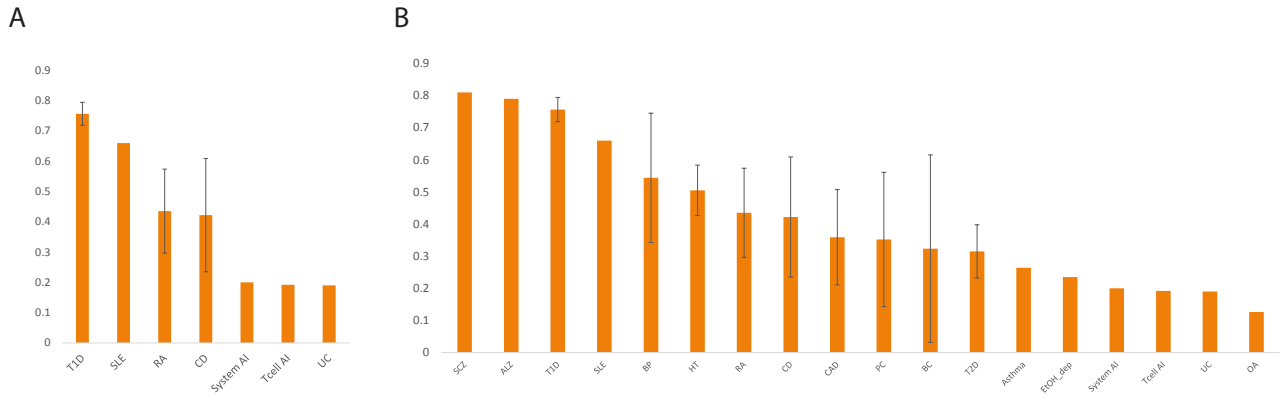
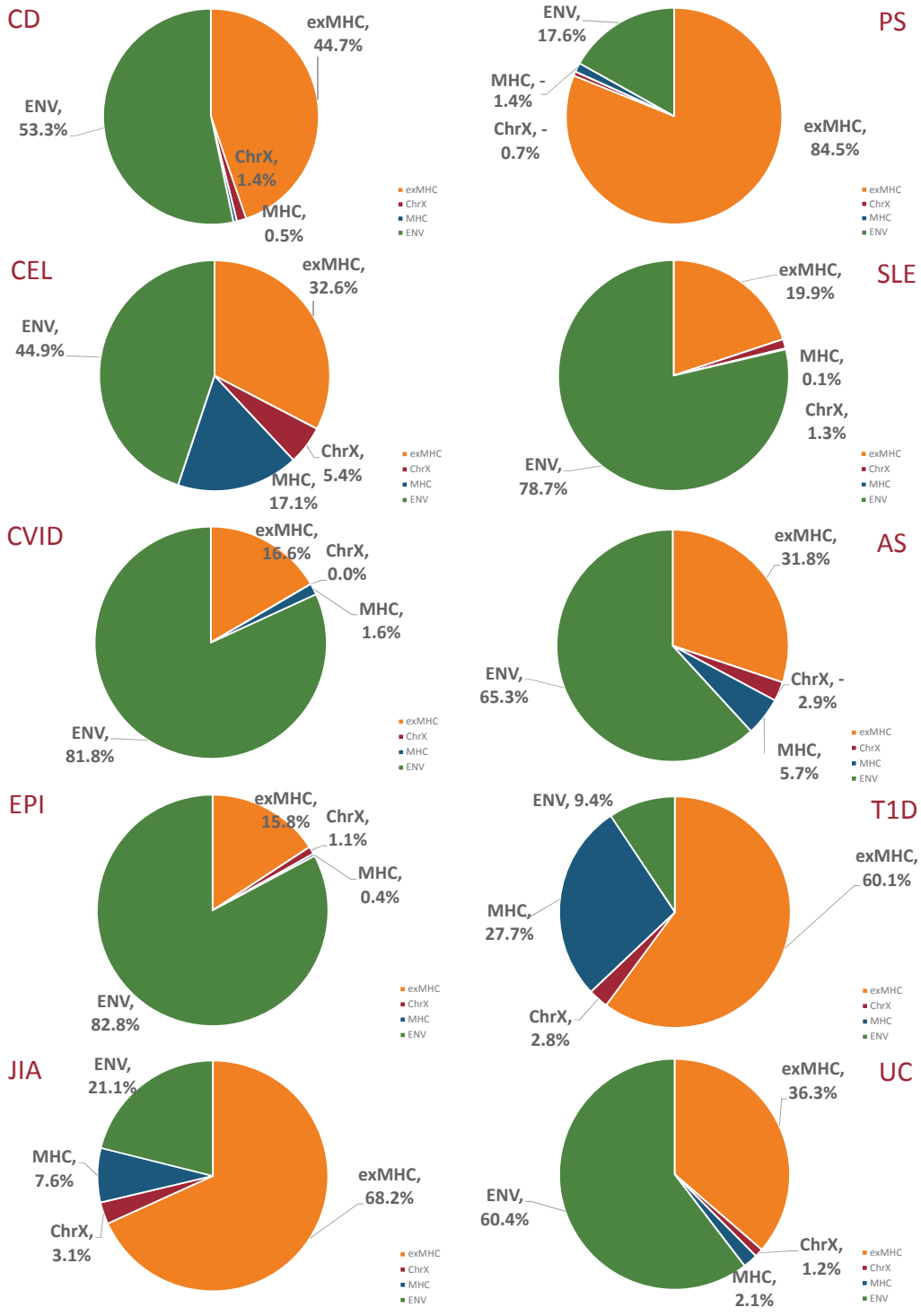
Supplementary Figure 1. SNP-heritability calculations reported by prior studies for A. Relevant AI diseases and B. All available diseases curated.



