

Table S5

Disease	Chr.	Region (Mb)	Reference	SNP	PPAA	P-Value
CAD	9	22.01-22.12	[1–6]	rs9632884	0.64	2.53E-13
CD	1	67.38-67.46	[1, 4, 6, 7]	rs10489629	0.39	3.71E-12
CD	2	233.94-233.97	[1, 4, 6, 7]	rs6431654	0.30	7.37E-14
CD	3	49.43-49.87	[1, 4–7]	rs6784820	0.28	2.93E-05
CD	5	40.43-40.64	[1, 4–7]	rs10213846	0.37	3.84E-12
CD	6	32.82-32.84	[1, 4, 7]	rs7768538	0.13	2.24E-06
CD	10	79.20-79.29	N/A	rs2579176	0.14	2.76E-04
CD	10	101.26-101.28	[1, 4, 6, 7]	rs7081330	0.13	1.85E-06
CD	16	49.30-49.36	[4–7]	rs17221417	0.29	8.06E-12
HT	14	45.46-45.66	N/A	rs762015	0.12	1.96E-03
RA	1	114.02	[1, 4–6, 8, 9]	rs6679677	0.17	1.55E-26
RA	2	100.19	[10]	rs11694875	0.14	3.15E-04
RA	6	HLA	[1, 4–6, 8, 9]	rs6457617*	1.00	6.22E-79
RA	17	4.10	N/A	rs9913077	0.14	1.29E-04
T1D	1	113.80-114.15	[1, 4–6, 9, 11, 12]	rs1217396	0.39	1.62E-10
T1D	2	206.67-206.85	N/A	rs4147713	0.22	1.82E-03
T1D	2	215.52-215.65	N/A	rs6737675	0.43	3.49E-04
T1D	3	12.51-12.58	N/A	rs1618545	0.19	3.11E-04
T1D	3	46.26-46.37	[12]	rs1799865	0.33	4.89E-05
T1D	3	82.74-82.82	N/A	rs1097157	0.25	2.33E-04
T1D	3	97.03-97.09	N/A	rs10934261	0.16	1.16E-04
T1D	6	HLA	[1, 4–6, 9, 11, 12]	rs9273363*	1.00	0.00E+00
T1D	6	120.74-120.84	N/A	rs12660882	0.16	3.50E-04
T1D	12	109.82-111.40	[1, 4–6, 11, 12]	rs17696736	0.92	2.10E-15
T1D	15	48.08-48.11	N/A	rs9302151	0.23	3.10E-03
			N/A	rs2414005	0.21	2.60E-03
T1D	16	10.96-11.34	[1, 4, 6, 9, 11, 12]	rs243327	0.28	1.87E-04
T2D	4	104.04-104.30	N/A	rs7698608	0.10	5.02E-04
T2D	5	153.62-153.63	N/A	rs11167666	0.06	3.99E-03
T2D	10	114.74-114.80	[1, 4, 6, 11]	rs11196205	0.13	5.10E-11

Table of regions with at least two SNPs having PPAA's satisfying the 5% FWER threshold in the analysis of the WTCCC Data. Listed for all regions are the SNPs with the highest PPAA and their corresponding marginal p-values. The marginal p-values reported are found via linear regression and used as a direct comparison. The reference column gives literature sources that have previously suggested some level of association between a given region and disease. Rows listed in bold are those for which we did not find any sources that previously suggested association with that disease. These regions could potentially be novel. Note that some of the listed references [4, 11, 13] are works that utilize methods that consider pairwise interactions between SNPs. *Multiple SNPs in the HLA region are significant, so we choose the SNP with the lowest marginal p-value and report that as the most extreme.

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