Supplementary Methods

Control Datasets

Shared controls from the United States (NARAC), Sweden (EIRA), Spain and Netherlands were provided by the Rheumatoid Arthritis Consortium International (RACI),[1] with control samples from the United Kingdom provided by the Welcome Trust Case Control Consortium (WTCCC).[2] Controls from Italy, Norway, Belgium and France were provided by the International Multiple Sclerosis Genetics Consortium (IMSGC).[3] Polish and Hungarian controls were provided from the Celiac Consortium,[4] and German controls from the KORAgen consortium.[5]

Genotyping and quality control

Samples were clustered together and called using the GenTrain2 clustering algorithm in the GenomeStudio Data Analysis Software package with the Immuno_BeadChip_1149691_B.bpm manifest file (NCBI Build 36). Poorly performing assays were identified as those with call rate <98% and a cluster separation score of <0.4. Samples were then excluded based on a call rate <98%, those with discordant genotype/reported sex and extreme heterozygosity. Duplicate individuals or first- or second-degree relatives were also removed using identity by decent analysis. Principal components analysis (PCA) was performed on an independent subset of SNPs using EIGENSOFT v4.2 to identify ancestry outliers.[6, 7] Further quality control excluded SNPs based on minor allele frequency (<5%), deviation from Hardy-Weinberg equilibrium in controls ($p<0.001$) and differences in missing data between cases and controls ($p<0.01$).

Functional annotation

Evidence for functional effects was investigated using for the lead SNP in each region, and SNPs in high linkage disequilibrium (LD) ($r^2 \geq 0.9$) using 1000 Genomes data. Published expression quantitative trait loci (eQTL) studies aggregated in three databases were interrogated;

RegulomeDB,[8] Genevar,[9] and the Pritchard lab eQTL browser (http://eqtl.uchicago.edu/cgi-bin/gbrowse/eqtl/). Evidence of eQTLs is reported when linked to expression of a gene in cells with an immune function (Lymphoblastoid and Monocytes).

Potentially functionally important residues was assessed by the online tools PolyPhen-2,[10] SIFT,[11] and phastCons17-way,[12] which use the physical properties of the amino acids, sequence homology and conservation to assess the impact of an amino acid substitution.

MHC imputation and association analysis

Classical human leukocyte antigen (*HLA*) alleles and corresponding amino acid sequences were imputed using SNP2HLA using reference data collected by the Type 1 Diabetes Genetics Consortium.[13] Analysis was performed on the dosage of variants passing the quality control thresholds; information score ≥0.9 and minor allele frequency ≥0.01. Single-test association was performed for HLA alleles, as well as omnibus tests for amino acids. A logistic regression assuming an additive model was used to test for association and generate odds ratios, with the top ten principal components included as covariates to account for population stratification. To test for independent effects, a forward stepwise logistic regression was used conditional on the variant of interest by including it as a covariate. Classical 4-digit HLA alleles were preferentially reported, unless an amino acid association explained more risk than HLA alleles alone. Significance was defined as $p<6.8x10^{-6}$ based on a Bonferroni correction of the 7,323 makers imputed by SNP2HLA.[14]

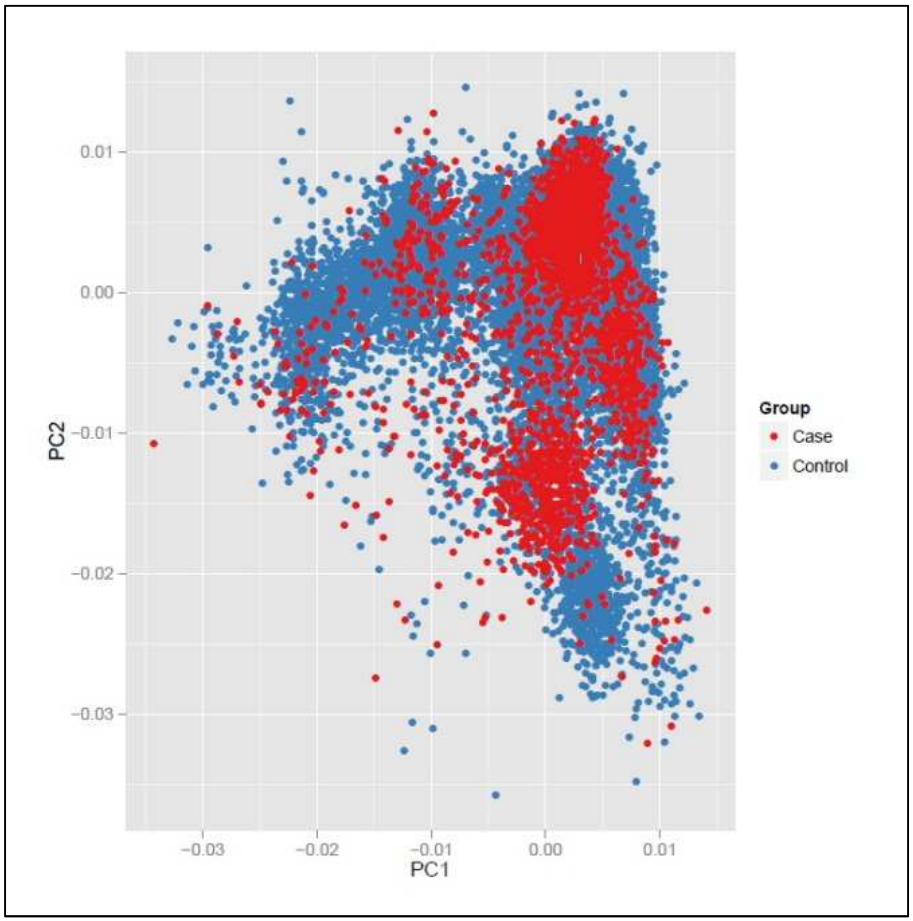


Figure S1: First two principal components of 2,566 IIM cases and controls after QC.

A scaled λGC_{1000} of 1.05 on a null set of SNPs indicates that the cases and controls are well matched (1.23 unscaled).

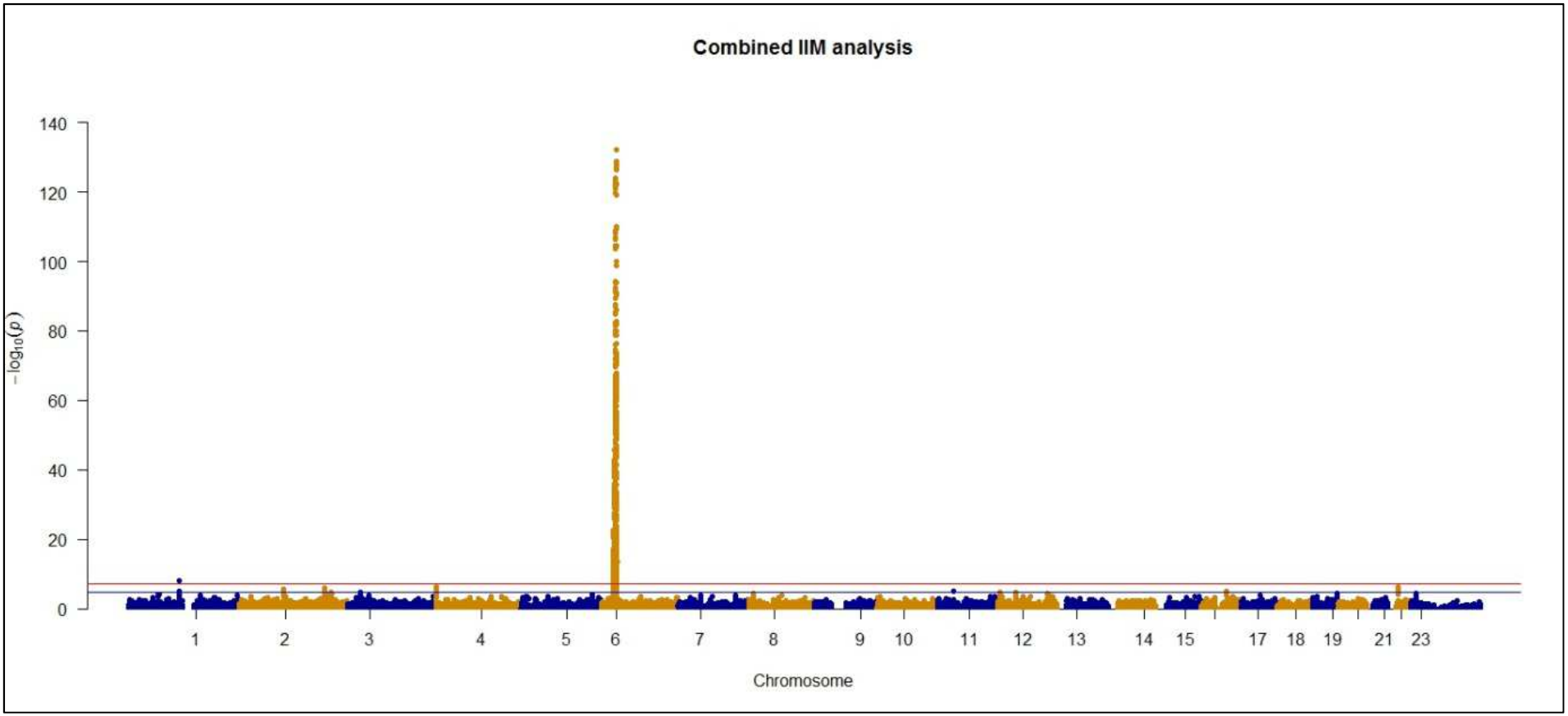
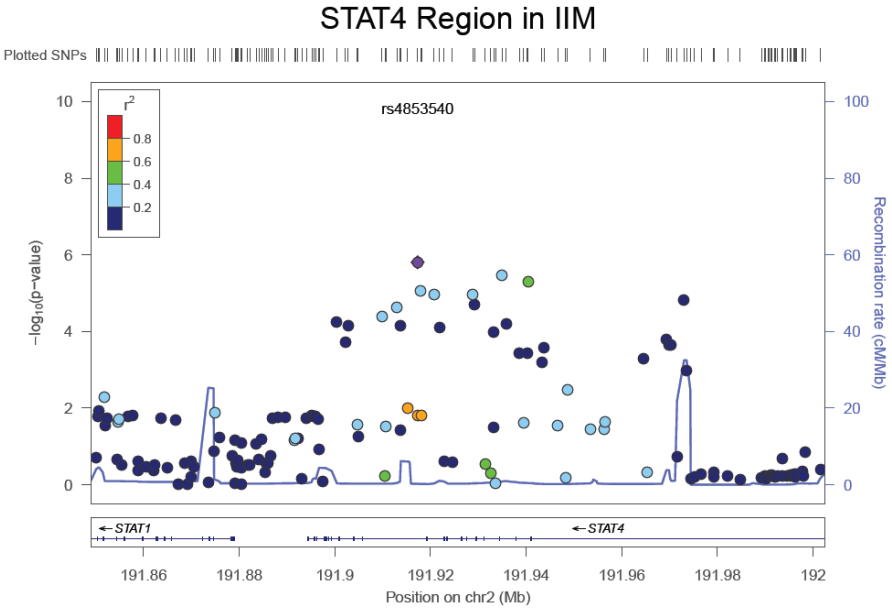
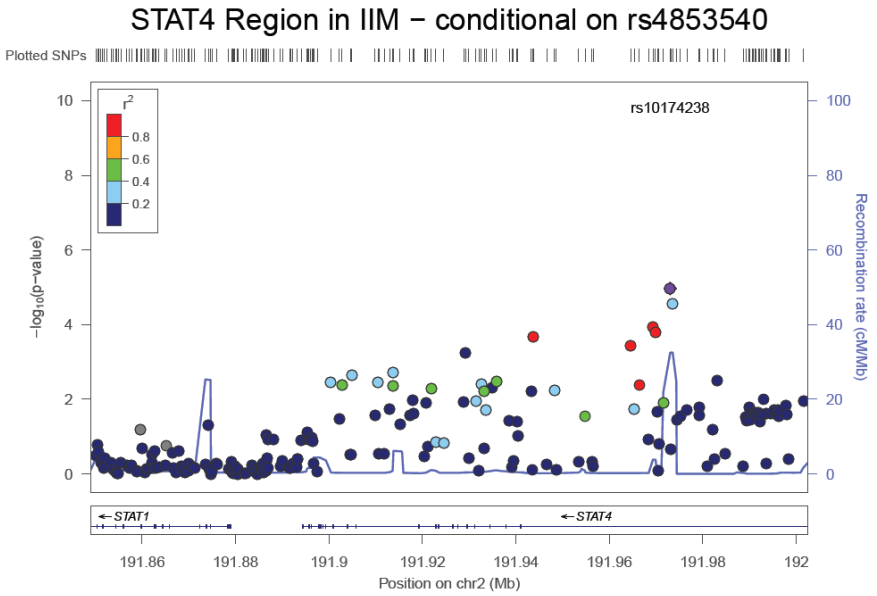


