

Supplemental Table 1. Most significant HLA association with cardiac NL

SNP	Chr	Pos (Mb)	MAF			P-value	Genetic model	OR [95% CI]	HWE P-value	
			Case	Control	CEU HapMap				Case	Control
rs3099844	6	31.557	0.26	0.11	0.15	4.52E-10	dom	3.34 [2.29-4.89]	0.2294	0.0002
rs7775397	6	32.369	0.24	0.10	0.09	1.35E-09	dom	3.3 [2.24-4.86]	0.6076	0.0004
rs2857595	6	31.676	0.34	0.17	0.21	1.96E-09	add	2.37 [1.79-3.14]	0.4086	0.1258
rs3131379	6	31.829	0.23	0.10	0.10	3.95E-09	add	2.59 [1.89-3.56]	0.6090	0.0042
rs558702	6	31.978	0.23	0.10	0.10	5.06E-09	dom	3.16 [2.15-4.65]	0.6106	0.0021
rs3117582	6	31.728	0.23	0.10	0.09	6.13E-09	add	2.55 [1.86-3.5]	0.6106	0.0039
rs389884	6	32.049	0.23	0.10	0.09	7.21E-09	dom	3.13 [2.12-4.6]	0.6106	0.0006
rs3135353	6	32.501	0.27	0.13	0.11	2.78E-08	dom	2.92 [2-4.26]	0.1574	0.0213
rs1980493	6	32.471	0.28	0.14	0.11	4.47E-08	dom	2.86 [1.96-4.17]	0.1038	0.0003
rs7750641	6	31.237	0.24	0.11	0.16	1.58E-07	dom	2.79 [1.9-4.09]	0.3027	0.0464
rs3134942	6	32.277	0.25	0.12	0.10	1.71E-07	dom	2.74 [1.88-4]	0.4522	0.0104
rs3130544	6	31.166	0.24	0.11	0.15	1.94E-07	dom	2.77 [1.89-4.07]	0.3027	0.0258
rs8321	6	30.141	0.19	0.09	0.14	5.02E-07	dom	2.73 [1.85-4.04]	0.0700	0.1203
rs9261290	6	30.147	0.19	0.09	0.14	1.06E-06	dom	2.65 [1.79-3.93]	0.0700	0.2257
rs3129963	6	32.488	0.29	0.16	0.12	1.51E-06	dom	2.53 [1.73-3.69]	0.1700	0.0145
rs3130350	6	30.436	0.19	0.09	0.14	1.55E-06	dom	2.65 [1.78-3.94]	0.2404	0.0694
rs2844657	6	30.938	0.31	0.18	0.26	3.04E-06	dom	2.45 [1.68-3.56]	0.1260	0.0466
rs3130380	6	30.387	0.19	0.09	0.14	6.31E-06	dom	2.49 [1.68-3.7]	0.2404	0.2643
rs3128982	6	31.525	0.44	0.29	0.34	7.98E-06	add	1.85 [1.41-2.43]	0.2618	0.2926
rs3129939	6	32.445	0.28	0.16	0.16	8.54E-06	add	1.98 [1.47-2.67]	0.8176	0.3963
rs3094054	6	30.441	0.19	0.10	0.13	9.71E-06	dom	2.45 [1.65-3.64]	0.3595	0.0343
rs13195509	6	26.572	0.15	0.07	0.11	1.40E-05	dom	2.54 [1.67-3.88]	0.0711	0.2501
rs3095314	6	31.198	0.57	0.42	0.45	1.43E-05	add	1.78 [1.37-2.31]	0.8493	0.0465
rs2071474	6	32.891	0.16	0.29	0.27	1.71E-05	dom	0.41 [0.27-0.61]	0.4850	0.8345
rs2523987	6	30.188	0.22	0.12	0.18	2.00E-05	dom	2.3 [1.57-3.37]	0.1837	0.0384
