Supplementary Table 3. Conditioning Studies for MHC Associations in EOMG[a]

Marker/Amino Acid/HLA determinant[b]	base pair position (HG18)	Genotype Posterior Prob.[c]	Inf[d]	Allele 1 (Minor Allele)	Allele 2	MAF (Case)[e]	MAF (Control)
6-30018489	30018489	0.998	0.979	G	A	0.06	0.03
HLA-A AA97	30018729	0.999	0.989	T	I	0.06	0.03
6-30018795	30018795	0.998	0.979	G	A	0.06	0.03
6-30018845	30018845	0.998	0.977	G	A	0.06	0.03
6-30019484	30019484	0.999	0.994	C	G	0.06	0.03
6-30019836	30019836	0.999	0.994	G	T	0.06	0.03
HLA-A*3101	30019970	0.999	0.991	SPEC	other	0.06	0.03
6-30020128	30020128	1.000	0.995	G	C	0.06	0.03
6-30020864	30020864	0.999	0.995	C	A	0.06	0.03
6-30020869	30020869	0.999	0.994	G	C	0.06	0.03
6-30020871	30020871	1.000	0.995	C	A	0.06	0.03
6-30020872	30020872	0.999	0.994	T	A	0.06	0.03
6-30020875	30020875	0.999	0.993	G	A	0.06	0.03
6-30020876	30020876	0.999	0.993	G	A	0.06	0.03
6-30020879	30020879	0.999	0.994	C	A	0.06	0.03
6-30020880	30020880	1.000	0.995	T	C	0.06	0.03
rs1061235	30021277	0.999	0.989	T	A	0.06	0.03
rs6930977	30543267	typed	typed	A	G	0.19	0.17
rs2157605	30562055	0.997	0.992	T	C	0.20	0.18
rs3130117	30616935	0.988	0.958	G	A	0.33	0.12
rs12665339	30709211	1.000	1.000	A	G	0.18	0.17
rs9262130	30711498	0.994	0.982	C	T	0.34	0.13
rs9262135	30726885	0.996	0.987	A	G	0.34	0.13
rs9405048	30778271	0.974	0.917	C	T	0.19	0.17
rs3129973	30829122	0.992	0.978	C	T	0.35	0.13
rs3130673	30854498	0.994	0.983	G	T	0.35	0.13
rs3131050	30868004	0.995	0.986	T	C	0.35	0.13
rs886424	30889981	typed	typed	C	T	0.37	0.14
rs1264353	30895741	0.999	0.997	C	A	0.37	0.14
rs2517578	30919244	0.966	0.905	G	C	0.37	0.15
rs2535334	30920975	0.969	0.912	G	A	0.38	0.15
rs2535333	30921076	0.964	0.917	G	A	0.46	0.22
rs2535332	30921228	0.974	0.922	C	T	0.37	0.14
rs2517576	30923014	0.971	0.935	G	A	0.46	0.20
rs2263298	30928352	0.974	0.923	C	T	0.37	0.14
rs2844659	30932511	typed	typed	C	T	0.46	0.20
rs2535328	30933973	0.980	0.942	C	T	0.37	0.13
rs2844657	30937501	typed	typed	A	G	0.46	0.20
rs2844656	30942310	0.981	0.943	A	G	0.37	0.13
rs1264326	30959888	0.972	0.915	C	A	0.37	0.14
rs1264322	30965873	0.999	0.998	G	A	0.37	0.13
rs1264319	30970402	0.968	0.929	C	T	0.46	0.21
rs1264318	30971509	0.955	0.904	C	G	0.47	0.22
rs886422	30972258	0.999	0.997	C	T	0.37	0.13
rs1264310	30981584	0.971	0.918	C	A	0.37	0.14
rs1264308	30987966	0.999	0.998	C	T	0.37	0.13

rs4678	31001920	typed	typed	G	A	0.45	0.20
rs3094088	31002944	0.980	0.944	T	A	0.37	0.15
rs3095155	31007030	0.980	0.939	G	C	0.37	0.15
rs3095154	31007031	0.976	0.947	G	A	0.47	0.22
rs3095153	31007174	0.980	0.940	G	A	0.37	0.15
rs3131787	31007503	0.979	0.952	T	C	0.45	0.20
rs3095152	31007629	0.980	0.940	G	A	0.37	0.15
rs3132581	31021437	0.987	0.964	G	A	0.37	0.14
rs3130781	31022531	0.969	0.933	T	C	0.47	0.21
rs3094086	31027370	0.990	0.972	G	A	0.37	0.14
rs3132580	31028103	typed	typed	G	A	0.38	0.14
rs3095089	31041773	typed	typed	G	T	0.45	0.18
rs3132579	31048968	0.990	0.979	T	C	0.45	0.17
rs12179536	31101569	typed	typed	A	G	0.19	0.18
rs3130544	31166319	typed	typed	C	A	0.40	0.13
rs2233974	31187995	0.996	0.992	C	G	0.46	0.18
rs2233956	31189184	typed	typed	T	C	0.43	0.18
rs3130557	31202682	0.999	0.997	C	T	0.41	0.14
rs1265115	31225054	0.992	0.982	C	A	0.28	0.32
rs1265109	31227568	typed	typed	G	T	0.26	0.27
rs743401	31233137	0.974	0.953	T	C	0.22	0.41
rs3095239	31234769	0.954	0.925	G	A	0.27	0.49
rs3094187	31234923	0.954	0.926	T	C	0.27	0.50
rs7750641	31237289	typed	typed	C	T	0.41	0.13
rs885948	31248511	0.998	0.997	G	A	0.28	0.51
rs1265156	31250276	typed	typed	C	A	0.29	0.32
rs887464	31253899	typed	typed	T	C	0.29	0.54
rs6921663	31262599	1.000	1.000	A	G	0.23	0.24
rs4713444	31263527	0.968	0.938	A	G	0.34	0.41
rs6899874	31270307	0.976	0.942	C	A	0.23	0.24
rs28397282	31273825	0.970	0.928	C	T	0.23	0.24
rs9391711	31274273	0.971	0.929	C	T	0.22	0.24
rs4122189	31275906	typed	typed	C	T	0.23	0.24
rs9366769	31277268	0.965	0.914	T	C	0.23	0.24
HLA-C*12	31346171	0.999	0.989	SPEC	other	0.06	0.04
HLA-C*1203	31346171	0.999	0.988	SPEC	other	0.05	0.03
6-31346738	31346738	0.994	0.989	T	C	0.57	0.47
6-31346974	31346974	0.999	0.987	G	A	0.05	0.03
6-31347428	31347428	0.961	0.914	C	G	0.45	0.21
HLA-C AA91	31347429	0.961	0.913	K	N	0.45	0.21
rs2524069	31352768	0.999	0.997	A	T	0.42	0.16
rs3134792	31420305	0.977	0.927	T	G	0.40	0.13
6-31430295	31430295	0.993	0.944	A	C	0.08	0.06
6-31430432	31430432	0.993	0.944	A	C	0.08	0.06
6-31430769	31430769	0.997	0.993	T	A	0.41	0.14
HLA-B*08	31431272	0.998	0.994	SPEC	other	0.41	0.13
HLA-B*40	31431272	0.999	0.994	SPEC	other	0.10	0.08
HLA-B*4001	31431272	0.993	0.944	SPEC	other	0.08	0.06
6-31431395	31431395	0.996	0.989	G	C	0.41	0.13
6-31431485	31431485	0.997	0.991	C	T	0.41	0.14
HLA-B AA172	31432030	0.992	0.940	W	L	0.08	0.06
HLA-B AA168	31432042	0.992	0.940	T	S	0.08	0.06
6-31432043	31432043	0.992	0.941	T	A	0.08	0.06
HLA-B AA139	31432129	0.982	0.972	other	N	0.68	0.41