Figure S2: Manhattan plot with the combined IIM cohort.

Analysis of 2,566 IIM cases and 15,651 controls. The red and blue lines represent genome-wide level of significance ($p=5x10^{-8}$) and suggestive significance ($p=2.25x10^{-5}$) respectively





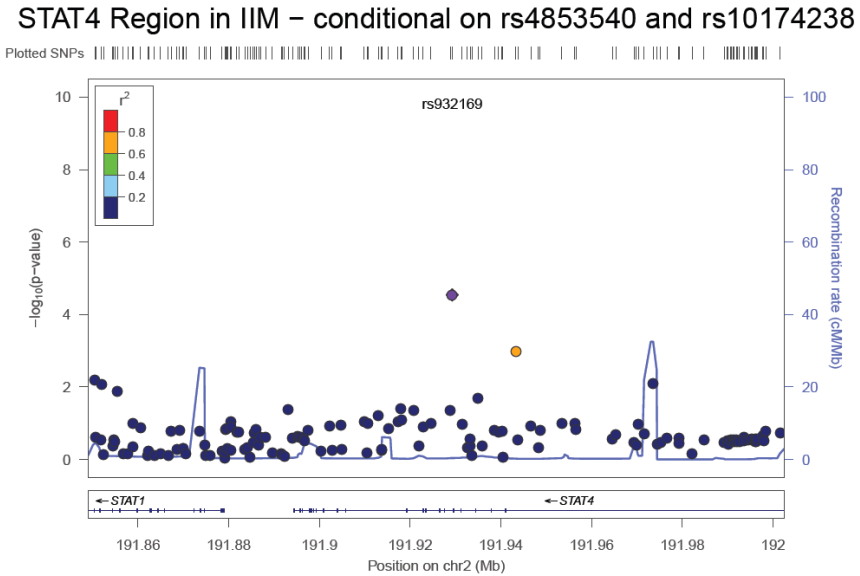


Figure S3: Stepwise logistic regression analysis in the *STAT4* region.

Independent effects within *STAT4* are shown with rs4853540, rs10174238 and rs932169

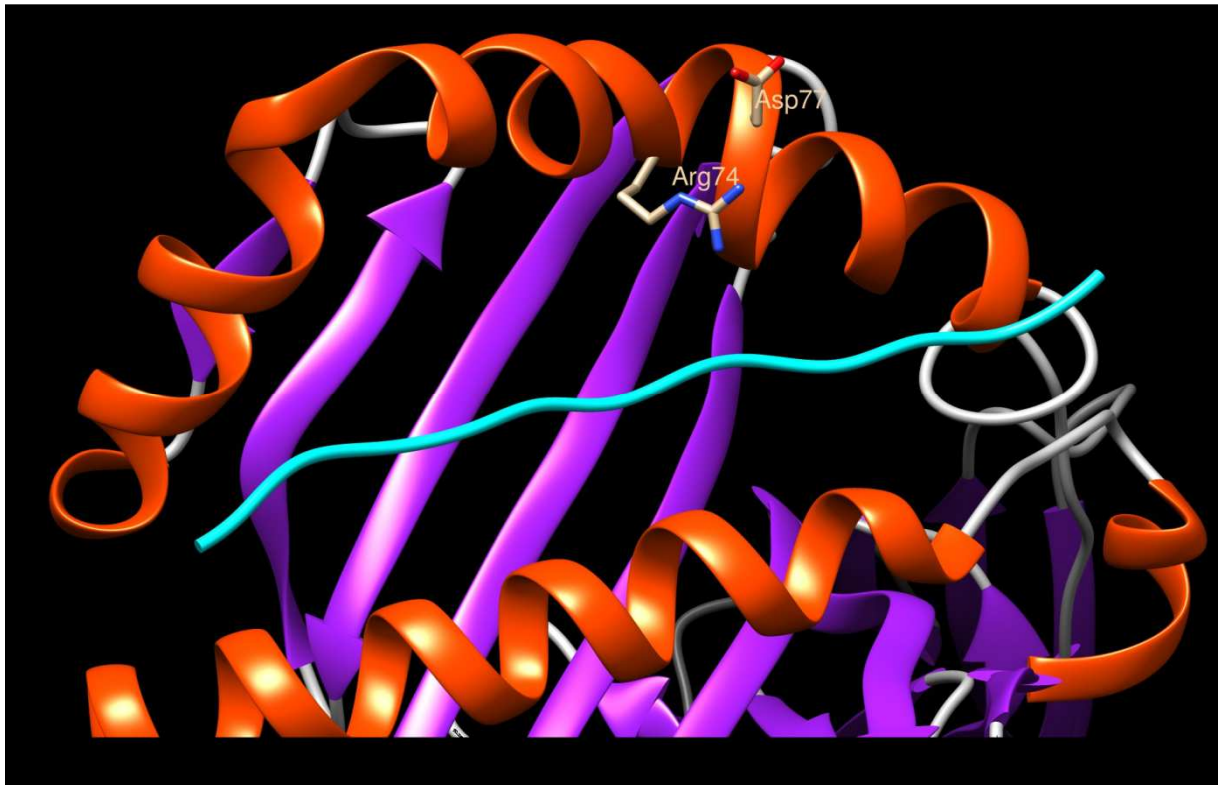


Figure S4: The location of Asp-77 and Arg-74 within the HLA-DRB1 molecule

HLA-DRB1*03:01 is associated with IIM, PM and JDM. Amino acids Asp-77 and Arg-74 are associated at a similar level of significance. This figure shows the location of these amino acids within the HLA-DRB1 molecule.