rs3132610	6	30.652	0.21	0.11	0.15	2.10E-05	dom	2.34 [1.58-3.46]	0.3967	0.0904
rs204991	6	32.269	0.30	0.19	0.14	2.26E-05	dom	2.26 [1.55-3.29]	0.1288	0.0553
rs1003878	6	32.408	0.33	0.21	0.19	2.42E-05	add	1.85 [1.39-2.46]	0.5351	1.0000
rs2844697	6	31.040	0.48	0.34	0.38	2.88E-05	add	1.74 [1.34-2.26]	1.0000	0.1241
rs2233956	6	31.189	0.29	0.17	0.24	3.23E-05	dom	2.23 [1.53-3.25]	0.5043	0.0108
rs2517598	6	30.188	0.25	0.15	0.19	3.52E-05	dom	2.21 [1.52-3.22]	0.2079	0.0836
rs241440	6	32.905	0.14	0.27	0.23	4.26E-05	dom	0.41 [0.27-0.63]	0.6989	0.5069
rs6457536	6	32.382	0.32	0.20	0.21	4.51E-05	add	1.8 [1.36-2.38]	0.8316	0.1603
rs241448	6	32.905	0.14	0.27	0.23	4.64E-05	dom	0.41 [0.27-0.63]	0.4566	0.8583
rs6935269	6	32.368	0.33	0.21	0.20	6.16E-05	add	1.77 [1.34-2.33]	1.0000	0.0748
rs3130893	6	29.089	0.16	0.08	0.11	6.55E-05	dom	2.3 [1.53-3.45]	0.0729	0.2643
rs3129791	6	29.062	0.16	0.08	0.11	6.63E-05	dom	2.29 [1.53-3.45]	0.0729	0.2653
rs3115553	6	32.354	0.33	0.21	0.21	6.67E-05	add	1.76 [1.33-2.33]	1.0000	0.0600
rs2746150	6	29.551	0.16	0.09	0.12	7.42E-05	dom	2.27 [1.51-3.4]	0.0397	0.5198
rs3131093	6	28.945	0.16	0.09	0.11	7.97E-05	dom	2.27 [1.51-3.41]	0.0729	0.2709
rs3095150	6	31.041	0.26	0.40	0.33	8.06E-05	add	0.55 [0.41-0.74]	0.2278	0.5133
rs3129943	6	32.447	0.36	0.24	0.24	8.20E-05	add	1.74 [1.32-2.29]	0.8408	0.6659
rs1619376	6	31.091	0.10	0.20	0.25	8.30E-05	add	0.42 [0.27-0.64]	0.5987	0.6290
rs2050190	6	32.447	0.46	0.33	0.26	8.43E-05	add	1.7 [1.3-2.21]	0.8518	0.1584
rs3094694	6	30.560	0.28	0.17	0.23	9.25E-05	add	1.81 [1.34-2.44]	1.0000	1.0000
rs3749971	6	29.451	0.17	0.09	0.12	1.02E-04	dom	2.22 [1.49-3.32]	0.1899	0.4032
rs9379897	6	26.710	0.18	0.10	0.14	1.09E-04	dom	2.18 [1.47-3.23]	0.1164	0.7780
rs1633021	6	29.855	0.33	0.24	0.27	1.23E-04	dom	2.11 [1.44-3.08]	0.0106	0.0241
rs4324798	6	28.884	0.16	0.09	0.11	1.29E-04	dom	2.23 [1.48-3.37]	0.0701	0.3166
rs2523608	6	31.431	0.26	0.38	0.43	1.42E-04	add	0.56 [0.41-0.75]	0.4754	0.6061

Chr – chromosome, Pos – position, MAF – Minor Allele Frequency, genetic transmission model: add – additive, rec - recessive, dom – dominant, OR – odds ratio, CI – 95% confidence interval, HWE – Hardy Weinberg Equilibrium.