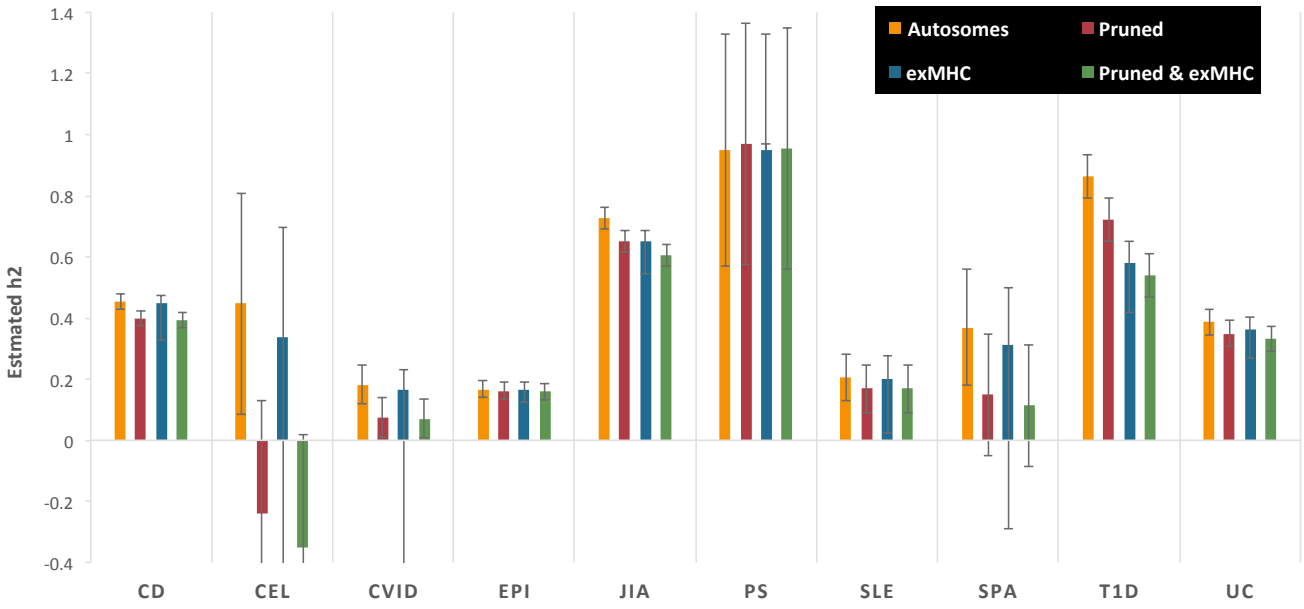
Raw data used from prior GWAS SNP-heritability estimates are provided in **Supplementary Table 1C.**

Supplementary Figure 2 Partitioning phenotypic variance to genetic and non-genetic components for all ten traits examined.



Pie chart includes Non-genetic *(ENV, Green)* and Genetic components, which is sub-divided into contributions from the autosomal regions excluding the extended *MHC* (ex*MHC*, Orange), the extended *MHC* (*MHC*, Blue), and the *X-chromosome* (*ChrX*, Red).

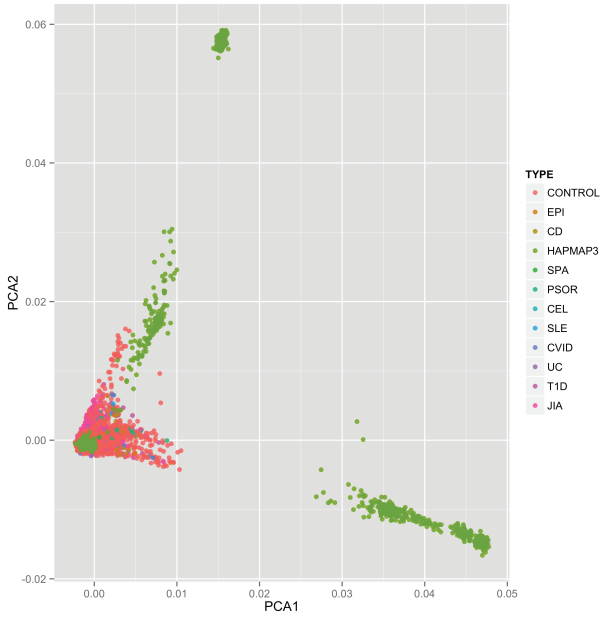
Supplementary Figure 3 Effect of LD-pruning on SNP-heritability estimates.