6-31432130	31432130	0.982	0.972	A	G	0.68	0.41
6-31432354	31432354	0.993	0.944	G	T	0.08	0.06
6-31432394	31432394	0.996	0.989	A	C	0.43	0.17
6-31432729	31432729	0.992	0.943	G	A	0.09	0.07
rs1811197	31435639	0.996	0.990	G	A	0.47	0.19
rs2523567	31437994	0.999	0.998	G	C	0.53	0.23
rs2844559	31448054	0.987	0.963	C	T	0.42	0.14
rs3099844	31556955	typed	typed	C	A	0.39	0.13
rs3094011	31559815	0.991	0.972	T	C	0.39	0.13
rs3132451	31690004	0.996	0.990	C	G	0.44	0.20
rs3130070	31699787	0.972	0.931	A	G	0.43	0.18
rs3130624	31705854	0.974	0.936	A	G	0.42	0.18
rs3130626	31706468	0.976	0.943	A	G	0.43	0.18
rs2736157	31708799	0.984	0.961	A	G	0.43	0.19
rs3130627	31708830	0.981	0.952	G	T	0.43	0.19
rs3115663	31709822	typed	typed	T	C	0.44	0.19
rs11229	31711749	typed	typed	A	G	0.44	0.19
rs10885	31712570	0.984	0.960	C	T	0.44	0.19
rs3130628	31717251	0.975	0.942	T	C	0.42	0.18
rs3130047	31718458	0.978	0.947	C	T	0.43	0.19
rs3117583	31727555	0.969	0.925	A	G	0.43	0.19
rs3117582	31728499	0.978	0.933	T	G	0.36	0.12
rs3132449	31733992	0.981	0.941	C	T	0.36	0.12
rs3117580	31738947	0.990	0.974	G	A	0.43	0.19
rs3130618	31740113	typed	typed	C	A	0.44	0.19
rs9267531	31744721	0.981	0.941	A	G	0.36	0.12
rs3131383	31812273	0.998	0.995	G	T	0.37	0.12
rs3132445	31820175	0.993	0.978	G	A	0.36	0.12
rs3130484	31823861	0.994	0.980	T	C	0.36	0.12
rs3131379	31829012	typed	typed	G	A	0.37	0.12
rs3117574	31833209	0.994	0.981	G	A	0.36	0.12
rs3117575	31834232	0.992	0.973	T	C	0.36	0.12
rs3117577	31835453	0.998	0.993	A	G	0.37	0.12
rs3115671	31842324	0.997	0.992	C	A	0.37	0.12
rs915652	31857121	0.997	0.991	C	T	0.37	0.12
rs599707	31916415	0.998	0.995	C	T	0.37	0.12
rs558702	31978305	typed	typed	G	A	0.36	0.12
rs497309	32000463	0.980	0.941	A	C	0.34	0.12
rs1270942	32026839	typed	typed	A	G	0.35	0.12
rs389884	32048876	typed	typed	A	G	0.35	0.12
rs1150752	32172704	0.997	0.992	T	C	0.35	0.12
rs7775397	32369230	typed	typed	T	G	0.35	0.12
rs1265754	32411670	0.999	0.998	A	T	0.34	0.12
rs3117103	32457535	0.999	0.996	T	A	0.35	0.13
rs3129953	32469799	0.965	0.919	C	T	0.43	0.19
rs1980493	32471193	0.999	0.999	T	C	0.42	0.17
rs3135353	32500855	typed	typed	C	T	0.41	0.16
rs3129891	32523058	0.999	0.997	G	A	0.46	0.21
rs2760991	32623336	0.986	0.933	C	T	0.04	0.12
6-32656528	32656528	0.999	0.997	G	A	0.04	0.12
6-32657541	32657541	0.997	0.992	G	A	0.35	0.13
DRB1 AA107	32659917	0.997	0.993	T	N	0.35	0.13
DRB1 AA104	32659926	0.999	0.997	other	Q	0.04	0.12
DRB1 AA104	32659926	0.997	0.993	other	R	0.35	0.13
6-32659931	32659931	0.998	0.967	A	G	0.04	0.03

6-32659988	32659988	0.999	0.997	C	T	0.04	0.12
HLA-DRB1*0301	32660042	0.997	0.992	SPEC	other	0.35	0.13
HLA-DRB1*07	32660042	0.999	0.997	SPEC	other	0.04	0.12
HLA-DRB1*16	32660042	1.000	0.988	SPEC	other	0.03	0.01
DRB1 AA60	32660058	0.999	0.997	other	L	0.04	0.12
DRB1 AA56	32660070	0.997	0.991	other	Y	0.36	0.14
DRB1 AA55	32660073	0.999	0.997	R	Q	0.04	0.12
DRB1 AA44	32660106	0.999	0.997	E	K	0.04	0.12
6-32660107	32660107	0.999	0.997	C	T	0.04	0.12
DRB1 AA43	32660109	0.999	0.997	other	Y	0.04	0.12
DRB1 AA41	32660115	0.999	0.997	other	G	0.04	0.12
HLA-DQA1*02	32716284	1.000	0.999	SPEC	other	0.04	0.12
DQA1 AA48	32717125	0.993	0.981	Y	F	0.08	0.19
DQA1 AA70	32717191	1.000	0.999	other	K	0.04	0.12
DQA1 AA75	32717206	1.000	0.999	other	H	0.04	0.12
6-32717211	32717211	1.000	0.999	T	C	0.04	0.12
DQA1 AA77	32717212	1.000	0.999	F	L	0.04	0.12
6-32737909	32737909	1.000	0.996	C	G	0.03	0.01
DQB1 AA159	32737910	1.000	0.996	Q	H	0.03	0.01
HLA-DQB1*0502	32739039	1.000	0.996	SPEC	other	0.03	0.01
HLA-DQB1*0604	32739039	0.995	0.962	SPEC	other	0.07	0.04
6-32740565	32740565	0.990	0.977	A	G	0.22	0.20
DQB1 AA120	32740576	0.990	0.977	other	Y	0.22	0.20
DQB1 AA90	32740666	1.000	0.996	other	S	0.03	0.01
6-32740667	32740667	1.000	0.996	C	T	0.03	0.01
DPB1 AA65	33156520	0.967	0.946	A	V	0.50	0.45
DPB1 AA84	33156577	0.971	0.953	other	A	0.49	0.44

a. This Table provides a summary of results before and after conditioning on particular HLA
SNPs. Conditioning on HLA-DRB1*0301 is shown for comparison. Results for conditionin
SNPs (see Table S2) and imputed SNPs. All imputed SNPs had posterior probablilities an
(see methods) and used the genotype probabilites. P values are provided for the most sig
B*08.