Supplemental Table 2. Most significant non-HLA associations with cardiac NL

SNP	Chr	Pos (Mb)	MAF			P-value	Genetic Model	Odds Ratio [95%CI]	HWE P-value	
			Case	Control	CEU HapMap				Case	Control
rs2403106	12	82.532	0.15	0.07	0.08	2.62E-06	add	2.48 [1.7-3.61]	1.0000	0.8935
rs1890645	1	193.798	0.38	0.30	0.34	3.52E-06	rec	2.98 [1.88-4.73]	0.0007	0.0905
rs743446	21	38.978	0.64	0.49	0.48	5.45E-06	rec	2.4 [1.64-3.49]	0.4193	0.2999
rs1391511	10	4.710	0.50	0.36	0.38	6.62E-06	add	1.84 [1.41-2.4]	0.4572	0.9700
rs29911	5	93.779	0.19	0.10	0.11	1.18E-05	add	2.17 [1.53-3.07]	0.5548	0.2292
rs2832478	21	30.185	0.48	0.36	0.33	1.19E-05	dom	2.81 [1.77-4.46]	0.0027	0.5243
rs9960	1	43.090	0.29	0.18	0.16	1.21E-05	add	1.94 [1.44-2.62]	0.8232	0.2113
rs463877	21	21.012	0.22	0.12	0.14	1.25E-05	add	2.03 [1.48-2.79]	0.0989	0.7428
rs3746314	19	34.889	0.19	0.10	0.13	1.31E-05	dom	2.37 [1.61-3.48]	0.2370	0.3057
rs6438101	3	113.936	0.59	0.48	0.47	2.47E-05	rec	2.29 [1.56-3.36]	0.0852	0.9724
rs1737145	6	97.733	0.38	0.49	0.49	2.63E-05	dom	0.44 [0.3-0.65]	0.0297	0.8353
rs4781956	16	17.579	0.17	0.30	0.31	2.67E-05	add	0.47 [0.33-0.67]	0.5232	0.3668
rs12114973	8	20.959	0.40	0.27	0.33	2.97E-05	add	1.76 [1.35-2.29]	1.0000	0.0650
rs11633486	15	21.640	0.17	0.09	0.13	3.16E-05	dom	2.34 [1.57-3.49]	0.5191	0.8286
rs6767890	3	16.483	0.22	0.13	0.14	3.17E-05	dom	2.25 [1.54-3.3]	0.5875	0.5368
rs1487982	15	90.796	0.26	0.17	0.19	3.37E-05	dom	2.2 [1.52-3.19]	0.0174	0.7071
rs869439	2	26.577	0.31	0.44	0.38	3.67E-05	dom	0.46 [0.31-0.66]	0.0541	0.3099
rs29926	5	93.760	0.19	0.10	0.12	3.79E-05	add	2.03 [1.45-2.84]	0.7653	0.7788
rs1349224	2	142.601	0.22	0.13	0.09	4.03E-05	add	2 [1.43-2.78]	1.0000	0.2173
rs2999138	1	59.034	0.13	0.06	0.06	4.13E-05	dom	2.49 [1.61-3.86]	0.2097	0.2433
rs4790823	17	1.151	0.45	0.38	0.46	4.21E-05	rec	2.41 [1.58-3.67]	0.0014	0.7391
rs12499874	4	111.349	0.37	0.25	0.28	4.29E-05	add	1.76 [1.34-2.3]	0.4315	0.0192
rs2432143	5	52.167	0.16	0.09	0.11	4.54E-05	dom	2.31 [1.54-3.45]	0.3019	0.0686
rs6735174	2	217.609	0.24	0.15	0.22	4.92E-05	dom	2.19 [1.5-3.19]	0.6076	0.0589
rs651241	13	97.448	0.31	0.45	0.42	5.06E-05	add	0.55 [0.41-0.74]	0.5124	0.7259
rs1470191	4	77.319	0.12	0.06	0.05	5.23E-05	add	2.34 [1.55-3.52]	0.6674	0.7548
rs2242375	17	8.647	0.54	0.44	0.48	5.68E-05	rec	2.25 [1.51-3.33]	0.0388	0.0296
rs2034002	4	77.324	0.12	0.06	0.05	5.82E-05	add	2.32 [1.54-3.5]	0.6674	0.8751
rs4429873	5	97.197	0.16	0.08	0.09	5.91E-05	add	2.11 [1.46-3.03]	1.0000	0.8176
rs6434026	2	184.015	0.30	0.19	0.17	6.57E-05	add	1.82 [1.36-2.44]	0.2649	0.1643
rs11085829	19	13.035	0.43	0.36	0.35	6.97E-05	rec	2.42 [1.57-3.74]	0.0041	0.8505