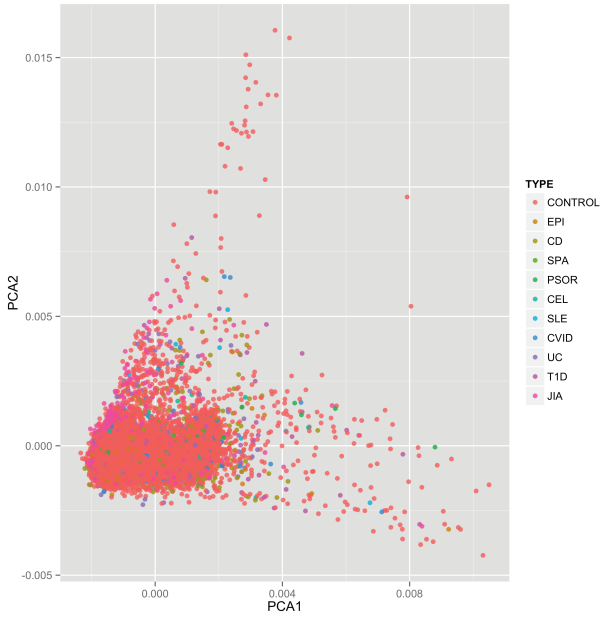
Autosomal SNP-h^2 estimations using all genotyped markers including the extended *MHC* (Orange) is significantly greater than when the markers are LD-pruned (Red). When the *MHC* is removed, the difference in SNP-h^2 calculated between using the full autosomal genotyped SNPs (Blue) as compared those that are LD-pruned (Green) is minimal.

Supplementary Figure 4 Genetically-inferred ancestry estimates of included cohorts based on principal components analysis (PCA)

A



B



Top two principal components from PCA of genome wide SNP genotypes in the genotyped study cohort with (A) and without (B) the HapMap 3 reference panel dataset subjects. Plots are color-coded by the pAID cohorts either with or without the HapMap subjects. Populations and cohorts sizes are as specified in **Table 1A.**

Supplementary Table 1 Reported pAID prevalence in the Western Hemisphere in Caucasoid populations

pAID	Data 1	REF	Data 2	REF	Data 3	REF	Data 4	REF
SPA	687/217,000	1	62/10000	2	52/10000	3		
PS	10788/5,472,032	4	114,521/7,533,475	5	548/21,921	6	33981/1359240	7
CEL	2722/5,472,032	4	6/813	8	4/2230	9	10/1002	10
SLE	1732/5,472,032	4	62/2,210,389	11	51/100,000	12		
CVID	87500/297,386,000	13	52.5/1,000,000	14	1/30,000	15		
UC	20669/5,472,032	4	15,873/8,997,731	16	8/100,000	17		
T1D	51783/5,472,032	4	980/11,194,478	18	4808/1,885,451	19		
JIA	87/445856	20	294,000/295,753,000	21	78/364,939	22		
CD	12309/5,472,032	4	13,918/8,997,731	16	140/496,280	23		

Supplementary Table 2 Reported pAID heritability estimates in the Western Hemisphere in Caucasoid populations

pAID	Data 1	Ref 1*	Data 2	Ref 2*	Data 3	Ref 3*
CD	58%	24	80%	25		
CEL	59%	26	87%	27	0.57	28
JIA	65%	29	53%	30	0.6	30
PS	68%	31	91%	32		
SLE	66%	33	66%	34		
SPA	90%	35	90%	36		
T1D	88%	37	88%	38		
UC	42%	24	53%	25		

Supplementary Table 3 Published SNP-h^2 estimates from literature.

Trait	*So*[39]	*Zaitlen*[40]	*Yang*[41]	*Chen*[42]	*Lee*[43]	*Speed*[44]	*Speed*[45]
Method	Variants	REML	REML	GREML	GREML	GREML	LDAK
Scale	Liability	Liability	Liability	Liability	Liability	Observed	Observed
ALZ	0.79	--	--	--	--	--	--
BP	0.77	--	0.32	--	0.35	0.69	0.59
BC	0.53	0.117	--	--	--	--	--
CAD	0.49	0.146	--	--	--	0.39	0.41
CD	0.55	--	0.18	0.26	--	0.54	0.58
PC	0.5	0.204	--	--	--	--	--
SCZ	0.81	--	--	--	--	--	--
SLE	0.66	--	--	--	--	--	--
T1D	0.8	--	0.25 (exMHC)	--	--	0.73	0.74
T2D	0.42	0.254	--	--	0.21	0.35	0.34
AI (T-cell)*	--	0.192	--	--	--	--	--
AI (Systemic)*	--	0.2	--	--	--	--	--
Asthma	--	0.264	--	--	--	--	--
RA	--	0.261	--	--	0.39	0.57	0.52
OA	--	0.126	--	--	--	--	--
Alcohol Dependence	--	0.235	--	--	--	--	--
UC	--	--	--	0.19	--	--	--
HT	--	--	--	--	0.575	0.42	0.52

See text for details and discussion. Disease or trait is listed on left and each column heading corresponding to first author last name of a reference as cited by superscript. *Per *Zaitlen* et al, AI disease that the authors classified as being 'T-cell mediated' or 'Systemic' (ie. RA/SLE/SSc/AS). References for each citation are as annotated in superscripts following each first author's last name.

