Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Jin Y, Birlea SA, Fain PR, et al. Variant of *TYR* and autoimmunity susceptibility loci in generalized vitiligo. N Engl J Med 2010;362:1686-97. DOI: 10.1056/NEJMoa0908547.

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METHODS

SUBJECTS

The genomewide association study included 1514 non-Hispanic/Latino European-derived white (CEU) generalized vitiligo patients whose single-nucleotide polymorphism (SNP) genotypes were determined and compared to those of 2813 "public" CEU control individuals genotyped using the Illumina 1M BeadChip: 502 from the CIDR: Collaborative Study on the Genetics of Alcoholism (COGA) dataset and 2731 from the Study of Addiction: Genetics and Environment (SAGE) dataset, obtained from the Database of Genotypes and Phenotypes (dbGaP), and 82 obtained from the Illumina iControlDB. Clinical history of vitiligo and other autoimmune diseases for these controls was not available.

Replication set 1 included 677 unrelated patients and 1106 CEU non-vitiligo controls from North America and Europe, principally spouses of vitiligo patients from the genomewide association study and replication set 1, all with no known relatives with vitiligo. Replication set 2 included 183 simplex parents-affected offspring trios and 332 unrelated multiplex families, consisting of two or more affected family members and relevant unaffected relatives (1383 individuals), from North America and Europe. Patients, relatives, and replication set 1 controls provided clinical history regarding vitiligo and other autoimmune diseases.

Written informed consent was obtained from all study subjects. This study was approved by each institutional review board and was conducted according to Declaration of Helsinki principles.

GENOTYPING AND QUALITY CONTROL

Genomic DNA was prepared from peripheral-blood specimens by standard methods or from saliva specimens with use of a DNA self-collection kit using the manufacturer's instructions

(Oragene, DNA Genotek). For genomewide genotyping, DNA concentrations were assayed by both ultraviolet A_{260} spectrophotometry (Nanodrop, Thermo Scientific) and fluorescence staining (PicoGreen method, Invitrogen). For genotyping individual SNPs, DNA concentrations were assayed by ultraviolet A_{260} spectrophotometry (NanoDrop).

Quality control filtering of the genomewide genotyping data was performed using Illumina GenomeStudio, version 3 and PLINK software,[1] version 1.05 (http://pngu.mgh.harvard.edu/purcell/plink/). Cases were excluded on the basis of SNP call rates < 98.5% (*N* = 30), discordance between reported and observed sex (*n* = 13), and/or inadvertent subject duplication (*N* = 12). Beyond prior quality control procedures, controls were excluded on the basis of SNP call rates < 95% (*N* = 0). Additional cases (*N* = 19) and controls (*N* = 2) were excluded on the basis of cryptic relatedness based on pair-wise identity-by-descent estimation (Pi-hat > 0.05), in which case the individual with lower SNP call rate was excluded. SNPs were excluded on the basis of observed minor allele frequency < 0.01 (*N* = 30,773), significant deviation ($P < 10^{-5}$) from Hardy-Weinberg equilibrium in the control dataset (*N* = 3,275), missing rate of 2% overall (*N* = 13,153) in cases plus controls, and/or significant difference ($P < 10^{-5}$) in missing rate in cases versus controls (*N* = 13,985). Data for SNPs with P values < 10^{-15} were reviewed with respect to allele calls, genotype clusters, and minor allele frequency in controls compared to data in public data sources, and were excluded if there were apparent data quality problems (*N* = 21). To control for population stratification, we used genetic matching (GEM),[2] which removes genetic outliers and unmatchable cases and controls based on genetic similarities derived from eigenvector decomposition (EVD). We selected a subset of 21,642 independent SNPs in controls by using the H-clust algorithm[3] with an r^2 cut-off value of 0.04. The initial, outlier-removal step of GEM created a matrix of data for these SNPs in all cases and

controls, detecting 25 significant eigenvector axes, and excluded as outliers 7 cases and 79 controls with ancestry coefficients > 6 SD in at least one of these eigenvector axes. After re-computing EVD, there were 4 significant eigenvector axes, and 38 additional cases and 95 controls were excluded for whom distances from the case to the nearest control (and vice-versa) defined by significant eigenvectors were greater than the cut-off value of 0.02. EVD was then recalculated, identifying 3 significant eigenvectors. Hierarchical groups of mutually exclusive subsets based on these significant EVD were formed using Ward's algorithm, inter-individual distances were rescaled, and 4 additional cases and 8 controls were removed.

In replication sets 1 and 2 we successfully determined genotypes for 48 SNPs that showed genomewide significant ($P < 5 \times 10^{-8}$) or near-significant P values in the genomewide association study by use of the Sequenom MassArray iPLEX genotyping system. SNP genotypes were subjected to quality control filters similar to those in the genomewide association study, as appropriate. In addition, for replication set 2 family data were subjected to Mendelian error-checking, and incompatibilities were either resolved or the incompatible individual or entire family was excluded. SNP genotypes could not be determined for MHC SNPs rs12206499 and rs34518860 for technical reasons. Therefore, genotypes for MHC SNP rs12206499 in replication set 1 were imputed by use of MaCH,[4] ver.1.0 (http://www.sph.umich.edu/csg/abecasis/MACH/download/) based on patterns of haplotype variation in the HapMap[5] CEU samples (release 24); genotypes for rs34518860 could not be reliably imputed. Genotypes were also imputed for *NALP1* region SNPs rs12150220, rs11078575, rs878329, and rs4790796 in the genomewide association study, and for *TYR* SNP rs1126809 in the genomewide association study and replication set 1.

STATISTICAL ANALYSES

For the genomewide association study, after quality control filtering of subjects and SNP data, we first compared allele frequencies of the remaining 520,460 SNPs in the 1441 remaining patients and 2811 controls using the Cochran-Armitage trend test implemented in PLINK,[1] which yielded a genomic inflation factor (λ) of 1.054. After removing genetic outliers and unmatchable individuals using GEM,[2] we then compared SNP allele frequencies in the final 1392 patients and 2629 controls using the unadjusted Cochran-Armitage trend test implemented in PLINK[1] and the adjusted Cochran-Armitage trend test implemented in EIGENSTRAT,[6] in which both phenotypes and genotypes of subjects were adjusted for ancestry using the top ten eigenvectors. Both of these tests yielded a genomic inflation factor of 1.048, indicating that residual population stratification was minimal. We then used the genomic control method[7] to correct the PLINK and EIGENSTRAT test statistics for this inflation factor. Odds ratios and 95% confidence limits were calculated by logistic regression analysis by use of PLINK.[1]

For replication set 1, after quality control filtering, we compared allele frequencies for genotyped and imputed SNPs in the remaining 647 patients and 1056 controls using the unadjusted Cochran-Armitage trend test. Odds ratios and 95% confidence limits were calculated by logistic regression analysis. For replication set 2, we calculated the association of each SNP with vitiligo using the family-based association test (FBAT),[8] version 1.5.5. Odds ratios and 95% confidence limits were calculated by conditional logistic regression analysis, which uses family-based data to create a matched case-pseudocontrol dataset.[9] To obtain combined ORs and P values, we performed meta-analysis using a Cochran-Mantel-Haenszel test with cases and controls from the genomewide association study and replication set 1, and cases and pseudocontrols from replication set 2 families. Genotype data for patients from the genomewide

association study and summary statistical results can be obtained by application to dbGaP [http://www.ncbi.nlm.nih.gov/sites/Entrez?Db-gap], accession number phs000224.v1.p1.

Calculation of linkage disequilibrium between SNPs in regions of association was carried out with Haploview software,[10] version 4.1. To distinguish independent associations in the MHC from secondary association due to linkage disequilibrium, we applied logistic regression analysis to the 22 MHC SNPs that showed strongest association with disease in the genomewide association study. As a test of the independent effect of a given locus conditioned on the effect of another locus, we compared the fit of a model containing both loci to a model containing only the conditioning locus, assuming a multiplicative genotypic effect for the high-risk allele of each locus. Analyses were performed using STATA, version 10.0 (http://www.stata.com).

We tested interaction between *HLA-A* SNP rs12206499 and *TYR* SNP rs1393350, and between *HLA-A* SNP rs12206499 and HLA class II region SNP rs532098 by logistic regression analysis, comparing the fit of a model containing both the main effects and interaction of the two loci to a model containing only the marginal effects of the two loci, using log-additive coding for each genotype and interaction between the two loci.[11] These analyses included SNP genotypes from the genomewide association study and replication set 1 and were performed using STATA.

The fraction of genetic variance accounted for by each of the two MHC region SNPs that showed independent association and the eight independent signals on other chromosomes, and by all ten loci combined, was calculated as Pseudo R^2 by logistic regression analysis of genomewide association study and replication set 1 data using STATA, assuming an multiplicative model for each SNP and a polygenic multiplicative model for all ten loci combined.[12]

RESULTS

ANALYSIS OF *NALP1* (*NLRP1*) REGION SNPs

We[13] and others[14] previously detected genetic linkage of generalized vitiligo with microsatellite markers on chromosome 17p13, specifically in families with both vitiligo and other autoimmune diseases, and by family-based association analysis of SNPs genotyped across the linkage region in the same families we then localized this signal to the *NALP1* (*NLRP1*) gene region, and then replicated these associations in a second cohort of multiplex families.[15] We subsequently verified association with the same high-risk alleles of the same *NALP1* SNPs in an independent cohort of generalized vitiligo cases and controls collected in northwest Romania.[16] *NALP1* encodes a key component of the NALP1 inflammasome that mediates innate immune responses to environmental triggers.[17]

In the present genomewide association study, only one of the previous highly associated *NALP1* SNPs was present on the Illumina 610 microarray, rs6502867 (P = 0.17, odds ratio 1.09); see Supplementary Table 7). Four other of the previous highly associated *NALP1* region SNPs were imputed; rs12150220 (P = 0.09, odds ratio 1.09), rs11078575 (P = 0.08, odds ratio 1.09); rs878329 (P = 0.11, odds ratio 1.08); and rs4790796 (P = 0.14, odds ratio 1.08), all showing at-best marginal association with the same high-risk allele as observed previously.[15,16] Stratification of cases into those with versus without concomitant other autoimmune diseases did not identify a more significantly-associated subset of patients.

In replication sets 1 and 2 we genotyped the four previously most-associated *NALP1* SNPs (see Supplementary Table 7). In the case-control replication set 1, none of the previous high-risk alleles of these SNPs were significantly associated with vitiligo. In contrast, in the family-based replication set 2 the high-risk alleles of all four markers were significantly

associated: rs6502867, P = 5.84 x 10^{-3}; rs12150220, P = 3.52 x 10^{-3}; rs2670660, P = 1.33 x 10^{-3}; rs8182352, P = 1.13 x 10^{-3}.