b. The nucleotide is shown for SNPs (rs numbers and chromosomal base pair postions). F
Where the AA is compared with multiple other AAs, "other" is used to represent all alternat
74 without the leader sequence). Where HLA classical alleles are provided, the specificity

c. Post Prob: The maximum posterior probabilities estimated from the imputed probabilities

d. Information (Inf) is a measure of the observed statistical information for the estimate of S
were genotyped.

e. MAF: Minor allele frequencies were estimated from probabilities (SNPTEST V2).

f. p values before conditioning using population substructure and gender as covariates.

g. p value after conditioning on the allele(s) listed in the heading line.

h. Odds ratios after conditioning on the alleles listed in the heading line,

i. COND: Indicates the gene(s) or marker(s) used in the conditional analyses. For all cond

p-value[f]	Odds Ratio minor allele, L95%, U95% Confidence Limits			Cond. p-value HLA B*08[g]	Odds Ratio minor allele, L95%, U95% Confidence Limits, After Conditioning on B*08[h]			Cond. p-value HLA DRB1*0301[g]	Cond. p-value All HLA B[g]	Cond. p-value HLA B*08 B*07 B*4001 B*4402[g]
1.1E-06	2.30	1.65	3.22	1.5E-08	2.88	2.00	4.15	1.4E-07	3.5E-05	8.5E-06
5.5E-06	2.09	1.52	2.86	4.7E-08	2.63	1.86	3.71	1.3E-06	6.3E-05	1.7E-05
1.1E-06	2.30	1.65	3.22	1.5E-08	2.88	2.00	4.15	1.4E-07	3.5E-05	8.4E-06
1.1E-06	2.30	1.65	3.22	1.5E-08	2.88	2.00	4.15	1.4E-07	3.5E-05	8.4E-06
5.2E-06	2.10	1.53	2.89	5.1E-08	2.64	1.86	3.74	1.7E-06	6.3E-05	1.8E-05
5.2E-06	2.10	1.53	2.89	5.1E-08	2.64	1.86	3.74	1.7E-06	6.3E-05	1.8E-05
9.0E-07	2.40	1.69	3.40	3.2E-08	2.90	1.99	4.23	2.6E-07	5.1E-05	1.7E-05
5.3E-06	2.10	1.53	2.89	5.4E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.2E-06	2.10	1.53	2.89	5.4E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.3E-06	2.10	1.53	2.89	5.4E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.2E-06	2.10	1.53	2.89	5.4E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.3E-06	2.10	1.52	2.89	5.5E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.3E-06	2.10	1.52	2.89	5.5E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.3E-06	2.10	1.52	2.89	5.5E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.3E-06	2.10	1.53	2.89	5.5E-08	2.63	1.86	3.73	1.8E-06	6.5E-05	1.9E-05
5.5E-06	2.10	1.52	2.88	5.5E-08	2.63	1.86	3.72	1.9E-06	6.5E-05	1.9E-05
9.0E-02	1.15	0.98	1.36	4.5E-07	1.61	1.34	1.94	2.8E-05	1.7E-03	1.9E-03
1.6E-01	1.12	0.96	1.32	3.8E-07	1.60	1.34	1.92	6.1E-05	1.7E-03	1.5E-03
1.3E-70	4.74	3.99	5.62	3.2E-01	0.87	0.67	1.14	3.4E-16	3.3E-01	3.5E-01
1.3E-01	1.14	0.96	1.34	3.9E-07	1.62	1.35	1.95	5.1E-05	8.9E-04	1.8E-03
2.2E-70	4.50	3.81	5.32	3.0E-01	0.87	0.67	1.13	2.6E-16	3.2E-01	3.2E-01
2.2E-70	4.44	3.77	5.24	2.8E-01	0.86	0.67	1.12	1.8E-16	2.9E-01	3.0E-01
1.1E-01	1.15	0.97	1.36	1.9E-07	1.66	1.37	2.02	3.3E-05	8.3E-04	1.7E-03
1.5E-73	4.54	3.85	5.34	2.4E-01	0.85	0.65	1.12	7.9E-18	2.5E-01	2.6E-01
2.0E-72	4.44	3.77	5.22	1.9E-01	0.84	0.64	1.09	2.0E-17	1.5E-01	2.1E-01
6.0E-73	4.45	3.79	5.24	2.0E-01	0.84	0.64	1.10	1.3E-17	1.6E-01	2.2E-01
2.0E-75	4.43	3.78	5.19	2.6E-01	0.85	0.65	1.12	3.8E-19	2.2E-01	3.0E-01
7.6E-76	4.47	3.81	5.24	2.6E-01	0.85	0.65	1.13	2.3E-19	2.2E-01	3.0E-01
6.6E-81	4.99	4.23	5.89	1.8E-01	0.80	0.58	1.11	1.1E-21	2.0E-01	1.8E-01
7.6E-81	4.95	4.20	5.83	1.9E-01	0.80	0.58	1.11	9.9E-22	2.1E-01	1.8E-01
4.1E-72	3.74	3.24	4.32	6.4E-03	1.36	1.09	1.70	2.5E-24	1.7E-01	9.2E-02
2.5E-84	5.22	4.42	6.17	1.5E-01	0.78	0.56	1.09	4.7E-23	1.6E-01	1.3E-01
2.1E-75	3.84	3.33	4.44	3.7E-03	1.39	1.11	1.73	1.0E-25	1.2E-01	6.3E-02
2.8E-84	5.22	4.42	6.16	1.5E-01	0.78	0.56	1.09	5.0E-23	1.6E-01	1.3E-01
2.6E-73	3.66	3.18	4.21	4.2E-03	1.37	1.11	1.71	2.3E-25	1.3E-01	6.8E-02
7.6E-85	5.20	4.40	6.13	1.7E-01	0.79	0.57	1.10	4.6E-23	1.9E-01	1.6E-01
6.2E-74	3.66	3.18	4.21	3.4E-03	1.38	1.11	1.71	2.2E-25	1.0E-01	5.7E-02
5.4E-85	5.17	4.39	6.10	2.0E-01	0.80	0.58	1.12	3.0E-23	2.2E-01	1.8E-01
6.2E-83	5.10	4.32	6.02	1.1E-01	0.77	0.55	1.07	2.7E-22	1.5E-01	1.0E-01
3.8E-84	4.90	4.17	5.75	2.3E-01	0.82	0.60	1.13	3.0E-23	2.9E-01	2.4E-01
9.4E-76	3.82	3.31	4.41	1.4E-03	1.43	1.15	1.78	2.6E-26	5.4E-02	2.6E-02
2.9E-73	3.75	3.25	4.33	2.7E-03	1.39	1.12	1.73	3.9E-25	7.7E-02	4.6E-02
3.6E-84	4.91	4.18	5.77	2.0E-01	0.81	0.58	1.12	4.0E-23	2.4E-01	2.0E-01
2.7E-82	5.04	4.27	5.94	1.1E-01	0.77	0.55	1.06	4.5E-22	1.6E-01	9.9E-02
4.8E-84	4.90	4.18	5.76	1.9E-01	0.80	0.58	1.11	5.3E-23	2.3E-01	1.9E-01

