E-01	0.00041915	3.71E-04	0.1059262
S	R	R	0.37333811	3.29E-01	4.23E-01	0.00796386	6.98E-03	5.4459E-15
V	F	R	0.34841626	3.34E-01	3.63E-01	0.10627794	8.54E-02	6.009E-140
V	S	E	0.33521011	3.15E-01	3.57E-01	0.04005216	3.04E-02	5.0701E-69
D	G	R	0.32383004	3.04E-01	3.45E-01	0.03902757	2.94E-02	2.6324E-71
S	F	R	0.28593292	8.78E-02	9.31E-01	0.00013972	6.18E-05	0.2891969
D	H	K	0.27424326	2.60E-01	2.89E-01	0.06832154	4.18E-02	5.078E-132
V	F	E	0.23674079	2.10E-01	2.67E-01	0.01271423	6.49E-03	1.4495E-33
A	Y	R	0.18334782	1.74E-01	1.93E-01	0.10320417	4.26E-02	1.055E-251
V	S	R	0.13582202	4.40E-02	4.19E-01	0.00018629	6.18E-05	0.07632222
D	S	E	0.11298365	1.05E-01	1.22E-01	0.05770306	1.46E-02	1.749E-183
D	F	E	0.07579911	5.48E-02	1.05E-01	0.00414493	6.79E-04	1.7044E-15
D	H	R	0.06223769	5.24E-02	7.39E-02	0.01709203	2.41E-03	5.8672E-59
D	S	K	0.06018088	4.82E-02	7.52E-02	0.01019933	1.42E-03	1.2931E-36
V	R	A	0.05775748	2.00E-02	1.67E-01	0.00041915	6.18E-05	0.00721181
D	S	R	0.05459938	5.02E-02	5.94E-02	0.0826658	1.03E-02	2.751E-257
D	Y	R	0.02908179	2.48E-02	3.41E-02	0.04051788	2.66E-03	2.971E-110
D	R	A	0.01788334	1.60E-02	2.00E-02	0.14008942	5.50E-03	2.668E-291
S	S	R	2.0647E-06	9.02E-69	4.73E+56	0.00023286	0.00E+00	0.9273609
V	S	K	1.763E-06	7.96E-64	3.90E+51	0.00027943	0.00E+00	0.9200792

Supplementary Table 6B. All DRB1-DQA1-DQB1 Haplotypes (with at least 4 counts in the dataset)