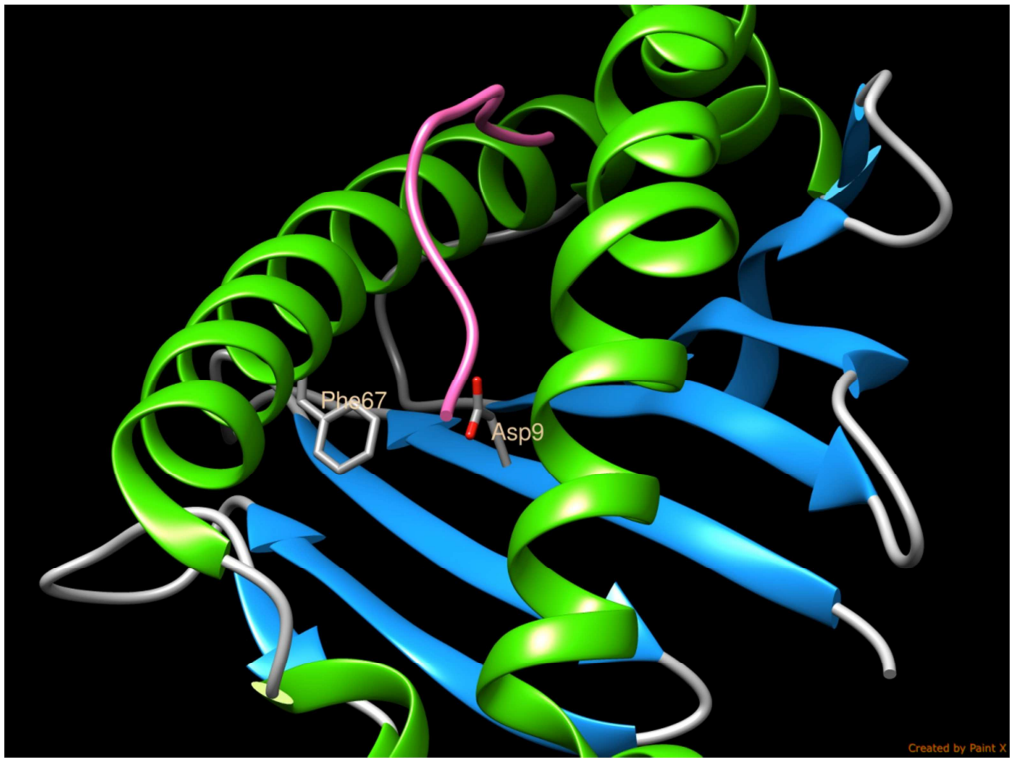


Figure S5: The location of Phe-67 and Asp-9 within the HLA-B molecule

HLA-B*08:01 is consistently associated with IIM. Amino acids Phe-67 and Asp-9 are associated at a similar level of significance. This figure shows the location of these amino acids within the HLA-B molecule.

Table S1: Sample numbers of IIM patients included in the combined Immunochip analysis

Diagnosis	Number
Anti-synthetase syndrome	11
Dermatomyositis	879
Inclusion Body Myositis	252
Juvenile Dermatomyositis	481
Juvenile Polymyositis	12
Polymyositis	931
Total	**2,566**

Antisynthetase syndrome patients were included in the combined analysis, however clinical data was not available to classify as PM or DM. These were not included in the clinical subgroup analysis.

Table S2: Overlap of IIM associations with other autoimmune diseases

Analysis Subgroup	Gene Region	Lead SNP in IIM	Disease Overlap	Reported SNP	P-value	Alleles	OR	LD (r^2) with IIM association	Reference
IIM/PM	***PTPN22***	rs2476601			7.22×10^{-9}	G>A	IIM=1.32 / PM=1.58		
			SLE	rs2476601	3.40×10^{-12}	G>A	1.35	1	[15]
			CRO	rs6679677	2.03×10^{-15}	C>A	0.84	0.92	[16]
			JIA	rs6679677	3.19×10^{-25}	C>A	1.59	0.92	[17]
			ATD	rs2476601	9.69×10^{-23}	G>A	1.63	1	[18]
			IBD	rs6679677	3.15×10^{-3}	C>A	0.94	1	[16]
			T1D	rs2476601	5.93×10^{-80}	G>A	1.96	1	[19]
			SSC	rs76853721	7.10×10^{-3}	G>A	0.62	1	[20]
			RA	rs2476601	6.60×10^{-170}	G>A	1.8	1	[21]
			VIT	rs2476601	6.10×10^{-13}	G>A	NR	1	[22]
IIM	*YDJC*	rs5754467			4.67×10^{-7}	A>G	1.21		
			CEL	rs4821124	5.70×10^{-11}	T>C	1.16	0.94	[4]
			SLE	rs5754217	2.30×10^{-6}	G>T	1.2	0.94	[15]
			PSO	rs4821124	3.80×10^{-8}	T>C	1.13	0.94	[23]
			CRO	rs2266959	3.89×10^{-16}	G>T	1.13	0.94	[16]
			JIA	rs2266959	6.20×10^{-9}	C>A	1.24	0.94	[17]
			UC	rs2266959	4.65×10^{-7}	G>T	1.08	0.94	[16]
			IBD	rs2266959	1.39×10^{-16}	G>T	1.11	0.90	[16]
			RA	rs5754217	4.80×10^{-5}	G>T	1.09	0.90	[24]
IIM	*STAT4*	rs4853540			1.57×10^{-6}	G>T	0.83		
			CEL	rs6715106	8.40×10^{-9}	A>G	0.79	0.37	[4]
			CRO	rs1517352	1.93×10^{-10}	C>A	0.91	0.42	[16]
			UC	rs1517352	1.55×10^{-6}	C>A	0.95	0.42	[16]
			IBD	rs1517352	3.28×10^{-11}	C>A	0.93	0.42	[16]
IIM	*STAT4*	rs10174238			1.08×10^{-5}	A>G	1.17		
			SLE	rs7574865	1.40×10^{-41}	G>T	1.57	0.79	[15]
			PBC	rs7574865	1.38×10^{-13}	G>T	1.31	0.79	[25]
			JIA	rs10174238	1.28×10^{-13}	A>G	1.29	1	[17]
			RA	rs11889341	3.60×10^{-19}	C>T	1.13	0.75	[21]
			SLE	rs7574865	5.10×10^{-9}	T>G	1.51	0.79	[26]
IIM	*STAT4*	rs932169			2.88×10^{-5}	G>C	1.25		
			PBC	rs3024921	2.59×10^{-18}	A>T	1.62	0.62	[25]
IIM	*CD28*	rs3116494			1.54×10^{-5}	A>G	1.16		
			PSC	rs7426056	1.89×10^{-20}	G>A	1.3	0.91	[27]
			RA	rs1980422	3.00×10^{-14}	T>C	1.12	0.91	[21]
PM	*SL26A1/IDUA*	rs4690220			7.47×10^{-6}	A>G	1.25		
			SJO	rs4690326	1.05×10^{-5}	C>A	0.84	0.72	[28]
PM	*RGS1*	rs7535818			1.37×10^{-5}	A>G	0.74		
			T1D	rs2209014	2.16×10^{-4}	A>G	0.89	0.69	[19]
			T1D	rs2816316	3.10×10^{-5}	A>C	NR	1	[29]
			CEL	rs1359062	2.50×10^{-25}	G>C	0.77	0.95	[4]
			MS	rs1323292	2.30×10^{-8}	A>G	0.89	1	[30]
			MS	rs1359062	4.80×10^{-20}	C>G	0.87	0.95	[3]
			CEL	rs2816316	2.20×10^{-17}	A>C	0.8	1	[31]
DM+JDM	*GSDMB*	rs1008723			9.05×10^{-6}	G>T	1.20		
			PBC	rs8067378	6.05×10^{-14}	A>G	0.79	1	[25]
			CRO	rs12946510	3.58×10^{-25}	C>T	1.15	0.77	[16]
			UC	rs12946510	3.39×10^{-26}	C>T	1.16	0.77	[16]
			IBD	rs12946510	4.10×10^{-38}	C>T	1.16	0.77	[16]
			UC	rs2872507	5.44×10^{-11}	G>A	1.15	0.90	[32]
			T1D	rs12453507	1.00×10^{-8}	G>C	0.9	0.94	[33]
			RA	rs2872507	2.80×10^{-9}	G>A	1.1	0.90	[1]
			MS	rs12946510	2.90×10^{-9}	G>A	1.07	0.77	[3]

Overlap reported between associations in IIM and the lead association in another autoimmune disease (as reported on www.immunobase.org). Overlap reported where LD (r^2>0.7), except for *STAT4* independent effects where moderate LD is also reported. Alleles and odds ratios reported where available and coloured as risk (red) and

protective (blue). ATD – Autoimmune Thyroid Disease, CEL – Celiac Disease, CRO - Crohn's disease, IBD – Inflammatory Bowel Disease, JIA – Juvenile Idiopathic Arthritis, MAF – minor allele frequency, MS – Multiple Sclerosis, NR - not reported, OR – Odds ratio, PBC – Primary Biliary Cirrhosis, PSC - Primary Sclerosing Cholangitis, PSO – Psoriasis, RA – Rheumatoid Arthritis, SJO - Sjogren Syndrome, SLE – Systemic Lupus Erythematosus, SSC - Systemic Scleroderma, T1D – Type 1 Diabetes, UC - Ulcerative colitis, VIT – Vitiligo