rs10827096	10	19.558	0.26	0.16	0.16	7.12E-05	dom	2.13 [1.47-3.09]	0.2315	0.1271
rs1354681	4	114.174	0.20	0.11	0.12	7.73E-05	add	1.97 [1.41-2.75]	0.3888	1.0000
rs3860243	6	97.012	0.47	0.35	0.43	7.74E-05	add	1.72 [1.31-2.25]	0.5815	0.0668
rs2472299	15	72.820	0.39	0.27	0.31	8.47E-05	add	1.72 [1.31-2.25]	1.0000	0.5144
rs4934471	10	91.062	0.37	0.49	0.50	8.55E-05	add	0.58 [0.44-0.76]	0.3172	0.6003
rs9830337	3	77.554	0.50	0.37	0.38	8.72E-05	add	1.71 [1.31-2.24]	0.5756	0.2815
rs762960	22	41.881	0.20	0.32	0.29	9.60E-05	add	0.52 [0.38-0.72]	1.0000	0.9684
rs1378942	15	72.864	0.47	0.35	0.33	9.95E-05	add	1.68 [1.29-2.19]	0.5750	0.1276
rs7770889	6	96.965	0.48	0.36	0.44	1.15E-04	add	1.69 [1.3-2.21]	0.8540	0.1224
rs7873018	9	76.312	0.22	0.33	0.31	1.17E-04	add	0.54 [0.39-0.74]	1.0000	0.5866
rs7853479	9	76.312	0.22	0.33	0.31	1.18E-04	add	0.54 [0.39-0.74]	1.0000	0.5864
rs4576485	9	112.855	0.28	0.18	0.13	1.20E-04	add	1.79 [1.33-2.4]	1.0000	0.7204
rs635567	6	75.886	0.40	0.29	0.25	1.23E-04	add	1.71 [1.3-2.25]	0.7010	0.1779
rs4392700	6	162.644	0.24	0.15	0.16	1.28E-04	add	1.84 [1.35-2.51]	0.7988	0.8343
rs6963754	7	9.292	0.31	0.22	0.20	1.29E-04	dom	2.08 [1.43-3.03]	0.0308	0.6911
rs627524	10	91.107	0.38	0.49	0.49	1.35E-04	add	0.59 [0.45-0.77]	1.0000	0.5115
rs6658098	1	4.627	0.56	0.43	0.48	1.37E-04	add	1.66 [1.28-2.16]	0.4515	0.0901
rs4475568	9	73.376	0.52	0.42	0.42	1.37E-04	rec	2.2 [1.47-3.3]	0.0650	0.0130
rs7689511	4	31.015	0.16	0.09	0.09	1.37E-04	add	2.03 [1.41-2.93]	0.5031	0.4592

rs12114477	8	66.546	0.58	0.46	0.48	1.38E-04	add	1.69 [1.29-2.22]	0.8487	0.0198
rs2183770	9	78.765	0.54	0.47	0.49	1.39E-04	rec	2.13 [1.44-3.14]	0.0026	0.3133
rs2399985	10	13.685	0.28	0.40	0.38	1.43E-04	add	0.57 [0.42-0.76]	0.4885	0.5176
rs6480311	10	69.627	0.24	0.34	0.31	1.43E-04	dom	0.48 [0.33-0.7]	0.0104	0.7880
rs13198474	6	25.982	0.13	0.06	0.10	1.46E-04	dom	2.33 [1.51-3.61]	0.2103	0.3086
rs4428477	6	88.690	0.21	0.13	0.16	1.47E-04	add	1.91 [1.37-2.68]	1.0000	0.2211
rs1609761	19	1.799	0.31	0.22	0.24	1.53E-04	dom	2.06 [1.42-2.99]	0.0481	0.4744
rs1451078	2	147.518	0.34	0.23	0.26	1.57E-04	add	1.71 [1.29-2.25]	0.1012	0.6593
rs4796096	17	30.874	0.17	0.10	0.09	1.57E-04	add	1.98 [1.39-2.83]	0.7380	0.8454
rs2090281	1	163.943	0.36	0.49	0.48	1.61E-04	add	0.59 [0.45-0.78]	0.8395	0.1755
rs5759197	22	41.880	0.21	0.33	0.34	1.72E-04	add	0.54 [0.39-0.74]	0.7788	1.0000
rs2503256	1	88.137	0.12	0.06	0.06	1.87E-04	add	2.18 [1.45-3.29]	0.0588	0.7647
rs7557667	2	107.319	0.26	0.16	0.14	1.93E-04	dom	2.03 [1.4-2.95]	0.4754	0.1260
rs1998484	1	59.065	0.12	0.06	0.07	2.03E-04	dom	2.33 [1.49-3.64]	0.3584	0.2254