Haplotype	OR	OR.low	OR.high	CtrlFreq	CaseFreq	P
RQRTVRHVTRSHSKHVVYNRGKQLYADFFVNNHFYDYRHESTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTSRADRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	1	1	1	0.1454537	0.33191042	NA
TQRTVRQMALSHSKQVVYTAAAQIYADFFVSNYFYDFRHERKPQWRSATLKLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYYTLRMGFSLLSMAAVDA	0.013806712	0.01214986	0.015689507	0.13269788	0.00414501	4.755E-246
TQRMVRQVARSHAEHGVVTQGRDISAVYFVFNYFLEFQHKYKGQWQAAALKMYSFTEERVKLLFHRLRxFTILILSTHSFDIEAVLRQHHISTSRAGRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	0.183762982	0.17478754	0.193199322	0.10321465	0.04262559	6.907E-251
TQRTVRQVARSHSKEGVYTAARQLYADYFVSNYICELRHEFKLQWRAATLKLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	0.372442832	0.35655961	0.389033584	0.0917204	0.07838406	1.055E-113
TQRTLRQVTRNHAEYGVYTAAKQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.272655803	0.25857009	0.287508837	0.0683581	0.04157387	1.49E-132
TQRTLRQVTRNHAEYGVYTAAKQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	2.133726959	2.04618609	2.225013036	0.05036912	0.24845335	3.7659E-73
RQRTVRHVTRSHSKHVVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRLCFFTQEKARWEFSKFGGGRMAIMYTHAFDIQAVFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYHTLRMGYSLLSMAAVDA	0.10584913	0.09739346	0.115038918	0.04962153	0.01175452	2.983E-160
TQRTLRQVTRNHAEYVVYTAARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	0.752563232	0.7160733	0.790912637	0.04532287	0.07603316	1.0688E-08
RQRTVRHVTRSHSKHGVYTAARDFYEDFFVYNYFYDFRHESTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.068579006	0.06166271	0.076271055	0.04186525	0.00655778	3.288E-140
TQRMVRQVARSHAEHGVVTQGRDISAVYFVFNYFLEFQHKYKGQWQAAALKMYSFTEERVKLLFHRLRxFTILILSTHSFDIEAVLRQHHISINRTDRQAVTTLELQTLETRVEDPPLPYVGAYYTLRMGYSVPTMAAVGA	0.025635828	0.02162314	0.030393161	0.03962247	0.00228904	9.513E-103
RQRTVRHVTRSHSKHGVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADQQGVIGYGVETLETRVEVPRQPYVGAYHTLRMGYSxxxxxxxxx	0.416809535	0.38975881	0.445737685	0.02934305	0.02814897	7.0702E-39
RQRTVRHVTRSYSKHVVYTEARRLHAAYFVFNHFYDFRHESTSYERAVALRLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEDPRQPYVGVYHTGRLGYSLSSIAAVDS	0.01963275	0.01519896	0.025359951	0.02280161	0.00098985	3.2586E-53
xxxxxRHVTRSHSKHGVYTLARDFYASYFVYNYFYDFRYEGTSYERxxxxxLYSYTQGRVCLVLRQFRxFTITILSTHSFDIEAVFRQHHISINRTDRQAVTTLELQTVSDEIDDLRLPYVGAYYTGRMGFSVPTMAAVGA	0.502973682	0.46598987	0.542892753	0.01976451	0.0231997	2.2974E-19
RQRTVRHVTRSHSKHVVYTAARDFYEDFFVYNYFYDFRHESTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.062888886	0.05328405	0.074225064	0.01756845	0.00259837	1.5017E-62
RQRTVRHVTRSHSKHVAYTAARDISAVFFLLNHFHELRYEGTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.151171375	0.13373773	0.170877618	0.01611999	0.00556793	1.2202E-53
TQRTVRQVARSHSKEGVYTAAEDIYADYFVSNYICELRHEFKLQWRAATLKLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	0.235908553	0.20927497	0.265931687	0.01266237	0.00643405	1.7924E-33
TQRMVRQVARSHAEHGVVTEARRFSAVYFVNNYIGHYRHEFKDQKQAAALKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEDPPLPYVGAYYTLRMGYSVPTMAAVGA	0.480983816	0.43683	0.529600598	0.0121484	0.01373422	2.9326E-14
TQRTLRQVTRNHAEYGVYTEARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.0372055	0.02868018	0.048265008	0.01200822	0.00098985	1.1672E-36
RQRTVRHVTRSHSKHGVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADQQGVIGYGVETLETRVEVPRQPYVGAYYTLRMGYSLLSMAAVDA	0.096333876	0.0798496	0.116221198	0.01046631	0.00210344	1.1159E-35
xxxTVRHVTRSHSKHGVYTAAKDIYASYFVYNYFYDFRHESTSYERxxxxxMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.059822033	0.04740481	0.075491822	0.0092982	0.00129918	9.8594E-34
TQRTVRQVARSHSKEVAYTAARQLYADYFVSNYICELRHEFKLQWRAATLKLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	0.267142761	0.23442073	0.304432349	0.00915802	0.00575353	5.4181E-24
TQRTVRQMALSHSKQGVYTAARDFYADYFVSNYFYDFRHERKPQWRAATLKLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQRQRVSTSRADRHSIIGYAVERVSAGVESPRQPYVGVYHTGRLGYSLSSIAAVDS	0.379294652	0.33429586	0.430350621	0.00794318	0.00699084	1.6349E-14
TPRMVQQVTRNHSKQGVYTAARRLYADYYAYNHVRELRHEFKVEERAVALRLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	0.097140178	0.07637738	0.123547231	0.00560695	0.00129918	3.1332E-22
RQRTVRHVTRSHSKHVVYTAAEDFYEDFFVYNYFYDFRHESTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.148517424	0.11914059	0.185137781	0.00476591	0.00167038	5.0265E-18
TQRTLRQVTRNHAEYVVYTAAEDIYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	1.341711656	1.18780591	1.515559195	0.00476591	0.01552833	0.01583954
TQRTVRQMALSHSKQGVYTAAAQIYADFFVSNYFYDFRHERKPQWRSATLKLCFFTQEKARWEFSKFGGGRMAIMYTHAFDIQAVFQQQRINTSHADRQGVIGFAVETLETRIDDPRQPYVGVDYTYRMALPVPTMAPAGA	0.079794502	0.05914764	0.107648629	0.00434539	0.00080426	3.0652E-17
TQRTVRQVARSHSKEGVYTAAEDIYADYFVSNYICELRHEFKLQWRAATLKMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.068719579	0.04902314	0.096329617	0.00415849	0.00061866	2.2215E-15
TQRTLRQVTRNHAEYGVYTAARQLYASYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	2.339368766	2.06871526	2.64543233	0.00415849	0.02190052	4.7712E-12
TQRTLRQVTRNHAEYGVYTAARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.131367276	0.10130869	0.170344341	0.00373797	0.00117545	5.6277E-15
TQRTVRQMALSHSKQVVYTAAAQIYADFFVSNYFYDFRHERKPQWRSATLKLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYHTLRMGYSLLSMAAVDA	0.067624542	0.04530377	0.100942553	0.00313055	0.00043306	1.7595E-11
TQRTLRQVTRNHAEYVVYTEARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	0.440706891	0.36064727	0.538538847	0.00294365	0.00284583	4.3685E-05
RQRTVRHVTRSHSKHVVYTAAEDIYEDFFVYNYFYDFRHESTSYERxxxxxMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.176974198	0.13220621	0.236901625	0.00242968	0.00098985	2.886E-09
TQSTVRHVTRSHSKHGVYTLARDIYASYFVYNYFYDFRYEGTSYERAVALRLYSFTQGRVCLVLRQFRxFTITILSTHSFDIEAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.026361461	0.0127541	0.054486506	0.00205588	0.00012373	5.508E-07
xxxTVRHVTRSHSKHVVYTLARDFYADYFVYNYFYDFRYEGTSYERxxxxxLYSYTQGRVCLVLRQFRxFTITILSTHSFDIEAVFRQHHISINRTDRQAVTTLELQTVSDEIDDLRLPYVGAYYTGRMGFSVPTMAAVGA	0.308706235	0.19640515	0.485219144	0.00065414	0.00049493	0.00934536
RQRTVRHVTRSHSKHVVYNRGKQLYADFFVNNHFYDYRHESTSYERAVALRLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYYTLRMGFSLLSMAAVDA	0.053401643	0.01876817	0.151945314	0.00060742	6.1866E-05	0.00507988
TQRTLRQVTRNHAEYGVYTAARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRxxxxSTNHTDRQAVTTLELQTLETRVEAPPLPYVEAYYTYRMAYSxxxxxxxxx	1.248275435	0.86931216	1.792441921	0.00051397	0.00167038	0.53993158
RQRTVRHVTRSHSKHVVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRLCFFTQEKARWEFSKFGGGRMAIMYTHAFDIQAVFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYYTLRMGFSLLSMAAVDA	8.10936E-07	1.0425E-82	6.30795E+69	0.00042052	0	0.93603037
TQRTLRQVTRNHAEYGVYTAARQLYASYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISTSRADRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	2.142474397	1.47066898	3.121162272	0.00042052	0.0023509	0.04284901
TQRMVRQVARSHAEHGVVTQGRDISAVYFVFNYFLEFQHKYKGQWQAAALKMYSFTEERVKLLFHRLRxFTILILSTHSFDIEAVFRQHHISINRTDRQAVTTLELQTVSDEIDDLRLPYVGAYYTGRMGFSVPTMAAVGA	0.075942693	0.02615581	0.220497529	0.0003738	6.1866E-05	0.01558951
TQRMVRQVARSHAEHGVVTEARRFSAVYFVNNYIGHYRHEFKDQKQAAALKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISTSRADRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	0.852824105	0.53538283	1.358483903	0.0003738	0.00080426	0.73238873
TQRTLRQVTRNHAEYGVYTAARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	1.757548001	1.15771084	2.668174879	0.0003738	0.00148478	0.1767638
RQRTVRHVTRSHSKHGVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	0.169867072	0.07560678	0.381643308	0.00032707	0.00012373	0.0285243
TQRTVRQMALSHSKQVVYTAAAQIYADFFVSNYFYDFRHERKPQWRSATLKLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQRQRVSTSRADRHSIIGYAVERVSAGVESPRQPYVGVYHTGRLGYSLSSIAAVDS	0.486840316	0.26774366	0.885225417	0.00032707	0.00030933	0.2286283
TQRMVRQVARSHAEHGVVTEARRFSAVYFVNNYIGHYRHEFKDQKQAAALKMYSFTEERVKLLFHRLRxFTILILSTHSFDIEAVLRQHHISTSRAGRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	8.13428E-07	2.313E-101	2.86061E+88	0.00028035	0	0.94864407
TQRTVRQMALSHSKQVVYTAAAQIYADFFVSNYFYDFRHERKPQWRSATLKLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	8.39527E-07	3.805E-100	1.85238E+87	0.00028035	0	0.94810043
TQRTLRQVTRNHAEYGVYTAARQLYASYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTVSDEIDDLRLPYVGAYYTGRMGFSVPTMAAVGA	0.154972987	0.06829894	0.351639815	0.00028035	0.00012373	0.02287167
TQRTLRQVTRNHAEYVVYTAARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTVSDEIDDLRLPYVGAYYTGRMGFSVPTMAAVGA	0.155743923	0.05249814	0.462038628	0.00028035	6.1866E-05	0.08726117
RQRTVRHVTRSHSKHVVYTAARDFYEDFFVYNYFYDFRHESTSYERAVALRLCFFTQEKARWEFSKFGGGRMAIMYTHAFDIQAVFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYHTLRMGYSLLSMAAVDA	0.174865612	0.07654763	0.39946349	0.00028035	0.00012373	0.03478993
TQRMVRQVARSHAEHGVVTQGRDISAVYFVFNYFLEFQHKYKGQWQAAALKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEDPPLPYVGAYYTLRMGYSVPTMAAVGA	7.79139E-07	2.176E-106	2.78994E+93	0.00023362	0	0.95107448
TQRTLRQVTRNHAEYVVYTEARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	8.67569E-07	6.972E-109	1.07963E+96	0.00023362	0	0.95265493
xxxTVRHVTRSHSKHVVYTLARDFYADYFVYNYFYDFRYEGTSYERxxxxxLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYYTLRMGFSLLSMAAVDA	0.132662148	0.04411068	0.398979238	0.00023362	6.1866E-05	0.0665832
TQRMVRQVARSHAEHGVVTQGRDISAVYFVFNYFLEFQHKYKGQWQAAALKMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.496421488	0.24651303	0.999680616	0.00023362	0.00024746	0.31708972
RQRTVRHVTRSHSKHVVYNRGKQLYADFFVNNHFYDYRHESTSYERAVALRLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	7.4433E-07	3.315E-170	1.6714E+157	0.0001869	0	0.97007384
RQRTVRHVTRSYSKHVVYTEARRLHAAYFVFNHFYDFRHESTSYERAVALRLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRQSIIGYAVERVSAGVEVPRQPYVGVYHTGRLGYSLSSIAAVDS	0.136463972	0.04425862	0.420763568	0.0001869	6.1866E-05	0.07692616
RQRTVRHVTRSHSKHGVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQQQRVSTSRADRQGVIGFAVETLETGVEDPRQPYVGAYYTLRMGFSLLSMAAVDA	0.140631721	0.04569504	0.432810265	0.0001869	6.1866E-05	0.08099099
RQRTVRHVTRSHSKHVVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRMYSFTEERVKLLFHRLRxFTILILSTHSFDIEAVLRQHHISTSRADRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	0.611366032	0.27769611	1.345962072	0.0001869	0.0001856	0.53294528
RQRTVRHVTRSHSKHGVYTAARDFYEDFFVYNYFYDFRHESTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	0.916945975	0.48751985	1.724627058	0.0001869	0.00043306	0.89082883
RQRTVRHVTRSHSKHGVYTAARDFYEDFFVYNYFYDFRHESTSYERAVALRLCFYTQERARWEFSKFGGGRMAIMYTQSFDIQAMFQRQRVSTSRADRHSIIGYAVERVSAGVESPRQPYVGVYHTGRLGYSLSSIAAVDS	8.17927E-07	3.79E-139	1.765E+126	0.00014017	0	0.96331073
TQRTLRQVTRNHAEYGVYTAAKQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEDPPLPYVGAYYTLRMGYSVPTMAAVGA	0.240735992	0.07499474	0.772771754	0.00014017	6.1866E-05	0.22207854
RQRTVRHVTRSHSKHVVYNRGKQLYADFFVNNHFYDYRHESTSYERAVALRMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTNHTDRQAVTTLELQTLETRVEDPPLPYVEAYYTYRMAYSVPTMAAAGA	0.262667221	0.08157522	0.845772409	0.00014017	6.1866E-05	0.252937
TQRTVRQVARSHSKEGVYTAARQLYADYFVSNYICELRHEFKLQWRAATLKLCFYTEERARWEFSKFGGGRMAIMYTQSFDIQAVFQRQRVSTSRADRHSIIGYAVERVSAGVESPRQPYVGVYHTGRLGYSLSSIAAVDS	0.28666943	0.08803023	0.933535687	0.00014017	6.1866E-05	0.28994022
RQRTVRHVTRSHSKHVVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEDPPLPYVGAYYTLRMGYSVPTMAAVGA	0.543684221	0.23799616	1.242005444	0.00014017	0.0001856	0.46072448
RQRTVRHVTRSHSKHVVYTAAEDIYEDFFVYNYFYDFRHESTSYERxxxxxMYSYTQGRVCLVLRQFRxFTILSLSIHSLESKAVFRQHHISTSRADRQAVTTLELQRVAKRIDAPLLLFEGVISSLRMGYSVPTMSAAGA	0.822821415	0.3294278	2.055185034	9.3449E-05	0.0001856	0.83129311
TQRTLRQVTRNHAEYGVYTEARQLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	1.131985389	0.44854836	2.856750864	9.3449E-05	0.0001856	0.89346435
RQRTVRHVTRSHSKHGVYTAAEDIYADFFVNNHFYDFRHESTSYERAVALRMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	1.277575781	0.40030136	4.077427783	4.6725E-05	0.0001856	0.83282108
xxxxxRHVTRSHSKHGVYTLARDFYASYFVYNYFYDFRYEGTSYERxxxxxMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	4.030805871	1.39445253	11.6514515	4.6725E-05	0.00049493	0.18909931
RQRTVRHVTRSHSKHGVYTAARDLYADYFVYHYFYDFRHEHKVQERAAAFKMYSYSEERVQLLFRRFRRFTILIVSTHSFDIETVLRQHHISINRTDRQAVTTLELQTLETRVEAPPLPYVGAYYTLRMGYSVPTMAAVGA	431285.7966	4.959E-99	3.7506E+109	0	0.00030933	0.95676621

