

# A genome-wide association study identifies vitiligo susceptibility loci at *MHC* and 6q27

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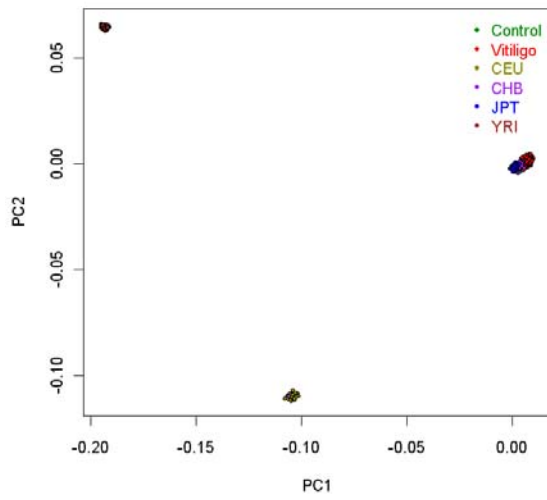
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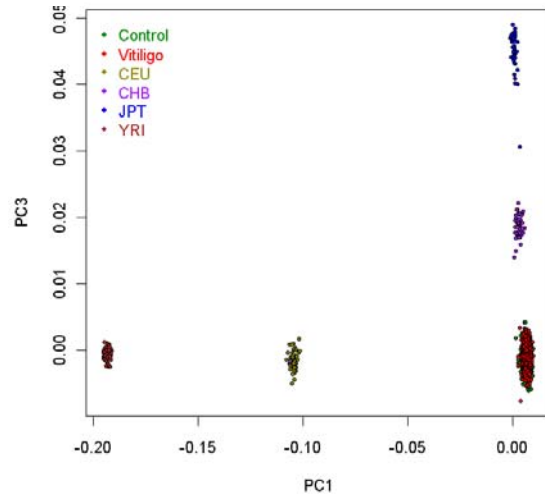
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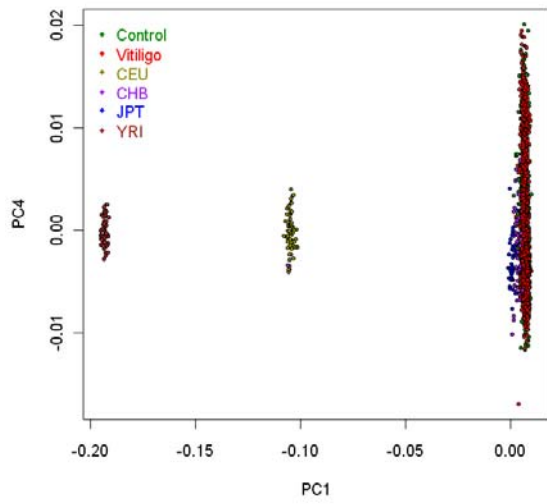
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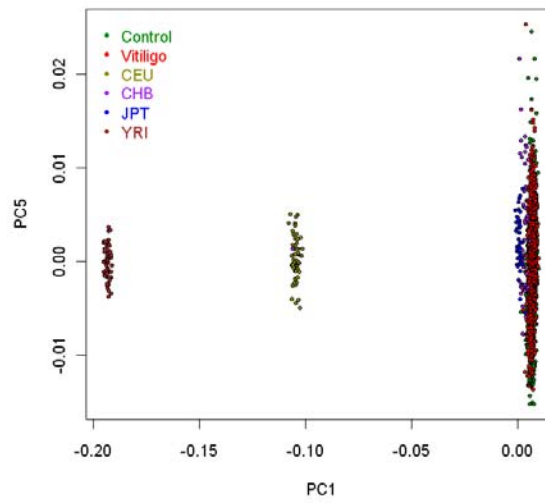
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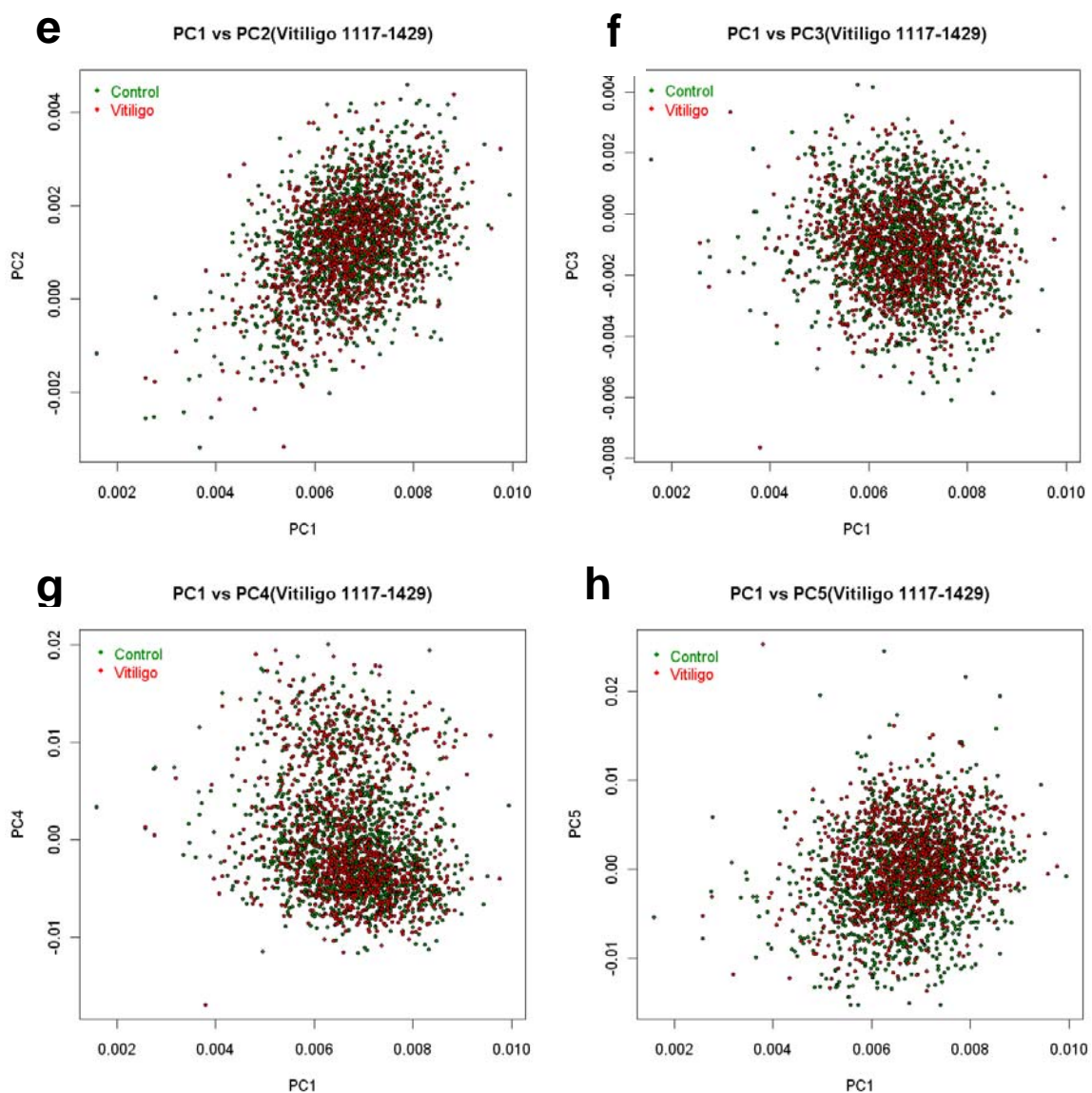