These results suggest that *NALP1* may be differentially associated with generalized vitiligo in the context of multiplex families versus singleton cases, consistent with the fact that the chromosome 17p13 signal was initially detected by genetic linkage analysis, particularly in the subset of multiplex families with concomitant other autoimmune diseases,[13,14] which are not typical among all vitiligo cases. However, this interpretation is biased by the fact that the present replication set 2 included the 114 multiplex families in which we originally detected linkage and association.[15] Nevertheless, we subsequently detected association with the same high-risk alleles of these *NALP1* SNPs in singleton generalized vitiligo cases versus controls from three adjacent counties in northwestern Romania, unselected with respect to concomitant autoimmune disease.[16] To determine whether high-risk *NALP1* alleles are particularly associated with disease in this limited geographical region, we stratified multiplex families and trios from this geographical region of Romania that were included in replication set 2 and were not included in the previous family-based study.[16] As shown in Supplementary Table 7, all four of these SNPs showed significant association in the Romanian family subset: rs6502867, P = 8.72 x 10^{-3}, odds ratio 1.58; rs12150220, 2.42 x 10^{-3}, odds ratio 1.84; rs2670660, P = 8.34 x 10^{-3}, odds ratio 1.92; rs8182352, P = 8.92 x 10^{-3}, odds ratio 1.99; these odds ratios were even higher in the subset of families with other concomitant autoimmune diseases. These Romanian families derive from the same limited geographical region as the previous Romanian case-control cohort,[16] and show association to the same high-risk SNP alleles, suggesting that the population from this geographically delimited region may be relatively homogeneous with respect to *NALP1* and vitiligo, with particularly high risk for patients and families with concomitant other autoimmune

diseases. Overall, these results support association of generalized vitiligo with *NALP1*, but suggest the likelihood of genetic heterogeneity with respect to *NALP1* association with generalized vitiligo in the wider CEU population.

ADDITIONAL STUDY INFORMATION

The study was designed by Dr. Spritz and Dr. Fain. The data were gathered by Dr. Jin, Dr. Birlea, Ms. Gowan, and Ms. Riccardi. The data were analyzed and are vouched for by Dr. Jin, Dr. Birlea, Dr. Fain, and Dr. Spritz. The manuscript was written by Dr. Spritz, Dr. Fain, and Dr. Jin, and all authors decided to publish the paper; Dr. Spritz wrote the first draft. This study was performed with prior agreement between the sponsor (National Institutes of Health) and Dr. Spritz that de-identified data from the genomewide association study would be submitted to the Database of Genotypes and Phenotypes (dbGaP) for the purpose of data sharing with qualified approved investigators, subject to limitations given the consents by which the samples were originally obtained.

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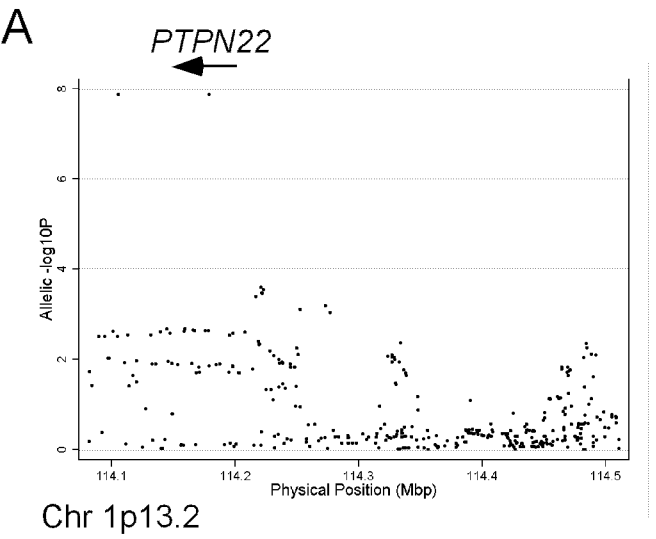
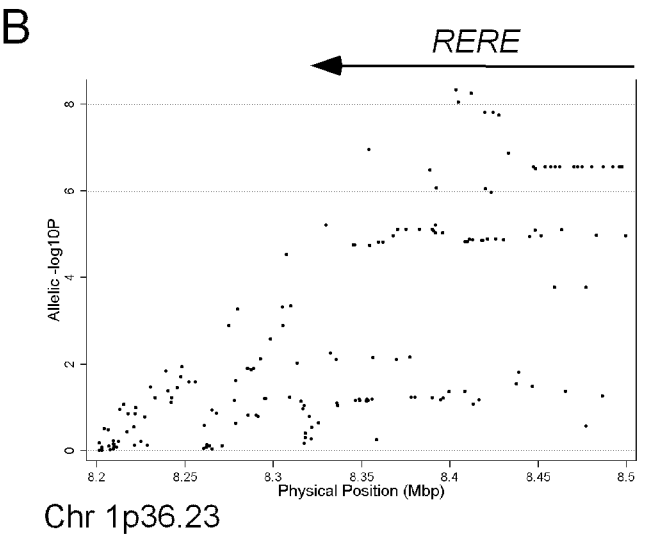
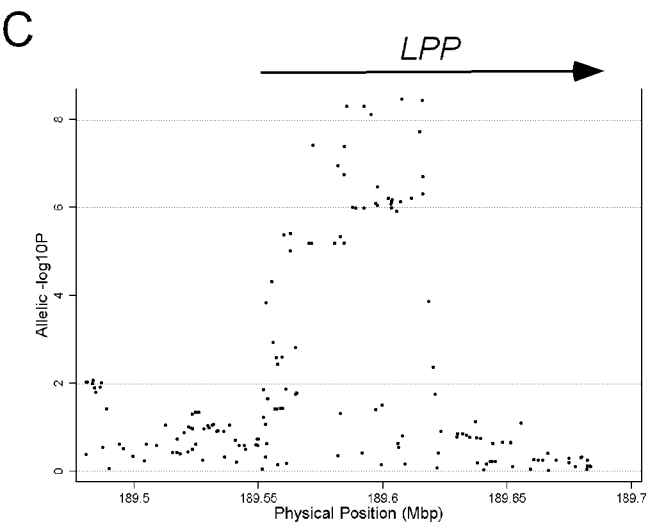
Legends to Supplementary Figures

Supplementary Appendix Figure 1. Detailed association results from the genomewide association study for the most significant association signals. $-\log_{10}$(P values) for SNPs located in chromosome segments A, 1p13.2; B, 1p36.23; C, 3q28; D, 10p15.1; E, 11q14.3; F, 14q12; G, 21q22.3; H, 22q13.1.

Supplementary Appendix Figure 2. Linkage disequilibrium plot across the *TYR* region of chromosome 11q14.3. Linkage disequilibrium (r^2) for 8 *TYR* SNPs, of which 7 were highly associated with generalized vitiligo, graphed against the physical positions of the markers (Build 36.1 from the National Center for Biotechnology Information).


A
PTPN22
Allelic -log10P
Physical Position (Mbp)
Chr 1p13.2


B
RERE
Allelic -log10P
Physical Position (Mbp)
Chr 1p36.23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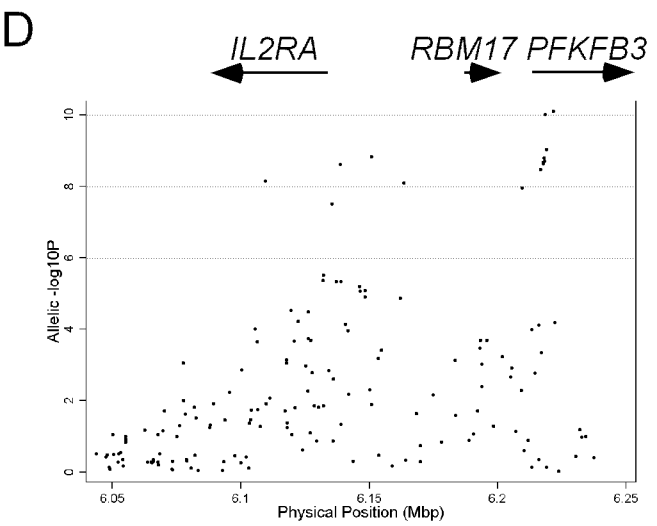
LPP
Allelic -log10P
Physical Position (Mbp)
Chr 3q28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IL2RA
RBM17 PFKFB3
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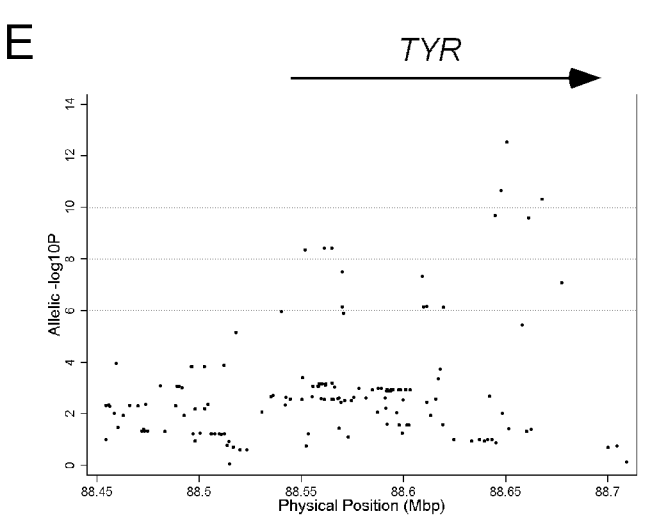
Physical Position (Mbp)
Chr 10p15.1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TYR
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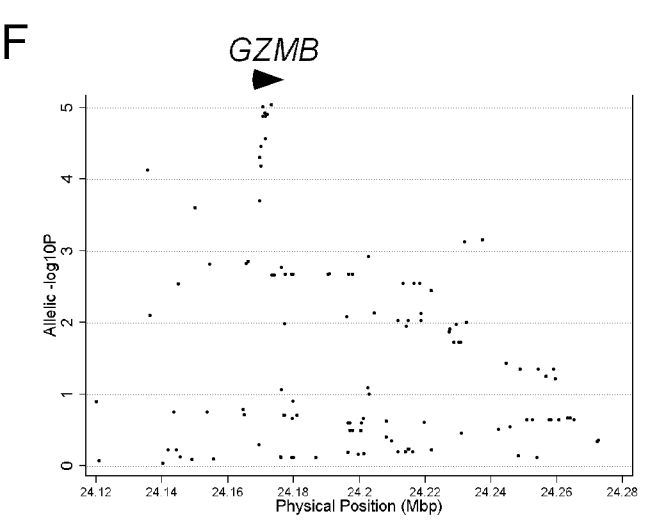
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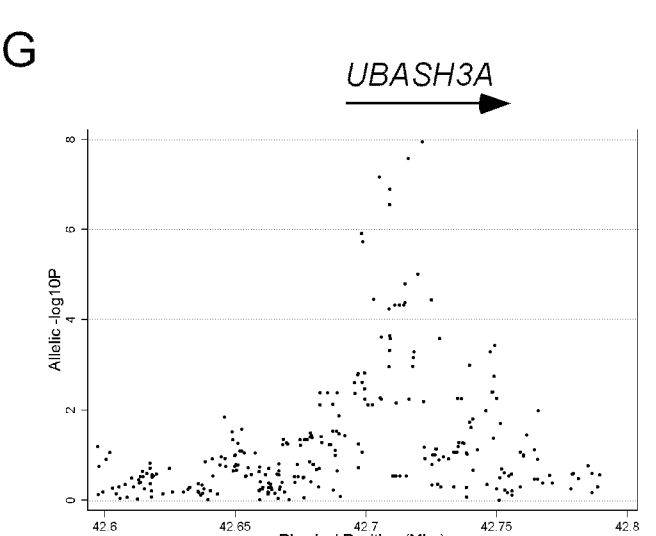
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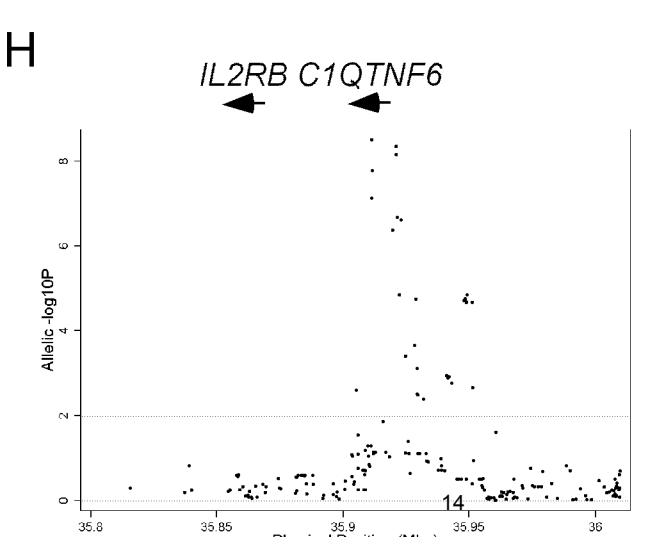
H
IL2RB C1QTNF6
Allelic -log10P
Physical Position (Mbp)
Chr 22q13.1