6.2E-74	3.72	3.23	4.29	1.5E-02	1.31	1.05	1.64	1.0E-23	1.1E-01	1.8E-01
3.6E-77	4.62	3.93	5.43	1.1E-01	0.78	0.58	1.05	3.4E-20	2.1E-01	9.4E-02
9.0E-78	4.66	3.97	5.48	1.1E-01	0.78	0.58	1.06	2.0E-20	2.2E-01	1.0E-01
2.2E-70	3.54	3.08	4.07	4.4E-03	1.36	1.10	1.67	5.7E-24	6.4E-02	6.6E-02
8.0E-78	4.66	3.97	5.48	1.1E-01	0.78	0.58	1.06	1.9E-20	2.2E-01	1.0E-01
2.4E-74	3.81	3.30	4.40	2.7E-02	1.29	1.03	1.61	6.4E-24	1.6E-01	2.5E-01
7.6E-78	4.66	3.97	5.48	1.1E-01	0.78	0.58	1.06	1.9E-20	2.2E-01	1.0E-01
1.1E-77	4.63	3.94	5.44	7.2E-02	0.76	0.56	1.03	3.5E-20	1.6E-01	7.1E-02
4.1E-76	3.84	3.33	4.42	6.9E-03	1.36	1.09	1.71	8.1E-26	5.6E-02	9.7E-02
2.8E-77	4.56	3.89	5.35	8.9E-02	0.77	0.57	1.04	3.4E-20	1.8E-01	8.6E-02
3.6E-77	4.44	3.79	5.19	1.7E-01	0.81	0.61	1.09	1.2E-20	3.1E-01	1.7E-01
1.1E-88	4.41	3.81	5.11	3.3E-05	1.70	1.32	2.19	2.4E-33	1.7E-02	8.4E-03
3.7E-93	4.67	4.03	5.41	6.4E-05	1.74	1.33	2.28	3.3E-35	2.2E-02	1.7E-02
6.5E-01	1.04	0.88	1.22	2.6E-07	1.63	1.36	1.97	1.5E-03	1.9E-01	2.7E-02
7.7E-105	5.90	5.03	6.93	2.7E-01	1.35	0.79	2.29	1.6E-38	2.2E-01	2.8E-01
1.5E-94	4.63	4.00	5.36	9.2E-05	1.79	1.34	2.41	1.1E-36	1.5E-03	6.2E-05
2.8E-73	3.95	3.40	4.58	1.5E-01	0.80	0.59	1.08	8.4E-20	6.9E-01	1.2E-01
1.6E-106	5.90	5.03	6.91	1.2E-01	1.56	0.90	2.72	5.1E-41	6.8E-02	1.2E-01
6.8E-03	0.83	0.72	0.95	2.7E-07	1.54	1.31	1.82	6.2E-02	5.0E-03	1.2E-02
4.3E-01	0.94	0.82	1.09	1.2E-10	1.75	1.48	2.08	6.6E-04	2.5E-03	7.7E-05
2.2E-35	0.44	0.39	0.50	5.0E-07	0.66	0.56	0.77	7.5E-18	6.1E-05	1.5E-02
1.1E-43	0.41	0.36	0.46	3.5E-07	0.65	0.55	0.77	5.7E-21	8.9E-04	1.3E-02
6.5E-44	0.41	0.36	0.46	3.1E-07	0.65	0.55	0.76	4.3E-21	8.5E-04	1.3E-02
4.2E-108	6.02	5.13	7.06	2.7E-01	1.40	0.77	2.54	6.7E-41	1.7E-01	2.5E-01
2.2E-43	0.42	0.37	0.47	3.7E-07	0.66	0.56	0.77	4.3E-21	4.6E-04	1.2E-02
1.1E-02	0.84	0.73	0.96	3.1E-07	1.53	1.30	1.81	8.4E-02	4.7E-02	1.1E-02
1.8E-53	0.38	0.33	0.43	3.0E-10	0.59	0.51	0.70	1.5E-27	4.6E-04	7.9E-05
2.3E-01	0.91	0.79	1.06	7.1E-08	1.62	1.36	1.94	1.2E-02	4.8E-02	2.7E-02
3.0E-06	0.73	0.64	0.83	3.1E-07	1.54	1.31	1.82	8.2E-01	8.3E-03	1.1E-02
3.9E-01	0.94	0.81	1.09	7.5E-09	1.70	1.42	2.03	3.7E-03	1.3E-02	9.4E-03
2.2E-01	0.91	0.78	1.06	5.0E-08	1.66	1.38	2.00	1.1E-02	4.8E-02	2.7E-02
2.2E-01	0.91	0.78	1.06	5.3E-08	1.66	1.38	1.99	1.2E-02	5.0E-02	2.8E-02
2.5E-01	0.92	0.79	1.06	6.0E-08	1.63	1.36	1.94	1.1E-02	4.6E-02	2.6E-02
3.1E-01	0.92	0.79	1.08	7.8E-09	1.71	1.43	2.06	4.7E-03	1.5E-02	1.0E-02
3.1E-03	1.59	1.17	2.17	3.4E-07	2.43	1.73	3.41	1.8E-05	1.7E-05	1.2E-07
3.7E-03	1.63	1.17	2.28	1.9E-07	2.69	1.85	3.91	1.5E-05	1.6E-05	7.3E-08
3.1E-11	1.55	1.36	1.76	4.3E-07	0.65	0.55	0.77	7.2E-01	2.8E-04	2.9E-02
3.6E-03	1.64	1.18	2.28	2.0E-07	2.69	1.85	3.90	1.5E-05	1.6E-05	7.6E-08
1.7E-74	3.97	3.43	4.61	8.1E-01	0.96	0.71	1.31	1.6E-23	4.1E-01	9.9E-01
1.7E-74	3.98	3.43	4.61	8.1E-01	0.96	0.71	1.31	1.7E-23	4.1E-01	9.9E-01
4.1E-87	4.61	3.96	5.37	5.1E-01	0.88	0.60	1.29	1.6E-28	4.8E-01	4.5E-01
5.2E-112	6.75	5.71	7.97	7.4E-01	0.75	0.14	4.00	5.6E-44	7.5E-01	8.0E-01
2.7E-03	1.49	1.15	1.94	9.9E-09	2.36	1.76	3.17	2.5E-05	1.0E+00	1.0E+00
2.7E-03	1.49	1.15	1.94	1.0E-08	2.36	1.76	3.17	2.5E-05	1.0E+00	1.0E+00
6.1E-106	5.85	4.99	6.85	5.7E-01	0.78	0.33	1.85	6.2E-40	9.0E-01	5.3E-01
2.9E-113	6.41	5.46	7.53	COND[i]	COND[i]	COND[i]	COND[i]	4.7E-45	COND[i]	COND[i]
6.1E-03	1.38	1.10	1.74	2.3E-08	2.09	1.61	2.70	8.9E-05	COND[i]	5.0E-01
2.7E-03	1.49	1.15	1.94	1.0E-08	2.36	1.76	3.17	2.5E-05	COND[i]	COND[i]
1.1E-107	6.02	5.13	7.06	3.2E-01	0.57	0.19	1.71	5.7E-41	2.2E-01	3.0E-01
2.9E-106	5.89	5.03	6.91	6.3E-01	0.81	0.34	1.93	3.9E-40	9.4E-01	5.9E-01
2.3E-03	1.50	1.16	1.95	1.0E-08	2.36	1.76	3.16	2.4E-05	9.5E-01	9.6E-01
2.3E-03	1.50	1.16	1.95	1.0E-08	2.36	1.76	3.16	2.4E-05	9.5E-01	9.6E-01
2.4E-03	1.50	1.15	1.95	1.0E-08	2.36	1.76	3.16	2.4E-05	9.6E-01	9.6E-01
2.9E-63	2.91	2.57	3.30	1.0E-10	1.76	1.48	2.09	1.5E-29	5.6E-01	6.0E-04