Supplementary Table 7A. Top 1000 combinations of 2AA's

AA1	AA2	DeltaDeviance	df	P	Residues
AA_DQB1_57	AA_DRB1_13	9661.011751	19	-2071.624	aa1 ADVS aa2 SRHFGY
AA_DQB1_57	AA_DRB1_11	9404.827094	18	-2017.4585	aa1 ADVS aa2 SPVLGD
AA_DQB1_57	AA_DRB1_37	9324.046636	15	-2004.1168	aa1 ADVS aa2 NSYFL
AA_DQA1_47	AA_DQB1_57	9245.520421	10	-1994.3595	aa1 CRQK aa2 ADVS
AA_DQB1_57	AA_DRB1_9	9111.50804	9	-1966.7992	aa1 ADVS aa2 EWK
AA_DQA1_52	AA_DQB1_57	9032.194409	8	-1951.1297	aa1 RSH aa2 ADVS
AA_DQB1_57	AA_DRB1_74	8768.560717	15	-1883.6679	aa1 ADVS aa2 RALQE
AA_DQB1_57	AA_DRB1_181	8564.448428	8	-1849.6292	aa1 ADVS aa2 TxM
AA_DQB1_57	AA_DRB1_67	8533.010207	11	-1838.3027	aa1 ADVS aa2 LIF
AA_DQB1_57	AA_DRB1_57	8507.090134	12	-1831.2261	aa1 ADVS aa2 DSVA
AA_DQB1_57	AA_DRB1_140	8501.312677	7	-1837.4868	aa1 ADVS aa2 TA
AA_DQB1_57	AA_DRB1_30	8477.663278	13	-1823.41	aa1 ADVS aa2 YCLRGH
AA_DQB1_26	AA_DRB1_13	8421.998337	17	-1805.7772	aa1 LYG aa2 SRHFGY
AA_DQB1_57	AA_DRB1_28	8365.142172	9	-1804.8578	aa1 ADVS aa2 DEH
AA_DQA1_47	AA_DQB1_26	8342.880208	11	-1797.0605	aa1 CRQK aa2 LYG
AA_DQB1_57	AA_DRB1_71	8236.643941	13	-1771.1422	aa1 ADVS aa2 KAER
AA_DQA1_54	AA_DQB1_57	8236.287389	5	-1783.1885	aa1 FL aa2 ADVS
AA_DQB1_57	AA_DRB1_25	8219.411599	5	-1779.5253	aa1 ADVS aa2 RQ
AA_DQB1_57	AA_DRB1_14	8219.411599	5	-1779.5253	aa1 ADVS aa2 EK
AA_DQB1_57	AA_DRB1_60	8193.263316	9	-1767.5663	aa1 ADVS aa2 YSH
AA_DQA1_25	AA_DQB1_57	8178.191553	5	-1770.5778	aa1 YF aa2 ADVS
AA_DQB1_26	AA_DRB1_37	8159.262554	12	-1755.7869	aa1 LYG aa2 NSYFL
AA_DQB1_71	AA_DRB1_11	8130.699637	20	-1738.6359	aa1 KTAD aa2 SPVLGD
AA_DQB1_26	AA_DRB1_11	8119.857477	15	-1743.0207	aa1 LYG aa2 SPVLGD
AA_DQB1_57	AA_DRB1_4	8100.501681	5	-1753.7138	aa1 ADVS aa2 RQ
AA_DQB1_57	AA_DRB1_78	8099.534066	5	-1753.5038	aa1 ADVS aa2 YV
AA_DQB1_135	AA_DQB1_57	8099.27327	4	-1755.1273	aa1 DG aa2 ADVS
AA_DQB1_71	AA_DRB1_13	8063.92442	21	-1722.8598	aa1 KTAD aa2 SRHFGY
AA_DQB1_74	AA_DRB1_13	8059.423028	16	-1728.5462	aa1 AES aa2 SRHFGY
AA_DQA1_52	AA_DQB1_26	8049.653735	8	-1737.9237	aa1 RSH aa2 LYG
AA_DQB1_185	AA_DRB1_74	8048.663141	9	-1736.1938	aa1 TI aa2 RALQE
AA_DQB1_30	AA_DRB1_13	7927.16276	16	-1699.8766	aa1 SYH aa2 SRHFGY
AA_DQB1_-10	AA_DRB1_13	7924.307845	14	-1702.0107	aa1 SAx aa2 SRHFGY
AA_DQB1_57	AA_DRB1_70	7901.711484	11	-1701.3681	aa1 ADVS aa2 QDR
AA_DQB1_74	AA_DRB1_11	7813.522727	16	-1675.2438	aa1 AES aa2 SPVLGD
AA_DQB1_26	AA_DRB1_67	7803.595344	8	-1684.5332	aa1 LYG aa2 LIF
AA_DRB1_74	AA_DRB1_13	7788.515928	10	-1678.2728	aa1 RALQE aa2 SRHFGY
AA_DQB1_57	AA_DRB1_180	7781.584219	8	-1679.7572	aa1 ADVS aa2 VLx
AA_DQB1_57	AA_DRB1_96	7764.845381	14	-1667.4368	aa1 ADVS aa2 HQYE
AA_DQA1_56	AA_DQB1_57	7761.859123	8	-1675.4773	aa1 xGR aa2 ADVS
AA_DQA1_76	AA_DQB1_57	7761.859123	8	-1675.4773	aa1 LMV aa2 ADVS
AA_DQB1_30	AA_DRB1_11	7735.351279	16	-1658.2997	aa1 SYH aa2 SPVLGD

AA_DRB1_70	AA_DRB1_13	7728.548278	11	-1663.8095	aa1 QDR aa2 SRHFGY
AA_DQB1_-18	AA_DRB1_37	7724.607689	11	-1662.9548	aa1 AVx aa2 NSYFL
AA_DQB1_-18	AA_DRB1_13	7712.879107	15	-1654.7916	aa1 AVx aa2 SRHFGY
AA_DRB1_71	AA_DRB1_13	7704.333349	11	-1658.5574	aa1 KAER aa2 SRHFGY
AA_DQB1_55	AA_DRB1_13	7701.634198	16	-1650.9914	aa1 LRP aa2 SRHFGY
AA_DQA1_47	AA_DQB1_167	7697.122294	7	-1662.9669	aa1 CRQK aa2 RH
AA_DQA1_47	AA_DQB1_13	7694.046593	7	-1662.2995	aa1 CRQK aa2 GA
AA_DQA1_47	AA_DQB1_45	7685.605546	6	-1662.0395	aa1 CRQK aa2 GE
AA_DRB1_74	AA_DRB1_11	7684.834392	10	-1655.7819	aa1 RALQE aa2 SPVLGD
AA_DQB1_57	AA_DRB1_-24	7677.184535	9	-1655.6001	aa1 ADVS aa2 LFx
AA_DQB1_26	AA_DRB1_71	7675.602012	11	-1652.3258	aa1 LYG aa2 KAER
AA_DRB1_70	AA_DRB1_11	7652.002895	11	-1647.2073	aa1 QDR aa2 SPVLGD
AA_DQB1_167	AA_DRB1_71	7627.834085	7	-1647.931	aa1 RH aa2 KAER
AA_DQB1_13	AA_DRB1_71	7626.192522	7	-1647.5748	aa1 GA aa2 KAER
AA_DQB1_45	AA_DRB1_71	7609.986933	7	-1644.0581	aa1 GE aa2 KAER
AA_DQB1_55	AA_DRB1_11	7598.06204	16	-1628.5421	aa1 LRP aa2 SPVLGD
AA_DQB1_67	AA_DRB1_13	7593.07385	11	-1634.4261	aa1 IV aa2 SRHFGY
AA_DQB1_66	AA_DRB1_13	7593.07385	11	-1634.4261	aa1 DE aa2 SRHFGY
AA_DQB1_140	AA_DQB1_57	7575.150444	5	-1639.6789	aa1 AT aa2 ADVS
AA_DQB1_182	AA_DQB1_57	7574.970429	5	-1639.6399	aa1 SN aa2 ADVS
AA_DRB1_96	AA_DRB1_74	7534.904342	8	-1626.2334	aa1 HQYE aa2 RALQE
AA_DQB1_37	AA_DRB1_13	7508.125843	11	-1616.0019	aa1 IYD aa2 SRHFGY
AA_DQB1_52	AA_DRB1_13	7505.964505	10	-1616.9817	aa1 LP aa2 SRHFGY
AA_DQB1_47	AA_DRB1_13	7503.520838	10	-1616.4517	aa1 FY aa2 SRHFGY
AA_DQB1_46	AA_DRB1_13	7503.520838	10	-1616.4517	aa1 EV aa2 SRHFGY
AA_DQB1_28	AA_DRB1_13	7503.520838	10	-1616.4517	aa1 ST aa2 SRHFGY
AA_DQB1_-10	AA_DRB1_11	7503.185891	15	-1609.3351	aa1 SAx aa2 SPVLGD
AA_DQA1_47	AA_DQB1_30	7490.357445	9	-1615.0685	aa1 CRQK aa2 SYH
AA_DQA1_187	AA_DQB1_57	7476.085635	6	-1616.5669	aa1 AT aa2 ADVS
AA_DQA1_26	AA_DQB1_57	7476.085635	6	-1616.5669	aa1 TS aa2 ADVS
AA_DQB1_87	AA_DRB1_70	7458.645072	7	-1611.2164	aa1 LFY aa2 QDR
AA_DQB1_167	AA_DRB1_13	7437.465104	11	-1600.6766	aa1 RH aa2 SRHFGY
AA_DQB1_13	AA_DRB1_13	7434.444209	11	-1600.0214	aa1 GA aa2 SRHFGY
AA_DQB1_45	AA_DRB1_13	7430.342615	11	-1599.1318	aa1 GE aa2 SRHFGY
AA_DQB1_-5	AA_DRB1_70	7428.904028	9	-1601.7366	aa1 PLSx aa2 QDR
AA_DQB1_185	AA_DRB1_71	7421.53715	7	-1603.1639	aa1 TI aa2 KAER
AA_DQB1_67	AA_DRB1_11	7421.021835	11	-1597.1103	aa1 IV aa2 SPVLGD
AA_DQB1_66	AA_DRB1_11	7421.021835	11	-1597.1103	aa1 DE aa2 SPVLGD
AA_DQB1_71	AA_DQB1_57	7389.861665	7	-1596.2903	aa1 KTAD aa2 ADVS
AA_DQB1_-18	AA_DRB1_71	7382.667329	11	-1588.7918	aa1 AVx aa2 KAER
AA_DQA1_52	AA_DQB1_167	7363.8063	5	-1593.8046	aa1 RSH aa2 RH
AA_DQA1_52	AA_DQB1_13	7361.576811	5	-1593.3206	aa1 RSH aa2 GA
AA_DRB1_26	AA_DRB1_13	7354.631484	8	-1587.1191	aa1 YFL aa2 SRHFGY
AA_DQA1_52	AA_DQB1_45	7353.177516	4	-1593.1566	aa1 RSH aa2 GE