**c** PC1 vs PC4(2546Chinese Samples vs 206hapmap)

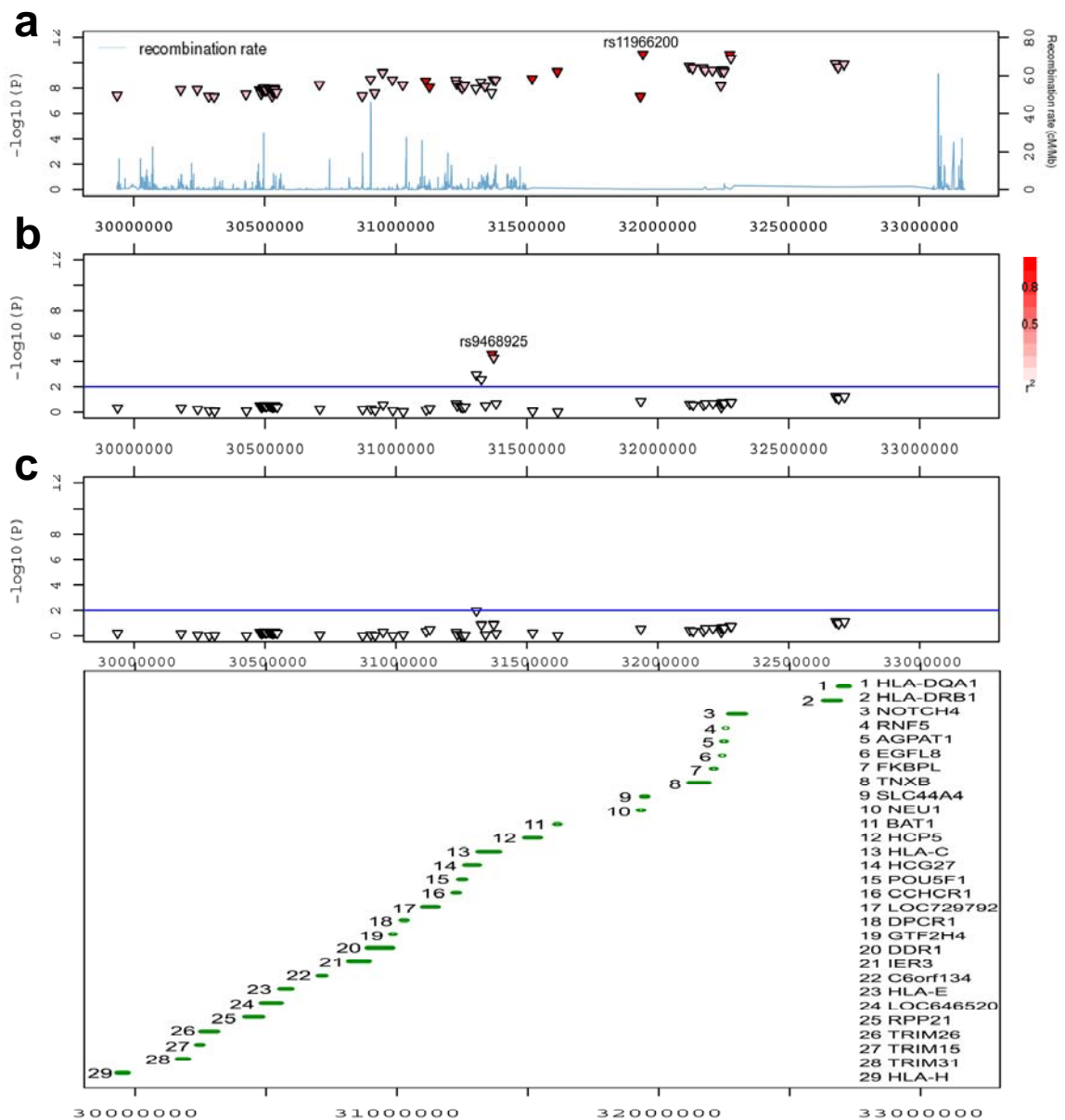


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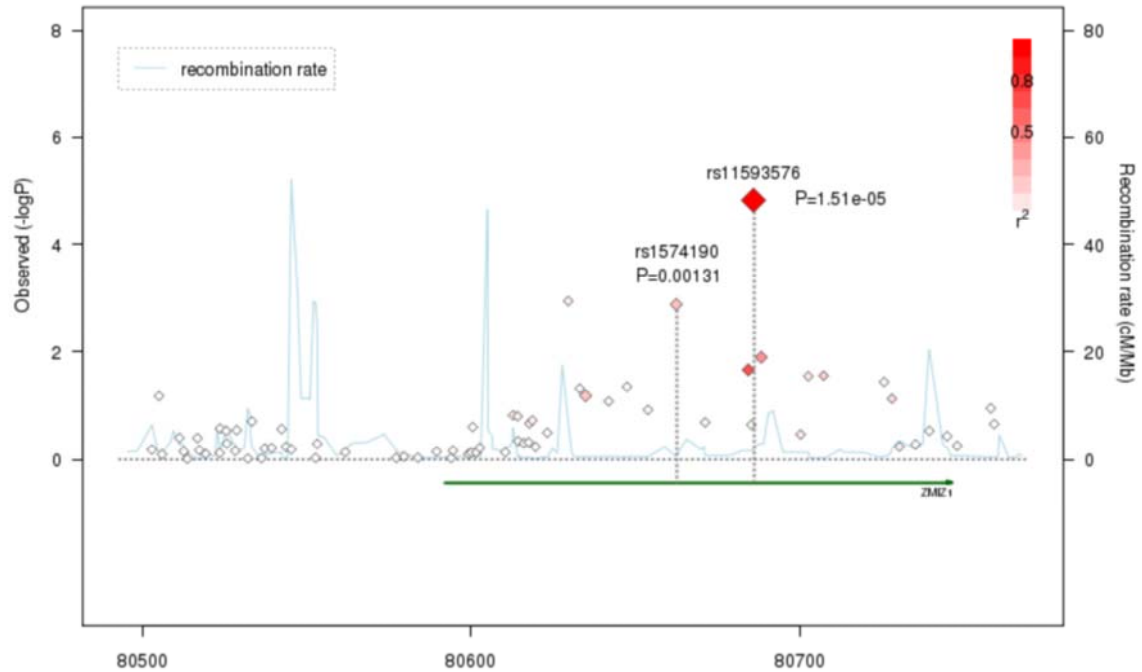




**Supplementary Figure 1** The principal components analysis (PCA) of 2,546 GWAS samples. (a-d) The PCA of 2,546 samples and 206 reference DNA samples from the HapMap. Cases are in red, controls are in green, CHB samples are in violet, JPT samples are in blue, CEU samples are in yellow and YRI samples are in brown. (e-h) The pair-wise PCA of 2,546 participant samples (1,117 cases, 1,429 healthy controls). The red points are the cases, and the green points are the controls.



**Supplementary Figure 2** Conditional logistic regression analysis for 70 SNPs in MHC region. The  $P$  values ( $-\log_{10}P$ ) shown as in y-axis were plotted against their map positions (x-axis). The color of each SNP spot reflects its  $r^2$  with the top SNP, changing from red to white. Estimated recombination rates were plotted in light blue. **a.** The 70 SNPs with  $P$  values of Cochran-Armitage trend test less than  $5 \times 10^{-8}$ ; **b.** After controlling for the effect of rs11966200; **c.** After controlling for the effect of rs11966200 and rs9468925.



**Supplementary Figure 3** The scatter plot of the association evidences within *ZMIZ1* at 10q22 for vitiligo. The  $P$  values ( $-\log_{10}P$ ) shown as in y-axis were plotted against their map positions (x-axis). The color of each SNP spot reflects its  $r^2$  with the top SNP, changing from red to white. Estimated recombination rates were plotted in light blue.

**Supplementary Table 1 Results of conditional logistic regression analysis for 70 SNPs in MHC region**

Gene	SNP	BP	A1	F_A	F_U	$P_{trend}$	OR	Controlling rs11966200		Controlling rs11966200 and rs9468925	
								$P$	OR	$P$	OR
HLA-H	rs9295822	29936859	A	0.123	0.077	3.52E-08	1.68	4.57E-01	1.11	6.08E-01	1.08
TRIM31	rs11964542	30179739	G	0.116	0.070	1.28E-08	1.75	4.59E-01	1.12	6.70E-01	1.07
TRIM15	rs17188127	30243081	A	0.116	0.070	1.24E-08	1.74	5.93E-01	1.09	8.46E-01	1.03
TRIM26	rs11967808	30287167	C	0.115	0.071	4.26E-08	1.71	7.38E-01	1.06	1.00E+00	1.00
TRIM26	rs17188268	30307337	A	0.116	0.072	4.57E-08	1.70	8.27E-01	1.04	9.12E-01	0.98
RPP21	rs3132649	30429036	A	0.118	0.072	2.85E-08	1.71	7.71E-01	1.05	9.59E-01	0.99
RPP21	rs3094061	30429168	C	0.118	0.072	2.85E-08	1.71	7.71E-01	1.05	9.59E-01	0.99
RPP21	rs9261761	30480966	A	0.135	0.085	1.34E-08	1.68	2.97E-01	1.15	5.11E-01	1.10
LOC646520	rs9261817	30486580	C	0.135	0.085	1.34E-08	1.68	2.97E-01	1.15	5.11E-01	1.10
LOC646520	rs9261821	30487053	G	0.133	0.085	2.59E-08	1.66	4.03E-01	1.12	6.30E-01	1.07
LOC646520	rs9261846	30490419	G	0.135	0.085	1.45E-08	1.67	3.18E-01	1.15	5.24E-01	1.09
LOC646520	rs9261858	30492296	A	0.135	0.085	1.38E-08	1.68	3.16E-01	1.15	5.22E-01	1.09
LOC646520	rs9261862	30492717	G	0.135	0.085	1.38E-08	1.68	3.16E-01	1.15	5.22E-01	1.09
LOC646520	rs9261871	30493873	G	0.135	0.085	1.22E-08	1.68	3.23E-01	1.15	5.32E-01	1.09
HLA-E	rs28750192	30495447	A	0.135	0.085	9.99E-09	1.68	2.86E-01	1.16	4.84E-01	1.10
LOC646520	rs9261919	30499702	A	0.135	0.085	9.99E-09	1.68	2.86E-01	1.16	4.84E-01	1.10
LOC646520	rs9261923	30500139	A	0.135	0.085	9.99E-09	1.68	2.86E-01	1.16	4.84E-01	1.10
LOC646520	rs9261926	30500385	A	0.135	0.085	9.33E-09	1.69	2.84E-01	1.16	4.79E-01	1.10
LOC646520	rs9261947	30502607	A	0.134	0.084	1.36E-08	1.68	3.35E-01	1.14	5.43E-01	1.09
LOC646520	rs9501447	30505819	G	0.134	0.084	1.43E-08	1.68	3.37E-01	1.14	5.45E-01	1.09
LOC646520	rs1079541	30514735	A	0.135	0.085	9.99E-09	1.68	2.86E-01	1.16	4.84E-01	1.10
LOC646520	rs9295871	30519068	G	0.135	0.085	9.99E-09	1.68	2.86E-01	1.16	4.84E-01	1.10
LOC646520	rs9295873	30522214	G	0.134	0.084	1.36E-08	1.68	3.35E-01	1.14	5.43E-01	1.09
LOC646520	rs9295886	30529376	A	0.131	0.083	4.07E-08	1.66	3.85E-01	1.13	6.21E-01	1.07
LOC646520	rs35407515	30531202	G	0.134	0.084	1.36E-08	1.68	3.35E-01	1.14	5.43E-01	1.09
LOC646520	rs34101875	30531337	A	0.134	0.085	1.87E-08	1.67	3.78E-01	1.13	6.01E-01	1.08
LOC646520	rs33986393	30532053	G	0.134	0.084	1.34E-08	1.68	3.34E-01	1.14	5.40E-01	1.09
LOC646520	rs9501336	30535489	A	0.134	0.084	1.50E-08	1.68	3.39E-01	1.14	5.46E-01	1.09
LOC646520	rs11966619	30537012	C	0.135	0.085	9.99E-09	1.68	2.86E-01	1.16	4.84E-01	1.10
LOC646520	rs35792611	30538854	C	0.134	0.085	1.32E-08	1.68	3.24E-01	1.15	5.20E-01	1.09