Supplementary Table 4 Percentages of total phenotypic variance explained by genetic variance (the autosome excluding the *MHC*, the *MHC* and the X-chromosome) and non-genetic variance (ENV).

pAID	*Auto exMHC*	*ChrX*	*MHC*	ENV
CD	44.7%	1.4%	0.5%	53.3%
CEL	32.6%	5.4%	17.1%	44.9%
CVID	16.6%	0.0%	1.6%	81.8%
EPI	15.8%	1.1%	0.4%	82.8%
JIA	68.2%	3.1%	7.6%	21.1%
PS	84.5%	-0.7%	-1.4%	17.6%
SLE	19.9%	1.3%	0.1%	78.7%
AS	31.8%	-2.9%	5.7%	65.3%
T1D	60.1%	2.8%	27.7%	9.4%
UC	36.3%	1.2%	2.1%	60.4%

Supplementary Table 5 Lead GWAS association signals across the extended *MHC* for each pAID

pAID	Marker	POS (hg19)	MAF	A2	P	BETA	SE
CD	rs1626392	29840223	0.21	G	2.3E-07	-0.22	0.04
CEL	SNP_DQB1_32740731	32740731	0.22	C	1.0E-26	-1.60	0.15
CVID	SNP_B_31432003_C	31432003	0.19	A	3.8E-08	0.61	0.11
JIA	AA_DRB1_181_32657335_x	32657335	0.03	A	1.6E-99	-2.57	0.12
PSOR	HLA_B_1302	31431272	0.03	A	3.1E-04	-1.74	0.48
SLE	rs537160	32024379	0.30	C	4.5E-08	-0.55	0.10
SPA	HLA_B_2705	31431272	0.03	A	1.9E-11	-2.88	0.43
T1D	AA_DQB1_57_32740666_A	32740666	0.34	A	3.0E-170	-1.72	0.06
UC	SNP_DRB1_32660090	32660090	0.31	A	2.5E-15	0.43	0.05

* P (Presence) or A (Absence) of the indicated HLA 4-digit allele, AA (amino acid [ie. lysine (K) or alanine (A)]), deletion (x). Details of the notion for the markers are as described by *Jia et al*.[46] A2: Alternative allele or marker. For deletions, A denotes 'Absence of'. P: P-value. MAF: Minor Allele Frequency. POS: position in the hg19 human genome reference. BETA: effect size on logistic regression. SE: standard error.

Supplementary Table 6 Population-based estimates of heritability (POP-h^2) attributable to the *MHC* from literature

pAID	Total h^2 (1)	Total h^2 (2)	Mean h^2	% MHC	REF
SPA	0.90	0.90	0.90	0.25	[3]
PS	0.68	0.91	0.80	0.50	[47]
CEL	0.59	0.87	0.73	0.40	[48,49]
SLE	0.66	0.66	0.66	0.10	[50]
UC	0.42	0.53	0.48	0.60	[51]
T1D	0.40	0.62	0.88	0.50	[51]
JIA	0.65	0.53	0.59	0.33	[51]
CD	0.58	0.80	0.69	0.10	[51]

See Supplementary Table 1B for details of the total heritability references. REF refers to references of the percentage heritability attributable to the *MHC.*

Supplementary Table 7 Estimates of SNP-h^2 attributable to the *MHC* using other GWAS datasets

Disease	SNP-h^2	SNP-h^2 *MHC*	% *MHC*
BPD	0.98	0	0.00%
CAD	0.41	0	0.00%
CD	1	0.02	2.00%
HT	0.48	0	0.00%
RA	0.57	0.13	22.81%
T1D	0.65	0.44	67.69%
T2D	0.52	0	0.00%

Supplementary Table 8 Known HLA haplotypes associated with AI Diseases

Disease	HLA Associated	REF
Ankylosing spondylitis	Class I: - B27 Class II:	52
Asthma	Class I: Class II: - DRB1*03 haplotype Class III: - TNFA-308	53
Autoimmune thyroid diseases (Grave's & Hashimoto)	Class I: Class II: - DR3 (DRB1*03; DRB1*Arg74), - DR4 (in Hashimoto's thyroiditis)	52,54
Celiac disease	Class I: Class II: - DQ2 (DRB1*0301-DQA1*0501-DQB1*0201) - DQ8 (DRB1*04-DQA1*0301-DQB1*0302)	55,56
Crohn's disease	Class I: Class II: - DRB1*0103-DQB1*0501 - DRB1*04	51,57
Multiple sclerosis	Class I: - A*02:01 Class II: - DR2 (DRB1*1501, DQA1*0102, DQB1*0602) - DRBI* 0501 - DRB1*03:01, *13:03 - DQB1*02:01 - DPB1*03:01	58,59
Psoriasis	Class I: - HLA-B*57 - HLA-B*40 (Decreased susceptibility) - Cw*0602 - Cw*1203 Class II: Class III: - HCP5	60