AA_DRB1_96	AA_DRB1_70	7348.239491	9	-1584.2371	aa1 HQYE aa2 QDR
AA_DQB1_125	AA_DRB1_70	7313.373702	7	-1579.6925	aa1 AGS aa2 QDR
AA_DRB1_71	AA_DRB1_11	7302.464427	11	-1571.3973	aa1 KAER aa2 SPVLGD
AA_DRB1_71	AA_DRB1_-24	7290.619552	9	-1571.7371	aa1 KAER aa2 LFx
AA_DQB1_67	AA_DQB1_57	7274.072853	5	-1574.3272	aa1 IV aa2 ADVS
AA_DQB1_66	AA_DQB1_57	7274.072853	5	-1574.3272	aa1 DE aa2 ADVS
AA_DRB1_77	AA_DRB1_13	7267.766167	6	-1571.3554	aa1 NT aa2 SRHFGY
AA_DRB1_73	AA_DRB1_13	7267.766167	6	-1571.3554	aa1 GA aa2 SRHFGY
AA_DQB1_167	AA_DRB1_11	7263.989139	10	-1564.4944	aa1 RH aa2 SPVLGD
AA_DQB1_13	AA_DRB1_11	7261.231498	10	-1563.8962	aa1 GA aa2 SPVLGD
AA_DQB1_45	AA_DRB1_11	7257.128925	10	-1563.0063	aa1 GE aa2 SPVLGD
AA_DQB1_37	AA_DRB1_11	7256.620572	12	-1560.0352	aa1 IYD aa2 SPVLGD
AA_DQB1_75	AA_DRB1_13	7256.520167	11	-1561.433	aa1 VL aa2 SRHFGY

Supplementary Table 7B. Top 100 combinations of 3AA's

AA1	AA2	AA3	DeltaDeviance	df	P	Residues
AA_DQB1_57	AA_DRB1_71	AA_DRB1_13	10148.52492	31	-2161.51987	aa1 ADVS aa2 KAER aa3 SRHFGY
AA_DQB1_57	AA_DRB1_86	AA_DRB1_13	10124.62638	29	-2158.88828	aa1 ADVS aa2 VG aa3 SRHFGY
AA_DQB1_-18	AA_DRB1_71	AA_DRB1_37	10045.15659	25	-2146.85261	aa1 AVx aa2 KAER aa3 NSYFL
AA_DQB1_57	AA_DRB1_74	AA_DRB1_11	9987.049638	31	-2126.55694	aa1 ADVS aa2 RALQE aa3 SPVLGD
AA_DQB1_57	AA_DRB1_74	AA_DRB1_13	9962.368443	31	-2121.21307	aa1 ADVS aa2 RALQE aa3 SRHFGY
AA_DQB1_71	AA_DQB1_-18	AA_DRB1_13	9948.308347	32	-2116.91211	aa1 KTAD aa2 AVx aa3 SRHFGY
AA_DQB1_71	AA_DQB1_-18	AA_DRB1_11	9945.712378	30	-2118.8707	aa1 KTAD aa2 AVx aa3 SPVLGD
AA_DQB1_74	AA_DQB1_-18	AA_DRB1_13	9943.814444	27	-2122.29737	aa1 AES aa2 AVx aa3 SRHFGY
AA_DQB1_57	AA_DRB1_86	AA_DRB1_37	9941.233586	27	-2121.73836	aa1 ADVS aa2 VG aa3 NSYFL
AA_DQB1_75	AA_DQB1_-18	AA_DRB1_13	9938.438515	26	-2122.42833	aa1 VL aa2 AVx aa3 SRHFGY
AA_DQB1_26	AA_DQB1_-10	AA_DRB1_13	9937.416871	26	-2122.20702	aa1 LYG aa2 SAx aa3 SRHFGY
AA_DQB1_26	AA_DQB1_-18	AA_DRB1_13	9937.416871	26	-2122.20702	aa1 LYG aa2 AVx aa3 SRHFGY
AA_DQB1_-18	AA_DRB1_71	AA_DRB1_13	9921.150843	26	-2118.68343	aa1 AVx aa2 KAER aa3 SRHFGY
AA_DQB1_77	AA_DQB1_-18	AA_DRB1_13	9920.94159	26	-2118.6381	aa1 RT aa2 AVx aa3 SRHFGY
AA_DQB1_57	AA_DQB1_26	AA_DRB1_13	9919.325229	36	-2105.681	aa1 ADVS aa2 LYG aa3 SRHFGY
AA_DQB1_38	AA_DQB1_-18	AA_DRB1_13	9917.652795	26	-2117.92568	aa1 VA aa2 AVx aa3 SRHFGY
AA_DQB1_57	AA_DQB1_-18	AA_DRB1_13	9913.173462	33	-2108.05674	aa1 ADVS aa2 AVx aa3 SRHFGY
AA_DQB1_71	AA_DQB1_57	AA_DRB1_11	9895.272334	32	-2105.4303	aa1 KTAD aa2 ADVS aa3 SPVLGD
AA_DQB1_57	AA_DRB1_86	AA_DRB1_11	9878.48074	27	-2108.14612	aa1 ADVS aa2 VG aa3 SPVLGD
AA_DQB1_57	AA_DRB1_67	AA_DRB1_13	9877.598178	32	-2101.60405	aa1 ADVS aa2 LIF aa3 SRHFGY
AA_DQB1_57	AA_DRB1_37	AA_DRB1_13	9874.77381	30	-2103.5101	aa1 ADVS aa2 NSYFL aa3 SRHFGY
AA_DQB1_57	AA_DRB1_71	AA_DRB1_37	9860.880401	30	-2100.50175	aa1 ADVS aa2 KAER aa3 NSYFL
AA_DQB1_-18	AA_DRB1_67	AA_DRB1_13	9853.196755	27	-2102.66968	aa1 AVx aa2 LIF aa3 SRHFGY
AA_DQB1_70	AA_DQB1_57	AA_DRB1_11	9852.082476	30	-2098.59673	aa1 RGE aa2 ADVS aa3 SPVLGD
AA_DQB1_26	AA_DRB1_71	AA_DRB1_13	9849.506749	30	-2098.03901	aa1 LYG aa2 KAER aa3 SRHFGY
AA_DQB1_57	AA_DRB1_57	AA_DRB1_13	9847.747922	31	-2096.3964	aa1 ADVS aa2 DSVA aa3 SRHFGY
AA_DQB1_30	AA_DQB1_-18	AA_DRB1_13	9846.931118	27	-2101.31257	aa1 SYH aa2 AVx aa3 SRHFGY
AA_DQB1_185	AA_DQB1_57	AA_DRB1_11	9846.666692	26	-2102.54867	aa1 TI aa2 ADVS aa3 SPVLGD
AA_DQB1_67	AA_DQB1_57	AA_DRB1_11	9844.169272	26	-2102.00769	aa1 IV aa2 ADVS aa3 SPVLGD
AA_DQB1_66	AA_DQB1_57	AA_DRB1_11	9844.169272	26	-2102.00769	aa1 DE aa2 ADVS aa3 SPVLGD
AA_DQB1_57	AA_DRB1_74	AA_DRB1_71	9841.332662	24	-2104.00616	aa1 ADVS aa2 RALQE aa3 KAER
AA_DQB1_57	AA_DRB1_181	AA_DRB1_13	9839.466174	23	-2104.92214	aa1 ADVS aa2 TxM aa3 SRHFGY
AA_DQB1_-18	AA_DRB1_70	AA_DRB1_13	9839.076178	26	-2100.90443	aa1 AVx aa2 QDR aa3 SRHFGY
AA_DQB1_71	AA_DQB1_57	AA_DRB1_13	9838.411893	35	-2089.39892	aa1 KTAD aa2 ADVS aa3 SRHFGY
AA_DQB1_57	AA_DRB1_13	AA_DRB1_-17	9837.778761	25	-2101.92525	aa1 ADVS aa2 SRHFGY aa3 ATx
AA_DQB1_75	AA_DQB1_57	AA_DRB1_13	9837.003146	32	-2092.81577	aa1 VL aa2 ADVS aa3 SRHFGY
AA_DQB1_74	AA_DQB1_57	AA_DRB1_13	9836.545077	32	-2092.71661	aa1 AES aa2 ADVS aa3 SRHFGY
AA_DQB1_57	AA_DQB1_13	AA_DRB1_13	9835.79373	27	-2098.90026	aa1 ADVS aa2 GA aa3 SRHFGY
AA_DQB1_167	AA_DQB1_57	AA_DRB1_13	9834.898754	26	-2099.99953	aa1 RH aa2 ADVS aa3 SRHFGY
AA_DQB1_57	AA_DQB1_-5	AA_DRB1_13	9830.63102	34	-2088.94878	aa1 ADVS aa2 PLSx aa3 SRHFGY
AA_DQB1_185	AA_DQB1_57	AA_DRB1_13	9830.48712	29	-2095.18957	aa1 TI aa2 ADVS aa3 SRHFGY
AA_DQB1_57	AA_DQB1_9	AA_DRB1_11	9829.398728	24	-2101.42053	aa1 ADVS aa2 YFL aa3 SPVLGD
AA_DQA1_175	AA_DQB1_57	AA_DRB1_37	9829.272123	27	-2097.48771	aa1 KQE aa2 ADVS aa3 NSYFL
AA_DQB1_57	AA_DRB1_71	AA_DRB1_11	9827.752845	30	-2093.32865	aa1 ADVS aa2 KAER aa3 SPVLGD
AA_DQB1_57	AA_DQB1_56	AA_DRB1_11	9826.880899	22	-2103.5251	aa1 ADVS aa2 PL aa3 SPVLGD
AA_DQB1_57	AA_DRB1_60	AA_DRB1_13	9823.396243	26	-2097.50789	aa1 ADVS aa2 YSH aa3 SRHFGY
AA_DQB1_57	AA_DRB1_180	AA_DRB1_11	9819.456296	25	-2097.95589	aa1 ADVS aa2 VLx aa3 SPVLGD
AA_DQB1_57	AA_DQB1_45	AA_DRB1_13	9817.955714	27	-2095.03663	aa1 ADVS aa2 GE aa3 SRHFGY
AA_DQB1_57	AA_DRB1_181	AA_DRB1_11	9817.721847	21	-2102.88039	aa1 ADVS aa2 TxM aa3 SPVLGD
AA_DQB1_57	AA_DRB1_70	AA_DRB1_13	9815.851225	33	-2086.98989	aa1 ADVS aa2 QDR aa3 SRHFGY
AA_DQA1_175	AA_DQB1_57	AA_DRB1_11	9814.27034	32	-2087.89448	aa1 KQE aa2 ADVS aa3 SPVLGD
AA_DQB1_57	AA_DRB1_71	AA_DRB1_-24	9810.683359	26	-2094.75407	aa1 ADVS aa2 KAER aa3 LFx
AA_DQB1_57	AA_DRB1_30	AA_DRB1_13	9808.205314	23	-2098.14844	aa1 ADVS aa2 YCLRGH aa3 SRHFGY
AA_DQB1_57	AA_DRB1_13	AA_DRB1_-16	9801.241117	26	-2092.70873	aa1 ADVS aa2 SRHFGY aa3 VAx