2.9E-63	2.91	2.57	3.30	1.0E-10	1.76	1.48	2.09	1.5E-29	5.6E-01	6.0E-04
2.7E-03	1.49	1.15	1.94	1.0E-08	2.36	1.76	3.16	2.6E-05	9.7E-01	9.8E-01
6.7E-84	4.40	3.79	5.11	4.3E-01	0.87	0.60	1.24	5.6E-27	8.9E-01	3.9E-01
2.0E-02	1.35	1.05	1.73	1.3E-07	2.15	1.62	2.86	5.4E-04	2.7E-01	3.0E-01
2.7E-92	4.47	3.87	5.16	4.2E-03	1.56	1.15	2.11	1.4E-34	8.1E-02	4.4E-03
8.5E-86	3.77	3.30	4.31	1.0E-07	1.86	1.48	2.33	1.1E-35	6.6E-02	3.7E-01
8.4E-109	5.90	5.04	6.90	1.5E-01	1.59	0.85	2.95	2.5E-41	9.4E-03	2.0E-01
8.6E-97	5.51	4.69	6.47	8.8E-01	1.03	0.69	1.55	1.1E-29	6.9E-01	7.4E-01
7.5E-100	5.80	4.93	6.83	8.8E-01	1.03	0.68	1.56	1.9E-31	6.9E-01	7.5E-01
7.8E-72	3.73	3.23	4.31	4.2E-03	1.37	1.10	1.70	4.0E-15	3.6E-02	1.5E-01
4.9E-76	4.12	3.54	4.79	5.8E-03	1.38	1.10	1.73	5.2E-15	4.7E-02	1.9E-01
8.2E-74	4.07	3.50	4.74	6.7E-03	1.36	1.09	1.71	6.2E-14	4.7E-02	2.0E-01
3.9E-78	4.17	3.59	4.84	2.4E-03	1.42	1.13	1.79	3.2E-16	2.9E-02	1.1E-01
5.2E-76	4.02	3.47	4.66	3.4E-03	1.40	1.12	1.75	1.9E-15	3.0E-02	1.4E-01
3.1E-74	4.02	3.46	4.67	4.9E-03	1.38	1.10	1.72	1.9E-14	3.5E-02	1.7E-01
3.5E-74	3.84	3.32	4.44	2.7E-03	1.40	1.12	1.74	3.0E-15	2.1E-02	1.1E-01
9.2E-74	3.83	3.31	4.42	3.3E-03	1.39	1.12	1.73	4.8E-15	2.5E-02	1.3E-01
1.7E-75	3.98	3.43	4.61	2.3E-03	1.42	1.13	1.77	1.5E-15	2.6E-02	1.2E-01
1.0E-73	4.01	3.45	4.66	9.7E-03	1.34	1.07	1.68	7.6E-14	6.0E-02	2.4E-01
9.0E-75	3.99	3.44	4.62	3.1E-03	1.40	1.12	1.75	5.7E-15	2.4E-02	1.3E-01
1.4E-78	4.19	3.61	4.87	1.4E-03	1.45	1.15	1.82	1.6E-16	1.7E-02	7.8E-02
9.8E-99	6.54	5.49	7.78	1.2E-01	1.30	0.93	1.81	8.3E-25	8.5E-02	1.2E-01
9.5E-99	6.45	5.43	7.68	9.1E-02	1.33	0.96	1.85	4.2E-25	9.3E-02	1.0E-01
8.8E-75	3.93	3.39	4.55	3.3E-03	1.39	1.12	1.74	3.8E-15	2.6E-02	1.3E-01
4.0E-74	3.84	3.32	4.43	3.0E-03	1.39	1.12	1.73	3.7E-15	2.4E-02	1.2E-01
8.0E-99	6.48	5.45	7.71	1.1E-01	1.31	0.94	1.83	7.1E-25	1.1E-01	1.1E-01
7.8E-96	5.88	4.97	6.94	7.8E-02	1.33	0.97	1.83	1.4E-24	7.0E-02	7.4E-02
4.0E-97	6.09	5.14	7.22	7.5E-02	1.34	0.97	1.84	9.0E-25	6.2E-02	7.1E-02
4.4E-97	6.08	5.13	7.20	7.2E-02	1.34	0.97	1.85	8.1E-25	5.9E-02	6.7E-02
1.1E-94	5.81	4.92	6.87	7.8E-02	1.33	0.97	1.82	3.3E-24	7.1E-02	7.3E-02
4.2E-97	6.07	5.13	7.19	6.7E-02	1.35	0.98	1.85	7.0E-25	5.6E-02	6.3E-02
6.3E-98	6.21	5.23	7.36	5.0E-02	1.37	1.00	1.89	4.0E-25	4.2E-02	4.7E-02
7.4E-96	5.92	5.01	7.00	7.0E-02	1.34	0.98	1.85	2.4E-24	6.5E-02	6.8E-02
4.3E-96	5.94	5.02	7.03	6.2E-02	1.35	0.98	1.86	1.6E-24	6.0E-02	6.0E-02
2.8E-96	5.95	5.03	7.04	4.8E-02	1.38	1.00	1.89	1.1E-24	5.2E-02	4.7E-02
3.4E-94	5.76	4.87	6.80	9.2E-02	1.31	0.96	1.78	8.5E-23	8.9E-02	8.4E-02
6.4E-92	5.69	4.82	6.73	1.3E-01	1.27	0.93	1.72	2.6E-20	1.3E-01	1.2E-01
9.0E-90	6.17	5.16	7.36	6.0E-01	1.09	0.80	1.48	1.4E-15	5.8E-01	5.7E-01
1.4E-88	5.54	4.69	6.56	2.3E-01	1.20	0.89	1.62	1.3E-17	2.5E-01	2.2E-01
1.5E-88	5.55	4.69	6.56	1.6E-01	1.23	0.92	1.65	2.4E-17	2.2E-01	1.8E-01
5.3E-90	5.67	4.79	6.71	9.6E-02	1.28	0.96	1.72	4.7E-18	1.2E-01	1.0E-01
1.3E-82	5.25	4.44	6.22	1.4E-01	1.22	0.94	1.60	1.0E-10	2.3E-01	1.8E-01
3.9E-82	5.25	4.43	6.22	1.5E-01	1.22	0.93	1.59	2.0E-10	2.4E-01	1.9E-01
1.3E-76	4.78	4.05	5.64	1.1E-01	1.23	0.96	1.58	7.9E-08	1.5E-01	1.3E-01
6.9E-75	4.02	3.46	4.67	9.8E-06	1.60	1.30	1.97	2.4E-14	5.7E-03	1.8E-03
2.4E-76	4.00	3.45	4.63	6.8E-06	1.60	1.30	1.97	1.4E-14	5.7E-03	1.4E-03
1.6E-79	4.29	3.69	4.99	4.3E-06	1.64	1.33	2.02	1.6E-14	5.1E-03	1.2E-03
9.6E-70	3.50	3.05	4.03	1.3E-08	1.72	1.43	2.07	4.7E-16	1.7E-05	2.5E-06
1.1E-16	0.41	0.34	0.51	2.4E-08	0.50	0.39	0.64	5.3E-09	1.9E-07	1.4E-08
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
1.2E-73	4.69	3.97	5.54	2.1E-01	1.17	0.91	1.50	9.4E-01	3.6E-01	2.9E-01
1.2E-73	4.69	3.97	5.54	2.0E-01	1.17	0.92	1.50	9.9E-01	3.4E-01	2.8E-01
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
1.2E-73	4.69	3.97	5.54	2.0E-01	1.17	0.92	1.50	9.9E-01	3.4E-01	2.8E-01
2.3E-03	1.77	1.22	2.55	1.4E-07	3.11	2.04	4.75	3.1E-06	5.9E-08	6.0E-09