rs3753473	1	201.398	0.13	0.07	0.07	2.05E-04	dom	2.27 [1.47-3.51]	0.2103	1.0000
rs4132249	18	64.773	0.29	0.19	0.20	2.06E-04	add	1.75 [1.3-2.34]	0.1723	0.3954
rs2301249	15	72.879	0.39	0.28	0.28	2.07E-04	add	1.66 [1.27-2.17]	0.8459	0.0699
rs2071856	22	36.101	0.19	0.31	0.32	2.08E-04	add	0.54 [0.39-0.75]	0.7653	0.5455
rs9321046	6	125.909	0.45	0.34	0.30	2.09E-04	add	1.66 [1.27-2.17]	0.2623	0.8784
rs12874831	13	107.685	0.15	0.24	0.21	2.15E-04	dom	0.45 [0.29-0.68]	0.0224	0.4260
rs1981664	2	42.431	0.31	0.42	0.44	2.17E-04	dom	0.5 [0.34-0.72]	0.1894	0.0606
rs192710	10	70.983	0.43	0.33	0.30	2.21E-04	dom	2.18 [1.44-3.3]	0.0573	0.9687
rs6500110	16	58.817	0.47	0.34	0.38	2.23E-04	add	1.64 [1.26-2.14]	1.0000	0.2968
rs12403816	1	240.773	0.56	0.49	0.48	2.26E-04	rec	2.07 [1.4-3.04]	0.0025	0.2397
rs4886406	15	72.844	0.38	0.27	0.29	2.33E-04	add	1.66 [1.27-2.18]	1.0000	0.3795
rs10519311	15	64.018	0.28	0.18	0.13	2.34E-04	dom	2.01 [1.39-2.92]	0.4900	0.7219
rs2073577	9	134.852	0.43	0.36	0.38	2.43E-04	rec	2.26 [1.46-3.48]	0.0075	1.0000
rs538056	6	159.870	0.48	0.37	0.45	2.45E-04	add	1.64 [1.26-2.14]	0.7095	0.7383
rs1402898	18	18.504	0.22	0.13	0.13	2.46E-04	add	1.83 [1.32-2.52]	0.7895	0.7666
rs6772801	3	140.979	0.39	0.28	0.23	2.46E-04	dom	2.07 [1.4-3.06]	0.2405	0.7296
rs6448403	4	25.393	0.45	0.36	0.43	2.47E-04	dom	2.26 [1.46-3.5]	0.0050	0.6000
rs11260745	1	16.339	0.11	0.06	0.09	2.51E-04	add	2.27 [1.46-3.53]	0.6172	0.4033
rs306507	19	61.151	0.31	0.41	0.35	2.51E-04	dom	0.5 [0.34-0.72]	0.1341	0.0859
rs7543038	1	162.990	0.44	0.37	0.42	2.52E-04	rec	2.23 [1.45-3.43]	0.0083	0.0500
rs4128828	8	66.534	0.58	0.46	0.48	2.53E-04	add	1.66 [1.26-2.17]	1.0000	0.0286
rs2839586	21	43.124	0.13	0.12	0.16	2.57E-04	rec	4.63 [2.04-10.53]	0.0004	0.6848
rs9791781	7	51.475	0.20	0.13	0.12	2.62E-04	dom	2.03 [1.39-2.98]	0.0411	0.4114
rs6868665	5	73.148	0.44	0.33	0.32	2.65E-04	add	1.63 [1.25-2.12]	0.8512	0.2559
rs2478126	10	13.700	0.12	0.06	0.05	2.67E-04	add	2.19 [1.44-3.34]	1.0000	0.8784
rs763497	5	121.455	0.19	0.11	0.13	2.67E-04	add	1.88 [1.34-2.63]	0.5548	0.8607
rs2032224	18	59.327	0.42	0.31	0.28	2.68E-04	add	1.63 [1.25-2.12]	0.8509	0.0420
rs4990483	18	18.474	0.21	0.13	0.13	2.69E-04	add	1.83 [1.32-2.53]	0.5859	0.9384
rs11098195	4	114.684	0.19	0.31	0.34	2.70E-04	dom	0.48 [0.33-0.72]	0.7653	0.8718
rs1965961	12	82.394	0.16	0.09	0.08	2.73E-04	dom	2.13 [1.42-3.21]	0.3008	0.6751
rs10482941	21	24.026	0.14	0.07	0.06	2.75E-04	add	2.05 [1.39-3.01]	1.0000	0.8005
rs7456643	7	2.280	0.27	0.19	0.24	2.76E-04	dom	1.99 [1.37-2.89]	0.1562	0.0864
rs11125321	2	50.706	0.53	0.42	0.45	3.01E-04	dom	2.46 [1.51-4]	0.0397	0.6960