AA_DQB1_57	AA_DRB1_13	AA_DRB1_-25	9801.241117	26	-2092.70873	aa1 ADVS aa2 SRHFGY aa3 RKx
AA_DQB1_57	AA_DQB1_-9	AA_DRB1_13	9797.435732	29	-2088.03229	aa1 ADVS aa2 MIx aa3 SRHFGY
AA_DQB1_57	AA_DQB1_-27	AA_DRB1_13	9797.435732	29	-2088.03229	aa1 ADVS aa2 ASx aa3 SRHFGY
AA_DQB1_57	AA_DRB1_180	AA_DRB1_71	9797.37264	21	-2098.47018	aa1 ADVS aa2 VLx aa3 KAER
AA_DQB1_57	AA_DRB1_231	AA_DRB1_13	9796.745934	23	-2095.6654	aa1 ADVS aa2 QxP aa3 SRHFGY
AA_DQB1_57	AA_DQB1_9	AA_DRB1_13	9795.17846	26	-2091.39546	aa1 ADVS aa2 YFL aa3 SRHFGY
AA_DQA1_69	AA_DQB1_57	AA_DRB1_11	9795.161426	30	-2086.2717	aa1 LAT aa2 ADVS aa3 SPVLGD
AA_DQA1_75	AA_DQB1_57	AA_DRB1_13	9793.40984	29	-2087.16049	aa1 SI aa2 ADVS aa3 SRHFGY
AA_DQA1_107	AA_DQB1_57	AA_DRB1_13	9793.40984	29	-2087.16049	aa1 IT aa2 ADVS aa3 SRHFGY
AA_DQA1_156	AA_DQB1_57	AA_DRB1_13	9793.40984	29	-2087.16049	aa1 LF aa2 ADVS aa3 SRHFGY
AA_DQA1_161	AA_DQB1_57	AA_DRB1_13	9793.40984	29	-2087.16049	aa1 ED aa2 ADVS aa3 SRHFGY
AA_DQA1_163	AA_DQB1_57	AA_DRB1_13	9793.40984	29	-2087.16049	aa1 SI aa2 ADVS aa3 SRHFGY
AA_DQB1_57	AA_DRB1_86	AA_DRB1_9	9788.549018	17	-2102.03028	aa1 ADVS aa2 VG aa3 EWK
AA_DQB1_67	AA_DQB1_57	AA_DRB1_13	9788.543704	28	-2087.38244	aa1 IV aa2 ADVS aa3 SRHFGY
AA_DQB1_66	AA_DQB1_57	AA_DRB1_13	9788.543704	28	-2087.38244	aa1 DE aa2 ADVS aa3 SRHFGY
AA_DQB1_57	AA_DRB1_26	AA_DRB1_13	9779.927276	25	-2089.39241	aa1 ADVS aa2 YFL aa3 SRHFGY
AA_DQB1_30	AA_DQB1_-18	AA_DRB1_11	9778.261278	26	-2087.73095	aa1 SYH aa2 AVx aa3 SPVLGD
AA_DQB1_57	AA_DRB1_47	AA_DRB1_13	9777.25455	26	-2087.51288	aa1 ADVS aa2 FY aa3 SRHFGY
AA_DQB1_57	AA_DRB1_37	AA_DRB1_-16	9776.613635	25	-2088.67456	aa1 ADVS aa2 NSYFL aa3 VAx
AA_DQB1_57	AA_DRB1_37	AA_DRB1_-25	9776.613635	25	-2088.67456	aa1 ADVS aa2 NSYFL aa3 RKx
AA_DQB1_71	AA_DQB1_57	AA_DRB1_71	9772.876528	26	-2086.56454	aa1 KTAD aa2 ADVS aa3 KAER
AA_DQA1_47	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.07008	aa1 CRQK aa2 ADVS aa3 YFL
AA_DQB1_57	AA_DQB1_56	AA_DRB1_13	9771.082976	24	-2088.78585	aa1 ADVS aa2 PL aa3 SRHFGY
AA_DQB1_57	AA_DRB1_28	AA_DRB1_13	9770.924256	22	-2091.39906	aa1 ADVS aa2 DEH aa3 SRHFGY
AA_DQB1_57	AA_DRB1_233	AA_DRB1_13	9770.354597	27	-2084.72656	aa1 ADVS aa2 RTx aa3 SRHFGY
AA_DQB1_57	AA_DRB1_189	AA_DRB1_13	9769.06546	23	-2089.66756	aa1 ADVS aa2 RxS aa3 SRHFGY
AA_DQB1_26	AA_DRB1_71	AA_DRB1_37	9768.212989	26	-2085.55435	aa1 LYG aa2 KAER aa3 NSYFL
AA_DQB1_26	AA_DQB1_-4	AA_DRB1_11	9767.804059	27	-2084.17414	aa1 LYG aa2 VLx aa3 SPVLGD
AA_DQB1_26	AA_DQB1_-5	AA_DRB1_11	9767.804059	27	-2084.17414	aa1 LYG aa2 PLSx aa3 SPVLGD
AA_DQB1_26	AA_DQB1_-6	AA_DRB1_11	9767.804059	27	-2084.17414	aa1 LYG aa2 TSx aa3 SPVLGD
AA_DQB1_26	AA_DQB1_-21	AA_DRB1_11	9767.804059	27	-2084.17414	aa1 LYG aa2 GDx aa3 SPVLGD
AA_DQB1_57	AA_DRB1_32	AA_DRB1_13	9766.74347	24	-2087.84566	aa1 ADVS aa2 HY aa3 SRHFGY
AA_DQB1_57	AA_DRB1_38	AA_DRB1_13	9765.697356	21	-2091.60533	aa1 ADVS aa2 VAL aa3 SRHFGY
AA_DQB1_167	AA_DRB1_71	AA_DRB1_13	9763.464304	21	-2091.12137	aa1 RH aa2 KAER aa3 SRHFGY
AA_DQB1_57	AA_DRB1_13	AA_DRB1_-24	9762.906729	24	-2087.0144	aa1 ADVS aa2 SRHFGY aa3 LFx
AA_DQB1_57	AA_DRB1_180	AA_DRB1_13	9760.968322	24	-2086.59442	aa1 ADVS aa2 VLx aa3 SRHFGY
AA_DQB1_13	AA_DRB1_71	AA_DRB1_13	9759.772186	21	-2090.3212	aa1 GA aa2 KAER aa3 SRHFGY
AA_DQA1_25	AA_DQA1_175	AA_DQB1_57	9758.539195	11	-2104.16072	aa1 YF aa2 KQE aa3 ADVS
AA_DQB1_57	AA_DRB1_180	AA_DRB1_9	9758.149743	14	-2099.68207	aa1 ADVS aa2 VLx aa3 EWK
AA_DQB1_57	AA_DRB1_13	AA_DRB1_-1	9758.036271	23	-2087.27775	aa1 ADVS aa2 SRHFGY aa3 ASx
AA_DQB1_57	AA_DQB1_-17	AA_DRB1_13	9754.853591	24	-2085.26962	aa1 ADVS aa2 AxP aa3 SRHFGY
AA_DQB1_-18	AA_DRB1_96	AA_DRB1_67	9745.437543	21	-2087.21454	aa1 AVx aa2 HQYE aa3 LIF
AA_DQB1_45	AA_DRB1_71	AA_DRB1_13	9743.407869	21	-2086.77466	aa1 GE aa2 KAER aa3 SRHFGY
AA_DQB1_57	AA_DRB1_16	AA_DRB1_11	9740.489232	21	-2086.14212	aa1 ADVS aa2 HY aa3 SPVLGD
AA_DQB1_57	AA_DRB1_85	AA_DRB1_13	9731.818925	21	-2084.26306	aa1 ADVS aa2 VA aa3 SRHFGY