Rheumatoid arthritis	Class I: - HLB*08 Class II: - DRBI *0401, *0404, *0101, *0405, *0101, *1001, *0901 Class III: - TNF	61,62
Systemic lupus erythematosus	Class I: Class II: - DR3 (DRB1*0301-DQB1*0201), - DR2 (DRB1*1501-DQB1*0602), - DR8 (DRB1*0801-DQB1*0402) - DRBI*0301 Class III: - SCIV2L/ CFB/ RDBP/ DOM3Z/STK19 - C4A, C4B	63
Type 1 diabetes	Class I: - HLA-A - HLA-B. Protective effect – DQB1*0602 Class II: - DQ2 (DRB1*0301-DQA1*0501-DQB1*0201) - DQ8 (DRB1*04-DQA1*0301-DQB1*0302)	64
Ulcerative colitis	Class I: Class II: - DRB1*0103-DQB1*0501 - DRB1*1502-BTNL2) - DRB1* 0501	51,65,66
Multiple Autoimmune diseases	Class I: - HLA-A1 - HLA-B8 Class II: - HLA-DR3	51
Sarcoidosis	Class I: Class II: - HLA-DRB1*03	67

Supplementary Table 9 Prevalence of AI Disease comorbidities among Western Caucasoid populations

Prevalence	Data	REF	Data	REF	Data 3	REF	Data4	REF
CEL-CD	--	--	4/356	[8]	--	--	--	--
CEL-CVID	--	--	--	--	--	--	--	--
CEL-JIA	0/408	[4]	--	--	--	--	--	--
CEL-SLE	--	--	4/356	[8]	--	--	--	--
CEL-T1D	12/408	[4]	8/356	[8]	96/9243	[10]	921/28958	[5]
CEL-PS	--	--	46/356	[8]	--	--	401/28958	[5]
CEL-SPA	--	--	2/356	[8]	--	--	--	--
CEL-UC	--	--	3/356	[8]	--	--	--	--
CVID-CD	1/52	[68]	--	--	--	--	--	--
CVID-JIA	4/52	[68]	--	--	--	--	--	--
CVID-SLE	1/116	[69]	--	--	--	--	--	--
JIA-T1D	4/443	[20]	0/53	[70]	--	--	--	--
JIA-CEL	10/151	[71]	1/53	[70]	--	--	--	--
PS-CD	95/10788	[72]	116/ 1353	[73]	72/1402	[73]	64/12502	[74]
PS-CEL	--	--	--	--	--	--	36/12502	[75]
PS-SLE	19/10788	[72]	--	--	--	--	--	--
PS-T1D	442/10788	[72]	--	--	--	--	--	--
PS-SPA	--	--	--	--	--	--	--	--
PS-UC	122/10788	[72]	166/1353	[73]	74/1402	[73]	60/ 12502	[74]
SLE-CD	13/1732	[72]	--	--	--	--	--	--
SLE-PS	19/1732	[72]	--	--	--	--	--	--
SLE-CEL	3/1732	[72]	--	--	--	--	--	--
SLE-T1D	46/1732	[72]	--	--	--	--	--	--
SLE-UC	25/1732	[72]	--	--	--	--	--	--
T1D-PS	442/51783	[72]	--	--	--	--	--	--
T1D-SLE	46/51783	[72]	--	--	--	--	--	--
T1D-CEL	108/51783	[72]	9/52	[76]	917/ 41566	[77]	33/ 1000	[19]
T1D-CEL	22/ 492	[78]	9/ 281	[79]	7/509	[18]		
T1D-UC	435/51783	[72]	--	--	--	--	--	--
T1D-CD	217/51783	[72]	--	--	--	--	--	--
T1D-JIA	4/443	[16]	--	--	--	--	--	--
UC-CD	--	--	--	--	2676/20699	[72]	--	--
UC-T1D	84/12185	[80]	63/7525	[81]	435/20669	[72]	--	--
UC-SPA	117/12185	--	9/976	[23]	7/84	[82]	7/273	[83]
UC-SLE	10/12185	--	18/7525	[81]	25/20669	[72]	--	--
UC-CEL	--	--	--	--	77/20669	[72]	--	--
UC-PS	424/12185	--	138/7525	[81]	122/20669	[72]	--	--
CD-UC	--	--	--	--	2676/12309	[72]	--	--
CD-CEL	--	--	--	--	101/12309	[72]	--	--
CD-T1D	35/7988	[80]	43/4021	[81]	217/12309	[72]	--	--
CD-SLE	12/7988	[80]	8/4021	[81]	13/12309	[72]	--	--
CD-PS	317/7988	[80]	75/4021	[81]	95/12309	[72]	--	--
CD-SPA	107/7988	[80]	6/483	[23]	9/78	[82]	8/133	[83]

Supplementary Table 10 Full results from the bivariate co-heritability analysis showing genetic correlation estimates for all 45 pairwise AI disease combinations