LOC646520	rs9461612	30546535	A	0.134	0.085	2.11E-08	1.67	3.94E-01	1.13	6.08E-01	1.07
C6orf134	rs17195551	30709374	A	0.119	0.071	5.11E-09	1.76	5.66E-01	1.10	8.27E-01	1.04
IER3	rs1264377	30872886	A	0.137	0.089	3.89E-08	1.63	6.01E-01	1.08	9.86E-01	1.00
DDR1	rs1264350	30904524	G	0.121	0.072	1.96E-09	1.78	5.41E-01	1.12	8.29E-01	1.04
DDR1	rs7759803	30920498	A	0.134	0.086	2.31E-08	1.65	7.25E-01	1.06	9.50E-01	1.01
DDR1	rs7746003	30950873	A	0.130	0.078	5.74E-10	1.78	2.56E-01	1.21	4.96E-01	1.12
GTF2H4	rs3218822	30988315	G	0.121	0.072	2.18E-09	1.78	7.36E-01	1.07	9.68E-01	0.99
DPCR1	rs3132580	31028103	A	0.121	0.073	5.43E-09	1.75	9.23E-01	1.02	7.79E-01	0.95
LOC729792	rs12201301	31115536	A	0.123	0.073	2.71E-09	1.77	6.76E-01	0.91	4.40E-01	0.84
LOC729792	rs17190134	31129839	C	0.122	0.074	8.04E-09	1.73	5.02E-01	0.86	3.09E-01	0.79
CCHCR1	rs130065	31230479	A	0.166	0.105	2.22E-09	1.69	2.03E-01	1.17	5.11E-01	1.09
CCHCR1	rs3130455	31233957	T	0.159	0.103	4.45E-09	1.65	3.07E-01	1.15	7.89E-01	1.04
POU5F1	rs1265159	31248026	A	0.158	0.103	7.15E-09	1.64	3.65E-01	1.13	8.68E-01	1.02
POU5F1	rs3130457	31255173	G	0.158	0.103	9.53E-09	1.63	4.09E-01	1.12	9.29E-01	1.01
HCG27	rs1265181	31263764	G	0.156	0.101	5.85E-09	1.65	3.76E-01	1.13	8.77E-01	1.02
HCG27	rs3130473	31307187	A	0.385	0.309	1.04E-08	1.40	1.04E-03	1.24	1.08E-02	1.19
HLA-C	rs3130424	31326218	C	0.306	0.233	3.23E-09	1.46	2.53E-03	1.25	1.33E-01	1.13
HLA-C	rs2248902	31342093	A	0.169	0.112	7.06E-09	1.61	2.98E-01	1.14	8.17E-01	1.03
HLA-C	rs9468925	31366816	A	0.331	0.408	2.21E-08	0.72	2.52E-05	0.77	NA	NA
HLA-C	rs2524123	31373293	G	0.505	0.421	2.04E-09	1.41	5.26E-05	1.28	1.24E-01	1.14
HLA-C	rs10484554	31382534	A	0.168	0.110	2.31E-09	1.64	2.08E-01	1.18	6.51E-01	1.06
HCP5	rs12206131	31521989	G	0.127	0.075	1.73E-09	1.78	8.16E-01	0.95	5.78E-01	0.88
BAT1	rs2523505	31617981	G	0.127	0.075	4.73E-10	1.80	9.44E-01	0.98	9.36E-01	1.02
NEU1	rs13118	31935265	A	0.137	0.088	4.29E-08	1.64	1.32E-01	0.71	2.82E-01	0.78
SLC44A4	rs11966200	31945045	A	0.123	0.068	2.01E-11	1.92	NA	NA	NA	NA
TNXB	rs34214527	32122434	A	0.146	0.090	1.88E-10	1.74	2.26E-01	1.24	3.63E-01	1.17
TNXB	rs12198173	32134786	A	0.146	0.090	2.55E-10	1.74	2.66E-01	1.21	4.20E-01	1.15
TNXB	rs13199524	32174743	A	0.146	0.090	2.55E-10	1.74	2.66E-01	1.21	4.20E-01	1.15
TNXB	rs12153855	32182782	G	0.152	0.095	3.84E-10	1.71	1.99E-01	1.22	2.54E-01	1.20
FKBPL	rs13211318	32210658	C	0.152	0.095	3.84E-10	1.71	1.99E-01	1.22	2.54E-01	1.20
EGFL8	rs3096697	32242488	A	0.148	0.096	6.31E-09	1.65	4.09E-01	1.13	4.93E-01	1.11
EGFL8	rs3130347	32242634	G	0.154	0.097	4.64E-10	1.70	1.88E-01	1.22	2.35E-01	1.20
AGPAT1	rs3130284	32248465	G	0.154	0.097	3.57E-10	1.70	1.67E-01	1.23	2.11E-01	1.21

AGPAT1	rs3134947	32253183	A	0.154	0.097	4.02E-10	1.70	1.89E-01	1.22	2.36E-01	1.20
RNF5	rs3134945	32254470	A	0.154	0.097	4.93E-10	1.70	1.89E-01	1.22	2.36E-01	1.20
NOTCH4	rs3134942	32276749	A	0.134	0.077	2.12E-11	1.85	1.52E-01	1.38	1.60E-01	1.37
NOTCH4	rs3131296	32280971	A	0.138	0.080	4.44E-11	1.85	1.62E-01	1.32	1.71E-01	1.32
HLA-DRB1	rs2858870	32680229	G	0.161	0.102	1.18E-10	1.70	5.84E-02	1.30	7.59E-02	1.28
HLA-DQA1	rs13204672	32690774	G	0.161	0.102	2.18E-10	1.69	7.78E-02	1.28	1.03E-01	1.25
HLA-DQA1	rs28383344	32713045	G	0.161	0.102	1.28E-10	1.70	5.94E-02	1.30	7.72E-02	1.28

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**Supplementary Table 2a Results of association analysis for 11 top MHC SNPs in GWAS**

Gene	SNP	BP	A1	F_A	F_U	$P_{\text{trend}}$	OR
HLA-C	rs3130424	31326218	C	0.306	0.233	3.23E-09	1.46
HLA-C	rs2248902	31342093	A	0.169	0.112	7.06E-09	1.61
HLA-C	rs9468925	31366816	A	0.331	0.408	2.21E-08	0.72
HLA-C	rs2524123	31373293	G	0.505	0.421	2.04E-09	1.41
HLA-C	rs10484554	31382534	A	0.168	0.110	2.31E-09	1.64
SLC44A4	rs11966200	31945045	A	0.123	0.068	2.01E-11	1.92
NOTCH4	rs3134942	32276749	A	0.134	0.077	2.12E-11	1.85
NOTCH4	rs3131296	32280971	A	0.138	0.08	4.44E-11	1.85
HLA-DRB1	rs2858870	32680229	G	0.161	0.102	1.18E-10	1.7
HLA-DQA1	rs13204672	32690774	G	0.161	0.102	2.18E-10	1.69
HLA-DQA1	rs28383344	32713045	G	0.161	0.102	1.28E-10	1.7