Supplementary Table 7C. Top 100 combinations of 4AA's

AA1	AA2	AA3	AA4	DeltaDeviance	df	P	Residues
AA_DQA1_47	AA_DQA1_48	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 LW aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_50	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 VEL aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_51	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 LF aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_52	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 RSH aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_53	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 QKR aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_54	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 FL aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_55	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 RG aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_56	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 xGR aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_61	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 FG aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_64	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 TR aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_66	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 IM aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_69	AA_DQA1_129	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 LAT aa3 HQ aa4 ADVS
AA_DQA1_47	AA_DQA1_69	AA_DQA1_130	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 LAT aa3 SA aa4 ADVS
AA_DQA1_47	AA_DQA1_69	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 LAT aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_69	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 LAT aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_69	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 LAT aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_69	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 LAT aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_75	AA_DQA1_129	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 SI aa3 HQ aa4 ADVS
AA_DQA1_47	AA_DQA1_75	AA_DQA1_130	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 SI aa3 SA aa4 ADVS
AA_DQA1_47	AA_DQA1_75	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 SI aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_75	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 SI aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_75	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 SI aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_75	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 SI aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_76	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 LMV aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_80	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 SY aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_107	AA_DQA1_129	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 IT aa3 HQ aa4 ADVS
AA_DQA1_47	AA_DQA1_107	AA_DQA1_130	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 IT aa3 SA aa4 ADVS
AA_DQA1_47	AA_DQA1_107	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 IT aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_107	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 IT aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_107	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 IT aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_107	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 IT aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_129	AA_DQA1_156	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 HQ aa3 LF aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQA1_161	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 HQ aa3 ED aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQA1_163	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 HQ aa3 SI aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQA1_175	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 HQ aa3 KQE aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_185	AA_DQB1_57	9859.678114	18	-2116.0641	aa1 CRQK aa2 HQ aa3 TI aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_167	AA_DQB1_57	9860.41582	17	-2117.6121	aa1 CRQK aa2 HQ aa3 RH aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_75	AA_DQB1_57	9818.668311	21	-2103.0855	aa1 CRQK aa2 HQ aa3 VL aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_74	AA_DQB1_57	9817.806051	21	-2102.8986	aa1 CRQK aa2 HQ aa3 AES aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_71	AA_DQB1_57	9817.806051	21	-2102.8986	aa1 CRQK aa2 HQ aa3 KTAD aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_70	AA_DQB1_57	9817.45218	18	-2106.9097	aa1 CRQK aa2 HQ aa3 RGE aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_67	AA_DQB1_57	9817.135281	20	-2104.1042	aa1 CRQK aa2 HQ aa3 IV aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_66	AA_DQB1_57	9817.135281	20	-2104.1042	aa1 CRQK aa2 HQ aa3 DE aa4 ADVS
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_56	9815.838125	14	-2112.1936	aa1 CRQK aa2 HQ aa3 ADVS aa4 PL
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_55	9815.482941	18	-2106.4828	aa1 CRQK aa2 HQ aa3 ADVS aa4 LRP
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_45	9860.372614	16	-2119.0045	aa1 CRQK aa2 HQ aa3 ADVS aa4 GE
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_26	9868.620999	23	-2111.2395	aa1 CRQK aa2 HQ aa3 ADVS aa4 LYG
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_13	9861.306357	18	-2116.417	aa1 CRQK aa2 HQ aa3 ADVS aa4 GA
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_9	9824.92838	18	-2108.5305	aa1 CRQK aa2 HQ aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DQB1_-18	9875.680826	22	-2114.1004	aa1 CRQK aa2 HQ aa3 ADVS aa4 AVx
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DRB1_181	9898.38857	20	-2121.7159	aa1 CRQK aa2 HQ aa3 ADVS aa4 TxM
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DRB1_180	9859.91856	19	-2114.7408	aa1 CRQK aa2 HQ aa3 ADVS aa4 VLx
AA_DQA1_47	AA_DQA1_129	AA_DQB1_57	AA_DRB1_86	9861.779059	21	-2112.4288	aa1 CRQK aa2 HQ aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_130	AA_DQA1_156	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 SA aa3 LF aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQA1_161	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 SA aa3 ED aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQA1_163	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 SA aa3 SI aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQA1_175	AA_DQB1_57	9778.09246	13	-2105.4538	aa1 CRQK aa2 SA aa3 KQE aa4 ADVS