Table S3: Total Immunochip associations, stratified by PM, DM and JDM, and IBM

Association	SNP	Total IIM n=2,566 λGC_{null}=1.05		Polymyositis n=931 λGC_{null}=1.05		Adult and Juvenile Dermatomyositis n=1,360 λGC_{null}=1.00		Inclusion Body Myositis n=252 λGC_{null}=1.06	
		p-value	OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)
PTPN22	rs2476601	$7.22x10^{-9}$	1.32 (1.20-1.45)	$7.90x10^{-11}$	1.58 (1.38-1.81)	0.2	1.09 (0.96-1.25)	$3.67x10^{-5}$	1.74 (1.34-2.26)
YDJC	rs5754467	$4.67x10^{-7}$	1.21 (1.12-1.30)	0.0003	1.23 (1.10-1.38)	0.005	1.15 (1.04-1.27)	0.01	1.31 (1.06-1.62)
DGKQ	rs6599390	$6.48x10^{-7}$	0.85 (0.79-0.90)	$1.63x10^{-5}$*	0.79 (0.71-0.88)	0.009	0.89 (0.82-0.97)	0.005	0.75 (0.61-0.92)
STAT4	rs4853540	$1.57x10^{-6}$	0.83 (0.77-0.89)	0.002	0.83 (0.73-0.93)	$3.07x10^{-5}$	0.80 (0.72-0.89)	0.7	0.95 (0.76-1.20)
STAT4	rs10174238	$1.52x10^{-5}$	1.17 (1.09-1.25)	0.0004	1.22 (1.09-1.36)	0.008	1.14 (1.03-1.25)	0.4	1.09 (0.88-1.35)
STAT4	rs932169	$1.99x10^{-5}$	1.25 (1.13-1.38)	$2.42x10^{-5}$	1.39 (1.19-1.62)	0.02	1.18 (1.03-1.35)	0.3	1.19 (0.87-1.62)
MGAT4A	rs10189330	$2.68x10^{-6}$	1.16 (1.09-1.23)	0.0005	1.19 (1.08-1.30)	0.01	1.11 (1.03-1.20)	0.005	1.30 (1.08-1.56)
CCL17	rs223900	$9.97x10^{-6}$	1.17 (1.09-1.25)	0.0004	1.21 (1.09-1.35)	0.005	1.14 (1.04-1.25)	0.06	1.21 (0.99-1.48)
EOMES	rs376072	$1.45x10^{-5}$	0.86 (0.80-0.92)	0.004	0.85 (0.76-0.95)	0.002	0.86 (0.79-0.95)	0.05	0.81 (0.66-1.00)
CD28	rs3116494	$1.54x10^{-5}$	1.16 (1.09-1.24)	0.01	1.14 (1.03-1.27)	0.0008	1.17 (1.07-1.27)	0.02	1.28 (1.05-1.56)
RPL31P10	rs11064180	$1.61x10^{-5}$	0.87 (0.82-0.93)	0.01	0.89 (0.80-0.98)	$5.47x10^{-5}$	0.84 (0.78-0.92)	0.6	0.95 (0.79-1.14)
PRR5L | TRAF6	rs570676	$9.42x10^{-6}$	0.87 (0.82-0.92)	0.01	0.88 (0.80-0.98)	$2.67x10^{-5}$	0.84 (0.77-0.91)	1	1.00 (0.83-1.21)
UBE3B | MMAB	rs7956536	0.01	0.92 (0.87-0.98)	$3.66x10^{-6}$	0.80 (0.72-0.88)	0.7	1.02 (0.94-1.10)	0.3	0.91 (0.76-1.09)
NAB1	rs2286896	0.008	1.12 (1.03-1.22)	$3.76x10^{-6}$	1.35 (1.19-1.53)	0.5	0.96 (0.86-1.09)	0.2	1.19 (0.92-1.54)
IL18R1	rs1420095	0.0003	0.81 (0.72-0.91)	$6.16x10^{-6}$	0.63 (0.52-0.77)	0.2	0.91 (0.79-1.05)	0.5	0.88 (0.63-1.24)
SLC26A1 | IDUA	rs4690220	$8.05x10^{-7}$*	1.17 (1.10-1.24)	$7.47x10^{-6}$	1.25 (1.13-1.37)	0.009	1.12 (1.03-1.21)	0.08	1.18 (0.98-1.41)
RGS1	rs7535818	0.005	0.89 (0.82-0.97)	$1.37x10^{-5}$	0.74 (0.65-0.85)	0.2	0.93 (0.84-1.03)	0.05	1.24 (1.00-1.54)
LOC728073 | RPL38	rs9905921	$1.77x10^{-8}$*	1.19 (1.12-1.26)	$2.01x10^{-6}$	1.26 (1.14-1.38)	0.002	1.13 (1.05-1.23)	0.005	1.30 (1.08-1.56)
FAM167A | BLK	rs17799348	$3.92x10^{-5}$	0.88 (0.82-0.93)	$4.13x10^{-6}$	0.79 (0.71-0.87)	0.03	0.91 (0.84-0.99)	1	1.01 (0.84-1.21)
GSDMB	rs1008723	0.02209	1.07 (1.01-1.14)	0.4	1.05 (0.95-1.15)	$9.05x10^{-6}$	1.20 (1.11-1.30)	$1.80x10^{-5}$	1.50 (1.24-1.80)
ROPN1L | ANKRD33B	rs4702698	0.0004	1.13 (1.06-1.20)	0.5	1.04 (0.94-1.15)	$4.77x10^{-6}$	1.22 (1.12-1.33)	0.7	0.96 (0.78-1.17)
PTTG1 | ATP10B	rs4921293	$7.52x10^{-5}$	1.14 (1.07-1.21)	0.1	1.08 (0.98-1.19)	$8.27x10^{-6}$	1.21 (1.11-1.31)	0.5	0.94 (0.77-1.14)

Analysis of all IIM, PM, and DM and JDM associations, stratified by clinical subgroup. Analysis includes 2,566 IIM cases, 931 PM cases, and 1,360 DM and JDM cases, compared to 15,651 controls. 252 IBM cases were matched to a subset of 6,270 controls. *Association removed during QC, but included here for comparison.

Table S4 - HLA Imputation in the combined IIM cohort

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the combined IIM analysis (n=2,566)

Gene	Allele (HLA) / Amino acid (AA)	P-value
HLA_DRB1	HLA_DRB1_03	6.63E-135
DRB1	AA_DRB1_77	1.11E-134
HLA_DRB1	HLA_DRB1_0301	2.58E-134
DRB1	AA_DRB1_74	5.86E-133
HLA_DQB1	HLA_DQB1_0201	2.01E-132
HLA_B	HLA_B_08	1.92E-122
HLA_B	HLA_B_0801	2.08E-122
B	AA_B_9	9.36E-118
DRB1	AA_DRB1_26	1.52E-117
HLA_C	HLA_C_0701	9.04E-89
C	AA_C_66	7.74E-79
DQB1	AA_DQB1_71	1.93E-77
DQB1	AA_DQB1_74	5.08E-77
DQB1	AA_DQB1_67	3.82E-75
DQB1	AA_DQB1_66	3.84E-75
HLA_DQB1	HLA_DQB1_02	4.90E-73
DQB1	AA_DQB1_28	9.03E-73
DQB1	AA_DQB1_46	9.23E-73
DQB1	AA_DQB1_52	9.25E-73
DQB1	AA_DQB1_47	9.27E-73
DQB1	AA_DQB1_30	1.14E-72
DQB1	AA_DQB1_37	3.52E-71
DRB1	AA_DRB1_37	4.32E-71
DQB1	AA_DQB1_55	1.98E-70
DQB1	AA_DQB1_-10	3.39E-70
DRB1	AA_DRB1_71	9.32E-68
DQA1	AA_DQA1_51	8.79E-66
DQA1	AA_DQA1_40	8.79E-66
B	AA_B_67	3.58E-65
DQA1	AA_DQA1_47	1.38E-64
DQA1	AA_DQA1_50	3.25E-64
DQA1	AA_DQA1_53	3.32E-64
DQA1	AA_DQA1_75	8.14E-63
HLA_DQA1	HLA_DQA1_0501	8.83E-63
HLA_DQA1	HLA_DQA1_05	8.84E-63
DQA1	AA_DQA1_107	3.92E-62
DQA1	AA_DQA1_163	5.55E-62
DQA1	AA_DQA1_161	5.66E-62
DQA1	AA_DQA1_156	5.68E-62
B	AA_B_156	3.78E-61

DQA1	AA_DQA1_175	1.13E-60
DRB1	AA_DRB1_32	1.37E-57
DQB1	AA_DQB1_75	2.43E-56
DQB1	AA_DQB1_57	4.77E-55
B	AA_B_163	4.55E-54
DRB1	AA_DRB1_73	6.07E-53
DQB1	AA_DQB1_38	2.88E-51
DQB1	AA_DQB1_77	1.02E-50
DRB1	AA_DRB1_67	3.88E-49
DRB1	AA_DRB1_13	2.09E-45
DRB1	AA_DRB1_11	6.85E-45
DRB1	AA_DRB1_10	1.74E-44
DRB1	AA_DRB1_149	2.02E-44
DRB1	AA_DRB1_12	5.47E-44
B	AA_B_114	1.11E-43
DRB1	AA_DRB1_-25	7.96E-42
DRB1	AA_DRB1_-16	8.23E-42
DRB1	AA_DRB1_233	8.84E-42
B	AA_B_97	2.76E-39
DQA1	AA_DQA1_52	1.25E-37
DPB1	AA_DPB1_194	2.21E-32
HLA_DPB1	HLA_DPB1_01	2.30E-32
HLA_DPB1	HLA_DPB1_0101	2.30E-32
B	AA_B_74	1.65E-30
DQA1	AA_DQA1_56	6.08E-30
DQA1	AA_DQA1_76	6.81E-30
B	AA_B_180	3.20E-28
B	AA_B_177	3.28E-28
DRB1	AA_DRB1_140	4.51E-28
B	AA_B_131	1.05E-27
B	AA_B_45	1.45E-27
DQB1	AA_DQB1_-18	2.06E-27
HLA_A	HLA_A_0101	3.93E-27
DRB1	AA_DRB1_9	4.35E-27
HLA_A	HLA_A_01	8.60E-27
A	AA_A_158	9.32E-27
A	AA_A_150	9.63E-27
B	AA_B_-21	1.07E-26
B	AA_B_-23	1.11E-26
A	AA_A_67	1.17E-26
A	AA_A_44	1.25E-26
C	AA_C_-9	1.60E-26
HLA_C	HLA_C_07	1.62E-26
C	AA_C_194	2.13E-26
C	AA_C_184	2.33E-26
C	AA_C_339	2.77E-26

C	AA_C_326	2.82E-26
C	AA_C_307	2.94E-26
C	AA_C_261	2.95E-26
C	AA_C_273	2.98E-26
C	AA_C_285	2.98E-26
C	AA_C_305	2.99E-26
C	AA_C_295	3.47E-26
C	AA_C_147	1.74E-25
C	AA_C_-17	2.03E-25
B	AA_B_116	2.09E-25
C	AA_C_253	3.74E-25
C	AA_C_267	3.76E-25
C	AA_C_306	3.80E-25
A	AA_A_156	5.75E-25
DRB1	AA_DRB1_86	4.69E-24
C	AA_C_-15	5.02E-24
C	AA_C_152	1.27E-21
DRB1	AA_DRB1_96	5.69E-21
HLA_DRB1	HLA_DRB1_1501	1.09E-20
DRB1	AA_DRB1_-1	1.30E-20
DQB1	AA_DQB1_-5	1.64E-20
DQA1	AA_DQA1_34	1.93E-20
DQB1	AA_DQB1_125	2.04E-20
HLA_DRB1	HLA_DRB1_15	3.72E-19
B	AA_B_24	3.73E-19
DQB1	AA_DQB1_87	5.95E-19
B	AA_B_-10	9.53E-19
HLA_DQB1	HLA_DQB1_03	1.30E-18
HLA_DQB1	HLA_DQB1_06	1.66E-18
DRB1	AA_DRB1_98	1.90E-18
DRB1	AA_DRB1_104	1.91E-18
DQA1	AA_DQA1_215	2.51E-18
B	AA_B_70	7.14E-18
HLA_DQB1	HLA_DQB1_0602	1.05E-17
DQB1	AA_DQB1_203	2.64E-17
B	AA_B_152	3.40E-17
B	AA_B_63	3.97E-17
DRB1	AA_DRB1_70	5.95E-17
DPB1	AA_DPB1_76	6.00E-17
B	AA_B_178	6.40E-17
DQA1	AA_DQA1_11	7.01E-17
DQA1	AA_DQA1_218	7.03E-17
DQB1	AA_DQB1_90	7.60E-17
DQB1	AA_DQB1_89	7.60E-17
DQB1	AA_DQB1_84	7.62E-17
DQB1	AA_DQB1_85	7.62E-17