rs10830236
rs1042602
rs11018528
rs10765198
rs1847134
rs1393350
rs1126809
rs1806319
1
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7
8

Supplementary Appendix Table 1. **Summary description of the samples used in this study**

	Generalized vitiligo patients				Controls			Other family members		
	N	Mean age of onset ± s.d.	% Female	Occurrence of other autoimmune disease (%)[a]	N	% Female	Occurrence of other autoimmune disease (%)[a]	N	Female (%)	Occurrence of other autoimmune disease (%)[a]
Genomewide association study[b]	1514	24.41 ± 16.5	70.1	31.6	2813	55.2	Unknown			
Replication set 1	677	25.61 ± 15.93	63.4	20.58	1106	50.1	3.51			
Replication set 2	1032[c]	20.65 ± 15.01	63.2	22.7				1021[d]	51.5	24.2

The genomewide association study utilized data from public controls (see Methods), for whom clinical history regarding vitiligo and other autoimmune diseases was not available. Replication set 1 utilized non-vitiligo controls from North America and the United Kingdom, almost all spouses of patients from the genomewide association study and replication set 1, with no other known family history of vitiligo.

[a] Includes autoimmune thyroid disease, rheumatoid arthritis, psoriasis, adult-onset autoimmune diabetes, pernicious anemia, Addison's disease, and systemic lupus erythematosus, which are the principal autoimmune diseases that are epidemiologically associated with generalized vitiligo.[5,6]

[b] Twenty-four cases were excluded from the summary data due to inadvertent sample duplication or discordant sex.

[c] Genotyped affected family members

[d] Genotyped unaffected family members

SUPPLEMENTARY APPENDIX TABLE 2. Linkage disequilibrium among MHC SNPs strongly associated with generalized vitiligo

Locus 1	Locus 2	r^2	D'	lod	CI_{lower}	CI_{upper}	Distance (bp)
rs2975033	rs2517715	0.76	0.963	1074.3	0.95	0.98	95178
rs2975033	rs3903160	0.943	0.976	1461.6	0.96	0.99	110636
rs2975033	rs6457110	0.552	0.931	720.56	0.91	0.95	111620
rs2975033	rs3893464	0.334	0.958	435.74	0.94	0.98	112989
rs2975033	rs12206499	0.863	0.942	1249.73	0.93	0.96	114866
rs2975033	rs3823355	0.852	0.928	1223.42	0.91	0.94	119822
rs2975033	rs6904029	0.851	0.927	1222.75	0.91	0.94	120806
rs2975033	rs3823375	0.73	0.925	985.57	0.91	0.94	121897
rs2975033	rs4947244	0.886	0.977	1309.5	0.96	0.99	132103
rs2975033	rs4959039	0.885	0.976	1306.49	0.96	0.99	134808
rs2975033	rs9357092	0.876	0.969	1283.58	0.95	0.98	161991
rs2975033	rs9366752	0.673	0.968	887.02	0.95	0.98	202416
rs2975033	rs4711209	0.877	0.972	1286.32	0.96	0.99	225142
rs2975033	rs6909253	0.443	0.869	544.38	0.84	0.89	233382
rs2975033	rs9261394	0.438	0.869	535.8	0.84	0.89	242301
rs2975033	rs9262582	0.063	0.525	57.99	0.47	0.58	1192044
rs2975033	rs9263607	0.056	0.439	51.17	0.38	0.49	1249896
rs2975033	rs17190526	0.058	0.449	54.18	0.4	0.5	1259820
rs2975033	rs9263823	0.063	0.513	59.47	0.46	0.57	1324833
rs2975033	rs7758128	0.006	0.267	5.6	0.17	0.36	2523021
rs2975033	rs3806156	0.007	0.103	6.72	0.06	0.14	2551436
rs2975033	rs2395185	0.002	0.045	1.54	0.01	0.08	2610905
rs2975033	rs2516049	0.002	0.049	1.92	0.01	0.09	2748138
rs2975033	rs532098	0.009	0.136	7.74	0.09	0.18	2755790
rs2975033	rs34518860	0.003	0.098	2.67	0.04	0.15	2771841
rs2517715	rs3903160	0.732	0.95	1008.55	0.93	0.97	15458
rs2517715	rs6457110	0.733	0.972	1057.7	0.96	0.99	16442
rs2517715	rs3893464	0.41	0.962	543.54	0.94	0.98	17811
rs2517715	rs12206499	0.712	0.922	959.67	0.9	0.94	19688
rs2517715	rs3823355	0.709	0.925	955.95	0.91	0.94	24644
rs2517715	rs6904029	0.709	0.925	956.51	0.91	0.94	25628

rs2517715	rs3823375	0.591	0.785	728.82	0.76	0.81	26719
rs2517715	rs4947244	0.741	0.986	1055.54	0.97	1	36925
rs2517715	rs4959039	0.741	0.986	1053.24	0.97	1	39630
rs2517715	rs9357092	0.74	0.983	1050.62	0.97	1	66813
rs2517715	rs9366752	0.571	0.984	764.29	0.97	1	107238
rs2517715	rs4711209	0.739	0.985	1051.17	0.97	1	129964
rs2517715	rs6909253	0.372	0.721	422.45	0.69	0.75	138204
rs2517715	rs9261394	0.367	0.72	413.96	0.69	0.75	147123
rs2517715	rs9262582	0.051	0.525	47.33	0.46	0.58	1096866
rs2517715	rs9263607	0.044	0.43	40.09	0.37	0.49	1154718
rs2517715	rs17190526	0.048	0.449	44.2	0.39	0.5	1164642
rs2517715	rs9263823	0.05	0.505	46.96	0.44	0.56	1229655
rs2517715	rs7758128	0.005	0.269	4.51	0.16	0.37	2427843
rs2517715	rs3806156	0.007	0.094	6.7	0.06	0.13	2456258
rs2517715	rs2395185	0.002	0.046	1.88	0.01	0.08	2515727
rs2517715	rs2516049	0.004	0.063	3.34	0.03	0.1	2652960
rs2517715	rs532098	0.014	0.158	12.76	0.11	0.2	2660612
rs2517715	rs34518860	0.006	0.153	5.33	0.09	0.21	2676663
rs3903160	rs6457110	0.578	0.958	771.79	0.94	0.97	984
rs3903160	rs3893464	0.36	1	505.92	0.99	1	2353
rs3903160	rs12206499	0.902	0.969	1343.99	0.95	0.98	4230
rs3903160	rs3823355	0.885	0.951	1298.71	0.94	0.97	9186
rs3903160	rs6904029	0.885	0.95	1298.84	0.93	0.96	10170
rs3903160	rs3823375	0.772	0.956	1073.36	0.94	0.97	11261
rs3903160	rs4947244	0.923	0.992	1406.42	0.98	1	21467
rs3903160	rs4959039	0.922	0.991	1402.81	0.98	1	24172
rs3903160	rs9357092	0.912	0.984	1371.79	0.97	1	51355
rs3903160	rs9366752	0.706	0.986	950.78	0.97	1	91780
rs3903160	rs4711209	0.913	0.987	1375.52	0.97	1	114506
rs3903160	rs6909253	0.469	0.898	586.83	0.87	0.92	122746
rs3903160	rs9261394	0.462	0.898	576.69	0.87	0.92	131665
rs3903160	rs9262582	0.063	0.523	57.52	0.46	0.58	1081408
rs3903160	rs9263607	0.058	0.444	52.74	0.39	0.5	1139260
rs3903160	rs17190526	0.06	0.453	55.16	0.4	0.5	1149184

rs3903160	rs9263823	0.063	0.511	59.31	0.45	0.57	1214197
rs3903160	rs7758128	0.006	0.272	5.94	0.18	0.36	2412385
rs3903160	rs3806156	0.007	0.103	6.54	0.06	0.14	2440800
rs3903160	rs2395185	0.002	0.044	1.44	0.01	0.08	2500269
rs3903160	rs2516049	0.002	0.046	1.63	0.01	0.08	2637502
rs3903160	rs532098	0.008	0.129	6.82	0.08	0.18	2645154
rs3903160	rs34518860	0.003	0.093	2.4	0.04	0.15	2661205
rs6457110	rs3893464	0.571	1	837.69	0.99	1	1369
rs6457110	rs12206499	0.65	1	946.65	0.99	1	3246
rs6457110	rs3823355	0.643	0.999	931.4	0.98	1	8202
rs6457110	rs6904029	0.643	0.999	931.96	0.98	1	9186
rs6457110	rs3823375	0.5	0.814	596.64	0.79	0.84	10277
rs6457110	rs4947244	0.583	0.993	816.35	0.98	1	20483
rs6457110	rs4959039	0.583	0.992	814.94	0.98	1	23188
rs6457110	rs9357092	0.584	0.991	817.22	0.98	1	50371
rs6457110	rs9366752	0.45	0.992	607.33	0.98	1	90796
rs6457110	rs4711209	0.58	0.99	809.03	0.98	1	113522
rs6457110	rs6909253	0.235	0.505	244.34	0.48	0.53	121762
rs6457110	rs9261394	0.229	0.502	236.2	0.47	0.53	130681
rs6457110	rs9262582	0.048	0.574	44.65	0.51	0.64	1080424
rs6457110	rs9263607	0.041	0.472	38.08	0.41	0.53	1138276
rs6457110	rs17190526	0.044	0.488	40.93	0.42	0.55	1148200
rs6457110	rs9263823	0.047	0.553	44.38	0.49	0.61	1213213
rs6457110	rs7758128	0.004	0.277	3.82	0.16	0.39	2411401
rs6457110	rs3806156	0.011	0.111	10.35	0.08	0.15	2439816
rs6457110	rs2395185	0.004	0.072	3.5	0.03	0.11	2499285
rs6457110	rs2516049	0.007	0.095	5.77	0.06	0.13	2636518
rs6457110	rs532098	0.017	0.155	15.81	0.12	0.19	2644170
rs6457110	rs34518860	0.005	0.162	4.66	0.09	0.23	2660221
rs3893464	rs12206499	0.373	1	524.54	0.99	1	1877
rs3893464	rs3823355	0.367	0.999	515.5	0.98	1	6833
rs3893464	rs6904029	0.367	0.999	516.55	0.98	1	7817
rs3893464	rs3823375	0.253	0.767	279.32	0.73	0.8	8908
rs3893464	rs4947244	0.332	0.991	454.85	0.98	1	19114