AA_DQA1_47	AA_DQA1_130	AA_DQB1_185	AA_DQB1_57	9859.678114	18	-2116.0641	aa1 CRQK aa2 SA aa3 TI aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_167	AA_DQB1_57	9860.41582	17	-2117.6121	aa1 CRQK aa2 SA aa3 RH aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_75	AA_DQB1_57	9818.668311	21	-2103.0855	aa1 CRQK aa2 SA aa3 VL aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_74	AA_DQB1_57	9817.806051	21	-2102.8986	aa1 CRQK aa2 SA aa3 AES aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_71	AA_DQB1_57	9817.806051	21	-2102.8986	aa1 CRQK aa2 SA aa3 KTAD aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_70	AA_DQB1_57	9817.45218	18	-2106.9097	aa1 CRQK aa2 SA aa3 RGE aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_67	AA_DQB1_57	9817.135281	20	-2104.1042	aa1 CRQK aa2 SA aa3 IV aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_66	AA_DQB1_57	9817.135281	20	-2104.1042	aa1 CRQK aa2 SA aa3 DE aa4 ADVS
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_56	9815.838125	14	-2112.1936	aa1 CRQK aa2 SA aa3 ADVS aa4 PL
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_55	9815.482941	18	-2106.4828	aa1 CRQK aa2 SA aa3 ADVS aa4 LRP
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_45	9860.372614	16	-2119.0045	aa1 CRQK aa2 SA aa3 ADVS aa4 GE
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_26	9868.620999	23	-2111.2395	aa1 CRQK aa2 SA aa3 ADVS aa4 LYG
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_13	9861.306357	18	-2116.417	aa1 CRQK aa2 SA aa3 ADVS aa4 GA
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_9	9824.92838	18	-2108.5305	aa1 CRQK aa2 SA aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DQB1_-18	9875.680826	22	-2114.1004	aa1 CRQK aa2 SA aa3 ADVS aa4 AVx
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DRB1_181	9898.38857	20	-2121.7159	aa1 CRQK aa2 SA aa3 ADVS aa4 TxM
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DRB1_180	9859.91856	19	-2114.7408	aa1 CRQK aa2 SA aa3 ADVS aa4 VLx
AA_DQA1_47	AA_DQA1_130	AA_DQB1_57	AA_DRB1_86	9861.779059	21	-2112.4288	aa1 CRQK aa2 SA aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_156	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 LF aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_156	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 LF aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_156	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 LF aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_156	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 LF aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_161	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 ED aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_161	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 ED aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_161	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 ED aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_161	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 ED aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_163	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 SI aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_163	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 SI aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_163	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 SI aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_163	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 SI aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_175	AA_DQB1_57	AA_DRB1_86	9958.228094	22	-2131.9891	aa1 CRQK aa2 KQE aa3 ADVS aa4 VG
AA_DQA1_47	AA_DQA1_175	AA_DQB1_57	AA_DRB1_71	10079.93862	34	-2142.9113	aa1 CRQK aa2 KQE aa3 ADVS aa4 KAER
AA_DQA1_47	AA_DQA1_175	AA_DQB1_57	AA_DRB1_70	9866.021177	28	-2104.162	aa1 CRQK aa2 KQE aa3 ADVS aa4 QDR
AA_DQA1_47	AA_DQA1_175	AA_DQB1_57	AA_DRB1_37	9901.428811	35	-2103.0371	aa1 CRQK aa2 KQE aa3 ADVS aa4 NSYFL
AA_DQA1_47	AA_DQA1_187	AA_DQB1_57	AA_DQB1_9	9771.14175	15	-2101.0701	aa1 CRQK aa2 AT aa3 ADVS aa4 YFL
AA_DQA1_47	AA_DQA1_207	AA_DQB1_185	AA_DQB1_57	9800.584983	20	-2100.517	aa1 CRQK aa2 VM aa3 TI aa4 ADVS
AA_DQA1_47	AA_DQA1_207	AA_DQB1_167	AA_DQB1_57	9800.466847	20	-2100.4913	aa1 CRQK aa2 VM aa3 RH aa4 ADVS
AA_DQA1_47	AA_DQA1_207	AA_DQB1_75	AA_DQB1_57	9827.191857	23	-2102.2625	aa1 CRQK aa2 VM aa3 VL aa4 ADVS
AA_DQA1_47	AA_DQA1_207	AA_DQB1_74	AA_DQB1_57	9826.330091	23	-2102.0758	aa1 CRQK aa2 VM aa3 AES aa4 ADVS
AA_DQA1_47	AA_DQA1_207	AA_DQB1_71	AA_DQB1_57	9826.330091	23	-2102.0758	aa1 CRQK aa2 VM aa3 KTAD aa4 ADVS
AA_DQA1_47	AA_DQA1_207	AA_DQB1_57	AA_DQB1_45	9801.282018	19	-2102.0301	aa1 CRQK aa2 VM aa3 ADVS aa4 GE
AA_DQA1_47	AA_DQA1_207	AA_DQB1_57	AA_DQB1_26	9877.140892	26	-2109.15	aa1 CRQK aa2 VM aa3 ADVS aa4 LYG
AA_DQA1_47	AA_DQA1_207	AA_DQB1_57	AA_DQB1_-18	9873.734599	24	-2111.0264	aa1 CRQK aa2 VM aa3 ADVS aa4 AVx
AA_DQA1_47	AA_DQA1_207	AA_DQB1_57	AA_DRB1_181	9839.909347	23	-2105.0182	aa1 CRQK aa2 VM aa3 ADVS aa4 TxM

Supplementary Table 8. Common *HLA-DRB1-DQA1-DQB1 h*aplotype INFO scores

Haplotype	4-digit allele	INFO	4-digit allele	INFO	4-digit allele	INFO
1	**HLA-DRB1*01:01**	0.968	**HLA-DQA1*01:01**	0.978	**HLA-DQB1*05:01**	0.982
2	**HLA-DRB1*03:01**	0.991	**HLA-DQA1*05:01**	1.002	**HLA-DQB1*02:01**	0.982
3	**HLA-DRB1*04:01**	0.978	**HLA-DQA1*03:01**	0.997	**HLA-DQB1*03:02**	0.985
4	**HLA-DRB1*04:01**	0.978	**HLA-DQA1*03:01**	0.997	**HLA-DQB1*03:01**	1.012
5	**HLA-DRB1*04:04**	0.939	**HLA-DQA1*03:01**	0.997	**HLA-DQB1*03:02**	0.985
6	**HLA-DRB1*07:01**	0.997	**HLA-DQA1*02:01**	0.995	**HLA-DQB1*02:02**	1.000
7	**HLA-DRB1*15:01**	1.003	**HLA-DQA1*01:02**	1.011	**HLA-DQB1*06:02**	1.002

Supplementary Table 9. Pairwise haplotypic interactions

DRB1-DQA1-DQB1 Haplotype Interaction	P value for interaction	Expected OR (additive model)	95% CI		Fold change in OR due to interaction	95% CI		Total OR	95% CI	
03:01-05:01-02:01 x 04:01-03:01-03:01	9.20E-11	3.9647	2.7103	5.7996	0.3190	0.2258	0.4507	1.2647	0.7565	2.1144
04:01-03:01-03:01 x 04:04-03:01-03:02	2.38E-06	3.8897	2.3812	6.3538	0.2280	0.1234	0.4214	0.8870	0.4041	1.9467
03:01-05:01-02:01 x 15:01-01:02-06:02	1.16E-05	0.4392	0.2049	0.9414	0.0908	0.0311	0.2654	0.0399	0.0107	0.1487
03:01-05:01-02:01 x 04:01-03:01-03:02	1.21E-05	15.5091	10.6834	22.5145	1.9614	1.4505	2.6523	30.4198	18.8312	49.1400
04:01-03:01-03:02 x 04:04-03:01-03:02	3.48E-05	15.2159	9.3700	24.7088	0.3294	0.1947	0.5573	5.0122	2.4515	10.2476
04:01-03:01-03:02 x 07:01-02:01-02:02	4.17E-05	1.0182	0.4620	2.2440	5.0873	2.3365	11.0767	5.1801	1.7089	15.7021
04:01-03:01-03:01 x 07:01-02:01-02:02	1.14E-04	0.2603	0.1177	0.5757	4.7781	2.1586	10.5765	1.2437	0.4045	3.8240
01:01-01:01-05:01 x 04:01-03:01-03:02	1.20E-04	5.4859	4.0745	7.3862	2.1622	1.4595	3.2031	11.8612	7.2456	19.4171
03:01-05:01-02:01 x 04:04-03:01-03:02	1.93E-04	7.8414	5.0305	12.2230	2.1223	1.4288	3.1523	16.6418	9.1825	30.1605
01:01-01:01-05:01 x 04:01-03:01-03:01	7.74E-04	1.4024	1.0317	1.9062	1.9524	1.3218	2.8838	2.7380	1.6668	4.4978
04:01-03:01-03:01 x 04:01-03:01-03:02	1.12E-03	7.6932	5.0174	11.7960	0.4770	0.3056	0.7444	3.6693	1.9795	6.8017
01:01-01:01-05:01 x 15:01-01:02-06:02	0.0040	0.1554	0.0750	0.3219	0.1365	0.0352	0.5289	0.0212	0.0046	0.0987
04:01-03:01-03:02 x 15:01-01:02-06:02	0.0293	0.8523	0.3880	1.8720	0.3577	0.1419	0.9018	0.3049	0.0905	1.0266
03:01-05:01-02:01 x 07:01-02:01-02:02	0.0316	0.5247	0.2440	1.1285	2.2441	1.0740	4.6890	1.1776	0.4069	3.4083
04:01-03:01-03:01 x 15:01-01:02-06:02	0.0326	0.2179	0.0988	0.4803	0.2608	0.0760	0.8944	0.0568	0.0131	0.2457
01:01-01:01-05:01 x 07:01-02:01-02:02	0.0414	0.1856	0.0893	0.3860	2.3193	1.0335	5.2045	0.4305	0.1447	1.2810
04:04-03:01-03:02 x 07:01-02:01-02:02	0.0837	0.5148	0.2254	1.1761	2.1585	0.9026	5.1620	1.1113	0.3343	3.6937
01:01-01:01-05:01 x 04:04-03:01-03:02	0.1908	2.7737	1.8914	4.0675	0.7079	0.4219	1.1878	1.9636	1.0315	3.7377
04:04-03:01-03:02 x 15:01-01:02-06:02	0.3322	0.4309	0.1892	0.9813	0.6178	0.2335	1.6351	0.2662	0.0744	0.9523
07:01-02:01-02:02 x 15:01-01:02-06:02	0.7417	0.0288	0.0103	0.0810	0.7757	0.1713	3.5120	0.0224	0.0036	0.1394
01:01-01:01-05:01 x 03:01-05:01-02:01	0.7673	2.8271	2.2583	3.5392	1.0436	0.7866	1.3845	2.9504	2.0562	4.2334

Supplementary Table 10. DR3/DR4 pairwise allelic interactions

Allele 1	Allele 2	P value for interaction
DQB1*02:01	DQB1*03:02	5.57E-26
DRB1*03:01	DQB1*03:02	5.57E-26
DQA1*05:01	DQB1*03:02	1.71E-25
DQB1*02:01	DRB1*04:04	1.49E-22
DRB1*03:01	DRB1*04:04	1.49E-22
DQA1*05:01	DRB1*04:04	1.56E-21
DQB1*02:01	DQA1*03:01	5.74E-06
DRB1*03:01	DQA1*03:01	5.74E-06
DQA1*05:01	DQA1*03:01	1.69E-05
DQA1*05:01	DRB1*04:01	0.1455
DQB1*02:01	DRB1*04:01	0.19037
DRB1*03:01	DRB1*04:01	0.19037

SUPPLEMENTARY NOTE

Construction of pseudo-case/control samples

We constructed pseudo-controls from a set of 1,661 European families with at least 1 affected child and both healthy parents present. From each family, we selected one affected child (randomly selecting one if multiple affected children were present) to be the case (transmitted alleles).