**Supplementary Table 2b Results of haplotype analysis for 11 top MHC SNPs in GWAS**

Haoplype	F_A	F_U	HAPLOTYPE	Frequency	OR	Chi-Square	$P$
H1	0.32	0.39	AGAAGGCGAAC	0.36	0.72	29.15	6.71E-08
H2	0.18	0.18	AGGGGGCGAAC	0.18	1.01	0.07	7.97E-01
H3	0.16	0.17	AGGAGGCGAAC	0.16	0.93	0.85	3.57E-01
H4	0.14	0.13	CGGGGGCGAAC	0.14	1.14	2.85	9.14E-02
H5	0.11	0.06	CAGGAAAAGGG	0.08	1.85	36.22	1.76E-09
H6	0.03	0.02	CAGGAGCGAAC	0.02	1.07	0.15	7.00E-01
H7	0.02	0.01	CAGGAGCGGGG	0.01	1.82	4.54	3.30E-02

**Supplementary Table 3 Results of association analysis for 32 SNPs in the GWAS and Replication 1**

CHR	SNP	BP	Minor Allele	GWAS					GWAS using reference control				Replication 1 (Sequenom)				
				MAF		OR(95%CI)	$P_{HWE}$	$P_{trend}$	MAF	OR	$P_{HWE}$	$P_{trend}$	MAF		OR(95%CI)	$P_{HWE}$	$P_{trend}$
				Case	Control								Case	Control			
1	rs2493144	228882104	C	0.242	0.276	0.84(0.74-0.95)	0.13	5.21E-03	0.278	0.83	0.87	3.92E-04	0.269	0.272	0.99(0.93-1.05)	0.04	7.19E-01
1	rs6667430	232140314	A	0.243	0.293	0.77(0.68-0.88)	0.90	7.40E-05	0.278	0.83	0.38	5.36E-04	0.271	0.274	0.98(0.92-1.05)	0.30	6.20E-01
2	rs28678499	1218030	C	0.322	0.283	1.20(1.07-1.36)	0.95	2.98E-03	0.281	1.21	0.46	1.26E-04	0.291	0.292	1.00(0.93-1.06)	0.14	8.88E-01
2	rs3106720	180242341	G	0.361	0.424	0.77(0.68-0.86)	0.26	4.79E-06	0.399	0.85	0.48	6.48E-04	0.393	0.403	0.96(0.90-1.02)	0.88	1.54E-01
2	rs2276573	180250932	A	0.385	0.452	0.76(0.68-0.85)	0.36	2.13E-06	0.423	0.85	0.65	8.33E-04	0.423	0.430	0.97(0.91-1.03)	0.82	3.13E-01
2	rs12474620	206082269	A	0.458	0.514	0.80(0.71-0.89)	0.60	6.51E-05	0.498	0.85	0.28	3.97E-04	0.489	0.487	1.01(0.95-1.07)	0.61	7.94E-01
2	rs17639046	206131392	T	0.409	0.469	0.78(0.70-0.88)	0.29	2.12E-05	0.454	0.83	0.87	8.30E-05	0.440	0.444	0.98(0.93-1.04)	0.17	5.53E-01
2	rs4255961	216332808	A	0.446	0.402	1.20(1.07-1.34)	0.87	1.54E-03	0.399	1.21	0.22	3.63E-05	0.410	0.399	1.05(0.99-1.11)	0.81	1.22E-01
3	rs9842620	157331787	G	0.277	0.330	0.78(0.69-0.88)	0.68	4.56E-05	0.319	0.82	0.86	8.72E-05	0.312	0.316	0.98(0.92-1.05)	0.15	5.77E-01
3	rs4359774	157345287	G	0.294	0.348	0.78(0.69-0.88)	0.32	4.20E-05	0.336	0.82	0.45	8.65E-05	0.327	0.331	0.98(0.93-1.05)	0.78	6.07E-01
3	rs9816126	157347949	T	0.291	0.345	0.78(0.69-0.88)	0.27	4.29E-05	0.334	0.82	0.43	8.15E-05	0.326	0.330	0.98(0.92-1.04)	0.83	5.22E-01
6	rs2236313	167280379	T	0.458	0.402	1.26(1.13-1.41)	0.25	4.39E-05	0.393	1.31	0.41	8.36E-09	0.424	0.382	1.19(1.13-1.27)	0.81	2.63E-09
6	rs6902119	167425781	C	0.453	0.397	1.26(1.12-1.41)	0.29	5.95E-05	0.388	1.31	0.83	7.63E-09	0.419	0.381	1.17(1.11-1.24)	0.36	9.09E-08
6	rs1855025	167457584	C	0.346	0.409	0.77(0.68-0.86)	0.38	3.94E-06	0.401	0.79	0.62	1.06E-06	failed				
7	rs916940	51054516	C	0.364	0.409	0.83(0.74-0.93)	0.58	1.16E-03	0.406	0.84	0.15	2.05E-04	0.415	0.400	1.07(1.01-1.13)	0.09	3.30E-02
8	rs4329285	47266528	T	0.144	0.112	1.33(1.13-1.57)	0.18	7.79E-04	0.110	1.36	0.16	4.77E-06	0.115	0.120	0.95(0.87-1.04)	0.95	2.91E-01
8	rs13253936	47431930	T	0.144	0.113	1.33(1.12-1.56)	0.19	9.45E-04	0.111	1.35	0.14	9.45E-06	0.125	0.126	0.99(0.90-1.08)	0.43	8.09E-01
8	rs9314419	145020849	T	0.394	0.434	0.85(0.76-0.95)	0.96	3.89E-03	0.443	0.82	0.2	2.64E-05	failed				
9	rs10814339	36144678	C	0.137	0.110	1.29(1.09-1.52)	0.89	3.52E-03	0.107	1.33	0.37	4.08E-05	0.123	0.111	1.12(1.03-1.23)	0.03	1.20E-02
10	rs4948522	60004581	C	0.469	0.419	1.22(1.10-1.37)	0.38	4.32E-04	0.418	1.23	0.77	7.35E-06	0.416	0.429	0.95(0.89-1.01)	0.30	8.20E-02
10	rs6481407	60005096	C	0.469	0.419	1.22(1.09-1.37)	0.39	4.72E-04	0.418	1.23	0.75	7.60E-06	failed				
10	rs1574190	80662387	T	0.165	0.200	0.79(0.68-0.91)	0.87	1.31E-03	0.196	0.81	0.74	6.94E-04	0.180	0.195	0.91(0.84-0.98)	0.72	9.28E-03
10	rs11593576	80685902	T	0.152	0.199	0.72(0.62-0.84)	0.24	1.51E-05	0.198	0.73	0.41	3.95E-07	0.179	0.195	0.90(0.84-0.97)	0.05	5.01E-03
13	rs310935	61931782	C	0.095	0.125	0.74(0.62-0.88)	0.63	9.53E-04	0.128	0.72	0.38	1.76E-05	0.113	0.114	0.99(0.91-1.09)	0.62	9.13E-01
13	rs983634	61946963	T	0.095	0.125	0.73(0.61-0.88)	0.63	8.01E-04	0.128	0.72	0.32	1.90E-05	0.113	0.114	0.99(0.90-1.08)	0.53	7.87E-01
15	rs1991253	55853982	A	0.204	0.242	0.80(0.70-0.92)	0.56	1.28E-03	0.242	0.80	0.67	1.08E-04	0.229	0.233	0.98(0.92-1.05)	0.29	5.57E-01

19	rs7245564	17824878	G	0.064	0.042	1.56(1.22-2.01)	1	4.61E-04	0.041	1.58	0.41	2.67E-06	0.043	0.05	0.85(0.74-0.97)	0.77	1.70E-02
20	rs16986247	39963742	G	0.417	0.356	1.29(1.15-1.45)	0.39	1.12E-05	0.368	1.23	0.69	9.56E-06	0.384	0.382	1.01(0.95-1.07)	0.68	8.08E-01
20	rs1987336	39968258	G	0.413	0.353	1.29(1.15-1.45)	0.35	1.38E-05	0.364	1.23	0.57	1.60E-05	0.386	0.383	1.01(0.95-1.08)	0.31	6.88E-01
22	rs2072466	15669118	G	0.29	0.25	1.23(1.08-1.39)	0.94	1.40E-03	0.246	1.26	0.89	9.58E-06	0.251	0.262	0.95(0.89-1.01)	0.28	8.90E-02
22	rs11090195	21592360	C	0.326	0.387	0.76(0.68-0.86)	1	5.54E-06	0.376	0.8	0.58	7.28E-06	0.354	0.348	1.02(0.96-1.09)	0.27	4.53E-01
22	rs463235	21608593	C	0.296	0.351	0.78(0.69-0.88)	0.18	4.52E-05	0.344	0.8	0.19	1.28E-05	0.335	0.329	1.03(0.97-1.09)	0.1	4.12E-01

Reference control: The samples were genotyped in a series of GWAS of various diseases in Chinese Han population, including psoriasis, systemic lupus erythematosus, leprosy, atopic dermatitis, and esophageal cancer.