rs3893464	rs4959039	0.332	0.99	452.6	0.97	1	21819
rs3893464	rs9357092	0.333	0.99	455.48	0.97	1	49002
rs3893464	rs9366752	0.256	0.99	348	0.97	1	89427
rs3893464	rs4711209	0.33	0.989	450.34	0.97	1	112153
rs3893464	rs6909253	0.566	0.956	776.59	0.94	0.97	120393
rs3893464	rs9261394	0.552	0.937	738.01	0.92	0.96	129312
rs3893464	rs9262582	0.025	0.551	23.33	0.46	0.63	1079055
rs3893464	rs9263607	0.019	0.424	17.14	0.34	0.5	1136907
rs3893464	rs17190526	0.02	0.437	18.87	0.35	0.51	1146831
rs3893464	rs9263823	0.025	0.539	24.25	0.45	0.62	1211844
rs3893464	rs7758128	0.005	0.406	5.17	0.26	0.53	2410032
rs3893464	rs3806156	0.003	0.071	2.39	0.03	0.12	2438447
rs3893464	rs2395185	0.001	0.04	0.62	0	0.09	2497916
rs3893464	rs2516049	0.001	0.052	0.98	0	0.1	2635149
rs3893464	rs532098	0.009	0.108	8.27	0.07	0.15	2642801
rs3893464	rs34518860	0.007	0.256	7.04	0.17	0.33	2658852
rs12206499	rs3823355	0.984	0.998	1605.21	0.98	1	4956
rs12206499	rs6904029	0.983	0.998	1603.87	0.98	1	5940
rs12206499	rs3823375	0.828	0.981	1198.56	0.97	0.99	7031
rs12206499	rs4947244	0.894	0.992	1339.18	0.98	1	17237
rs12206499	rs4959039	0.894	0.991	1340.4	0.98	1	19942
rs12206499	rs9357092	0.886	0.985	1316.17	0.97	1	47125
rs12206499	rs9366752	0.681	0.985	912.08	0.97	1	87550
rs12206499	rs4711209	0.884	0.986	1311.08	0.97	1	110276
rs12206499	rs6909253	0.44	0.857	534.63	0.83	0.88	118516
rs12206499	rs9261394	0.435	0.858	525.88	0.83	0.88	127435
rs12206499	rs9262582	0.061	0.524	56.08	0.46	0.58	1077178
rs12206499	rs9263607	0.054	0.437	49.49	0.38	0.49	1135030
rs12206499	rs17190526	0.057	0.45	52.69	0.39	0.5	1144954
rs12206499	rs9263823	0.061	0.511	57.45	0.45	0.57	1209967
rs12206499	rs7758128	0.008	0.299	6.87	0.2	0.39	2408155
rs12206499	rs3806156	0.011	0.126	10.01	0.09	0.17	2436570
rs12206499	rs2395185	0.004	0.067	3.52	0.03	0.1	2496039
rs12206499	rs2516049	0.004	0.067	3.57	0.03	0.1	2633272

rs12206499	rs532098	0.011	0.156	10.27	0.11	0.2	2640924
rs12206499	rs34518860	0.003	0.093	2.32	0.04	0.15	2656975
rs3823355	rs6904029	0.998	0.999	1670.8	0.99	1	984
rs3823355	rs3823375	0.84	0.994	1243.01	0.98	1	2075
rs3823355	rs4947244	0.907	0.994	1374.22	0.98	1	12281
rs3823355	rs4959039	0.907	0.993	1374.27	0.98	1	14986
rs3823355	rs9357092	0.896	0.985	1340.42	0.97	1	42169
rs3823355	rs9366752	0.693	0.988	934.86	0.97	1	82594
rs3823355	rs4711209	0.897	0.988	1344.83	0.98	1	105320
rs3823355	rs6909253	0.45	0.872	553.09	0.85	0.9	113560
rs3823355	rs9261394	0.445	0.872	544.34	0.85	0.9	122479
rs3823355	rs9262582	0.061	0.52	55.76	0.46	0.58	1072222
rs3823355	rs9263607	0.054	0.435	49.51	0.38	0.49	1130074
rs3823355	rs17190526	0.057	0.447	52.71	0.39	0.5	1139998
rs3823355	rs9263823	0.061	0.508	57.2	0.45	0.56	1205011
rs3823355	rs7758128	0.008	0.305	7.14	0.21	0.4	2403199
rs3823355	rs3806156	0.01	0.123	9.48	0.08	0.16	2431614
rs3823355	rs2395185	0.004	0.065	3.25	0.03	0.1	2491083
rs3823355	rs2516049	0.004	0.063	3.2	0.03	0.1	2628316
rs3823355	rs532098	0.011	0.154	9.9	0.11	0.2	2635968
rs3823355	rs34518860	0.003	0.101	2.75	0.04	0.16	2652019
rs6904029	rs3823375	0.842	0.996	1250.36	0.98	1	1091
rs6904029	rs4947244	0.909	0.994	1380.75	0.98	1	11297
rs6904029	rs4959039	0.909	0.994	1380.76	0.98	1	14002
rs6904029	rs9357092	0.898	0.986	1346.52	0.97	1	41185
rs6904029	rs9366752	0.694	0.988	939.25	0.97	1	81610
rs6904029	rs4711209	0.899	0.989	1351.01	0.98	1	104336
rs6904029	rs6909253	0.453	0.873	557.31	0.85	0.9	112576
rs6904029	rs9261394	0.448	0.874	548.53	0.85	0.9	121495
rs6904029	rs9262582	0.061	0.52	55.69	0.46	0.58	1071238
rs6904029	rs9263607	0.054	0.435	49.42	0.38	0.49	1129090
rs6904029	rs17190526	0.056	0.444	51.78	0.39	0.5	1139014
rs6904029	rs9263823	0.061	0.508	57.12	0.45	0.56	1204027
rs6904029	rs7758128	0.008	0.308	7.32	0.21	0.4	2402215

rs6904029	rs3806156	0.01	0.123	9.51	0.08	0.16	2430630
rs6904029	rs2395185	0.004	0.066	3.34	0.03	0.1	2490099
rs6904029	rs2516049	0.004	0.064	3.24	0.03	0.1	2627332
rs6904029	rs532098	0.011	0.153	9.81	0.11	0.2	2634984
rs6904029	rs34518860	0.003	0.099	2.65	0.04	0.16	2651035
rs3823375	rs4947244	0.784	0.995	1136.21	0.98	1	10206
rs3823375	rs4959039	0.785	0.995	1137.66	0.98	1	12911
rs3823375	rs9357092	0.776	0.987	1109.44	0.97	1	40094
rs3823375	rs9366752	0.599	0.988	798.54	0.97	1	80519
rs3823375	rs4711209	0.775	0.989	1109.95	0.98	1	103245
rs3823375	rs6909253	0.357	0.722	399.2	0.69	0.75	111485
rs3823375	rs9261394	0.35	0.719	389.3	0.69	0.75	120404
rs3823375	rs9262582	0.064	0.576	60.65	0.52	0.63	1070147
rs3823375	rs9263607	0.068	0.523	64.02	0.47	0.58	1127999
rs3823375	rs17190526	0.072	0.539	68.4	0.48	0.59	1137923
rs3823375	rs9263823	0.065	0.565	62.88	0.51	0.62	1202936
rs3823375	rs7758128	0.006	0.298	5.93	0.19	0.4	2401124
rs3823375	rs3806156	0.009	0.106	7.91	0.07	0.14	2429539
rs3823375	rs2395185	0.003	0.052	2.47	0.02	0.09	2489008
rs3823375	rs2516049	0.002	0.046	1.83	0.01	0.08	2626241
rs3823375	rs532098	0.009	0.126	7.62	0.08	0.17	2633893
rs3823375	rs34518860	0.003	0.108	2.73	0.05	0.17	2649944
rs4947244	rs4959039	0.999	0.999	1641.53	0.98	1	2705
rs4947244	rs9357092	0.988	0.996	1593.47	0.98	1	29888
rs4947244	rs9366752	0.764	0.993	1049.5	0.98	1	70313
rs4947244	rs4711209	0.989	0.995	1598.76	0.98	1	93039
rs4947244	rs6909253	0.526	0.982	721.63	0.97	0.99	101279
rs4947244	rs9261394	0.52	0.983	711.87	0.97	1	110198
rs4947244	rs9262582	0.061	0.499	54.2	0.44	0.55	1059941
rs4947244	rs9263607	0.056	0.424	49.89	0.37	0.48	1117793
rs4947244	rs17190526	0.058	0.432	52.3	0.38	0.48	1127717
rs4947244	rs9263823	0.062	0.49	56.22	0.43	0.54	1192730
rs4947244	rs7758128	0.006	0.258	5.67	0.16	0.35	2390918
rs4947244	rs3806156	0.007	0.103	6.21	0.06	0.14	2419333