3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
9.7E-74	4.70	3.98	5.56	2.0E-01	1.18	0.92	1.50	COND[i]	3.3E-01	2.7E-01
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
2.1E-08	4.91	2.81	8.56	1.3E-11	8.33	4.51	15.39	3.8E-10	3.7E-10	9.1E-12
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
6.0E-71	4.37	3.72	5.14	1.1E-01	1.21	0.96	1.53	1.5E-01	2.5E-01	1.8E-01
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
3.7E-16	0.42	0.34	0.52	3.2E-08	0.51	0.40	0.64	6.1E-09	2.1E-07	1.6E-08
3.2E-16	0.42	0.35	0.52	3.0E-08	0.51	0.40	0.65	5.7E-09	2.4E-07	1.7E-08
2.2E-19	0.46	0.39	0.55	1.0E-08	0.57	0.47	0.69	2.0E-08	4.4E-08	9.8E-09
3.2E-16	0.42	0.35	0.52	3.0E-08	0.51	0.40	0.65	5.7E-09	2.4E-07	1.7E-08
3.2E-16	0.42	0.35	0.52	3.0E-08	0.51	0.40	0.65	5.7E-09	2.4E-07	1.7E-08
3.2E-16	0.42	0.35	0.52	3.0E-08	0.51	0.40	0.65	5.7E-09	2.4E-07	1.7E-08
3.2E-16	0.42	0.35	0.52	3.0E-08	0.51	0.40	0.65	5.7E-09	2.4E-07	1.7E-08
3.4E-07	4.01	2.35	6.84	6.6E-11	7.33	4.03	13.33	4.0E-09	2.0E-09	3.9E-11
3.4E-07	4.01	2.35	6.84	6.6E-11	7.33	4.03	13.33	4.0E-09	2.0E-09	3.9E-11
3.4E-07	4.01	2.35	6.84	6.6E-11	7.33	4.03	13.33	4.0E-09	2.0E-09	3.9E-11
4.9E-05	1.89	1.39	2.56	1.2E-07	2.49	1.77	3.49	9.1E-09	9.9E-04	7.0E-04
1.1E-01	1.14	0.97	1.34	1.0E-08	1.70	1.42	2.03	2.0E-09	4.4E-07	5.7E-07
1.0E-01	1.14	0.97	1.34	1.0E-08	1.70	1.42	2.03	2.1E-09	4.4E-07	5.7E-07
7.8E-07	3.70	2.20	6.23	3.5E-10	6.36	3.57	11.33	1.6E-08	8.6E-09	2.8E-10
7.8E-07	3.70	2.20	6.23	3.5E-10	6.36	3.57	11.33	1.6E-08	8.6E-09	2.8E-10
4.7E-03	1.20	1.06	1.37	4.0E-07	1.43	1.25	1.64	1.5E-07	1.4E-05	4.6E-06
4.0E-03	1.21	1.06	1.37	4.1E-07	1.43	1.24	1.64	1.4E-07	1.5E-05	4.7E-06

A determinants. Most of the data is after conditioning on HLA-B*08 with or without additional
g on HLA B*08 showed that most of the MHC signal is due to HLA B*08. Results include both
d information scores >0.9 (see Supplementary Methods). The p values were determined usi
nificant 100 markers prior to conditioning on HLA B*08 and all markers with p < 5E-07 after c

For sequences designated with amino acid (AA) numbers the symbol refers to the standard A
tive AAs. The AA position includes the leader sequence (e.g. DRB1* position 104 is the same
 (SPEC) is compared with all alternative alleles.

s of the genotypes. Posterior probablities of genotyped markers are 1.0.

SNP allele frequency determined by the SNPTEST v2 algorithm (see methods). SNPs with 1.

itioned genes/markers the p values and odds ratios were 1.0.