**Supplementary Table 4 Association analysis for candidate loci/variants of vitiligo and autoimmune diseases in GWAS dataset**

CHR	SNP	BP	A1	F_A	F_U	$P_{trend}$	OR	$P_{HWE}$	Disease/Trait	Region	Reported Gene(s)
1	rs301819	8424373	A	0.159	0.160	8.65E-01	0.99	3.02E-02	Vitiligo	1p36.23	RERE
1	rs4908760	8448729	G	0.169	0.165	6.90E-01	1.03	6.92E-03	Vitiligo	1p36.23	RERE
1	rs11121194	8492493	G	0.167	0.163	7.22E-01	1.03	1.48E-02	Vitiligo	1p36.23	RERE
1	rs10489494*	63571349	A	0.127	0.146	6.05E-02	0.85	1.10E-01	Vitiligo	1p31.3-p32.2	FOXD3
1	rs2476601	114179091	A	0.000	0.001	1.26E-01	0.00	1.00E+00	Vitiligo	1p13.2	PTPN22
1	rs1800871 <sup>#</sup>	205011934	C	0.334	0.341	6.33E-01	0.97	7.24E-01	Vitiligo	1q31-q32	IL10
1	rs1800896	205013520	G	0.075	0.09	4.82E-02	0.81	4.21E-01	Vitiligo	1q31-q32	IL10
2	rs3732191*	47893789	C	0.053	0.065	6.45E-02	0.8	8.30E-01	Vitiligo	2p16.3	FBXO11
2	rs231775 <sup>#</sup>	204429997	G	0.31	0.317	6.26E-01	0.97	7.62E-02	Vitiligo	2q33	CTLA4
3	rs12490563*	69841116	G	0.097	0.08	4.46E-02	1.22	2.00E-01	Vitiligo	3p14.1-p12.3	MITF
3	rs13076312	189571948	G	0.3196	0.3663	4.67E-04	0.8125	7.76E-01	Vitiligo	3q28	LPP
3	rs1464510	189595248	C	0.3639	0.4098	7.59E-04	0.8239	1.00E+00	Vitiligo	3q28	LPP
3	rs13091753	189597283	A	0.448	0.428	1.58E-01	1.09	2.49E-01	Vitiligo	3q28	LPP
3	rs1559810	189607048	A	0.451	0.433	1.96E-01	1.08	1.00E+00	Vitiligo	3q28	LPP
4	rs2646325*	55363497	A	0.047	0.036	4.03E-02	1.33	1.00E+00	Vitiligo	4q11-q12	KIT
5	rs3806933 <sup>#</sup>	110433574	G	0.357	0.35	5.86E-01	1.03	9.54E-01	Vitiligo	5q22.1	TSLP
6	rs8643 <sup>#</sup>	7831904	G	0.132	0.136	6.78E-01	0.97	9.16E-02	Vitiligo	6p24.3	TXNDC5
6	rs5370 <sup>#</sup>	12403800	A	0.277	0.259	1.54E-01	1.1	9.75E-02	Vitiligo	6p24.1	EDN1
6	rs1325116*	12598432	G	0.16	0.144	1.01E-01	1.14	3.90E-01	Vitiligo	9p23	TYRP1
6	rs6960920 <sup>#</sup>	44433254	C	0.487	0.493	6.69E-01	0.98	8.32E-01	Vitiligo	7p13	CAMK2B,NUDCD3
6	rs2234693 <sup>#</sup>	152199574	A	0.392	0.377	2.92E-01	1.06	7.78E-01	Vitiligo	6q25.1	ESR1
6	rs1801132 <sup>#</sup>	152293261	A	0.489	0.5	4.17E-01	0.95	8.74E-01	Vitiligo	6q25.1	ESR1
6	rs2228480	152461788	A	0.214	0.217	7.88E-01	0.98	8.15E-01	Vitiligo	6q25.1	ESR1
6	rs13208776	168684473	A	0.004	0.005	5.92E-01	0.79	1.00E+00	Vitiligo	6q27	SMOC2
6	rs1402	168686225	C	0.085	0.086	8.95E-01	0.99	7.37E-01	Vitiligo	6q27	SMOC2
6	rs2144749	168695540	G	0.001	0.003	1.30E-01	0.38	1.00E+00	Vitiligo	6q27	SMOC2
9	rs4744411 <sup>#</sup>	96692051	G	0.369	0.364	7.02E-01	1.02	3.96E-02	Vitiligo	9q22	C9orf3
10	rs706779	6138830	G	0.355	0.371	2.25E-01	0.93	5.71E-01	Vitiligo	10p15.1	IL2RA
10	rs7090530	6150881	C	0.274	0.280	6.07E-01	0.97	6.46E-01	Vitiligo	10p15.1	IL2RA
10	rs12251307	6163501	A	0.198	0.211	2.70E-01	0.93	3.83E-01	Vitiligo	10p15.1	IL2RA-RBM17
10	rs4750005	6209691	G	0.278	0.300	7.64E-02	0.90	9.00E-01	Vitiligo	10p15.1	RBM17

10	rs3920615	6216786	G	0.372	0.368	7.51E-01	1.02	6.09E-01	Vitiligo	10p15.1	RBM17-PFKB3
10	rs4747887	6217688	G	0.368	0.366	9.12E-01	1.01	6.48E-01	Vitiligo	10p15.1	RBM17-PFKB3
10	rs4750012	6217800	A	0.367	0.366	9.60E-01	1.00	6.48E-01	Vitiligo	10p15.1	RBM17-PFKB3
10	rs7099083	6218242	A	0.368	0.366	8.80E-01	1.01	5.69E-01	Vitiligo	10p15.1	RBM17-PFKB3
10	rs1800450 <sup>#</sup>	54200073	A	0.355	0.315	3.07E-03	1.2	5.40E-01	Vitiligo	10q11.2-q21	MBL2
11	rs7943316 <sup>#</sup>	34424222	A	0.3	0.314	3.14E-01	0.94	9.51E-01	Vitiligo	11p13	CAT
11	rs769217 <sup>#</sup>	34427255	A	0.468	0.457	4.66E-01	1.04	3.11E-01	Vitiligo	11p13	CAT
11	rs10830236	88540464	A	0.193	0.179	2.08E-01	1.10	1.00E+00	Vitiligo	11q14.3	TYR
11	rs11018528	88570025	G	0.180	0.173	5.03E-01	1.05	3.10E-01	Vitiligo	11q14.3	TYR
11	rs10765198	88609422	G	0.177	0.171	5.85E-01	1.04	6.42E-01	Vitiligo	11q14.3	TYR
11	rs1847134	88644901	C	0.171	0.173	8.57E-01	0.99	7.81E-01	Vitiligo	11q14.3	TYR
11	rs1393350	88650694	A	0.002	0.001	4.79E-01	1.60	1.00E+00	Vitiligo	11q14.3	TYR
11	rs1806319	88677584	G	0.319	0.313	6.09E-01	1.03	7.12E-01	Vitiligo	11q14.3	TYR
12	rs7975232 <sup>#</sup>	46530451	C	0.272	0.28	5.51E-01	0.96	6.58E-02	Vitiligo	12q12-q14	VDR
13	rs17196261*	93936176	A	0.051	0.044	2.17E-01	1.18	1.10E-01	Vitiligo	13q32.1	TYRP2
14	rs8192917	24172000	G	0.276	0.254	8.60E-02	1.12	1.85E-01	Vitiligo	14q12	GZMB
14	rs2273844	24173254	A	0.272	0.254	1.45E-01	1.10	1.63E-01	Vitiligo	14q12	GZMB
14	rs3783637*	54417868	A	0.41	0.382	4.46E-02	1.12	5.40E-01	Vitiligo	14q22.1-q22.2	GCH1
16	rs3212358*	88512240	A	0.117	0.11	4.66E-01	1.07	2.80E-01	Vitiligo	16q24.3	MC1R
17	rs6502867	5361052	G	0.046	0.047	8.82E-01	0.98	5.44E-01	Vitiligo	17p13	NLRP1
17	rs8066276*	58942997	G	0.256	0.232	5.31E-02	1.14	7.70E-01	Vitiligo	17q23	ACE
20	rs2378132*	32309697	G	0.224	0.213	3.23E-01	1.07	2.70E-01	Vitiligo	20q11.2-q12	ASIP
21	rs11203203	42709255	A	0.039	0.039	8.74E-01	1.02	1.00E+00	Vitiligo	21q22.3	UBASH3A
21	rs2839511	42721590	A	0.036	0.034	7.07E-01	1.06	6.81E-01	Vitiligo	21q22.3	UBASH3A
21	rs2075877*	44534480	A	0.423	0.395	3.62E-02	1.12	8.00E-02	Vitiligo	21q22.3	AIRE
22	rs4680	18331271	A	0.27	0.254	1.80E-01	1.09	4.42E-01	Vitiligo	22q11.2	COMT
22	rs2269577 <sup>#</sup>	27543011	G	0.397	0.363	1.24E-02	1.16	4.23E-01	Vitiligo	22q12	XBP1
22	rs229527	35911431	C	0.280	0.286	6.65E-01	0.97	3.80E-02	Vitiligo	22q13.1	C1QTNF6
22	rs5756546	35919751	A	0.122	0.102	2.06E-02	1.23	7.71E-01	Vitiligo	22q13.1	C1QTNF6
1	rs3806308	20015453	A	0.419	0.435	2.49E-01	0.94	7.47E-01	Ulcerative colitis	1p36.13	RNF186
1	rs6426833	20044447	G	0.27	0.265	6.96E-01	1.03	4.97E-01	Ulcerative colitis	1p36.13	OTUD3, PLA2G2E
1	rs7524102	22571034	G	0.215	0.189	2.27E-02	1.18	1.00E+00	Ulcerative colitis	1p36.12	Intergenic
1	rs10889677	67497708	C	0.271	0.267	7.37E-01	1.02	8.39E-01	Ulcerative colitis	1p31.3	IL23R