rs4947244	rs2395185	0.002	0.048	1.67	0.01	0.09	2478802
rs4947244	rs2516049	0.002	0.046	1.6	0.01	0.08	2616035
rs4947244	rs532098	0.008	0.133	6.88	0.08	0.18	2623687
rs4947244	rs34518860	0.003	0.097	2.71	0.04	0.15	2639738
rs4959039	rs9357092	0.988	0.996	1593.45	0.98	1	27183
rs4959039	rs9366752	0.764	0.993	1049.54	0.98	1	67608
rs4959039	rs4711209	0.989	0.995	1598.75	0.98	1	90334
rs4959039	rs6909253	0.525	0.982	720.83	0.97	0.99	98574
rs4959039	rs9261394	0.52	0.983	711.55	0.97	1	107493
rs4959039	rs9262582	0.06	0.497	53.68	0.44	0.55	1057236
rs4959039	rs9263607	0.055	0.421	49.17	0.37	0.47	1115088
rs4959039	rs17190526	0.057	0.429	51.56	0.38	0.48	1125012
rs4959039	rs9263823	0.061	0.488	55.7	0.43	0.54	1190025
rs4959039	rs7758128	0.006	0.261	5.79	0.17	0.35	2388213
rs4959039	rs3806156	0.007	0.103	6.24	0.06	0.14	2416628
rs4959039	rs2395185	0.002	0.047	1.61	0.01	0.09	2476097
rs4959039	rs2516049	0.002	0.046	1.57	0.01	0.08	2613330
rs4959039	rs532098	0.008	0.134	6.98	0.09	0.18	2620982
rs4959039	rs34518860	0.003	0.098	2.82	0.04	0.15	2637033
rs9357092	rs9366752	0.766	0.998	1064.36	0.98	1	40425
rs9357092	rs4711209	0.99	0.998	1605.11	0.98	1	63151
rs9357092	rs6909253	0.528	0.981	724.45	0.97	0.99	71391
rs9357092	rs9261394	0.522	0.982	714.61	0.97	0.99	80310
rs9357092	rs9262582	0.061	0.499	54.07	0.44	0.55	1030053
rs9357092	rs9263607	0.056	0.426	50.24	0.37	0.48	1087905
rs9357092	rs17190526	0.058	0.434	52.65	0.38	0.49	1097829
rs9357092	rs9263823	0.062	0.49	56.15	0.43	0.54	1162842
rs9357092	rs7758128	0.007	0.267	5.99	0.17	0.36	2361030
rs9357092	rs3806156	0.007	0.104	6.33	0.06	0.14	2389445
rs9357092	rs2395185	0.001	0.043	1.35	0.01	0.08	2448914
rs9357092	rs2516049	0.001	0.042	1.33	0	0.08	2586147
rs9357092	rs532098	0.008	0.133	6.89	0.08	0.18	2593799
rs9357092	rs34518860	0.004	0.104	3.14	0.05	0.16	2609850
rs9366752	rs4711209	0.766	0.995	1056.37	0.98	1	22726

rs9366752	rs6909253	0.405	0.98	537.57	0.96	0.99	30966
rs9366752	rs9261394	0.401	0.981	531.04	0.96	1	39885
rs9366752	rs9262582	0	0.019	0.1	-0.01	0.08	989628
rs9366752	rs9263607	0.001	0.041	0.6	0	0.09	1047480
rs9366752	rs17190526	0.001	0.044	0.7	0	0.1	1057404
rs9366752	rs9263823	0.001	0.039	0.47	-0.01	0.09	1122417
rs9366752	rs7758128	0.008	0.258	6.99	0.17	0.34	2320605
rs9366752	rs3806156	0.001	0.052	1.24	0.01	0.1	2349020
rs9366752	rs2395185	0.001	0.051	0.47	0	0.12	2408489
rs9366752	rs2516049	0.001	0.061	0.62	0	0.13	2545722
rs9366752	rs532098	0.002	0.081	1.96	0.03	0.13	2553374
rs9366752	rs34518860	0.008	0.138	6.85	0.09	0.19	2569425
rs4711209	rs6909253	0.533	0.989	741.46	0.97	1	8240
rs4711209	rs9261394	0.527	0.99	731.81	0.98	1	17159
rs4711209	rs9262582	0.061	0.501	54.78	0.44	0.56	966902
rs4711209	rs9263607	0.057	0.426	50.6	0.37	0.48	1024754
rs4711209	rs17190526	0.059	0.436	53.45	0.38	0.49	1034678
rs4711209	rs9263823	0.062	0.491	56.89	0.43	0.55	1099691
rs4711209	rs7758128	0.006	0.254	5.5	0.16	0.35	2297879
rs4711209	rs3806156	0.007	0.102	6.19	0.06	0.14	2326294
rs4711209	rs2395185	0.001	0.043	1.34	0.01	0.08	2385763
rs4711209	rs2516049	0.001	0.042	1.3	0	0.08	2522996
rs4711209	rs532098	0.007	0.132	6.74	0.08	0.18	2530648
rs4711209	rs34518860	0.004	0.103	3.09	0.05	0.16	2546699
rs6909253	rs9261394	0.98	0.996	1716.18	0.98	1	8919
rs6909253	rs9262582	0.027	0.448	24.45	0.37	0.52	958662
rs6909253	rs9263607	0.022	0.364	20.5	0.29	0.43	1016514
rs6909253	rs17190526	0.022	0.362	20.61	0.29	0.43	1026438
rs6909253	rs9263823	0.029	0.454	27.04	0.38	0.52	1091451
rs6909253	rs7758128	0.005	0.322	5.22	0.2	0.43	2289639
rs6909253	rs3806156	0.001	0.025	0.5	-0.01	0.06	2318054
rs6909253	rs2395185	0	0.016	0.17	-0.01	0.06	2377523
rs6909253	rs2516049	0	0.004	0.01	-0.01	0.05	2514756
rs6909253	rs532098	0.003	0.061	2.65	0.02	0.1	2522408

rs6909253	rs34518860	0.004	0.152	3.86	0.08	0.22	2538459
rs9261394	rs9262582	0.027	0.451	24.28	0.38	0.52	949743
rs9261394	rs9263607	0.022	0.363	20.06	0.29	0.43	1007595
rs9261394	rs17190526	0.022	0.361	20.02	0.29	0.43	1017519
rs9261394	rs9263823	0.029	0.456	26.8	0.38	0.52	1082532
rs9261394	rs7758128	0.005	0.323	5.19	0.21	0.43	2280720
rs9261394	rs3806156	0	0.023	0.4	-0.01	0.06	2309135
rs9261394	rs2395185	0	0.013	0.11	-0.01	0.06	2368604
rs9261394	rs2516049	0	0.001	0	-0.01	0.05	2505837
rs9261394	rs532098	0.003	0.058	2.39	0.02	0.1	2513489
rs9261394	rs34518860	0.004	0.154	3.86	0.08	0.22	2529540
rs9262582	rs9263607	0.754	0.998	657.08	0.98	1	57852
rs9262582	rs17190526	0.777	0.994	684.8	0.98	1	67776
rs9262582	rs9263823	0.884	0.966	745.65	0.95	0.98	132789
rs9262582	rs7758128	0.002	0.073	1.64	0.02	0.13	1330977
rs9262582	rs3806156	0.021	0.364	17.26	0.29	0.43	1359392
rs9262582	rs2395185	0.015	0.282	13.11	0.21	0.35	1418861
rs9262582	rs2516049	0.023	0.341	19.65	0.27	0.41	1556094
rs9262582	rs532098	0.015	0.381	13.27	0.29	0.46	1563746
rs9262582	rs34518860	0	0.134	0.27	0.01	0.33	1579797
rs9263607	rs17190526	0.887	0.957	822.58	0.94	0.97	9924
rs9263607	rs9263823	0.737	0.962	628.91	0.94	0.98	74937
rs9263607	rs7758128	0.004	0.122	3.52	0.06	0.19	1273125
rs9263607	rs3806156	0.038	0.436	32.76	0.37	0.5	1301540
rs9263607	rs2395185	0.018	0.27	15.36	0.21	0.33	1361009
rs9263607	rs2516049	0.027	0.327	23.15	0.27	0.39	1498242
rs9263607	rs532098	0.02	0.392	18.26	0.31	0.46	1505894
rs9263607	rs34518860	0	0.001	0	-0.01	0.04	1521945
rs17190526	rs9263823	0.77	0.963	671.64	0.94	0.98	65013
rs17190526	rs7758128	0.004	0.12	3.43	0.06	0.19	1263201
rs17190526	rs3806156	0.028	0.376	24.44	0.31	0.44	1291616
rs17190526	rs2395185	0.017	0.267	15.33	0.21	0.33	1351085
rs17190526	rs2516049	0.027	0.327	23.7	0.27	0.39	1488318
rs17190526	rs532098	0.025	0.433	22.79	0.36	0.5	1495970

rs17190526	rs34518860	0	0.017	0.24	-0.01	0.06	1512021
rs9263823	rs7758128	0.005	0.115	3.96	0.06	0.18	1198188
rs9263823	rs3806156	0.022	0.368	19.25	0.3	0.44	1226603
rs9263823	rs2395185	0.013	0.25	11.02	0.18	0.32	1286072
rs9263823	rs2516049	0.02	0.306	16.82	0.24	0.37	1423305
rs9263823	rs532098	0.016	0.38	13.95	0.29	0.46	1430957
rs9263823	rs34518860	0	0.028	0.01	-0.01	0.25	1447008
rs7758128	rs3806156	0.059	1	72.17	0.97	1	28415
rs7758128	rs2395185	0.018	0.887	19.27	0.76	0.95	87884
rs7758128	rs2516049	0.017	0.875	17.26	0.74	0.94	225117
rs7758128	rs532098	0.028	0.844	32.48	0.75	0.91	232769
rs7758128	rs34518860	0.188	0.827	135.56	0.77	0.87	248820
rs3806156	rs2395185	0.337	0.645	363.95	0.62	0.67	59469
rs3806156	rs2516049	0.409	0.723	460.78	0.7	0.75	196702
rs3806156	rs532098	0.446	0.815	534.9	0.79	0.84	204354
rs3806156	rs34518860	0	0.004	0	-0.01	0.08	220405
rs2395185	rs2516049	0.867	0.95	1286.72	0.93	0.96	137233
rs2395185	rs532098	0.426	0.884	529.66	0.86	0.91	144885
rs2395185	rs34518860	0.085	1	108.3	0.98	1	160936
rs2516049	rs532098	0.525	1	760.31	0.99	1	7652
rs2516049	rs34518860	0.081	1	102.71	0.98	1	23703
rs532098	rs34518860	0.144	1	187.94	0.99	1	16051

Notes:

Locus 1 and Locus 2 are the two loci under comparison

r^2 is the correlation coefficient between the two loci

D' is the value of D prime between the two loci

lod is the log of the likelihood odds ratio, a measure of confidence in the value of D'

CI_{lower} is 95% confidence lower bound on D'

CI_{upper} is the 95% confidence upper bound on D'

Distance is bp separating the two loci

SUPPLEMENTARY APPENDIX TABLE 3. Second locus effect tests of strongly-associated HLA region SNPs in a forward stepwise-regression procedure for the vitiligo phenotype, based on data from the genomewide association study