rs11961755	6	121.808	0.15	0.26	0.23	3.08E-04	dom	0.47 [0.31-0.71]	0.7207	0.8920
rs9310499	3	16.539	0.39	0.28	0.33	3.09E-04	add	1.64 [1.25-2.15]	0.6973	0.7958
rs13431590	2	2.741	0.09	0.18	0.18	3.12E-04	dom	0.38 [0.23-0.65]	0.0389	0.0565
rs12940055	17	59.076	0.19	0.11	0.12	3.12E-04	add	1.87 [1.33-2.62]	1.0000	0.5465
rs1796236	7	157.187	0.19	0.11	0.11	3.12E-04	add	1.88 [1.33-2.65]	1.0000	0.6042
rs762143	21	37.816	0.13	0.07	0.06	3.14E-04	add	2.03 [1.38-2.97]	0.4255	0.1330
rs4977467	9	18.917	0.23	0.14	0.14	3.17E-04	dom	2.02 [1.38-2.96]	0.7920	0.1190
rs1481789	8	72.203	0.11	0.21	0.15	3.17E-04	add	0.47 [0.31-0.71]	1.0000	0.9171
rs7768473	6	22.540	0.39	0.28	0.31	3.18E-04	dom	2.05 [1.39-3.04]	0.1739	0.5233
rs4464193	19	57.855	0.31	0.42	0.38	3.29E-04	dom	0.51 [0.35-0.73]	0.1894	0.9151

rs1105191	9	15.361	0.34	0.43	0.42	3.33E-04	dom	0.51 [0.35-0.73]	0.0209	0.4805
rs8063008	16	85.621	0.33	0.44	0.49	3.35E-04	dom	0.51 [0.35-0.73]	0.4016	0.3096
rs10141611	14	38.046	0.56	0.44	0.50	3.36E-04	add	1.63 [1.25-2.13]	0.4528	0.4404
rs11659241	18	44.842	0.36	0.49	0.46	3.38E-04	add	0.6 [0.46-0.8]	0.3137	0.5112
rs7222435	17	14.270	0.16	0.10	0.07	3.40E-04	dom	2.09 [1.4-3.14]	0.2984	0.3203
rs4606122	9	73.376	0.33	0.43	0.45	3.46E-04	dom	0.51 [0.35-0.73]	0.0362	0.6211
rs847057	20	44.666	0.30	0.42	0.45	3.48E-04	add	0.6 [0.45-0.79]	0.8275	0.0646
rs1433185	8	108.517	0.25	0.38	0.31	3.49E-04	add	0.58 [0.43-0.78]	0.3264	0.7404
rs11732418	4	137.983	0.16	0.08	0.10	3.52E-04	dom	2.13 [1.41-3.22]	1.0000	0.0400
rs3106594	13	60.558	0.33	0.44	0.40	3.54E-04	add	0.6 [0.45-0.79]	0.6740	0.5064
rs2116531	7	14.421	0.46	0.34	0.35	3.67E-04	add	1.62 [1.24-2.12]	0.7063	0.9692
rs10513111	3	141.607	0.16	0.10	0.10	3.72E-04	dom	2.08 [1.39-3.1]	0.3019	0.2153
rs505930	18	62.459	0.44	0.33	0.33	3.72E-04	add	1.63 [1.25-2.14]	0.8502	0.0503
rs12591953	15	69.787	0.50	0.38	0.36	3.75E-04	add	1.62 [1.24-2.1]	0.8539	0.9124
rs12352103	9	132.285	0.16	0.10	0.07	3.85E-04	dom	2.08 [1.39-3.12]	0.2984	0.6195
rs12410615	1	57.005	0.30	0.21	0.19	3.90E-04	add	1.69 [1.26-2.26]	0.5134	0.9160
rs729371	2	240.023	0.34	0.42	0.49	3.91E-04	dom	0.51 [0.35-0.74]	0.0020	0.8034
rs7339191	13	60.528	0.42	0.31	0.36	3.92E-04	add	1.64 [1.25-2.15]	0.3468	0.0301
rs2457278	17	0.751	0.48	0.36	0.43	3.93E-04	add	1.61 [1.24-2.09]	0.8540	0.6515
rs171227	5	62.466	0.25	0.36	0.38	3.96E-04	add	0.58 [0.43-0.78]	1.0000	1.0000
rs2689700	10	95.937	0.08	0.17	0.16	4.02E-04	dom	0.39 [0.23-0.66]	0.1603	0.6215
rs1433174	8	108.587	0.29	0.41	0.37	4.08E-04	add	0.6 [0.45-0.79]	0.2673	0.3173
rs971256	14	54.319	0.33	0.45	0.39	4.13E-04	add	0.6 [0.45-0.8]	0.6741	0.8054
rs1742296	6	90.228	0.15	0.08	0.06	4.17E-04	add	1.97 [1.35-2.88]	1.0000	0.7200