1	rs1801274	159746369	G	0.355	0.34	2.68E-01	1.07	9.06E-01	Ulcerative colitis	1q23.3	FCGR2A
6	rs9263739	31219335	A	0.067	0.098	1.18E-04	0.66	1.32E-01	Ulcerative colitis	6p21.33	HLA
6	rs2395185	32541145	A	0.423	0.4	9.94E-02	1.1	4.41E-01	Ulcerative colitis	6p21.32	Intergenic
7	rs2108225	107240339	A	0.397	0.381	2.64E-01	1.07	9.11E-01	Ulcerative colitis	7q31.1	SLC26A3
7	rs4730273	107266755	A	0.418	0.418	9.81E-01	1	7.27E-02	Ulcerative colitis	7q31.1	Intergenic
7	rs4730276	107271673	A	0.408	0.405	8.24E-01	1.01	1.54E-01	Ulcerative colitis	7q31.1	multiple gene
7	rs4598195	107290677	C	0.326	0.339	3.31E-01	0.94	1.00E+00	Ulcerative colitis	7q31.1	multiple gene
7	rs2158836	107368075	A	0.159	0.151	4.23E-01	1.07	9.18E-01	Ulcerative colitis	7q31.1	multiple gene
9	rs10975003	5203687	G	0.21	0.216	6.62E-01	0.97	1.83E-01	Ulcerative colitis	9p24.1	multiple gene
9	rs668853	84500967	G	0.28	0.263	1.65E-01	1.09	8.91E-01	Ulcerative colitis	9q21.32	Intergenic
9	rs10781500	138389159	A	0.291	0.29	8.94E-01	1.01	9.49E-01	Ulcerative colitis	9q34.3	CARD9
12	rs1558744	66790859	A	0.116	0.116	9.80E-01	1	3.65E-01	Ulcerative colitis	12q15	multiple gene
12	rs2870946	66882928	G	0	0.002	3.01E-02	0	1.00E+00	Ulcerative colitis	12q15	IL26
13	rs17085007	26429267	G	0.237	0.231	6.27E-01	1.03	8.64E-02	Ulcerative colitis	13q12.13	USP12
1	rs1983853	85083780	A	0	0.001	7.13E-01	0.64	1.00E+00	Type 1 diabetes	1p22.3	EDG7
1	rs3024505	205006527	A	0.034	0.049	5.95E-03	0.67	3.88E-01	Type 1 diabetes	1q32.1	IL10
2	rs1534422	12558192	G	0.24	0.238	8.77E-01	1.01	3.43E-01	Type 1 diabetes	2p25.1	Intergenic
2	rs1990760	162832297	A	0.208	0.201	5.68E-01	1.04	8.05E-01	Type 1 diabetes	2q24.2	IFIH1
4	rs10517086	25694609	A	0.007	0.01	2.31E-01	0.68	1.00E+00	Type 1 diabetes	4p15.2	Intergenic
4	rs4505848	123351942	G	0.455	0.465	4.96E-01	0.96	4.57E-01	Type 1 diabetes	4q27	IL2
5	rs1445898	35946286	G	0.251	0.258	5.65E-01	0.96	2.40E-01	Type 1 diabetes	5p13.2	CAPSL
6	rs3757247	91014184	A	0.489	0.477	4.05E-01	1.05	3.40E-01	Type 1 diabetes	6q15	BACH2
6	rs9388489	126740412	A	0.019	0.016	4.55E-01	1.17	1.00E+00	Type 1 diabetes	6q22.32	C6orf173
7	rs7804356	26858190	G	0.11	0.111	9.20E-01	0.99	2.25E-01	Type 1 diabetes	7p15.2	Intergenic
9	rs10758593	4282083	A	0.401	0.413	3.85E-01	0.95	5.86E-01	Type 1 diabetes	9p24.2	GLIS3
10	rs12251307	6163501	A	0.198	0.211	2.70E-01	0.93	3.83E-01	Type 1 diabetes	10p15.1	IL2RA
10	rs10509540	90013013	G	0.24	0.233	6.02E-01	1.04	2.35E-01	Type 1 diabetes	10q23.31	C10orf59
11	rs1004446	2126719	A	0.285	0.268	1.74E-01	1.09	5.90E-01	Type 1 diabetes	11p15.5	INS
11	rs7111341	2169742	A	0.082	0.083	8.96E-01	0.99	8.63E-01	Type 1 diabetes	11p15.5	INS
12	rs3764021	9724895	A	0.372	0.396	7.79E-02	0.9	7.40E-01	Type 1 diabetes	12p13.31	NR
12	rs11052552	9747225	A	0.373	0.397	7.64E-02	0.9	9.12E-01	Type 1 diabetes	12p13.31	NR
12	rs4763879	9801431	A	0.479	0.435	1.89E-03	1.19	6.28E-01	Type 1 diabetes	12p13.31	CD69
12	rs1701704	54698754	C	0.273	0.24	7.51E-03	1.19	7.17E-01	Type 1 diabetes	12q13.2	multiple gene

12	rs3184504	110368991	A	0.003	0.005	2.78E-01	0.59	1.00E+00	Type 1 diabetes	12q24.12	SH2B3
12	rs17696736	110971201	G	0.002	0.004	3.07E-01	0.58	1.00E+00	Type 1 diabetes	12q24.13	C12orf30
14	rs1465788	68333352	A	0.277	0.258	1.20E-01	1.11	7.82E-01	Type 1 diabetes	14q24.1	Intergenic
14	rs4900384	97568704	A	0.343	0.335	5.54E-01	1.04	3.73E-01	Type 1 diabetes	14q32.2	Intergenic
15	rs8035957	36625556	A	0.433	0.419	2.91E-01	1.06	2.11E-01	Type 1 diabetes	15q14	RASGRP1
16	rs2903692	11146284	A	0.247	0.247	9.81E-01	1	8.31E-01	Type 1 diabetes	16p13.13	KIAA0350
16	rs4788084	28447349	A	0.267	0.273	6.04E-01	0.97	5.50E-01	Type 1 diabetes	16p11.2	IL27
16	rs7202877	73804746	C	0.192	0.203	3.40E-01	0.93	4.12E-01	Type 1 diabetes	16q23.1	Intergenic
17	rs2290400	35319766	G	0.259	0.278	1.22E-01	0.91	3.56E-01	Type 1 diabetes	17q12	ORMDL3
18	rs1893217	12799340	G	0.191	0.154	4.61E-04	1.3	9.19E-01	Type 1 diabetes	18p11.21	PTPN2
18	rs763361	65682622	A	0.325	0.35	7.12E-02	0.9	1.46E-01	Type 1 diabetes	18q22.2	CD226
19	rs425105	51900321	G	0.182	0.19	4.39E-01	0.94	8.64E-01	Type 1 diabetes	19q13.32	Intergenic
21	rs11203203	42709255	A	0.039	0.039	8.74E-01	1.02	1.00E+00	Type 1 diabetes	21q22.3	UBASH3A
21	rs9976767	42709459	G	0.321	0.313	5.45E-01	1.04	1.96E-01	Type 1 diabetes	21q22.3	UBASH3A
22	rs5753037	28911722	G	0.432	0.427	6.97E-01	1.02	6.66E-01	Type 1 diabetes	22q12.2	Intergenic
1	rs12141391	72047061	A	0	0	3.77E-01	0	1.00E+00	SLE	1p31.1	NEGR1
1	rs2205960	171458098	A	0.267	0.261	6.19E-01	1.03	9.45E-01	SLE	1q25.1	TNFSF4
1	rs10798269	171576336	A	0.346	0.316	2.33E-02	1.14	2.98E-01	SLE	1q25.1	Intergenic
2	rs13385731	33555394	G	0.145	0.149	6.83E-01	0.97	2.51E-01	SLE	2p22.3	RASGRP3
2	rs3821236	191611003	A	0.459	0.448	4.28E-01	1.05	7.89E-01	SLE	2q32.3	STAT4
2	rs7574865	191672878	A	0.346	0.327	1.60E-01	1.09	8.10E-01	SLE	2q32.3	STAT4
3	rs6445975	58345217	C	0.218	0.207	3.08E-01	1.07	5.72E-01	SLE	3p14.3	PXK
4	rs10516487	102970099	A	0.141	0.139	8.44E-01	1.02	2.26E-01	SLE	4q24	BANK1
5	rs979233	42411000	A	0.107	0.086	1.26E-02	1.27	1.00E+00	SLE	5p12	GHR
5	rs10036748	150438339	G	0.249	0.255	6.28E-01	0.97	1.86E-01	SLE	5q33.1	TNIP1
6	rs3131379	31829012	A	0	0.001	4.47E-01	0.43	1.00E+00	SLE	6p21.33	HLA region
6	rs9271100	32684456	A	0.17	0.178	4.13E-01	0.94	3.67E-01	SLE	6p21.32	HLA-DRB1
6	rs548234	106674727	G	0.276	0.264	3.14E-01	1.07	1.00E+00	SLE	6q21	PRDM1, ATG5
7	rs4917014	50276409	C	0.334	0.32	2.88E-01	1.07	3.62E-01	SLE	7p12.2	IKZF1
7	rs1167796	75011116	A	0.285	0.282	8.16E-01	1.02	3.26E-01	SLE	7q11.23	NR
7	rs4728142	128361203	A	0.129	0.136	4.54E-01	0.94	3.68E-01	SLE	7q32.1	IRF5
7	rs10488631	128381419	G	0.002	0	5.12E-02	6.41	1.00E+00	SLE	7q32.1	IRF5, TNPO3
7	rs12537284	128505142	A	0.002	0.001	1.41E-01	3.2	1.00E+00	SLE	7q32.1	IRF5, TNPO3