Null Model	Alternative Model	P_{logit}	Null Model	Alternative Model	P_{logit}	Null Model	Alternative Model	P_{logit}	Null Model	Alternative Model	P_{logit}
F	F+A	NS	A	A+F	1.75E-5	U	U+A	5.59E-13	A	A+U	1.14E-27
F	F+B	NS	B	B+F	1.87E-8	U	U+B	1.92E-9	B	B+U	4.07E-27
F	F+C	NS	C	C+F	2.22E-4	U	U+C	3.14E-14	C	C+U	1.52E-27
F	F+D	NS	D	D+F	2.57E-8	U	U+D	3.94E-9	D	D+U	8.99E-27
F	F+E	NS	E	E+F	4.42E-9	U	U+E	3.36E-10	E	E+U	4.90E-28
…	F	1.78E-20	…	…	…	U	U+F	3.55E-16	F	F+U	2.56E-26
F	F+G	NS	G	G+F	NS	U	U+G	4.38E-16	G	G+U	7.13E-27
F	F+H	NS	H	H+F	5.95E-2	U	U+H	1.40E-15	H	H+U	7.24E-27
F	F+I	NS	I	I+F	5.21E-6	U	U+I	7.36eE-13	I	I+U	3.05E-28
F	F+J	NS	J	J+F	2.42E-5	U	U+J	1.78E-13	J	J+U	7.28E-28
F	F+K	NS	K	K+F	4.18E-6	U	U+K	3.03E-13	K	K+U	9.08E-28
F	F+L	NS	L	L+F	1.42E-4	U	U+L	4.33E-14	L	L+U	1.02E-27
F	F+M	NS	M	M+F	1.81E-8	U	U+M	4.18E-12	M	M+U	2.36E-29
F	F+N	NS	N	N+F	9.77E-5	U	U+N	5.26E-14	N	N+U	9.22E-28
F	F+O	NS	O	O+F	3.83E-8	U	U+O	9.37E-13	O	O+U	4.55E-29
F	F+P	NS	P	P+F	8.42E-8	U	U+P	3.06E-13	P	P+U	3.08E-29
F	F+Q	2.07E-12	Q	Q+F	8.98E-18	U	U+Q	8.91E-9	Q	Q+U	4.21E-25
F	F+R	1.13E-15	R	R+F	5.09E-17	U	U+R	NS	R	R+U	9.49E-15

F	F+S	7.26E-12	S	S+F	1.16E-18	U	U+S	NS	S	S+U	5.30E-20
F	F+T	1.03E-13	T	T+F	1.25E-18	U	U+T	NS	T	T+U	6.98E-18
F	F+U	2.26E-26	U	U+F	3.55E-16	…	U	4.10E-31	…	…	…
F	F+V	9.75E-14	V	V+F	3.33E-19	U	U+V	1.41E-4	V	V+U	5.43E-21

A, rs2975033; B, rs2517715; C, rs3903160; D, rs6457110; E, rs13893464; F, rs12206499; G, rs3823355; H, rs6904029; I, rs3823375; J, rs4947244; K, rs4959039; L, rs9357092; M, rs9366752; N, rs4711209; O, rs6906253; P, rs9261394; Q, rs7758128; R, rs3806156; S, rs2395185; T, rs2516049; U, rs532098; V, rs34518860 P_{logit}, P values from logistic regression analyses. NS, not significant (P > 0.05). A multiplicative genetic model for the high risk allele of each locus was assumed.

SUPPLEMENTARY APPENDIX TABLE 4A. Allelic association analyses of most significant SNPs comparing generalized vitiligo patients with concomitant other autoimmune diseases versus controls (genomewide association study data)

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
1	rs301819	8424373	A	0.49	0.41	G	5.84E-05	1.35	1.17	1.56
1	rs4908760	8448729	G	0.43	0.37	A	4.60E-04	1.30	1.12	1.51
1	rs11121194	8492493	C	0.43	0.37	T	5.77E-04	1.29	1.12	1.50
1	rs2476601	114179091	A	0.17	0.09	G	7.37E-12	2.01	1.64	2.46
3	rs13076312	189571948	T	0.53	0.44	C	9.92E-07	1.43	1.24	1.65
3	rs1464510	189595248	T	0.54	0.44	G	1.37E-07	1.47	1.27	1.70
3	rs13091753	189597283	T	0.49	0.40	G	3.61E-07	1.45	1.25	1.67
3	rs1559810	189607048	T	0.49	0.40	G	4.37E-07	1.44	1.25	1.67
6	rs2975033	29930240	T	0.36	0.29	C	1.29E-04	1.34	1.15	1.56
6	rs2517715	30025418	G	0.41	0.34	A	1.55E-04	1.33	1.15	1.54
6	rs3903160	30040876	T	0.35	0.29	C	1.38E-04	1.34	1.15	1.56
6	rs6457110	30041860	A	0.45	0.40	T	7.34E-03	1.22	1.06	1.41
6	rs3893464	30043229	C	0.59	0.54	T	2.01E-03	1.26	1.09	1.46
6	rs12206499	30045106	G	0.36	0.29	A	4.50E-05	1.37	1.18	1.59
6	rs3823355	30050062	T	0.36	0.29	C	4.42E-05	1.37	1.18	1.60
6	rs6904029	30051046	A	0.36	0.29	G	7.60E-05	1.36	1.17	1.58
6	rs3823375	30052137	C	0.38	0.33	T	9.46E-04	1.29	1.11	1.49
6	rs4947244	30062343	G	0.33	0.28	C	3.87E-04	1.32	1.13	1.54
6	rs4959039	30065048	G	0.33	0.28	A	4.19E-04	1.32	1.13	1.53
6	rs9357092	30092231	A	0.34	0.28	G	3.00E-04	1.33	1.14	1.55
6	rs9366752	30132656	T	0.27	0.23	C	3.46E-03	1.27	1.08	1.49
6	rs4711209	30155382	A	0.33	0.28	G	3.06E-04	1.33	1.14	1.55
6	rs6909253	30163622	G	0.49	0.42	T	1.31E-04	1.32	1.15	1.53
6	rs9261394	30172541	A	0.49	0.42	G	1.50E-04	1.32	1.14	1.52
6	rs7758128	32453261	A	0.05	0.03	C	1.01E-03	1.80	1.26	2.57
6	rs3806156	32481676	T	0.47	0.37	G	6.28E-08	1.50	1.30	1.74
6	rs2395185	32541145	T	0.43	0.33	G	5.20E-08	1.50	1.30	1.74
6	rs2516049	32678378	G	0.42	0.32	A	2.02E-09	1.57	1.35	1.82

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
6	rs532098	32686030	T	0.58	0.46	C	1.90E-10	1.61	1.39	1.86
6	rs34518860	32702081	A	0.14	0.11	G	9.98E-03	1.32	1.07	1.64
10	rs706779	6138830	A	0.60	0.53	G	5.24E-04	1.30	1.12	1.50
10	rs7090530	6150881	A	0.66	0.60	C	3.40E-04	1.32	1.13	1.53
10	rs12251307	6163501	C	0.92	0.87	T	4.71E-05	1.70	1.31	2.20
10	rs4750005	6209691	T	0.58	0.52	C	5.30E-04	1.29	1.12	1.49
10	rs3920615	6216786	A	0.62	0.55	G	1.05E-04	1.33	1.15	1.54
10	rs4747887	6217688	T	0.62	0.55	C	1.07E-04	1.33	1.15	1.54
10	rs4750012	6217800	C	0.62	0.55	T	1.10E-04	1.33	1.15	1.54
10	rs7099083	6218242	G	0.62	0.55	A	8.84E-05	1.34	1.16	1.55
11	rs10830236	88540464	C	0.73	0.67	T	9.74E-05	1.38	1.17	1.62
11	rs11018528	88570025	A	0.77	0.71	G	2.82E-05	1.44	1.21	1.71
11	rs10765198	88609422	T	0.78	0.71	C	1.64E-05	1.46	1.23	1.74
11	rs1847134	88644901	A	0.77	0.68	C	2.78E-07	1.55	1.31	1.84
11	rs1393350	88650694	G	0.83	0.73	A	1.06E-09	1.79	1.48	2.16
11	rs1806319	88677584	A	0.71	0.63	G	2.37E-05	1.40	1.20	1.63
14	rs8192917	24172000	G	0.28	0.23	A	6.76E-03	1.25	1.06	1.47
14	rs2273844	24173254	A	0.28	0.23	G	7.56E-03	1.25	1.06	1.47
21	rs11203203	42709255	A	0.42	0.37	G	2.90E-03	1.25	1.08	1.45
21	rs2839511	42721590	A	0.29	0.23	G	2.48E-05	1.41	1.20	1.66
22	rs229527	35911431	T	0.48	0.42	G	1.06E-03	1.27	1.10	1.47
22	rs5756546	35919751	T	0.28	0.22	C	1.12E-04	1.38	1.17	1.62

SUPPLEMENTARY APPENDIX TABLE 4B. Allelic association analyses of most significant SNPs comparing generalized vitiligo patients without concomitant other autoimmune diseases versus controls (genomewide association study data)

CHR	SNP	Position (bp)	A1	F_A	F_U	A2	trend P	OR	L95	U95
1	rs301819	8424373	A	0.48	0.4143	G	5.62E-07	1.313	1.18	1.462
1	rs4908760	8448729	G	0.429	0.3711	A	1.02E-05	1.269	1.141	1.411
1	rs11121194	8492493	C	0.4311	0.3721	T	7.21E-06	1.274	1.146	1.417
1	rs2476601	114179091	A	0.1193	0.09216	G	0.0006785	1.336	1.13	1.58
3	rs13076312	189571948	T	0.4989	0.4446	C	4.82E-05	1.243	1.119	1.381

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
3	rs1464510	189595248	T	0.4958	0.4392	G	2.23E-05	1.255	1.13	1.395
3	rs13091753	189597283	T	0.4436	0.4011	G	0.001396	1.187	1.068	1.319
3	rs1559810	189607048	T	0.4427	0.3997	G	0.001205	1.19	1.071	1.322
6	rs2975033	29930240	T	0.3943	0.2909	C	4.28E-16	1.564	1.403	1.744
6	rs2517715	30025418	G	0.429	0.3394	A	7.24E-12	1.448	1.302	1.611
6	rs3903160	30040876	T	0.3947	0.2872	C	1.45E-17	1.606	1.439	1.793
6	rs6457110	30041860	A	0.5011	0.3987	T	2.09E-14	1.505	1.354	1.673
6	rs3893464	30043229	C	0.6351	0.5383	T	4.26E-13	1.49	1.337	1.661
6	rs12206499	30045106	G	0.4103	0.2911	A	7.05E-21	1.679	1.504	1.873
6	rs3823355	30050062	T	0.4069	0.2894	C	1.55E-20	1.672	1.498	1.866
6	rs6904029	30051046	A	0.4064	0.2903	G	4.77E-20	1.661	1.488	1.853
6	rs3823375	30052137	C	0.4332	0.3258	T	1.04E-16	1.579	1.416	1.76
6	rs4947244	30062343	G	0.3801	0.2758	C	7.10E-17	1.593	1.427	1.78
6	rs4959039	30065048	G	0.3796	0.2761	A	1.30E-16	1.587	1.421	1.772
6	rs9357092	30092231	A	0.3828	0.276	G	1.31E-17	1.61	1.442	1.798
6	rs9366752	30132656	T	0.3181	0.2288	C	3.54E-14	1.558	1.388	1.749
6	rs4711209	30155382	A	0.3812	0.275	G	1.91E-17	1.607	1.439	1.795
6	rs6909253	30163622	G	0.5137	0.4175	T	6.95E-13	1.469	1.322	1.632
6	rs9261394	30172541	A	0.5189	0.4204	G	1.87E-13	1.484	1.335	1.65
6	rs7758128	32453261	A	0.0694	0.02683	C	5.40E-17	2.777	2.167	3.56
6	rs3806156	32481676	T	0.479	0.3749	G	2.20E-15	1.538	1.382	1.712
6	rs2395185	32541145	T	0.4106	0.332	G	1.18E-09	1.395	1.252	1.553
6	rs2516049	32678378	G	0.4041	0.321	A	8.29E-11	1.431	1.283	1.595
6	rs532098	32686030	T	0.6084	0.461	C	1.08E-27	1.813	1.627	2.021
6	rs34518860	32702081	A	0.1872	0.1076	G	1.81E-18	1.892	1.636	2.188
10	rs706779	6138830	A	0.6109	0.5347	G	9.17E-09	1.371	1.23	1.527
10	rs7090530	6150881	A	0.6725	0.5991	C	2.25E-08	1.368	1.225	1.527
10	rs12251307	6163501	C	0.9106	0.8701	T	2.63E-06	1.529	1.279	1.827
10	rs4750005	6209691	T	0.5904	0.5205	C	1.88E-07	1.325	1.192	1.474
10	rs3920615	6216786	A	0.6158	0.5451	G	1.20E-07	1.334	1.199	1.485
10	rs4747887	6217688	T	0.6157	0.5452	C	1.31E-07	1.333	1.198	1.484
10	rs4750012	6217800	C	0.6157	0.5453	T	1.35E-07	1.333	1.197	1.483
10	rs7099083	6218242	G	0.6157	0.5455	A	1.49E-07	1.331	1.196	1.482