rs824241	9	28.776	0.19	0.11	0.15	4.22E-04	add	1.82 [1.3-2.54]	0.0308	0.3455
rs10774085	12	2.930	0.24	0.35	0.28	4.24E-04	dom	0.5 [0.34-0.74]	0.0779	0.0783
rs7268140	20	48.841	0.33	0.22	0.22	4.29E-04	add	1.67 [1.25-2.22]	0.3982	0.7637
rs9998709	4	186.954	0.37	0.26	0.30	4.29E-04	add	1.64 [1.24-2.15]	1.0000	0.7218
rs10508581	10	19.560	0.32	0.23	0.20	4.34E-04	add	1.66 [1.25-2.2]	0.5233	0.7669
rs11970088	6	23.381	0.26	0.38	0.30	4.43E-04	dom	0.51 [0.35-0.74]	0.3418	0.3057
rs1554973	9	119.521	0.35	0.25	0.20	4.46E-04	add	1.65 [1.25-2.18]	0.5390	0.8183
rs1364449	5	22.511	0.47	0.41	0.46	4.46E-04	rec	2.11 [1.39-3.19]	0.0086	0.0705
rs8070753	17	9.205	0.47	0.36	0.30	4.48E-04	add	1.6 [1.23-2.07]	0.5759	0.5010
rs586205	13	21.264	0.10	0.11	0.13	4.49E-04	rec	4.95 [2.03-12.1]	0.0002	0.6705
rs10493716	1	82.636	0.44	0.33	0.33	4.49E-04	add	1.59 [1.23-2.07]	0.5709	0.0335
rs9296582	6	47.863	0.37	0.26	0.29	4.52E-04	add	1.63 [1.24-2.13]	0.8408	0.2207
rs10107938	8	127.223	0.14	0.08	0.08	4.54E-04	dom	2.13 [1.4-3.26]	0.6923	0.3274
rs6491682	13	101.865	0.26	0.16	0.15	4.57E-04	dom	1.95 [1.34-2.84]	0.4754	0.3774
rs1795240	1	169.358	0.40	0.49	0.47	4.64E-04	dom	0.51 [0.35-0.74]	0.0526	0.5113
rs564351	6	47.928	0.26	0.17	0.21	4.66E-04	add	1.72 [1.27-2.33]	0.4754	0.5750
rs678957	11	117.556	0.10	0.05	0.07	4.71E-04	add	2.24 [1.42-3.52]	0.3005	0.7190
rs8001181	13	97.409	0.33	0.45	0.40	4.72E-04	add	0.61 [0.46-0.8]	0.5342	0.6503
rs12405458	1	82.625	0.23	0.14	0.15	4.75E-04	add	1.75 [1.28-2.4]	0.6018	0.6758
rs10072558	5	166.323	0.59	0.47	0.44	4.75E-04	add	1.62 [1.23-2.12]	0.4427	0.7026
rs12784034	10	37.362	0.11	0.06	0.09	4.75E-04	dom	2.24 [1.42-3.52]	0.3550	0.0319
rs2725201	4	89.218	0.57	0.45	0.49	4.79E-04	add	1.61 [1.23-2.09]	0.2620	0.6253
rs11648723	16	21.893	0.11	0.06	0.06	4.79E-04	add	2.15 [1.4-3.3]	1.0000	0.6179
rs7814057	8	81.289	0.45	0.35	0.37	4.80E-04	add	1.61 [1.23-2.09]	0.4533	0.7037
rs164288	1	158.871	0.16	0.09	0.10	4.86E-04	add	1.93 [1.33-2.8]	0.1460	0.4590
rs2121881	6	127.952	0.41	0.49	0.48	4.87E-04	rec	0.33 [0.17-0.61]	0.0019	0.8626
rs7831778	8	66.600	0.55	0.44	0.44	4.90E-04	add	1.61 [1.23-2.1]	0.4551	0.6237
rs11124005	2	104.831	0.34	0.46	0.44	4.93E-04	add	0.61 [0.46-0.81]	1.0000	0.2802
rs4904729	14	90.318	0.19	0.12	0.08	4.94E-04	add	1.84 [1.3-2.59]	0.3695	0.0395
rs10516798	4	89.103	0.39	0.29	0.35	4.98E-04	add	1.62 [1.23-2.12]	1.0000	0.8657

Chr – chromosome, Pos – position, MAF – minor allele frequency, genetic transmission model: add – additive, rec - recessive, dom – dominant, OR – odds ratio, CI – 95% confidence interval, HWE – Hardy Weinberg Equilibrium.