DQA1	AA_DQA1_129	7.67E-17
DQB1	AA_DQB1_220	8.77E-17
DQB1	AA_DQB1_-21	8.84E-17
DQB1	AA_DQB1_221	9.06E-17
DQB1	AA_DQB1_-6	1.03E-16
DQB1	AA_DQB1_-4	1.05E-16
DQA1	AA_DQA1_61	1.16E-16
DQB1	AA_DQB1_53	1.19E-16
DQA1	AA_DQA1_66	1.20E-16
DQA1	AA_DQA1_18	1.28E-16
DQA1	AA_DQA1_45	1.28E-16
DQA1	AA_DQA1_48	1.30E-16
HLA_DQA1	HLA_DQA1_01	1.30E-16
DQA1	AA_DQA1_64	1.31E-16
DQA1	AA_DQA1_55	1.32E-16
DQA1	AA_DQA1_80	1.37E-16
DQA1	AA_DQA1_207	1.51E-16
HLA_DPA1	HLA_DPA1_0201	2.14E-16
DRB1	AA_DRB1_60	2.14E-16
DRB1	AA_DRB1_57	2.23E-16
DQA1	AA_DQA1_69	2.25E-16
A	AA_A_76	3.30E-16
DQB1	AA_DQB1_86	3.61E-16
DPA1	AA_DPA1_83	8.75E-16
DPA1	AA_DPA1_50	1.03E-15
HLA_DQA1	HLA_DQA1_0102	1.08E-15
HLA_DPA1	HLA_DPA1_01	1.19E-15
HLA_DPA1	HLA_DPA1_02	1.29E-15
DPA1	AA_DPA1_31	1.30E-15
A	AA_A_90	1.79E-15
A	AA_A_163	1.92E-15
DPA1	AA_DPA1_228	2.85E-15
DPA1	AA_DPA1_160	2.90E-15
DPA1	AA_DPA1_127	2.97E-15
DPA1	AA_DPA1_111	3.73E-15
DRB1	AA_DRB1_30	4.94E-15
B	AA_B_69	6.51E-15
HLA_B	HLA_B_0702	6.91E-15
DQB1	AA_DQB1_182	8.48E-15
DQB1	AA_DQB1_140	9.07E-15
HLA_B	HLA_B_07	9.14E-15
HLA_DPA1	HLA_DPA1_0103	9.46E-15
HLA_C	HLA_C_0702	1.05E-14
C	AA_C_99	1.26E-14
A	AA_A_152	1.28E-14
B	AA_B_71	2.06E-14

B	AA_B_11	4.22E-14
DRB1	AA_DRB1_181	5.29E-14
B	AA_B_12	6.01E-14
A	AA_A_167	6.48E-14
A	AA_A_166	6.49E-14
DRB1	AA_DRB1_4	1.28E-13
C	AA_C_24	1.47E-13
DQA1	AA_DQA1_-16	3.15E-13
DRB1	AA_DRB1_47	3.32E-13
DRB1	AA_DRB1_28	5.31E-13
DQB1	AA_DQB1_70	5.39E-13
DRB1	AA_DRB1_78	8.61E-13
DPB1	AA_DPB1_35	9.79E-13
C	AA_C_9	9.87E-13
DRB1	AA_DRB1_133	1.09E-12
DRB1	AA_DRB1_142	1.13E-12
C	AA_C_304	1.20E-12
HLA_DQA1	HLA_DQA1_02	1.72E-12
HLA_DQA1	HLA_DQA1_0201	1.74E-12
DQA1	AA_DQA1_54	1.75E-12
B	AA_B_95	2.09E-12
DRB1	AA_DRB1_25	2.16E-12
DRB1	AA_DRB1_14	2.19E-12
HLA_DRB1	HLA_DRB1_0701	2.22E-12
HLA_DRB1	HLA_DRB1_07	2.23E-12
DPB1	AA_DPB1_87	5.13E-12
DPB1	AA_DPB1_85	5.15E-12
DPB1	AA_DPB1_86	5.20E-12
A	AA_A_105	6.01E-12
DPB1	AA_DPB1_84	6.85E-12
DPB1	AA_DPB1_96	7.64E-12
DPB1	AA_DPB1_170	7.82E-12
C	AA_C_116	2.94E-11
B	AA_B_-8	3.01E-11
B	AA_B_46	3.11E-11
DQB1	AA_DQB1_9	3.88E-11
B	AA_B_94	4.07E-11
DRB1	AA_DRB1_-17	4.23E-11
DPB1	AA_DPB1_8	6.98E-11
C	AA_C_156	8.86E-11
B	AA_B_-11	9.00E-11
DQA1	AA_DQA1_25	2.48E-10
HLA_DRB1	HLA_DRB1_0401	3.93E-10
HLA_DQB1	HLA_DQB1_0301	5.68E-10
DQB1	AA_DQB1_45	6.23E-10
C	AA_C_77	6.50E-10

C	AA_C_80	6.50E-10
DPB1	AA_DPB1_9	7.19E-10
C	AA_C_90	8.52E-10
DQB1	AA_DQB1_167	1.02E-09
DQB1	AA_DQB1_13	1.07E-09
HLA_DQB1	HLA_DQB1_0303	2.29E-09
DQB1	AA_DQB1_26	5.67E-09
A	AA_A_77	9.48E-09
B	AA_B_41	1.69E-08
B	AA_B_325	3.91E-08
C	AA_C_73	6.08E-08
HLA_B	HLA_B_5701	8.41E-08
HLA_B	HLA_B_57	1.05E-07
HLA_DPB1	HLA_DPB1_04	1.25E-07
B	AA_B_81	1.50E-07
B	AA_B_83	3.19E-07
B	AA_B_82	3.19E-07
HLA_C	HLA_C_0602	3.60E-07
HLA_C	HLA_C_06	3.60E-07
B	AA_B_77	4.52E-07
A	AA_A_70	5.24E-07
C	AA_C_97	6.27E-07
B	AA_B_80	1.10E-06
C	AA_C_1	1.91E-06
HLA_B	HLA_B_15	2.42E-06
A	AA_A_321	3.46E-06
A	AA_A_97	3.52E-06
A	AA_A_276	3.73E-06
B	AA_B_32	4.20E-06
B	AA_B_62	5.09E-06
C	AA_C_95	6.42E-06
DQB1	AA_DQB1_135	6.72E-06

Table S5 - HLA Imputation in the combined IIM cohort conditional on HLA-DRB1*03:01

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the combined IIM analysis (n=2,566)

Gene	Allele (HLA) / Amino acid (AA)	P-value
B	AA_B_9	2.93E-14
HLA_B	HLA_B_08	3.09E-14
HLA_B	HLA_B_0801	3.23E-14
DRB1	AA_DRB1_-1	1.70E-11
B	AA_B_114	1.73E-11
B	AA_B_67	1.79E-11
HLA_DRB1	HLA_DRB1_1501	9.50E-10
HLA_C	HLA_C_0701	1.90E-09
DRB1	AA_DRB1_71	5.35E-09
DQB1	AA_DQB1_71	6.36E-09
B	AA_B_156	7.49E-09
C	AA_C_66	9.30E-09
DQB1	AA_DQB1_26	2.11E-08
HLA_DRB1	HLA_DRB1_15	2.84E-08
DQB1	AA_DQB1_74	4.18E-08
HLA_DQB1	HLA_DQB1_0602	4.95E-08
HLA_DRB1	HLA_DRB1_16	9.39E-08
HLA_DRB1	HLA_DRB1_1601	1.57E-07
DRB1	AA_DRB1_67	2.25E-07
HLA_C	HLA_C_0702	2.95E-07
B	AA_B_70	3.34E-07
DRB1	AA_DRB1_57	3.46E-07
C	AA_C_99	5.01E-07
B	AA_B_97	5.67E-07
HLA_B	HLA_B_0702	6.62E-07
DQB1	AA_DQB1_126	7.52E-07
HLA_DQB1	HLA_DQB1_0502	9.02E-07
HLA_B	HLA_B_07	1.06E-06
DRB1	AA_DRB1_74	1.77E-06
DQB1	AA_DQB1_57	1.89E-06
DRB1	AA_DRB1_-24	1.97E-06
DQB1	AA_DQB1_75	2.82E-06
DQB1	AA_DQB1_56	2.82E-06
HLA_DRB1	HLA_DRB1_08	3.28E-06
HLA_DQB1	HLA_DQB1_04	4.07E-06
HLA_DQB1	HLA_DQB1_0402	4.44E-06
DRB1	AA_DRB1_-25	5.83E-06
DRB1	AA_DRB1_-16	5.96E-06
DRB1	AA_DRB1_-17	5.99E-06

Table S6 - HLA Imputation in the combined IIM cohort conditional on HLA-DRB1*03:01 and HLA-B*08:01

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the combined IIM analysis (n=2,566)