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
11	rs10830236	88540464	C	0.715	0.6676	T	0.0001403	1.251	1.114	1.403
11	rs11018528	88570025	A	0.7597	0.7056	G	5.81E-06	1.325	1.173	1.496
11	rs10765198	88609422	T	0.7655	0.7136	C	1.20E-05	1.314	1.163	1.486
11	rs1847134	88644901	A	0.7461	0.6845	C	4.81E-07	1.357	1.205	1.529
11	rs1393350	88650694	G	0.796	0.7319	A	2.73E-08	1.438	1.264	1.635
11	rs1806319	88677584	A	0.6861	0.63	G	1.55E-05	1.277	1.142	1.426
14	rs8192917	24172000	G	0.2829	0.2347	A	2.89E-05	1.289	1.144	1.452
14	rs2273844	24173254	A	0.2808	0.2341	G	4.95E-05	1.28	1.136	1.442
21	rs11203203	42709255	A	0.4363	0.3727	G	9.67E-07	1.308	1.174	1.456
21	rs2839511	42721590	A	0.2813	0.2254	G	1.17E-06	1.341	1.191	1.511
22	rs229527	35911431	T	0.4947	0.4186	G	1.08E-08	1.359	1.223	1.511
22	rs5756546	35919751	T	0.2676	0.2202	C	2.75E-05	1.295	1.147	1.462

SUPPLEMENTARY APPENDIX TABLE 4C. Allelic association analyses of most significant SNPs comparing generalized vitiligo patients with concomitant other autoimmune diseases versus controls (replication set 1 data)

CHR	SNP	Position (bp)	A1	F_A	F_U	A2	TREND P	OR	L95	U95
1	rs301819	8424373	A	0.5512	0.4396	G	0.0009119	1.546	1.193	2.004
1	rs4908760	8448729	G	0.5	0.3842	A	0.0004447	1.586	1.223	2.056
1	rs11121194	8492493	C	0.5039	0.3906	T	0.0005728	1.57	1.212	2.033
1	rs2476601	114179091	A	0.1523	0.09034	G	0.001753	1.791	1.236	2.595
3	rs13076312	189571948	T	0.543	0.4433	C	0.002052	1.52	1.163	1.986
3	rs1464510	189595248	T	0.5273	0.4408	G	0.00746	1.436	1.1	1.875
3	rs13091753	189597283	T	0.4878	0.4079	G	0.0124	1.424	1.078	1.882
3	rs1559810	189607048	T	0.468	0.401	G	0.03405	1.346	1.022	1.773
6	rs2975033	29930240	T	0.3611	0.2945	C	0.02855	1.36	1.032	1.792
6	rs2517715	30025418	G	0.3849	0.3391	A	0.1513	1.216	0.9304	1.59
6	rs3903160	30040876	T	0.3492	0.3009	C	0.1112	1.255	0.9485	1.661
6	rs6457110	30041860	A	0.4435	0.4082	T	0.2821	1.158	0.886	1.514
6	rs3893464	30043229	C	0.6157	0.5168	T	0.004682	1.466	1.123	1.914

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
6	rs3823355	30050062	T	0.3508	0.3025	C	0.1164	1.252	0.9453	1.657
6	rs6904029	30051046	A	0.3427	0.3004	G	0.168	1.218	0.9197	1.614
6	rs3823375	30052137	C	0.372	0.3498	T	0.481	1.104	0.8381	1.455
6	rs4947244	30062343	G	0.3125	0.2859	C	0.3711	1.138	0.8571	1.511
6	rs4959039	30065048	G	0.316	0.2845	A	0.2956	1.165	0.8752	1.55
6	rs9357092	30092231	A	0.316	0.2836	G	0.2792	1.171	0.8794	1.56
6	rs9366752	30132656	T	0.2642	0.2452	C	0.5116	1.106	0.8185	1.495
6	rs4711209	30155382	A	0.3175	0.2846	G	0.2724	1.173	0.8821	1.559
6	rs6909253	30163622	G	0.4802	0.4148	T	0.042	1.321	1.009	1.729
6	rs9261394	30172541	A	0.488	0.4195	G	0.03491	1.334	1.02	1.746
6	rs7758128	32453261	A	0.02419	0.0278	C	0.7386	0.8635	0.3644	2.046
6	rs3806156	32481676	T	0.3849	0.3601	G	0.4465	1.108	0.8503	1.445
6	rs2395185	32541145	T	0.373	0.2933	G	0.008067	1.455	1.101	1.922
6	rs2516049	32678378	G	0.364	0.2936	A	0.02132	1.382	1.048	1.824
6	rs532098	32686030	T	0.46	0.4061	C	0.1177	1.223	0.9499	1.575
10	rs706779	6138830	A	0.5984	0.5321	G	0.04747	1.304	1.002	1.698
10	rs7090530	6150881	A	0.656	0.6111	C	0.1641	1.218	0.9222	1.609
10	rs12251307	6163501	C	0.8952	0.8975	T	0.9095	0.9756	0.6366	1.495
10	rs4750005	6209691	T	0.3434	0.3794	C	0.3198	0.8293	0.5732	1.2
10	rs3920615	6216786	A	0.5708	0.5392	G	0.3613	1.132	0.8671	1.478
10	rs4747887	6217688	T	0.5586	0.5329	C	0.4272	1.114	0.8534	1.454
10	rs4750012	6217800	C	0.5656	0.5344	T	0.3458	1.14	0.8679	1.498
10	rs7099083	6218242	G	0.556	0.5328	A	0.4785	1.102	0.8421	1.443
11	rs10830236	88540464	C	0.7683	0.7058	T	0.04628	1.362	1.004	1.849
11	rs11018528	88570025	A	0.816	0.7422	G	0.01215	1.524	1.094	2.124
11	rs10765198	88609422	T	0.8175	0.7409	C	0.008144	1.567	1.121	2.191
11	rs1847134	88644901	A	0.7937	0.7091	C	0.005991	1.549	1.131	2.121
11	rs1393350	88650694	G	0.832	0.7591	A	0.01061	1.563	1.107	2.207
11	rs1806319	88677584	A	0.7417	0.6558	G	0.009798	1.473	1.096	1.981
14	rs8192917	24172000	G	0.252	0.2423	A	0.7358	1.053	0.7784	1.426
14	rs2273844	24173254	A	0.254	0.2435	G	0.7155	1.057	0.7834	1.427
21	rs11203203	42709255	A	0.5123	0.3959	G	0.0006459	1.57	1.209	2.04
21	rs2839511	42721590	A	0.296	0.2438	G	0.07671	1.291	0.9721	1.716

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
22	rs229527	35911431	T	0.5766	0.4348	G	1.55E-05	1.821	1.382	2.399
22	rs5756546	35919751	T	0.3095	0.2205	C	0.001162	1.631	1.211	2.198

SUPPLEMENTARY APPENDIX TABLE 4D. Allelic association analyses of most significant SNPs comparing generalized vitiligo patients without concomitant other autoimmune diseases versus controls (replication set 1 data)

CHR	SNP	BP	A1	F_A	F_U	A2	TREND P	OR	L95	U95
1	rs301819	8424373	A	0.5245	0.4396	G	1.97E-05	1.384	1.191	1.608
1	rs4908760	8448729	G	0.4806	0.3842	A	8.77E-07	1.457	1.253	1.695
1	rs11121194	8492493	C	0.4806	0.3906	T	4.54E-06	1.42	1.221	1.65
1	rs2476601	114179091	A	0.08299	0.09034	G	0.5046	0.9115	0.6941	1.197
3	rs13076312	189571948	T	0.502	0.4433	C	0.001979	1.279	1.094	1.495
3	rs1464510	189595248	T	0.4969	0.4408	G	0.003157	1.265	1.082	1.479
3	rs13091753	189597283	T	0.4494	0.4079	G	0.0293	1.195	1.018	1.402
3	rs1559810	189607048	T	0.4452	0.401	G	0.01774	1.212	1.034	1.421
6	rs2975033	29930240	T	0.352	0.2945	C	0.001466	1.297	1.104	1.523
6	rs2517715	30025418	G	0.4012	0.3391	A	0.001134	1.294	1.107	1.511
6	rs3903160	30040876	T	0.3592	0.3009	C	0.001315	1.304	1.109	1.535
6	rs6457110	30041860	A	0.4821	0.4082	T	0.0001587	1.347	1.153	1.573
6	rs3893464	30043229	C	0.5972	0.5168	T	8.57E-05	1.354	1.163	1.577
6	rs3823355	30050062	T	0.3624	0.3025	C	0.00109	1.312	1.114	1.544
6	rs6904029	30051046	A	0.3583	0.3004	G	0.001491	1.3	1.105	1.53
6	rs3823375	30052137	C	0.41	0.3498	T	0.001197	1.298	1.108	1.52
6	rs4947244	30062343	G	0.3385	0.2859	C	0.003327	1.277	1.084	1.505
6	rs4959039	30065048	G	0.3409	0.2845	A	0.001642	1.299	1.103	1.53
6	rs9357092	30092231	A	0.3395	0.2836	G	0.001711	1.299	1.103	1.531
6	rs9366752	30132656	T	0.3074	0.2452	C	0.0003568	1.362	1.149	1.615
6	rs4711209	30155382	A	0.3384	0.2846	G	0.002509	1.286	1.092	1.514
6	rs6909253	30163622	G	0.4793	0.4148	T	0.000668	1.311	1.121	1.534
6	rs9261394	30172541	A	0.4803	0.4195	G	0.001425	1.289	1.102	1.507