Cond. p-value HLA B*08 C*0304 C*0501 C*1203[g]	Cond. p-value All HLA B A*3101 DRB1*07 DRB1*16[g]	Cond. p-value Selected HLA B A*3101 DRB1*07 DRB1*16[g]	Cond. p-value HLA B*08 rs1265109[g]	Cond. p-value HLA B*0801 DRB1*07 DRB1*16 A3101 rs1265109[g]
1.4E-06	4.4E-01	3.4E-01	3.6E-06	2.7E-01
2.1E-06	7.4E-01	5.1E-01	4.7E-06	3.1E-01
1.4E-06	4.3E-01	3.3E-01	3.6E-06	2.7E-01
1.4E-06	4.4E-01	3.3E-01	3.6E-06	2.7E-01
2.3E-06	8.1E-01	5.5E-01	5.5E-06	3.6E-01
2.3E-06	8.1E-01	5.5E-01	5.5E-06	3.6E-01
3.4E-06	1.0E+00	1.0E+00	7.5E-06	1.0E+00
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.8E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.3E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	5.9E-06	3.8E-01
2.5E-06	8.2E-01	5.7E-01	6.0E-06	3.9E-01
3.0E-04	6.5E-03	1.7E-02	1.9E-04	4.3E-03
2.2E-04	5.9E-03	1.5E-02	1.5E-04	3.7E-03
3.6E-01	3.5E-01	4.4E-01	4.3E-01	5.2E-01
3.6E-04	3.2E-03	1.3E-02	2.7E-04	4.5E-03
3.4E-01	3.4E-01	4.3E-01	4.1E-01	5.2E-01
3.2E-01	3.1E-01	4.0E-01	3.8E-01	5.0E-01
2.6E-04	1.7E-03	7.8E-03	2.0E-04	2.3E-03
3.1E-01	2.2E-01	3.1E-01	3.4E-01	4.0E-01
2.6E-01	1.9E-01	2.9E-01	3.2E-01	4.0E-01
2.7E-01	2.0E-01	3.0E-01	3.3E-01	4.1E-01
3.8E-01	2.4E-01	3.8E-01	4.8E-01	5.7E-01
3.8E-01	2.5E-01	3.8E-01	4.8E-01	5.8E-01
2.7E-01	1.7E-01	2.3E-01	3.6E-01	4.2E-01
2.8E-01	1.8E-01	2.3E-01	3.8E-01	4.3E-01
4.1E-01	1.7E-01	1.4E-01	6.5E-02	1.2E-01
1.9E-01	1.1E-01	1.4E-01	2.6E-01	2.7E-01
3.7E-01	1.7E-01	1.3E-01	5.3E-02	1.3E-01
1.8E-01	1.1E-01	1.4E-01	2.6E-01	2.7E-01
3.7E-01	1.6E-01	1.3E-01	5.6E-02	1.2E-01
2.2E-01	1.3E-01	1.7E-01	3.0E-01	3.0E-01
3.3E-01	1.3E-01	1.1E-01	4.8E-02	1.1E-01
2.6E-01	1.6E-01	2.0E-01	3.5E-01	3.6E-01
1.6E-01	9.8E-02	1.2E-01	2.4E-01	2.6E-01
3.3E-01	2.0E-01	2.3E-01	4.1E-01	4.0E-01
1.7E-01	8.3E-02	5.7E-02	1.8E-02	4.7E-02
2.4E-01	7.7E-02	5.8E-02	3.1E-02	4.8E-02
2.8E-01	1.6E-01	2.0E-01	3.7E-01	3.6E-01
1.6E-01	1.0E-01	1.4E-01	2.4E-01	2.8E-01
2.7E-01	1.5E-01	1.9E-01	3.5E-01	3.5E-01

4.0E-01	1.5E-01	1.6E-01	9.6E-02	1.2E-01
1.8E-01	1.5E-01	2.3E-01	2.8E-01	4.8E-01
1.9E-01	1.5E-01	2.4E-01	2.9E-01	4.8E-01
2.4E-01	9.5E-02	5.8E-02	2.8E-02	3.2E-02
1.9E-01	1.5E-01	2.4E-01	2.9E-01	4.8E-01
5.6E-01	2.3E-01	2.2E-01	1.6E-01	1.9E-01
1.9E-01	1.5E-01	2.4E-01	2.9E-01	4.8E-01
1.4E-01	1.2E-01	1.9E-01	2.1E-01	4.0E-01
4.1E-01	7.4E-02	7.6E-02	6.5E-02	6.8E-02
1.7E-01	1.5E-01	2.3E-01	2.4E-01	4.6E-01
2.9E-01	2.3E-01	3.5E-01	4.0E-01	6.3E-01
5.0E-02	3.7E-02	1.5E-02	1.2E-03	3.6E-03
1.8E-01	3.6E-02	3.4E-02	4.8E-03	1.5E-02
2.5E-01	3.5E-01	1.6E-01	4.5E-03	5.9E-02
2.2E-01	4.5E-01	3.7E-01	1.5E-01	2.3E-01
5.4E-01	1.8E-02	4.7E-03	7.1E-03	6.5E-02
4.2E-01	7.6E-01	7.1E-01	6.3E-01	5.0E-01
8.3E-02	1.7E-01	1.4E-01	4.4E-02	6.0E-02
3.2E-01	4.1E-03	2.0E-03	1.4E-01	8.8E-01
1.9E-02	3.3E-03	3.2E-04	COND	COND
1.1E-01	6.5E-05	8.4E-04	2.6E-01	9.8E-03
1.6E-01	6.3E-04	3.8E-04	8.9E-01	4.0E-02
1.6E-01	6.0E-04	3.6E-04	8.8E-01	3.8E-02
1.8E-01	2.6E-01	1.8E-01	1.2E-01	8.9E-02
1.7E-01	3.4E-04	1.6E-04	8.3E-01	2.1E-02
3.2E-01	2.5E-01	2.5E-01	6.2E-01	3.3E-01
1.0E-02	2.4E-03	2.3E-03	1.9E-02	1.3E-01
8.7E-01	8.6E-02	7.7E-02	3.8E-02	8.9E-02
1.2E-01	3.4E-02	2.1E-01	1.7E-01	7.4E-01
4.5E-01	2.5E-02	2.8E-02	1.4E-02	3.5E-02
8.8E-01	8.9E-02	8.6E-02	4.1E-02	1.0E-01
9.0E-01	9.2E-02	8.8E-02	4.2E-02	1.1E-01
8.4E-01	8.3E-02	7.4E-02	3.6E-02	8.5E-02
5.0E-01	3.0E-02	3.3E-02	1.7E-02	4.2E-02
2.6E-01	3.5E-04	8.3E-05	5.3E-04	1.1E-02
COND	3.3E-04	6.7E-05	1.5E-03	2.4E-02
1.0E-01	3.0E-04	2.4E-02	2.4E-03	7.6E-04
9.5E-01	3.3E-04	6.8E-05	1.5E-03	2.4E-02
6.4E-01	1.8E-01	3.5E-01	9.6E-01	3.8E-01
6.5E-01	1.8E-01	3.5E-01	9.6E-01	3.8E-01
7.4E-01	3.8E-01	2.6E-01	8.1E-01	8.5E-01
7.0E-01	8.4E-01	9.0E-01	9.0E-01	7.9E-01
2.0E-03	1.0E+00	1.0E+00	2.7E-03	3.9E-02
2.0E-03	1.0E+00	1.0E+00	2.7E-03	3.9E-02
6.4E-01	9.0E-01	7.7E-01	4.3E-01	7.5E-01
COND[i]	COND[i]	COND[i]	COND[i]	COND[i]
1.6E-03	1.0E+00	8.3E-01	1.5E-03	3.2E-02
2.0E-03	COND[i]	COND[i]	2.7E-03	3.9E-02
3.5E-01	3.1E-01	4.3E-01	1.7E-01	3.2E-01
7.1E-01	9.5E-01	8.3E-01	4.7E-01	8.1E-01
2.1E-03	9.4E-01	9.4E-01	2.8E-03	4.1E-02
2.1E-03	9.4E-01	9.4E-01	2.8E-03	4.1E-02
2.1E-03	9.5E-01	9.5E-01	2.8E-03	4.0E-02
2.5E-05	7.9E-01	2.6E-03	1.1E-06	1.6E-05