Gene	Allele (HLA) / Amino acid (AA)	P-value
DRB1	AA_DRB1_-1	3.06E-11
HLA_DRB1	HLA_DRB1_1501	1.64E-09
B	AA_B_97	9.55E-09
DQB1	AA_DQB1_71	1.15E-08
DRB1	AA_DRB1_71	1.26E-08
DQB1	AA_DQB1_26	3.61E-08
HLA_DRB1	HLA_DRB1_15	4.72E-08
DQB1	AA_DQB1_74	7.16E-08
HLA_DQB1	HLA_DQB1_0602	7.43E-08
HLA_DRB1	HLA_DRB1_16	2.01E-07
HLA_DRB1	HLA_DRB1_1601	3.32E-07
DRB1	AA_DRB1_67	3.96E-07
DRB1	AA_DRB1_57	4.07E-07
DQB1	AA_DQB1_126	1.38E-06
HLA_DQB1	HLA_DQB1_0502	1.63E-06
C	AA_C_99	1.85E-06
DRB1	AA_DRB1_-24	2.09E-06
DQB1	AA_DQB1_57	2.68E-06
DRB1	AA_DRB1_74	2.84E-06
DQB1	AA_DQB1_75	3.03E-06
DQB1	AA_DQB1_56	3.87E-06
HLA_DRB1	HLA_DRB1_08	4.25E-06
B	AA_B_114	4.48E-06
HLA_DQB1	HLA_DQB1_04	5.54E-06
HLA_DQB1	HLA_DQB1_0402	6.03E-06

Table S7 - HLA Imputation in the polymyositis subgroup

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the polymyositis subgroup analysis (n=931)

Gene	Allele (HLA) / Amino acid (AA)	P-value
HLA_DRB1	HLA_DRB1_03	1.14E-80
DRB1	AA_DRB1_77	1.65E-80
HLA_DRB1	HLA_DRB1_0301	6.11E-80
HLA_DQB1	HLA_DQB1_0201	5.85E-78
DRB1	AA_DRB1_74	1.27E-75
HLA_B	HLA_B_08	4.81E-75
HLA_B	HLA_B_0801	5.44E-75
B	AA_B_9	4.30E-67
DRB1	AA_DRB1_26	1.74E-64
HLA_C	HLA_C_0701	4.41E-51
B	AA_B_67	6.33E-48
DQA1	AA_DQA1_50	1.02E-46
DQA1	AA_DQA1_53	1.02E-46
DQA1	AA_DQA1_175	1.22E-46
DQA1	AA_DQA1_47	3.23E-46
C	AA_C_66	3.74E-46
DQA1	AA_DQA1_75	4.47E-46
HLA_DQA1	HLA_DQA1_0501	5.04E-46
HLA_DQA1	HLA_DQA1_05	5.04E-46
DQA1	AA_DQA1_107	5.34E-45
DQA1	AA_DQA1_163	8.62E-45
DQA1	AA_DQA1_161	8.72E-45
DQA1	AA_DQA1_156	8.74E-45
DQA1	AA_DQA1_51	1.39E-44
DQA1	AA_DQA1_40	1.39E-44
DRB1	AA_DRB1_32	7.86E-41
DRB1	AA_DRB1_37	2.20E-40
DQB1	AA_DQB1_28	1.68E-36
DQB1	AA_DQB1_47	1.69E-36
DQB1	AA_DQB1_46	1.69E-36
DQB1	AA_DQB1_52	1.70E-36
HLA_DQB1	HLA_DQB1_02	1.73E-36
DRB1	AA_DRB1_10	3.11E-36
DRB1	AA_DRB1_13	3.97E-36
DRB1	AA_DRB1_149	6.24E-36
DQB1	AA_DQB1_74	8.46E-36
DRB1	AA_DRB1_11	1.23E-35
B	AA_B_156	1.29E-35
DRB1	AA_DRB1_-25	1.55E-35
DRB1	AA_DRB1_-16	1.58E-35

DRB1	AA_DRB1_12	1.68E-35
DQB1	AA_DQB1_37	8.28E-35
DQB1	AA_DQB1_71	9.27E-35
DQB1	AA_DQB1_55	1.20E-34
DQB1	AA_DQB1_30	1.28E-34
DQB1	AA_DQB1_-10	4.16E-34
DRB1	AA_DRB1_233	5.43E-34
DQB1	AA_DQB1_66	2.23E-33
DQB1	AA_DQB1_67	2.24E-33
DRB1	AA_DRB1_71	1.11E-32
B	AA_B_163	6.75E-31
B	AA_B_97	6.68E-30
DRB1	AA_DRB1_73	5.60E-27
DQB1	AA_DQB1_77	2.04E-25
DQB1	AA_DQB1_75	2.41E-25
DQB1	AA_DQB1_38	2.97E-25
DQA1	AA_DQA1_215	1.57E-23
DRB1	AA_DRB1_98	1.80E-23
DRB1	AA_DRB1_104	1.82E-23
DRB1	AA_DRB1_67	5.46E-23
B	AA_B_45	1.59E-22
DQA1	AA_DQA1_34	2.61E-22
B	AA_B_74	1.61E-21
DQA1	AA_DQA1_52	3.78E-21
B	AA_B_-21	4.18E-21
B	AA_B_-23	4.33E-21
DRB1	AA_DRB1_86	1.04E-20
B	AA_B_114	1.32E-20
B	AA_B_180	2.02E-20
B	AA_B_177	2.02E-20
B	AA_B_63	7.38E-20
HLA_C	HLA_C_07	9.70E-20
C	AA_C_-9	1.72E-19
B	AA_B_131	1.97E-19
C	AA_C_194	1.99E-19
C	AA_C_184	2.00E-19
DQA1	AA_DQA1_56	2.04E-19
C	AA_C_339	2.08E-19
C	AA_C_326	2.08E-19
C	AA_C_307	2.12E-19
C	AA_C_305	2.14E-19
C	AA_C_285	2.15E-19
C	AA_C_261	2.18E-19
C	AA_C_273	2.19E-19
DQA1	AA_DQA1_76	2.41E-19
C	AA_C_295	2.83E-19

DQB1	AA_DQB1_57	3.47E-19
DRB1	AA_DRB1_47	4.22E-19
C	AA_C_147	4.41E-19
C	AA_C_-17	7.70E-19
C	AA_C_306	9.50E-19
C	AA_C_253	9.68E-19
C	AA_C_267	9.76E-19
B	AA_B_116	2.28E-18
DRB1	AA_DRB1_140	1.24E-17
DQB1	AA_DQB1_-18	3.18E-17
DRB1	AA_DRB1_9	5.60E-17
B	AA_B_24	8.16E-17
C	AA_C_-15	1.97E-16
HLA_DPB1	HLA_DPB1_01	3.20E-16
HLA_DPB1	HLA_DPB1_0101	3.20E-16
DPB1	AA_DPB1_194	3.74E-16
C	AA_C_152	1.56E-14
HLA_A	HLA_A_0101	2.10E-14
DRB1	AA_DRB1_30	2.12E-14
HLA_A	HLA_A_01	2.95E-14
A	AA_A_158	2.97E-14
A	AA_A_150	2.99E-14
A	AA_A_67	3.45E-14
A	AA_A_44	3.56E-14
DRB1	AA_DRB1_96	3.83E-14
DRB1	AA_DRB1_60	8.09E-14
DRB1	AA_DRB1_28	1.09E-13
DRB1	AA_DRB1_4	1.59E-13
DRB1	AA_DRB1_57	4.89E-13
B	AA_B_-10	7.64E-13
C	AA_C_9	1.12E-12
A	AA_A_156	1.16E-12
DRB1	AA_DRB1_181	1.36E-12
HLA_DQB1	HLA_DQB1_03	4.66E-12
DRB1	AA_DRB1_78	7.63E-12
DQB1	AA_DQB1_140	7.72E-12
DQB1	AA_DQB1_182	7.90E-12
HLA_DQA1	HLA_DQA1_02	4.01E-11
DQA1	AA_DQA1_54	4.08E-11
HLA_DQA1	HLA_DQA1_0201	4.11E-11
C	AA_C_90	4.41E-11
DRB1	AA_DRB1_25	6.27E-11
DRB1	AA_DRB1_14	6.31E-11
HLA_DRB1	HLA_DRB1_0701	6.52E-11
HLA_DRB1	HLA_DRB1_07	6.57E-11
C	AA_C_24	9.15E-11

B	AA_B_46	4.76E-10
DQA1	AA_DQA1_25	7.16E-10
B	AA_B_41	1.08E-09
DQA1	AA_DQA1_187	1.48E-09
C	AA_C_304	2.33E-09
DRB1	AA_DRB1_70	2.62E-09
DRB1	AA_DRB1_120	4.97E-09
C	AA_C_156	5.02E-09
DQB1	AA_DQB1_185	6.83E-09
DQA1	AA_DQA1_26	6.91E-09
HLA_DQA1	HLA_DQA1_0301	6.93E-09
HLA_DQA1	HLA_DQA1_03	6.94E-09
A	AA_A_166	8.39E-09
A	AA_A_167	8.39E-09
C	AA_C_73	1.53E-08
HLA_DRB1	HLA_DRB1_04	3.80E-08
DRB1	AA_DRB1_33	3.93E-08
B	AA_B_32	4.76E-08
DRB1	AA_DRB1_180	5.35E-08
DRB1	AA_DRB1_-24	6.14E-08
DPB1	AA_DPB1_76	8.66E-08
DQB1	AA_DQB1_135	9.07E-08
A	AA_A_76	9.23E-08
HLA_DRB1	HLA_DRB1_0401	1.19E-07
B	AA_B_178	1.20E-07
B	AA_B_70	1.74E-07
B	AA_B_69	1.78E-07
B	AA_B_152	1.86E-07
B	AA_B_-8	2.28E-07
B	AA_B_-11	2.97E-07
B	AA_B_71	4.00E-07
B	AA_B_83	4.30E-07
B	AA_B_82	4.30E-07
HLA_DQB1	HLA_DQB1_0202	6.17E-07
B	AA_B_12	6.59E-07
B	AA_B_81	7.14E-07
B	AA_B_77	1.06E-06
B	AA_B_11	1.07E-06
B	AA_B_80	1.13E-06
HLA_DQB1	HLA_DQB1_0303	1.91E-06
A	AA_A_90	1.94E-06
B	AA_B_95	2.17E-06
B	AA_B_-16	2.40E-06
A	AA_A_163	2.56E-06
C	AA_C_116	2.94E-06
HLA_B	HLA_B_57	4.23E-06