	Auto *rG*	Auto *SE*	Auto *P*	exMHC *rG*	exMHC *SE*	exMHC *P*	chrX *rG*	chrX *SE*	chrX *P*
CEL-CD	0.192	0.162	1.00E-01	0.211	0.188	1.05E-01	-0.17	0.31	0.29
CEL-CVID	0.199	0.391	2.99E-01	0.245	0.475	2.94E-01	NA	NA	NA
CEL-JIA	0.013	0.182	4.71E-01	0.121	0.239	2.96E-01	0.44	0.19	0.01
CEL-SLE	0.008	0.415	4.92E-01	0.054	0.498	4.56E-01	0.02	0.15	0.45
CEL-T1D	0.072	0.200	3.57E-01	-0.084	0.285	3.82E-01	-0.03	0.31	0.46
CEL-UC	-0.018	0.259	4.73E-01	-0.051	0.323	4.38E-01	0.11	0.31	0.37
CVID-CD	0.101	0.109	1.75E-01	0.115	0.116	1.56E-01	-1.00	124.42	0.50
CVID-JIA	0.343	0.127	1.22E-03	0.354	0.142	2.47E-03	-1.00	3.78	0.50
CVID-T1D	0.177	0.130	7.89E-02	0.207	0.167	9.92E-02	-1.00	291.00	0.50
CVID-UC	0.138	0.158	1.89E-01	0.134	0.170	2.12E-01	-1.00	34.60	0.50
EPI-CD	0.023	0.075	3.79E-01	0.003	0.077	4.85E-01	0.89	0.39	0.00
EPI-CEL	-0.099	0.264	3.54E-01	-0.078	0.304	3.99E-01	-0.17	0.25	0.26
EPI-CVID	-0.122	0.183	2.52E-01	-0.095	0.196	3.14E-01	-1.00	219.03	0.50
EPI-JIA	-0.150	0.079	2.95E-02	-0.142	0.085	4.87E-02	-0.04	0.19	0.42
EPI-PSOR	0.087	0.188	3.23E-01	0.030	0.189	4.38E-01	-0.36	0.35	0.15
EPI-SLE	0.153	0.176	1.92E-01	0.187	0.183	1.52E-01	-0.21	0.15	0.10
EPI-SPA	0.090	0.215	3.37E-01	0.073	0.240	3.80E-01	0.05	2.15	0.49
EPI-T1D	-0.017	0.086	4.20E-01	0.022	0.105	4.18E-01	0.09	0.31	0.39
EPI-UC	0.197	0.103	2.77E-02	0.248	0.108	1.06E-02	-0.63	0.29	0.01
JIA-CD	0.019	0.049	3.50E-01	0.030	0.053	2.85E-01	0.02	0.21	0.47
PSOR-CD	-0.089	0.113	2.15E-01	-0.100	0.115	1.92E-01	0.31	0.45	0.25
PSOR-CEL	-0.092	0.428	4.14E-01	-0.058	0.495	4.53E-01	0.58	0.36	0.05
PSOR-CVID	0.271	0.269	1.50E-01	0.284	0.282	1.49E-01	NA	NA	NA
PSOR-JIA	0.006	0.123	4.81E-01	0.042	0.131	3.77E-01	0.03	0.22	0.44
PSOR-SLE	-0.115	0.260	3.29E-01	-0.065	0.262	4.02E-01	0.32	0.20	0.07
PSOR-T1D	-0.241	0.139	3.29E-02	-0.282	0.167	3.74E-02	-0.27	0.39	0.25
PSOR-UC	-0.316	0.169	2.31E-02	-0.289	0.171	3.76E-02	-0.15	0.39	0.36
SLE-CD	-0.266	0.120	8.25E-03	-0.255	0.121	1.15E-02	0.07	0.19	0.37
SLE-CVID	-0.149	0.261	2.82E-01	-0.187	0.280	2.49E-01	1.00	6.04	0.50
SLE-JIA	0.115	0.115	1.58E-01	0.091	0.123	2.28E-01	-0.19	0.11	0.05
SLE-T1D	-0.011	0.126	4.65E-01	-0.021	0.153	4.46E-01	-0.10	0.22	0.34
SLE-UC	-0.010	0.151	4.74E-01	-0.020	0.157	4.50E-01	-0.29	0.19	0.07
SPA-CD	-0.215	0.138	4.64E-02	-0.235	0.156	4.67E-02	1.00	5.50	0.36
SPA-CEL	0.284	0.520	2.84E-01	0.383	0.700	2.76E-01	0.77	3.18	0.26
SPA-CVID	-0.079	0.320	4.02E-01	-0.083	0.363	4.09E-01	NA	NA	NA
SPA-JIA	0.116	0.138	1.95E-01	0.091	0.158	2.80E-01	-1.00	0.66	0.00
SPA-PSOR	0.171	0.322	2.94E-01	0.214	0.357	2.69E-01	1.00	2.96	0.22
SPA-SLE	0.101	0.302	3.68E-01	0.096	0.334	3.86E-01	0.80	2.41	0.13
SPA-T1D	0.158	0.164	1.58E-01	0.229	0.223	1.37E-01	-1.00	1.72	0.16
SPA-UC	-0.012	0.181	4.73E-01	-0.049	0.204	4.05E-01	-1.00	2.99	0.19
T1D-CD	0.096	0.053	3.45E-02	0.142	0.064	1.33E-02	0.22	0.34	0.26
T1D-JIA	0.064	0.055	1.26E-01	0.112	0.070	5.59E-02	-0.01	0.20	0.48
UC-CD	0.659	0.069	0.00E+00	0.674	0.072	0.00E+00	0.29	0.33	0.19
UC-JIA	0.046	0.067	2.49E-01	0.024	0.073	3.72E-01	0.30	0.21	0.08
UC-T1D	-0.090	0.070	9.79E-02	-0.095	0.086	1.33E-01	-0.14	0.32	0.33