CHR	SNP	Position (nt)	A1	F_A	F_U	A2	trend P	OR	L95	U95
6	rs7758128	32453261	A	0.05532	0.0278	C	0.0002353	2.002	1.371	2.923
6	rs3806156	32481676	T	0.4055	0.3601	G	0.01827	1.202	1.031	1.401
6	rs2395185	32541145	T	0.3016	0.2933	G	0.6327	1.042	0.8808	1.232
6	rs2516049	32678378	G	0.32	0.2936	A	0.139	1.133	0.9602	1.336
6	rs532098	32686030	T	0.4719	0.4061	C	0.001224	1.275	1.1	1.478
10	rs706779	6138830	A	0.5443	0.5321	G	0.5365	1.048	0.9024	1.218
10	rs7090530	6150881	A	0.6124	0.6111	C	0.9471	1.005	0.8598	1.175
10	rs12251307	6163501	C	0.8789	0.8975	T	0.1351	0.8386	0.6654	1.057
10	rs4750005	6209691	T	0.4061	0.3794	C	0.1884	1.139	0.9379	1.384
10	rs3920615	6216786	A	0.5358	0.5392	G	0.8666	0.987	0.8472	1.15
10	rs4747887	6217688	T	0.5337	0.5329	C	0.9658	1.003	0.8605	1.17
10	rs4750012	6217800	C	0.5311	0.5344	T	0.8634	0.9865	0.845	1.152
10	rs7099083	6218242	G	0.5328	0.5328	A	1	1	0.8575	1.166
11	rs10830236	88540464	C	0.7473	0.7058	T	0.02231	1.223	1.029	1.454
11	rs11018528	88570025	A	0.7774	0.7422	G	0.03734	1.211	1.011	1.45
11	rs10765198	88609422	T	0.7832	0.7409	C	0.01137	1.263	1.054	1.513
11	rs1847134	88644901	A	0.7732	0.7091	C	0.000286	1.382	1.159	1.647
11	rs1393350	88650694	G	0.8233	0.7591	A	8.56E-05	1.466	1.21	1.777
11	rs1806319	88677584	A	0.7172	0.6558	G	0.00102	1.323	1.119	1.565
14	rs8192917	24172000	G	0.3078	0.2423	A	0.0001198	1.396	1.177	1.656
14	rs2273844	24173254	A	0.3102	0.2435	G	9.37E-05	1.401	1.182	1.661
21	rs11203203	42709255	A	0.4359	0.3959	G	0.04164	1.173	1.006	1.367
21	rs2839511	42721590	A	0.2597	0.2438	G	0.3504	1.085	0.9143	1.287
22	rs229527	35911431	T	0.5302	0.4348	G	6.59E-07	1.493	1.273	1.75
22	rs5756546	35919751	T	0.2818	0.2205	C	0.0001825	1.409	1.176	1.687

A1, minor allele; F_A, minor allele frequency in patients; F_U, minor allele frequency in controls; A2, major allele

Trend P values were calculated using the PLINK[1] unadjusted Cochran-Armitage trend test. Trend P values in Supplementary Appendix Tables 4A and 4B were further corrected by the genomic inflation factor of 1.048 using the genomic control method.[7]

SUPPLEMENTARY APPENDIX TABLE 5. Association Analysis of Non-Synonymous *TYR* SNPs

SNP	Location (nt)	Risk-Allele	Genomewide Association Study					Replication Sets				Combined Analysis (Genomewide Association Study + Replication Sets 1 & 2)	
								Replication Set 1		Replication Set 2			
			Risk-Allele Frequency		EIGENSTRAT P value	PLINK P value	Odds Ratio (95% CI)	P value	Odds Ratio (95% CI)	P value	Odds Ratio (95% CI)	P value	Odds Ratio (95% CI)
			patients (N =1392)	controls (N=2629)									
rs1042602 (S192Y)	88551344	C	0.64	0.63	1.65×10^{-8}	0.62	1.03 (0.93-1.13)	0.29	1.08 (0.94-1.24)	0.62	1.07 (0.87-1.31)	0.26	1.05 (0.97-1.13)
rs1126809 (R402Q)	88657609	G	0.76	0.69	nd	5.92×10^{-12}	1.46 (1.31-1.62)	4.28×10^{-7}	1.58 (1.32-1.88)	nd	nd	1.13×10^{-17}	1.48 (1.35-1.61)

Genotypes for rs1126809 in the genomewide association study and replication set 1 were imputed using MaCH,[4] ver.1.0 (http://www.sph.umich.edu/csg/abecasis/MACH/download/) based on patterns of haplotype variation in the HapMap[5] CEU samples (release 24). For rs1042602 the combined analysis was performed using data from the genomewide association study, replication set 1, and replication set 2. For rs1126809, the combined analysis is based only on data from the genomewide association study and replication set 1, as data for rs1126809 could not be imputed for replication set 2.

SUPPLEMENTARY APPENDIX TABLE 6. Linkage disequilibrium among *TYR* region SNPs

Locus 1	Locus 2	r^2	D'	lod	CI_{lower}	CI_{upper}	Distance (bp)
rs10830236	rs1042602	0.259	0.987	348.04	0.97	1	10880
rs10830236	rs11018528	0.772	0.967	1032.39	0.95	0.98	29561
rs10830236	rs10765198	0.71	0.944	906.66	0.93	0.96	68958
rs10830236	rs1847134	0.672	0.864	830.62	0.84	0.89	104437
rs10830236	rs1393350	0.614	0.937	747.57	0.92	0.96	110230
rs10830236	rs1126809	0.663	0.865	815.41	0.84	0.89	117145
rs10830236	rs1806319	0.674	0.89	863.22	0.87	0.91	137120
rs1042602	rs11018528	0.215	0.99	286.59	0.97	1	18681
rs1042602	rs10765198	0.206	0.988	269.53	0.97	1	58078
rs1042602	rs1847134	0.184	0.876	214.96	0.84	0.91	93557
rs1042602	rs1393350	0.182	0.991	239.31	0.97	1	99350
rs1042602	rs1126809	0.181	0.878	213.08	0.84	0.91	106265
rs1042602	rs1806319	0.233	0.865	277.81	0.83	0.89	126240
rs11018528	rs10765198	0.916	0.975	1287.01	0.96	0.99	39397
rs11018528	rs1847134	0.87	0.974	1207.46	0.96	0.99	74876
rs11018528	rs1393350	0.779	0.959	991.65	0.94	0.97	80669
rs11018528	rs1126809	0.859	0.96	1175.37	0.94	0.97	87584
rs11018528	rs1806319	0.652	0.962	849.32	0.94	0.98	107559
rs10765198	rs1847134	0.828	0.967	1114.35	0.95	0.98	35479
rs10765198	rs1393350	0.835	0.975	1094.39	0.96	0.99	41272
rs10765198	rs1126809	0.816	0.953	1083.04	0.94	0.97	48187
rs10765198	rs1806319	0.632	0.964	818.07	0.95	0.98	68162
rs1847134	rs1393350	0.775	0.998	1042.19	0.98	1	5793
rs1847134	rs1126809	0.983	0.999	1527.58	0.98	1	12708
rs1847134	rs1806319	0.749	0.988	1044.89	0.97	1	32683
rs1393350	rs1126809	0.789	1	1070.26	0.99	1	6915
rs1393350	rs1806319	0.588	0.992	772.06	0.98	1	26890
rs1126809	rs1806319	0.746	0.994	1048.81	0.98	1	19975

Notes:

Locus 1 and Locus 2 are the two loci under comparison

r^2 is the correlation coefficient between the two loci
D' is the value of D prime between the two loci
lod is the log of the likelihood odds ratio, a measure of confidence in the value of D'
CI_{lower} is 95% confidence lower bound on D'
CI_{upper} is the 95% confidence upper bound on D'
Distance is bp separating the two loci

Supplementary Table 7. Association of *NALP1* SNPs with Generalized Vitiligo in the Genomewide Association Study and Replication Analyses

SNP[a]	Location (nt)	Risk-Allele[a]	Genomewide Association Study (1392 patients, 2629 controls)				Replication Sets							
							Replication Set 1 (647 patients, 1056 controls)		Replication Set 2 (183 trios, 332 multiplex families)		Replication Set 2; Romania subset (36 trios, 43 multiplex families)		Replication Set 2; Romania subset with concomitant other autoimmune diseases (6 trios, 29 multiplex families)	
			Risk-Allele Frequency		PLINK P value[b]	Odds Ratio (95% CI)[c]	P value[d]	Odds Ratio (95% CI)[c]	P value[e]	Odds Ratio (95% CI)[f]	P value[e]	Odds Ratio (95% CI)[f]	P value[e]	Odds Ratio (95% CI)[f]
			patients	controls										
rs6502867	5361052	A	0.764	0.750	0.17	1.08 (0.97-1.20)	2.39×10^{-2}	0.83 (0.71-0.98)	2.92×10^{-3}	1.45 (1.15-1.84)	8.72×10^{-3}	1.58 (0.86-2.94)	1.00×10^{-2}	2.82 (1.02-8.29)
rs12150220	5426091	A	0.466	0.446	0.09	1.09 (0.99-1.19)	0.21	0.91 (0.79-1.05)	1.76×10^{-3}	1.33 (1.09-1.62)	2.42×10^{-3}	1.84 (1.08-3.15)	1.26×10^{-2}	2.72 (1.07-6.92)
rs11078575	5426509	C	0.488	0.470	0.08	1.09 (0.99-1.20)	nd		nd		nd			
rs2670660	5459730	C	nd	nd	nd		0.44	0.95 (0.82-1.09)	6.65×10^{-4}	1.43 (1.17-1.76)	8.34×10^{-3}	1.92 (1.10-3.36)	9.86×10^{-3}	2.89 (1.14-7.31)
rs878329	5493974	G	0.463	0.445	0.11	1.08 (0.99-1.19)	nd		nd		nd			
rs8182352	5495711	G	nd	nd	nd		0.72	0.98 (0.85-1.12)	5.64×10^{-4}	1.48 (1.22-1.80)	8.92×10^{-3}	1.99 (1.17-3.38)	1.86×10^{-2}	3.22 (1.25-8.31)
rs4790796	5496043	A	0.459	0.442	0.14	1.08 (0.98-1.18)	nd		nd		nd			

[a] SNP high-risk alleles are defined as those associated with generalized vitiligo in previous studies.[15,16] [b]PLINK[1] Cochran-Armitage trend test statistics, calculated after GEM[2] correction of the genomewide dataset, were adjusted for the genomic inflation factor of 1.048 by use of the genomic control method.[7] [c] Odds ratios were calculated from the coefficients of the logistic regression equations; parentheses indicate 95% confidence intervals. [d] P values were calculated using the Cochran-Armitage trend test. [e] P values were calculated using the family based association test (FBAT),[8] version 1.5.5. [f] Odds ratios were calculated by conditional logistic regression analysis.[9] Genotypes for rs12150220, rs11078575, rs878329, and rs4790796 were imputed in the genomewide association study by use of MaCH,[4] ver.1.0 (http://www.sph.umich.edu/csg/abecasis/MACH/download/), based on patterns of haplotype variation in the HapMap[5] CEU samples (release 24); SNPs rs2670660 and rs8182352 are not represented in the HapMap data and thus could not be imputed. SNP positions are from Build 36.1 from the National Center for Biotechnology Information. nd, not determined.