8	rs7812879	11377591	A	0.246	0.243	7.92E-01	1.02	3.47E-01	SLE	8p23.1	BLK
8	rs13277113	11386595	G	0.297	0.285	3.41E-01	1.06	3.30E-01	SLE	8p23.1	C8orf13, BLK
9	rs11243676	134086588	A	0	0.001	4.47E-01	0.43	1.00E+00	SLE	9q34.13	NTNG2
10	rs1913517	49789060	A	0.282	0.285	7.95E-01	0.98	5.59E-01	SLE	10q11.22	LRRC18, WDFY4
11	rs4963128	579564	A	0.058	0.057	9.56E-01	1.01	1.00E+00	SLE	11p15.5	KIAA1542
11	rs4639966	118078729	G	0.305	0.283	9.77E-02	1.11	2.67E-01	SLE	11q23.3	NR
11	rs6590330	127816269	A	0.34	0.344	7.67E-01	0.98	2.91E-01	SLE	11q24.3	ETS1
12	rs1385374	127866647	A	0.222	0.205	1.42E-01	1.11	9.35E-01	SLE	12q24.32	SLC15A4
16	rs7186852	30543160	G	0.078	0.068	1.39E-01	1.17	6.75E-01	SLE	16p11.2	NR
16	rs7197475	30550368	A	0.078	0.067	1.26E-01	1.18	6.75E-01	SLE	16p11.2	NR
16	rs9888739	31220754	A	0.003	0.002	8.68E-01	1.1	1.00E+00	SLE	16p11.2	ITGAM
16	rs11150610	31241737	C	0.266	0.261	6.96E-01	1.03	3.73E-01	SLE	16p11.2	ITGAM
16	rs11574637	31276375	G	0.003	0.002	6.43E-01	1.28	1.00E+00	SLE	16p11.2	ITGAM, ITGAX
17	rs12949531	13674531	A	0.326	0.32	6.47E-01	1.03	8.55E-01	SLE	17p12	Intergenic
18	rs17083844	66993223	A	0.057	0.051	3.66E-01	1.12	5.80E-01	SLE	18q22.3	SOCS6
22	rs131654	20247190	C	0.471	0.478	6.44E-01	0.97	3.68E-01	SLE	22q11.21	HIC2, UBE2L3
1	rs3890745	2543484	G	0.489	0.485	7.86E-01	1.02	5.97E-01	Rheumatoid arthritis	1p36.32	MMEL1-TNFRSF14
2	rs13017599	61017835	A	0.019	0.014	1.75E-01	1.35	2.53E-01	Rheumatoid arthritis	2p16.1	REL
2	rs231735	204402121	C	0.175	0.176	9.22E-01	0.99	1.01E-01	Rheumatoid arthritis	2q33.2	CTLA4
6	rs660895	32685358	G	0.213	0.222	4.59E-01	0.95	4.90E-01	Rheumatoid arthritis	6p21.32	HLA-DRB1
6	rs6457617	32771829	G	0.527	0.477	4.06E-04	1.22	2.44E-01	Rheumatoid arthritis	6p21.32	HLA-DQA1, HLA-DQA2
8	rs2736340	11381382	G	0.274	0.268	6.83E-01	1.03	4.19E-01	Rheumatoid arthritis	8p23.1	BLK
9	rs881375	122692719	A	0.302	0.28	8.56E-02	1.11	5.55E-01	Rheumatoid arthritis	9q33.2	TRAF1, C5
9	rs3761847	122730060	G	0.485	0.461	8.99E-02	1.1	4.89E-01	Rheumatoid arthritis	9q34	TRAF1-C5
18	rs2002842	74510585	C	0.16	0.174	1.85E-01	0.9	9.27E-01	Rheumatoid arthritis	18q23	SALL3
21	rs2837960	41433788	C	0.237	0.236	9.30E-01	1.01	7.69E-01	Rheumatoid arthritis	21q22.3	NR
1	rs2201841	67466790	A	0.272	0.266	6.34E-01	1.03	1.00E+00	Psoriasis	1p31.3	IL23R
1	rs4085613	150816642	A	0.43	0.426	7.95E-01	1.02	4.82E-01	Psoriasis	1q21.3	LCE3D, LCE3A
5	rs20541	132023863	A	0.296	0.311	2.59E-01	0.93	4.59E-01	Psoriasis	5q31.1	IL13
5	rs3213094	158683347	A	0.429	0.446	2.37E-01	0.94	7.08E-01	Psoriasis	5q33.3	IL12B
6	rs1265181	31263764	G	0.156	0.101	5.85E-09	1.65	4.67E-01	Psoriasis	6p21.33	HLA-C
6	rs10484554	31382534	A	0.168	0.11	2.31E-09	1.64	3.42E-01	Psoriasis	6p21.33	HLA-C
6	rs3134792	31420305	C	0.057	0.069	7.09E-02	0.81	3.07E-01	Psoriasis	6p21.33	HLA-C



6	rs2395029	31539759	C	0.015	0.012	3.69E-01	1.25	1.00E+00	Psoriasis	6p21.33	HLA-C
6	rs610604	138241110	C	0.092	0.091	8.80E-01	1.02	5.20E-01	Psoriasis	6q23.3	TNFAIP3
12	rs2066808	55024240	G	0.034	0.029	2.84E-01	1.19	1.07E-01	Psoriasis	12q13.2	IL23A, STAT2
13	rs7993214	39248912	A	0.23	0.241	3.54E-01	0.94	7.18E-01	Psoriasis	13q13.3	COG6
1	rs6604026	93076191	G	0.017	0.017	9.92E-01	1	1.00E+00	Multiple sclerosis	1p22.1	EVI5, RPL5
1	rs1335532	116902480	A	0.396	0.421	7.71E-02	0.9	3.02E-01	Multiple sclerosis	1p13.1	CD58
1	rs12047808	177735937	G	0.139	0.141	8.48E-01	0.98	7.42E-01	Multiple sclerosis	1q25.2	C1orf125
2	rs1109670	9167489	A	0.281	0.301	1.28E-01	0.91	4.51E-01	Multiple sclerosis	2p25.1	DDEF2
2	rs651477	119112161	G	0.172	0.176	7.47E-01	0.98	7.82E-01	Multiple sclerosis	2q14.2	EN1
2	rs1437898	133463100	A	0.389	0.392	8.39E-01	0.99	9.12E-01	Multiple sclerosis	2q21.2	FLJ34870
2	rs882300	136692725	A	0.221	0.181	2.87E-04	1.29	9.29E-01	Multiple sclerosis	2q22.1	CXCR4
3	rs908821	142023408	G	0.402	0.384	1.88E-01	1.08	5.02E-01	Multiple sclerosis	3q23	SLC25A36
3	rs1841770	149239376	C	0.173	0.164	4.12E-01	1.06	7.00E-01	Multiple sclerosis	3q24	ZIC1
3	rs12638253	158108785	G	0.248	0.246	8.42E-01	1.01	1.76E-01	Multiple sclerosis	3q25.32	FLJ16641
4	rs10518025	67747035	G	0.078	0.084	4.07E-01	0.92	1.00E+00	Multiple sclerosis	4q13.2	CENPC1
4	rs1478091	132009951	G	0.056	0.059	5.78E-01	0.94	4.76E-01	Multiple sclerosis	4q28.3	LOC132321
4	rs7672826	182636689	A	0.321	0.32	9.80E-01	1	7.81E-02	Multiple sclerosis	4q35.1	MGC45800
5	rs6897932	35910332	A	0.154	0.15	7.10E-01	1.03	5.33E-01	Multiple sclerosis	5p13.2	IL7R
5	rs4704970	155433570	A	0.002	0.002	8.77E-01	0.91	1.00E+00	Multiple sclerosis	5q33.2	SGCD
6	rs6941421	15197130	G	0.369	0.356	3.25E-01	1.06	7.73E-01	Multiple sclerosis	6p23	JARID2
6	rs3129934	32444165	A	0.083	0.074	2.39E-01	1.13	1.76E-01	Multiple sclerosis	6p21.32	HLA-DRB1
6	rs9271366	32694832	G	0.13	0.137	4.93E-01	0.95	8.23E-01	Multiple sclerosis	6p21.32	HLA-DRB1
7	rs10259085	7234956	G	0.287	0.292	7.30E-01	0.98	3.06E-01	Multiple sclerosis	7p21.3	C1GALT1
7	rs17157903	103415272	A	0.251	0.262	3.70E-01	0.94	1.15E-01	Multiple sclerosis	7q22.1	RELN
7	rs10243024	116133839	A	0.306	0.304	8.78E-01	1.01	2.60E-01	Multiple sclerosis	7q31.2	MET
8	rs1529316	3815546	G	0.201	0.214	2.75E-01	0.93	3.46E-01	Multiple sclerosis	8p23.2	CSMD1
8	rs2116078	73526543	C	0.285	0.298	3.22E-01	0.94	9.50E-01	Multiple sclerosis	8q13.3	KCNB2
9	rs1755289	17928351	A	0.381	0.396	2.68E-01	0.94	1.51E-01	Multiple sclerosis	9p22.2	SH3GL2
9	rs2842483	78095970	G	0.085	0.087	7.62E-01	0.97	3.18E-01	Multiple sclerosis	9q21.13	RFK
10	rs2104286	6139051	G	0.136	0.135	9.82E-01	1	6.52E-01	Multiple sclerosis	10p15.1	IL2RA
11	rs1386330	87459075	G	0.069	0.07	8.92E-01	0.99	6.84E-01	Multiple sclerosis	11q14.2	RAB38
12	rs1800693	6310270	G	0.113	0.109	6.50E-01	1.04	7.51E-02	Multiple sclerosis	12p13.31	TNFRSF1A
12	rs1458175	40252128	A	0.167	0.17	7.45E-01	0.98	9.25E-01	Multiple sclerosis	12q12	PDZRN4