Supplementary Table 11 Full AUC results from pAID liability prediction analysis

Trait	Training $P_{threshold}$	training			*VALIDATION*			
		min	avg	max	*MIN*	*AVG*	*MAX*	*STDEV*
JIA	1.00E-08	91.18%	91.50%	92.05%	*86.86%*	*89.27%*	*92.46%*	*2.06%*
JIA	1.00E-07	91.78%	92.35%	92.72%	*85.80%*	*88.65%*	*91.86%*	*2.21%*
JIA	1.00E-06	92.80%	93.16%	93.53%	*84.15%*	*88.09%*	*91.67%*	*2.58%*
JIA	1.00E-05	93.61%	93.88%	94.33%	*82.76%*	*87.06%*	*91.14%*	*2.56%*
JIA	1.00E-04	93.85%	94.29%	94.78%	*82.16%*	*86.13%*	*89.72%*	*2.62%*
JIA	1.00E-03	94.61%	95.07%	95.41%	*80.03%*	*84.80%*	*87.24%*	*2.60%*
CD	1.00E-08	69.65%	70.18%	71.34%	*64.69%*	*68.13%*	*70.69%*	*1.46%*
CD	1.00E-07	71.20%	72.07%	73.10%	*66.77%*	*69.42%*	*72.37%*	*1.59%*
CD	1.00E-06	74.94%	75.42%	76.29%	*67.90%*	*70.18%*	*73.69%*	*2.01%*
CD	1.00E-05	79.35%	80.02%	81.09%	*69.27%*	*71.84%*	*75.81%*	*1.95%*
CD	1.00E-04	84.36%	85.15%	85.87%	*70.28%*	*73.79%*	*76.69%*	*2.16%*
CD	1.00E-03	90.04%	90.61%	91.17%	*68.20%*	*70.96%*	*75.23%*	*2.28%*
UC	1.00E-08	61.55%	63.25%	64.78%	*56.96%*	*60.88%*	*64.77%*	*2.44%*
UC	1.00E-07	64.72%	66.23%	67.53%	*58.71%*	*62.51%*	*67.24%*	*2.47%*
UC	1.00E-06	70.24%	71.46%	72.66%	*59.27%*	*63.10%*	*67.73%*	*2.54%*
UC	1.00E-05	77.77%	79.42%	80.19%	*60.29%*	*64.99%*	*68.58%*	*2.89%*
UC	1.00E-04	86.38%	87.01%	87.64%	*62.96%*	*66.01%*	*69.39%*	*2.07%*
UC	1.00E-03	92.93%	93.59%	94.23%	*59.81%*	*64.45%*	*68.26%*	*2.87%*
T1D	1.00E-08	86.95%	87.28%	87.58%	*84.79%*	*87.29%*	*91.32%*	*2.12%*
T1D	1.00E-07	87.27%	87.59%	87.90%	*84.93%*	*87.48%*	*91.31%*	*1.98%*
T1D	1.00E-06	88.17%	88.34%	88.60%	*85.43%*	*87.54%*	*90.96%*	*1.82%*
T1D	1.00E-05	89.39%	89.90%	90.57%	*85.82%*	*87.37%*	*91.16%*	*1.81%*
T1D	1.00E-04	93.14%	93.65%	94.49%	*84.15%*	*85.74%*	*88.84%*	*1.55%*
T1D	1.00E-03	97.90%	98.01%	98.14%	*79.65%*	*82.02%*	*85.61%*	*1.63%*
CEL	1.00E-08	69.07%	70.83%	72.37%	*56.95%*	*71.25%*	*84.73%*	*7.57%*
CEL	1.00E-07	68.89%	71.02%	72.28%	*55.74%*	*70.62%*	*83.88%*	*7.70%*
CEL	1.00E-06	70.31%	71.81%	74.98%	*53.79%*	*69.74%*	*84.75%*	*8.39%*
CEL	1.00E-05	73.73%	75.61%	77.76%	*51.54%*	*67.50%*	*80.26%*	*8.06%*
CEL	1.00E-04	89.07%	90.65%	92.89%	*49.69%*	*63.37%*	*74.15%*	*7.75%*
CEL	1.00E-03	99.28%	99.50%	99.75%	*41.18%*	*56.87%*	*68.21%*	*8.07%*
PS	1.00E-08	54.09%	54.09%	54.09%	*42.67%*	*42.67%*	*42.67%*	*0.00%*
PS	1.00E-07	54.09%	57.32%	60.54%	*39.25%*	*40.96%*	*42.67%*	*2.42%*
PS	1.00E-06	54.56%	60.02%	67.04%	*33.00%*	*41.71%*	*54.52%*	*7.29%*
PS	1.00E-05	69.84%	78.70%	83.34%	*27.03%*	*38.49%*	*60.79%*	*9.19%*
PS	1.00E-04	94.43%	96.28%	97.30%	*31.41%*	*46.69%*	*60.78%*	*8.19%*
PS	1.00E-03	99.97%	99.98%	99.99%	*45.38%*	*51.31%*	*57.79%*	*3.39%*
SLE	1.00E-08	60.11%	61.39%	63.13%	*46.10%*	*46.98%*	*48.12%*	*0.84%*
SLE	1.00E-07	59.21%	62.31%	64.03%	*47.85%*	*52.39%*	*58.92%*	*3.68%*
SLE	1.00E-06	62.23%	64.80%	67.67%	*50.69%*	*57.02%*	*69.71%*	*5.42%*
SLE	1.00E-05	67.89%	71.98%	78.69%	*45.44%*	*57.40%*	*68.04%*	*6.31%*
SLE	1.00E-04	87.24%	89.77%	91.69%	*51.67%*	*56.40%*	*61.95%*	*3.46%*