C	AA_C_95	4.92E-06
DQB1	AA_DQB1_125	5.82E-06

Table S8 - HLA Imputation in the polymyositis subgroup conditional on HLA-DRB1*03:01

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the polymyositis subgroup analysis (n=931)

Gene	Allele (HLA) / Amino acid (AA)	P-value
B	AA_B_67	4.44E-12
HLA_B	HLA_B_08	3.92E-09
HLA_B	HLA_B_0801	4.17E-09
B	AA_B_9	2.45E-08
DQA1	AA_DQA1_215	8.32E-07
DRB1	AA_DRB1_98	8.86E-07
DRB1	AA_DRB1_104	8.89E-07
DRB1	AA_DRB1_57	1.75E-06
B	AA_B_45	2.72E-06
DQA1	AA_DQA1_50	2.87E-06
DQA1	AA_DQA1_53	2.87E-06
DQA1	AA_DQA1_47	3.17E-06
C	AA_C_11	3.59E-06
B	AA_B_97	5.38E-06
DRB1	AA_DRB1_60	6.15E-06

Table S9 - HLA Imputation in the polymyositis subgroup conditional on HLA-DRB1*03:01 and HLA-B*08:01

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the polymyositis subgroup analysis (n=931)

Gene	Allele (HLA) / Amino acid (AA)	P-value
C	AA_C_11	1.17E-07
DQA1	AA_DQA1_215	1.10E-06
DRB1	AA_DRB1_98	1.18E-06
DRB1	AA_DRB1_104	1.18E-06
B	AA_B_194	2.02E-06
C	AA_C_9	2.18E-06
DRB1	AA_DRB1_57	2.28E-06
DQA1	AA_DQA1_50	3.77E-06
DQA1	AA_DQA1_53	3.77E-06
DQA1	AA_DQA1_47	4.25E-06
C	AA_C_99	4.56E-06
B	AA_B_67	6.71E-06

Table S10 - HLA Imputation in the dermatomyositis subgroup

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the dermatomyositis subgroup analysis (n=879)

Gene	Allele (HLA) / Amino acid (AA)	P-value
HLA_B	HLA_B_08	2.43E-42
HLA_B	HLA_B_0801	2.46E-42
B	AA_B_9	3.53E-38
HLA_DQB1	HLA_DQB1_0201	4.97E-38
HLA_DRB1	HLA_DRB1_0301	6.91E-37
HLA_DRB1	HLA_DRB1_03	9.78E-37
DRB1	AA_DRB1_77	1.37E-36
DRB1	AA_DRB1_74	1.64E-34
HLA_C	HLA_C_0701	7.35E-34
DQB1	AA_DQB1_66	5.64E-32
DQB1	AA_DQB1_67	5.65E-32
DQB1	AA_DQB1_57	7.61E-32
DRB1	AA_DRB1_26	1.55E-30
DQB1	AA_DQB1_71	2.17E-30
DQB1	AA_DQB1_74	6.69E-30
HLA_DQB1	HLA_DQB1_02	3.53E-29
DQB1	AA_DQB1_28	7.89E-29
DQB1	AA_DQB1_47	7.90E-29
DQB1	AA_DQB1_46	7.91E-29
DQB1	AA_DQB1_52	7.94E-29
C	AA_C_66	3.99E-28
DQB1	AA_DQB1_37	1.75E-27
DQB1	AA_DQB1_30	1.25E-26
DQB1	AA_DQB1_55	2.40E-26
DQB1	AA_DQB1_-10	2.54E-26
DQB1	AA_DQB1_75	1.50E-23
DRB1	AA_DRB1_73	5.46E-23
DQB1	AA_DQB1_38	1.67E-20
DQB1	AA_DQB1_77	6.10E-20
B	AA_B_163	4.58E-19
DRB1	AA_DRB1_71	7.19E-19
B	AA_B_156	3.08E-17
B	AA_B_114	4.74E-17
DRB1	AA_DRB1_67	2.97E-14
DQB1	AA_DQB1_-5	1.55E-13
B	AA_B_74	1.61E-13
DQB1	AA_DQB1_125	4.47E-13
B	AA_B_67	6.76E-13
DQA1	AA_DQA1_50	9.52E-13
DQA1	AA_DQA1_53	9.68E-13
DRB1	AA_DRB1_37	1.84E-12

DPB1	AA_DPB1_194	2.68E-12
HLA_DPB1	HLA_DPB1_01	2.84E-12
HLA_DPB1	HLA_DPB1_0101	2.84E-12
DQB1	AA_DQB1_87	3.90E-12
DQA1	AA_DQA1_175	5.24E-12
DQA1	AA_DQA1_47	5.61E-12
HLA_DQB1	HLA_DQB1_06	6.52E-12
DQB1	AA_DQB1_203	1.93E-11
DQA1	AA_DQA1_52	3.65E-11
DQA1	AA_DQA1_11	5.10E-11
DQA1	AA_DQA1_218	5.14E-11
DQA1	AA_DQA1_56	6.49E-11
DQA1	AA_DQA1_76	6.51E-11
DQA1	AA_DQA1_51	6.52E-11
DQA1	AA_DQA1_40	6.52E-11
DQB1	AA_DQB1_220	6.56E-11
DQB1	AA_DQB1_221	6.75E-11
DQB1	AA_DQB1_90	7.03E-11
DQB1	AA_DQB1_89	7.04E-11
DQB1	AA_DQB1_84	7.16E-11
DQB1	AA_DQB1_85	7.17E-11
DQA1	AA_DQA1_61	9.26E-11
DQA1	AA_DQA1_66	9.40E-11
DQA1	AA_DQA1_18	9.75E-11
DQA1	AA_DQA1_45	9.76E-11
DQA1	AA_DQA1_48	9.81E-11
HLA_DQA1	HLA_DQA1_01	9.87E-11
DQA1	AA_DQA1_64	9.87E-11
DQA1	AA_DQA1_55	9.88E-11
DQA1	AA_DQA1_80	9.91E-11
DQB1	AA_DQB1_53	1.14E-10
DQB1	AA_DQB1_-21	1.28E-10
DQB1	AA_DQB1_-6	1.56E-10
DQB1	AA_DQB1_-4	1.62E-10
DQA1	AA_DQA1_69	1.97E-10
B	AA_B_97	2.60E-10
DQB1	AA_DQB1_86	5.09E-10
B	AA_B_180	8.23E-10
B	AA_B_177	8.24E-10
DQB1	AA_DQB1_13	9.25E-10
DQB1	AA_DQB1_167	9.63E-10
B	AA_B_-21	1.08E-09
DQB1	AA_DQB1_45	1.09E-09
B	AA_B_-23	1.09E-09
HLA_DQB1	HLA_DQB1_0301	1.10E-09
C	AA_C_152	1.12E-09

HLA_DPA1	HLA_DPA1_0201	2.19E-09
C	AA_C_-9	2.22E-09
B	AA_B_131	2.35E-09
HLA_C	HLA_C_07	2.43E-09
C	AA_C_194	2.77E-09
C	AA_C_184	2.89E-09
B	AA_B_-10	2.95E-09
C	AA_C_295	3.14E-09
HLA_DQA1	HLA_DQA1_0501	3.34E-09
DQA1	AA_DQA1_75	3.34E-09
HLA_DQA1	HLA_DQA1_05	3.34E-09
B	AA_B_45	3.36E-09
C	AA_C_339	3.44E-09
C	AA_C_326	3.44E-09
C	AA_C_261	3.47E-09
C	AA_C_273	3.47E-09
C	AA_C_307	3.49E-09
C	AA_C_285	3.50E-09
C	AA_C_305	3.51E-09
DQA1	AA_DQA1_107	5.36E-09
DQA1	AA_DQA1_163	5.43E-09
DQA1	AA_DQA1_161	5.45E-09
DQA1	AA_DQA1_156	5.45E-09
HLA_DRB1	HLA_DRB1_1501	5.88E-09
DQB1	AA_DQB1_70	7.26E-09
DQB1	AA_DQB1_26	7.41E-09
HLA_A	HLA_A_0101	7.53E-09
DRB1	AA_DRB1_32	7.86E-09
HLA_A	HLA_A_01	1.01E-08
A	AA_A_158	1.01E-08
A	AA_A_150	1.03E-08
HLA_DPA1	HLA_DPA1_02	1.07E-08
C	AA_C_147	1.07E-08
DPA1	AA_DPA1_50	1.07E-08
DPA1	AA_DPA1_31	1.08E-08
A	AA_A_67	1.09E-08
DQA1	AA_DQA1_-16	1.11E-08
C	AA_C_-17	1.11E-08
A	AA_A_44	1.14E-08
HLA_DPA1	HLA_DPA1_01	1.19E-08
DRB1	AA_DRB1_-1	1.32E-08
DPA1	AA_DPA1_83	1.39E-08
C	AA_C_99	1.53E-08
C	AA_C_253	1.73E-08
C	AA_C_267	1.73E-08
C	AA_C_306	1.75E-08