12	rs703842	56449006	A	0.366	0.372	6.43E-01	0.97	4.61E-01	Multiple sclerosis	12q14.1	METTL1, CYP27B1
13	rs9523762	92129887	G	0.442	0.446	7.79E-01	0.98	5.56E-01	Multiple sclerosis	13q31.3	GPC5
16	rs7191888	72138559	G	0.1	0.104	6.56E-01	0.96	1.54E-01	Multiple sclerosis	16q22.3	C16orf47
18	rs1557351	52903312	G	0.459	0.459	9.94E-01	1	9.15E-01	Multiple sclerosis	18q21.31	WDR7
18	rs337718	67925258	A	0.305	0.31	6.69E-01	0.97	4.96E-01	Multiple sclerosis	18q22.3	CBLN2
19	rs7253363	11543495	A	0	0	8.61E-01	1.28	1.00E+00	Multiple sclerosis	19p13.2	ACP5
19	rs299175	61005340	A	0.368	0.359	4.84E-01	1.04	9.07E-01	Multiple sclerosis	19q13.42	NLRP11
20	rs397020	1153886	G	0.304	0.309	7.46E-01	0.98	7.10E-01	Multiple sclerosis	20p13	C20orf46
20	rs6074022	44173603	G	0.386	0.38	6.63E-01	1.03	1.97E-01	Multiple sclerosis	20q13.12	CD40
6	rs477515	32677669	A	0.266	0.234	7.83E-03	1.19	4.59E-01	Inflammatory bowel disease	6p21.32	HLA-DQA1
9	rs6478109	116608587	G	0.476	0.511	1.34E-02	0.87	1.00E+00	Inflammatory bowel disease	9q32	TNFSF15
10	rs1250550	80730323	A	0.447	0.44	5.80E-01	1.03	1.19E-01	Inflammatory bowel disease	10q22.3	ZMIZ1
16	rs8049439	28745016	G	0.262	0.268	6.02E-01	0.97	7.36E-01	Inflammatory bowel disease	16p11.2	multiple gene
19	rs10500264	38442154	A	0.087	0.093	4.56E-01	0.93	2.73E-01	Inflammatory bowel disease	19q13.11	Intergenic
20	rs2315008	61814400	C	0.366	0.338	3.65E-02	1.13	6.79E-01	Inflammatory bowel disease	20q13.33	TNFRSF6B
21	rs2836878	39387404	A	0.219	0.222	8.27E-01	0.99	9.39E-01	Inflammatory bowel disease	21q22.2	PSMG1
22	rs2412973	28859631	A	0.307	0.297	4.29E-01	1.05	4.47E-01	Inflammatory bowel disease	22q12.2	multiple gene
1	rs7517847	67454257	C	0.424	0.409	2.59E-01	1.07	2.99E-01	Crohn's disease	1p31.3	IL23R
1	rs11465804	67475114	0	0	0	NA	NA	1.00E+00	Crohn's disease	1p31.3	IL23R
1	rs11209026	67478546	0	0	0	NA	NA	1.00E+00	Crohn's disease	1p31.3	IL23R
1	rs2476601	114179091	A	0	0.001	1.26E-01	0	1.00E+00	Crohn's disease	1p13.2	PTPN22
1	rs2274910	159118670	A	0.306	0.3	6.44E-01	1.03	4.12E-01	Crohn's disease	1q23.3	ITLN1
1	rs9286879	171128857	A	0.082	0.073	2.00E-01	1.14	5.55E-01	Crohn's disease	1q24.3	Intergenic
2	rs2241880	233848107	G	0.377	0.377	9.84E-01	1	7.36E-01	Crohn's disease	2q37.1	ATG16L1
3	rs3197999	49696536	A	0.061	0.062	8.78E-01	0.98	4.90E-01	Crohn's disease	3p21.31	MST1
5	rs4613763	40428485	G	0.001	0.001	8.05E-01	1.28	1.00E+00	Crohn's disease	5p13.1	PTGER4
5	rs17234657	40437266	C	0.001	0.001	8.05E-01	1.28	1.00E+00	Crohn's disease	5p13.1	Intergenic
5	rs1373692	40466940	C	0.152	0.159	4.87E-01	0.95	5.53E-01	Crohn's disease	5p13.1	Intergenic
5	rs2188962	131798704	A	0.003	0.003	7.62E-01	0.85	1.00E+00	Crohn's disease	5q31.1	Intergenic
5	rs10045431	158747111	A	0.103	0.101	7.58E-01	1.03	7.71E-01	Crohn's disease	5q33.3	IL12B
6	rs2301436	167357978	A	0.456	0.402	1.07E-04	1.25	2.48E-01	Crohn's disease	6q27	CCR6
7	rs1456893	50240218	A	0.344	0.337	6.23E-01	1.03	7.67E-01	Crohn's disease	7p12.2	Intergenic
9	rs10758669	4971602	C	0.313	0.306	6.08E-01	1.03	5.34E-01	Crohn's disease	9p24.1	JAK2

10	rs6601764	3852542	A	0.218	0.191	1.74E-02	1.18	6.69E-01	Crohn's disease	10p15.1	NR
10	rs1398024	23705444	A	0.122	0.125	7.43E-01	0.97	9.04E-01	Crohn's disease	10p12.2	C10orf67
10	rs224136	64140681	A	0.267	0.289	8.85E-02	0.9	7.97E-01	Crohn's disease	10q21.2	Intergenic
10	rs11190140	101281583	A	0.458	0.466	5.71E-01	0.97	7.95E-02	Crohn's disease	10q24.2	NKX2-3
13	rs3764147	43355925	G	0.313	0.308	7.22E-01	1.02	1.00E+00	Crohn's disease	13q14.11	Unknown
16	rs5743289	49314275	A	0.002	0.002	9.72E-01	1.02	1.00E+00	Crohn's disease	16q12.1	NOD2
16	rs2076756	49314382	G	0.008	0.006	3.64E-01	1.36	1.00E+00	Crohn's disease	16q12.1	CARD15
17	rs2872507	35294289	A	0.257	0.272	2.18E-01	0.92	5.04E-01	Crohn's disease	17q12	ORMDL3
17	rs744166	37767727	G	0.377	0.396	1.65E-01	0.92	1.00E+00	Crohn's disease	17q21.2	STAT3
21	rs2836754	39213610	G	0.341	0.362	1.21E-01	0.91	9.09E-01	Crohn's disease	21q22.2	Intergenic
21	rs762421	44439989	G	0.485	0.492	6.36E-01	0.97	9.16E-01	Crohn's disease	21q22.3	ICOSLG

\* Indicates SNPs with the most significant evidence in candidate genes previously reported.

# the variant is estimated by tag SNP ( $r^2 > 0.8$ ) from HapMap CHB database.

The candidate loci/variants of autoimmune diseases were available at: [www.genome.gov/gwastudies](http://www.genome.gov/gwastudies).