SLE	1.00E-03	98.99%	99.19%	99.66%	*51.49%*	*59.05%*	*70.54%*	*7.27%*
AS	1.00E-07	49.88%	55.32%	63.57%	*47.22%*	*54.53%*	*60.33%*	*4.44%*
AS	1.00E-06	57.16%	64.71%	68.91%	*47.99%*	*57.76%*	*67.43%*	*6.05%*
AS	1.00E-05	75.69%	78.57%	80.91%	*51.72%*	*59.99%*	*68.12%*	*4.86%*
AS	1.00E-04	94.32%	95.59%	96.75%	*45.23%*	*49.94%*	*59.43%*	*5.36%*
AS	1.00E-03	99.95%	99.99%	100.00%	*44.34%*	*53.28%*	*61.24%*	*5.46%*
THY	1.00E-08	62.62%	62.62%	62.62%	*48.14%*	*48.14%*	*48.14%*	*0.00%*
THY	1.00E-07	57.66%	62.00%	67.77%	*44.66%*	*48.91%*	*56.98%*	*4.77%*
THY	1.00E-06	59.48%	69.51%	75.99%	*42.32%*	*52.23%*	*61.36%*	*6.36%*
THY	1.00E-05	77.23%	82.02%	89.03%	*30.03%*	*50.14%*	*67.09%*	*11.91%*
THY	1.00E-04	96.49%	97.10%	97.96%	*35.56%*	*53.57%*	*67.67%*	*12.85%*
THY	1.00E-03	99.97%	99.99%	100.00%	*53.11%*	*60.88%*	*73.24%*	*6.48%*
CVID	1.00E-08	60.23%	61.57%	62.64%	*52.47%*	*60.65%*	*68.12%*	*4.14%*
CVID	1.00E-07	61.58%	62.77%	63.72%	*53.01%*	*60.43%*	*64.14%*	*3.79%*
CVID	1.00E-06	63.67%	68.46%	71.38%	*56.18%*	*61.82%*	*68.87%*	*4.37%*
CVID	1.00E-05	73.73%	77.66%	82.24%	*58.44%*	*63.57%*	*67.32%*	*3.39%*
CVID	1.00E-04	88.53%	91.41%	92.73%	*57.78%*	*64.18%*	*72.69%*	*4.57%*
CVID	1.00E-03	98.80%	99.11%	99.27%	*50.68%*	*59.55%*	*64.83%*	*5.04%*

Supplementary Table 12 ICD9 'diagnosis' search terms used to select subjects for inclusion from EMR datasets

pAID	ICD9 Search Terms and Codes
THY	%Chronic%Thyroiditis% | %Grave% | %Hashimoto% | 242.0% | 245.0% | 245.2%
SPA	%Ankyl%Spond%litis% | %Spondyloarthropathy% | 720% | 720%
PSOR	%Psoriasis% | 696.10%
CEL	%Celiac% | 579.00%
SLE	%Systemic%Lupus%Erythematosus% | 710.0%
CVID	%Variable%Immunodefi% | 279.06%
UC	%Ulcerative%Colitis% | 556%
T1D	%Type%1%Diabetes% | 250._1% | 250._3%
JIA	%Enthe%rthritis% | %Idiop%rthritis% | %Juvenile%rthritis% | %Mono%rthritis% | %Oligo%rthritis% | %Poly%rthritis% | %Psor%rthritis% | %Rheum%rthritis% | %System%Arthritis% | 714% | 716.2% | 716.5% | 716.6% | 716.8% | 716.9%
CD	%Crohn% | 555%

*NOTE: ICD9 codes used for EPIC-SQL case identification by patient diagnosis [% = wildcard (0 or more characters), _ = wildcard (exactly 1 character)]. *EMR: Electronic Medical Records*

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