We first determined the parent of origin for each of the child's two chromosomes, using heterozygous "checkpoints". Checkpoints consist of markers for which the child and only one parent are heterozygous. For example, if the mother's genotype at marker X is "AA", the father's is "AB", and the child's is "BA", we determine that the first allele at each marker came from the father. At each marker, the pseudo-case genotype is that of the affected child. Pseudo-control genotype consists of the two untransmitted allele from the parents, ordered by the parent of origin determined above. For example, if at a given marker, the father is "AA", the mother is "AB", the affected child is "AA", and the allele order in the child is determined to be mother/father, then the pseudo-control genotype must be "BA".

After applying HLA imputation, we also used the checkpoint results to identify phasing error. We observed that in about 5% of the samples, there was jumping (such that the class I segment of a chromosome in the child is from one parent, while the class II segment is from the other); no significant phasing error occurred within genes, within the class I region or within the class II region.

Quality control

After combining the UK and Eur datasets, we excluded a total of 344 binary markers due to allele missingness or rareness (frequency < 0.05%); we correspondingly removed individuals who carried the missing or rare alleles. The post-quality control final dataset consisted of 18,832 samples, including 8,095 cases and 10,737 controls (or pseudo-controls). The gender and region of origin of each sample is provided in **Table S1**.

Imputation quality was high for each dataset, quantified here as the allelic R^2 score reported by BEAGLE.

Dataset (post-QC)	**1st quartile**	**Median**	**Mean**	**3rd quartile**
UK	0.9970	1	0.9855	1
Eur-fam	0.9990	1	0.9934	1

Figure S1 shows the histograms of R^2 scores of all post-QC variants. **Table S2** provides the complete list of 8,617 tested binary variants and their allelic R^2 scores, as well as the unadjusted disease association statistics in the total dataset, the UK case-control dataset, and the European pseudo-case/control dataset

Accounting for population stratification

To account for population stratification, we included the 13 region codes as covariates. We had also assessed the correction by including genotype principal components (PC). We computed the PCs in the 16,086 UK case/control samples using EIGENSTRAT [1], using pruned genome-wide SNPs (excluding those on Chromosome 6). To calculate the genomic control inflation factor (λ_{GC}) within the UK dataset, we tested the association to T1D in a set of 1,469 (807 after LD-pruning) SNPs in non-autoimmune loci. These SNPs were included on the ImmunoChip array as a deep replication for a study investigating the genetic basis for reading and writing ability, thus not expected to significantly associate with immune traits. We included three sets of covariates in three trials, and observed the following genomic-control factor lambda values (Q-Q plots are shown in **Figure S2**):

Covariates included	$\boldsymbol{\lambda_{GC}}$
No covariate	1.1516
Gender only	1.1502
Gender + top 10 PCs	1.1374
Gender + region code	1.1034
Gender + region code + top 10 PCs	1.1028

As the including of up to 10 PCs did not significantly alter λ_{GC}, we elected to not include genotype principal components (PC) in our association analyses. This approach was consistent with that used for genome-wide association analysis by Onengut-Gumuscu[2].

To assess the statistical significance of a specific marker, we assessed the improvement of fit of a model over the null model (only region and gender covariates) when that marker is added to the model. We calculate as the deviance defined by
$\Delta \text{Deviance}_{alt\text{-}null} = -2\ln(\text{likelihood}_{alt}/\text{likelihood}_{null})$,
which follows a χ^2 distribution with $m-1$ degrees of freedom, from which we calculate the p-value. We considered $p = 5\text{x}10^{-8}$ as the significance threshold.

Analysis of amino acid positions considering non-additive effect

We wanted to show that the independently associated risk-modulating amino acid positions remained unchanged after including non-additive effects. To this end, we repeated the forward-search analysis after incorporating non-additive terms into the regression model. In this analysis, each variant is coded as 0/1/2 for allelic dosage; and an additional heterozygote factor is added, which equals 1 only if the individual is heterozygotic for this allele/haplotype.

Testing for discordance effect sizes between T1D and Rheumatoid Arthritis

DRB1#13 and #71 show strong independent effects in both T1D and RA. We tested whether the individual residues at each position confer differential risk or protection between the two diseases, using previously described method [3]. Given a multi-allelic amino acid position with m residues, we calculated the multivariate log-odds ratios (log-OR) of the residues by including in the logistic regression the binary markers corresponding to each residue [3]. We excluded the most common residue in controls as the reference (therefore the log-OR and variance for that residue are both 0). Let $a_1, a_2, \ldots a_{m-1}$ and $b_1, b_2, \ldots b_{m-1}$ be the multivariate log-ORs in the two diseases; and let $v_1, v_2, \ldots v_{m-1}$ and $u_1, u_2, \ldots u_{m-1}$ be the variances around the log-OR estimates. To test the discordance of effect sizes between the two diseases, we calculated the statistic

$$\sum\nolimits_{i=1\ldots m-1} \frac{(a_i - b_i)^2}{v_i + u_i}$$

This is χ^2 distributed with $m-1$ degrees of freedom under the null.

We note that the RA and T1D datasets likely shared a proportion of control samples (from the British 1958 Birth Cohort and Blood Service). However, we do not expect inflated discordance, as had any bias been introduced by shared controls, it would tend toward artificial concordance, rather than discordance.

Proportion of phenotypic variance explained

We assumed the liability threshold model, and calculated the proportion of phenotypic variance explained (h^2) by a combination of variants using previously described methods [4,5].

We used a model based on the biometrical model from Fisher [6] and the liability threshold model from Pearson and Lee [7]. We assumed that disease risk is the consequence of an underlying liability score; and that individuals with a score above a pre-specified threshold get disease [8]. We further assume that the population consists of genotype groups; and that liability score within each genotype group is normally distributed with an unknown mean and variance of 1. The value of h^2 is defined by the variance between genotypic groups (V_g) divided by the total population variance (V_t), which equals the sum of V_g and variance within group ($V_i = 1$); or,

$$h^2 = V_g/(V_g + V_i)$$

V_g, the between-group variance, is defined as

$$\sum p_i(\bar{x_i} - \bar{\bar{x}})^2$$

Where p_i is the population frequency of a genotypic group i; $\bar{x}_i$ is the mean of the group; and $\bar{\bar{x}}$ is the grand mean of the population.

To estimate the h^2 explained by *HLA-DRB1-DQA1-DQB1*, we estimated the multivariate ORs of 67 haplotypes (each occurring at least four times in the dataset) defined by all amino acids in the locus, using the most common haplotype in controls as the reference. Similarly, to calculate h^2 explained by DQβ1#57, DRβ1#13, DRβ1#71, we calculated the control frequencies and multivariate ORs of 29 haplotypes (with at least four copies) defined by these three positions.

We next assumed that the alleles are in Hardy-Weinberg equilibrium, and calculated the genotype frequency (p_i) and prevalence of disease within each possible diploid genotype (f_i). Given that the disease is rare, relative risk approximately equals the odds ratio, therefore

$$f_i = \frac{RR_i \times F}{\sum p_i \times RR_i}$$

We then determined the liability threshold within each genotype (T_i) using the normal inverse cumulative distribution function.

Next, we could assume that the shift of liability threshold of the reference genotype group, $T_{ref,}$ from the population threshold is 0. Assuming equal within-genotype variance of 1, the shift in liability threshold equals the difference in the genotypic means; that is, $\bar{x}_i = T_i - T_{\mathrm{ref.}}$ The grand mean of the population can then be updated as

$\bar{\bar{x}} = \sum p_i \times \bar{x}_i$.

INFO score calculation

To assess the imputation quality of a given variant, we calculated the INFO score from the ratio of the observed variance in dosage (of the minor allele) to the expected variance under Hardy-Weinberg equilibrium [9]:

$$INFO = \frac{var(x)}{2p(1-p)}$$

where *x* is the imputed best-guess dosage and *p* is the frequency of the minor allele. An INFO score close to 0 indicates poor imputation quality, while a score closer to 1 indicates higher quality; a value greater than 1 is also possible. Due to the presence of non-additive effects that inflated the disease risk in heterozygotes, the allele distribution in disease cases deviated from Hardy-Weinberg equilibrium. Therefore, we calculated INFO scores using the variance and allele frequency in controls only.

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