2.5E-05	7.9E-01	2.6E-03	1.1E-06	1.6E-05
2.1E-03	9.7E-01	9.7E-01	2.8E-03	4.0E-02
9.0E-01	3.5E-01	7.0E-01	8.7E-01	2.6E-01
1.5E-02	3.3E-01	4.2E-01	1.2E-02	8.5E-02
2.5E-01	6.4E-01	3.0E-02	2.8E-02	5.5E-02
8.7E-02	1.1E-01	6.6E-01	2.7E-03	4.1E-02
1.1E-01	9.8E-03	3.8E-01	8.3E-02	1.6E-01
7.8E-01	9.8E-01	8.6E-01	7.9E-01	8.8E-01
8.0E-01	9.1E-01	7.8E-01	7.8E-01	8.0E-01
1.1E-02	3.3E-02	5.7E-02	1.9E-02	9.2E-03
1.6E-02	1.1E-01	1.9E-01	1.6E-02	3.3E-02
1.6E-02	1.2E-01	1.9E-01	1.6E-02	3.3E-02
7.8E-03	8.2E-02	1.5E-01	8.1E-03	2.4E-02
9.7E-03	8.0E-02	1.4E-01	9.5E-03	2.2E-02
1.2E-02	9.3E-02	1.6E-01	1.2E-02	2.5E-02
7.0E-03	5.7E-02	1.0E-01	6.7E-03	1.4E-02
8.6E-03	6.7E-02	1.2E-01	8.2E-03	1.7E-02
7.5E-03	6.7E-02	1.2E-01	6.9E-03	1.6E-02
2.0E-02	1.3E-01	2.0E-01	2.1E-02	3.6E-02
8.9E-03	7.0E-02	1.3E-01	9.2E-03	1.9E-02
4.0E-03	5.2E-02	9.4E-02	4.3E-03	1.3E-02
9.5E-02	3.3E-01	4.4E-01	7.7E-02	3.5E-01
7.9E-02	3.6E-01	4.4E-01	5.9E-02	3.3E-01
9.1E-03	7.3E-02	1.2E-01	8.5E-03	1.8E-02
8.4E-03	7.0E-02	1.2E-01	7.9E-03	1.8E-02
9.1E-02	4.0E-01	4.7E-01	6.9E-02	3.6E-01
7.3E-02	2.7E-01	3.4E-01	5.0E-02	2.7E-01
6.4E-02	2.7E-01	3.5E-01	4.7E-02	2.8E-01
6.1E-02	2.6E-01	3.4E-01	4.5E-02	2.7E-01
6.9E-02	3.1E-01	3.8E-01	4.9E-02	3.0E-01
5.8E-02	2.5E-01	3.3E-01	4.1E-02	2.6E-01
3.8E-02	2.1E-01	2.8E-01	2.9E-02	2.1E-01
6.8E-02	2.5E-01	3.1E-01	4.6E-02	2.5E-01
5.9E-02	2.4E-01	2.9E-01	4.1E-02	2.3E-01
4.6E-02	2.4E-01	2.7E-01	3.3E-02	2.1E-01
8.6E-02	3.7E-01	4.3E-01	6.2E-02	3.7E-01
1.2E-01	4.4E-01	5.3E-01	9.1E-02	4.5E-01
5.5E-01	8.6E-01	7.7E-01	4.9E-01	8.5E-01
2.2E-01	7.6E-01	8.2E-01	1.8E-01	7.3E-01
1.7E-01	6.6E-01	7.0E-01	1.3E-01	5.8E-01
1.0E-01	4.6E-01	5.2E-01	7.0E-02	4.1E-01
1.8E-01	6.8E-01	7.0E-01	1.4E-01	6.0E-01
1.9E-01	7.1E-01	7.2E-01	1.5E-01	6.3E-01
1.1E-01	5.5E-01	5.2E-01	9.9E-02	4.3E-01
8.8E-04	1.1E-02	6.1E-03	3.0E-04	1.9E-03
8.5E-04	1.2E-02	4.9E-03	2.2E-04	1.6E-03
8.2E-04	7.4E-03	3.4E-03	2.1E-04	1.2E-03
2.1E-06	3.0E-02	2.2E-02	5.6E-07	1.1E-02
2.0E-07	7.5E-01	6.1E-01	1.7E-08	6.1E-01
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
1.5E-01	8.4E-01	8.3E-01	1.9E-01	6.3E-01
1.4E-01	8.1E-01	8.1E-01	1.8E-01	6.1E-01
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
1.4E-01	8.1E-01	8.1E-01	1.8E-01	6.1E-01
2.2E-07	1.9E-01	1.7E-01	8.6E-08	3.3E-01

2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
1.4E-01	8.0E-01	7.9E-01	1.8E-01	6.0E-01
2.3E-07	COND[i]	COND[i]	2.0E-08	COND[i]
2.4E-09	COND[i]	COND[i]	5.1E-11	COND[i]
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
9.0E-02	6.6E-01	6.3E-01	1.3E-01	5.2E-01
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
2.3E-07	1.0E+00	1.0E+00	2.0E-08	1.0E+00
2.1E-07	8.2E-01	7.8E-01	1.7E-08	6.1E-01
6.2E-08	3.6E-02	7.9E-02	8.9E-09	7.0E-02
2.1E-07	8.2E-01	7.8E-01	1.7E-08	6.1E-01
2.1E-07	8.2E-01	7.8E-01	1.7E-08	6.1E-01
2.1E-07	8.2E-01	7.8E-01	1.7E-08	6.1E-01
2.1E-07	8.2E-01	7.8E-01	1.7E-08	6.1E-01
1.2E-08	9.4E-01	9.2E-01	2.9E-10	9.9E-01
1.2E-08	9.4E-01	9.2E-01	2.9E-10	9.9E-01
1.2E-08	9.4E-01	9.2E-01	2.9E-10	9.9E-01
4.9E-05	9.4E-05	9.2E-05	1.8E-05	8.3E-06
8.3E-08	8.4E-04	2.2E-03	5.2E-08	3.6E-04
8.3E-08	8.4E-04	2.2E-03	5.2E-08	3.6E-04
4.0E-08	8.1E-01	7.8E-01	1.2E-09	8.3E-01
4.0E-08	8.1E-01	7.8E-01	1.2E-09	8.3E-01
9.9E-07	4.4E-05	2.8E-05	1.5E-06	1.1E-05
8.6E-07	5.2E-05	3.1E-05	1.4E-06	1.1E-05

determinants or

genotyped

ng SNPTEST V2

ontrolling for HLA

A nomenclature.

as AA position

00 information