DQA1	AA_DQA1_129	2.25E-08
DPA1	AA_DPA1_228	2.37E-08
DPA1	AA_DPA1_160	2.44E-08
DPA1	AA_DPA1_127	2.47E-08
DPA1	AA_DPA1_111	2.48E-08
HLA_DQB1	HLA_DQB1_0602	2.98E-08
HLA_DRB1	HLA_DRB1_15	3.08E-08
DRB1	AA_DRB1_58	1.14E-07
HLA_DPA1	HLA_DPA1_0103	1.24E-07
DPB1	AA_DPB1_87	1.30E-07
DPB1	AA_DPB1_85	1.31E-07
DPB1	AA_DPB1_86	1.35E-07
DPB1	AA_DPB1_84	1.74E-07
DPB1	AA_DPB1_76	1.99E-07
HLA_C	HLA_C_0702	2.74E-07
A	AA_A_156	2.90E-07
DPB1	AA_DPB1_8	2.94E-07
B	AA_B_24	3.41E-07
DQA1	AA_DQA1_207	3.85E-07
C	AA_C_77	4.72E-07
C	AA_C_80	4.72E-07
HLA_B	HLA_B_0702	5.37E-07
B	AA_B_116	5.38E-07
HLA_DRB1	HLA_DRB1_11	5.89E-07
HLA_B	HLA_B_07	7.41E-07
A	AA_A_90	8.12E-07
C	AA_C_-15	8.98E-07
DPB1	AA_DPB1_170	9.28E-07
DPB1	AA_DPB1_96	9.29E-07
HLA_DQA1	HLA_DQA1_0102	9.54E-07
A	AA_A_163	1.31E-06
B	AA_B_11	1.48E-06
A	AA_A_76	1.74E-06
DPB1	AA_DPB1_35	1.94E-06
B	AA_B_95	2.29E-06
DPB1	AA_DPB1_9	2.58E-06
B	AA_B_-8	3.04E-06
B	AA_B_70	3.40E-06
DQB1	AA_DQB1_-18	4.94E-06
B	AA_B_152	5.31E-06
A	AA_A_152	5.44E-06
B	AA_B_325	6.15E-06
B	AA_B_178	6.32E-06

Table S11 - HLA Imputation in the dermatomyositis subgroup conditional on HLA-B*08:01

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the dermatomyositis subgroup analysis (n=879)

Gene	Allele (HLA) / Amino acid (AA)	P-value
DQB1	AA_DQB1_57	8.95E-14
DQB1	AA_DQB1_71	7.03E-10
DQB1	AA_DQB1_66	1.23E-09
DQB1	AA_DQB1_67	1.23E-09
DQB1	AA_DQB1_75	1.64E-09
DQB1	AA_DQB1_74	3.59E-09
HLA_DQB1	HLA_DQB1_06	1.80E-07
DRB1	AA_DRB1_47	1.85E-07
DQB1	AA_DQB1_-5	4.17E-07
DQB1	AA_DQB1_38	4.42E-07
DQB1	AA_DQB1_125	1.19E-06
DQB1	AA_DQB1_77	1.34E-06
HLA_DQB1	HLA_DQB1_02	1.41E-06
HLA_DRB1	HLA_DRB1_1501	1.64E-06
DRB1	AA_DRB1_74	1.68E-06
DQB1	AA_DQB1_47	2.14E-06
DQB1	AA_DQB1_28	2.14E-06
DQB1	AA_DQB1_37	2.14E-06
DQB1	AA_DQB1_46	2.14E-06
DQB1	AA_DQB1_52	2.14E-06
DRB1	AA_DRB1_-1	4.67E-06
HLA_DQB1	HLA_DQB1_0602	4.69E-06

Table S12 - HLA Imputation in the dermatomyositis subgroup conditional on HLA-B*08:01 and HLA-DQB1 amino acid 57

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the dermatomyositis subgroup analysis (n=879)

Gene	Allele (HLA) / Amino acid (AA)	P-value
DQB1	AA_DQB1_56	1.23E-06
HLA_DQB1	HLA_DQB1_0402	2.01E-06
HLA_DQB1	HLA_DQB1_04	2.26E-06

Table S13 - HLA Imputation in the juvenile dermatomyositis subgroup

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the juvenile dermatomyositis subgroup analysis (n=481)

Gene	Allele (HLA) / Amino acid (AA)	P-value
DRB1	AA_DRB1_77	4.26E-14
HLA_DRB1	HLA_DRB1_03	4.58E-14
HLA_DRB1	HLA_DRB1_0301	7.91E-14
HLA_DQB1	HLA_DQB1_0201	3.34E-13
DRB1	AA_DRB1_74	2.26E-12
DRB1	AA_DRB1_37	4.76E-12
DRB1	AA_DRB1_71	6.82E-12
DRB1	AA_DRB1_26	9.55E-12
DRB1	AA_DRB1_140	5.23E-11
DQA1	AA_DQA1_52	1.36E-10
DQA1	AA_DQA1_47	2.51E-10
DRB1	AA_DRB1_9	3.06E-10
B	AA_B_9	8.40E-10
DPB1	AA_DPB1_194	1.59E-09
HLA_DPB1	HLA_DPB1_01	1.74E-09
HLA_DPB1	HLA_DPB1_0101	1.74E-09
DQA1	AA_DQA1_50	4.11E-09
DQA1	AA_DQA1_53	4.11E-09
HLA_B	HLA_B_0801	7.20E-09
HLA_B	HLA_B_08	7.24E-09
DQA1	AA_DQA1_51	1.14E-08
DQA1	AA_DQA1_40	1.14E-08
DQA1	AA_DQA1_175	1.25E-08
DRB1	AA_DRB1_13	1.54E-08
DRB1	AA_DRB1_11	1.84E-08
DQA1	AA_DQA1_129	1.92E-08
DQB1	AA_DQB1_67	2.69E-08
DQB1	AA_DQB1_66	2.69E-08
DQB1	AA_DQB1_57	4.71E-08
DRB1	AA_DRB1_-17	7.13E-08
DQB1	AA_DQB1_71	9.22E-08
DQB1	AA_DQB1_55	9.33E-08
HLA_DQA1	HLA_DQA1_0501	1.11E-07
HLA_DQA1	HLA_DQA1_05	1.11E-07
DQA1	AA_DQA1_75	1.12E-07
DQB1	AA_DQB1_28	1.29E-07
DQB1	AA_DQB1_46	1.29E-07
DQB1	AA_DQB1_52	1.29E-07
DQB1	AA_DQB1_47	1.30E-07
HLA_DQB1	HLA_DQB1_02	1.33E-07
DQA1	AA_DQA1_107	1.89E-07

DQA1	AA_DQA1_163	1.91E-07
DQA1	AA_DQA1_161	1.92E-07
DQA1	AA_DQA1_156	1.92E-07
DQA1	AA_DQA1_11	1.99E-07
DQA1	AA_DQA1_218	1.99E-07
DRB1	AA_DRB1_32	2.12E-07
DQB1	AA_DQB1_37	2.52E-07
DQB1	AA_DQB1_89	2.53E-07
DQB1	AA_DQB1_85	2.53E-07
DQB1	AA_DQB1_84	2.54E-07
DQB1	AA_DQB1_90	2.55E-07
DQB1	AA_DQB1_220	2.66E-07
DQB1	AA_DQB1_221	2.70E-07
DQB1	AA_DQB1_53	3.01E-07
DQA1	AA_DQA1_61	3.09E-07
DQA1	AA_DQA1_66	3.13E-07
DQA1	AA_DQA1_18	3.20E-07
HLA_DQA1	HLA_DQA1_01	3.20E-07
DQA1	AA_DQA1_45	3.20E-07
DQA1	AA_DQA1_48	3.21E-07
DQA1	AA_DQA1_64	3.22E-07
DQA1	AA_DQA1_55	3.22E-07
DQA1	AA_DQA1_80	3.22E-07
DQB1	AA_DQB1_203	3.49E-07
B	AA_B_114	3.80E-07
C	AA_C_16	3.84E-07
DQB1	AA_DQB1_30	5.94E-07
DQB1	AA_DQB1_74	7.25E-07
HLA_C	HLA_C_0202	7.53E-07
HLA_C	HLA_C_02	7.53E-07
DQA1	AA_DQA1_69	9.22E-07
B	AA_B_156	9.73E-07
DQB1	AA_DQB1_86	1.06E-06
DQB1	AA_DQB1_125	1.08E-06
DQA1	AA_DQA1_56	1.32E-06
DQA1	AA_DQA1_76	1.32E-06
DQB1	AA_DQB1_87	1.56E-06
DQB1	AA_DQB1_-10	1.62E-06
DQB1	AA_DQB1_-4	1.66E-06
DRB1	AA_DRB1_12	1.67E-06
DQB1	AA_DQB1_-6	1.70E-06
DQB1	AA_DQB1_-21	1.71E-06
DRB1	AA_DRB1_10	1.76E-06
DRB1	AA_DRB1_149	1.92E-06
DQB1	AA_DQB1_70	1.99E-06
DRB1	AA_DRB1_-16	2.40E-06

DRB1	AA_DRB1_-25	2.40E-06
DRB1	AA_DRB1_96	4.04E-06
C	AA_C_211	4.22E-06
DQA1	AA_DQA1_-16	4.22E-06
HLA_DPA1	HLA_DPA1_0103	4.74E-06
DQB1	AA_DQB1_-5	5.44E-06
HLA_C	HLA_C_0701	5.88E-06

Table S14 - HLA Imputation in the juvenile dermatomyositis subgroup conditional on HLA-DRB1*03:01

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the juvenile dermatomyositis subgroup analysis (n=481)

Gene	Allele (HLA) / Amino acid (AA)	P-value
C	AA_C_16	1.75E-07
C	AA_C_211	3.27E-07
HLA_C	HLA_C_0202	3.28E-07
HLA_C	HLA_C_02	3.28E-07
DRB1	AA_DRB1_-24	8.20E-07
C	AA_C_163	1.53E-06

Table S15 - HLA Imputation in the juvenile dermatomyositis subgroup conditional on HLA-DRB1*03:01 and HLA-C*02:02

HLA alleles and amino acids reaching significance ($p<6.8x10^{-6}$) in the juvenile dermatomyositis subgroup analysis (n=481)

Gene	Allele (HLA) / Amino acid (AA)	P-value
DRB1	AA_DRB1_-24	8.97E-07

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