Supplemental Table 3. Association of autoimmune disease GWAS SNPs with cardiac NL

SNP	Chr	Pos (Mb)	Region	maf case	maf ctrl	pvalue	model	OR [CI]	hwcase	hwctrl	Disease	Ref
rs6684	1	2.536	MMEL1	0.41	0.33	1.50E-02	add	1.39 [1.07-1.82]	0.567	0.938	RA	WTCCC, Nature 447, 2007
rs3890	1	2.543	MMEL1	0.37	0.31	9.60E-02	add	1.26 [0.96-1.66]	0.843	0.841	RA	www.genome.gov/gwastudies
rs1049	1	10.276	KIF1B	0.41	0.33	2.49E-02	add	1.36 [1.04-1.78]	1.000	0.510	MS	www.genome.gov/gwastudies
rs3806	1	20.015	RNF186	0.37	0.37	9.61E-01	add	0.99 [0.76-1.3]	0.689	0.370	UC	www.genome.gov/gwastudies
rs1075	1	20.036	HTR6	NA	NA	NA	NA	NA	NA	NA	UC	Silverberg et al, Nat Genet 2009
rs6426	1	20.044	several	0.46	0.45	7.89E-01	add	1.04 [0.8-1.35]	0.454	0.553	UC	www.genome.gov/gwastudies
rs6426	1	20.044	several	0.46	0.45	7.89E-01	add	1.04 [0.8-1.35]	0.454	0.553	UC	www.genome.gov/gwastudies
rs7524	1	22.571	Intergenic	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs1120	1	39.822	LOC100129342	0.42	0.42	9.48E-01	add	1.01 [0.77-1.32]	0.705	0.695	BD	Fei, Arthritis Res Ther
rs2269	1	63.881	PGM1	0.16	0.19	8.54E-02	dom	0.69 [0.46-1.05]	0.073	0.392	T1D	www.genome.gov/gwastudies
rs1004	1	67.443	IL23R	0.28	0.30	6.71E-01	add	0.94 [0.7-1.25]	0.820	0.541	CD	Duerr et al, Science 314, 2006
rs1004	1	67.443	IL23R	0.28	0.30	6.71E-01	add	0.94 [0.7-1.25]	0.820	0.541	UC	Silverberg et al, Nat Genet 2009
rs1180	1	67.448	IL23R	0.28	0.30	6.71E-01	add	0.94 [0.7-1.25]	0.820	0.541	CD	WTCCC, Nature 447, 2007
rs1180	1	67.448	IL23R	0.28	0.30	6.71E-01	add	0.94 [0.7-1.25]	0.820	0.541	UC	Franke et al, Nat Genet 40, 2008
rs7517	1	67.454	IL23R	0.42	0.42	5.47E-02	rec	0.56 [0.31-1.01]	0.004	0.645	CD	Duerr et al, Science 314, 2006
rs7517	1	67.454	IL23R	0.42	0.42	5.47E-02	rec	0.56 [0.31-1.01]	0.004	0.645	CD	Rioux, Nat Genet
rs7517	1	67.454	IL23R	0.42	0.42	5.47E-02	rec	0.56 [0.31-1.01]	0.004	0.645	IBD	Duerr, Science
rs1048	1	67.461	IL23R	0.45	0.46	6.72E-01	add	0.94 [0.73-1.23]	0.577	1.000	CD	Duerr et al, Science 314, 2006
rs2201	1	67.467	IL23R	0.30	0.31	9.47E-01	add	0.99 [0.74-1.32]	0.659	0.226	CD	Duerr et al, Science 314, 2006
rs2201	1	67.467	IL23R	0.30	0.31	9.47E-01	add	0.99 [0.74-1.32]	0.659	0.226	PS	Nair, Nat Genet
rs1146	1	67.475	IL23R	NA	NA	NA	NA	NA	NA	NA	CD	Duerr et al, Science 314, 2006
rs1146	1	67.475	IL23R	NA	NA	NA	NA	NA	NA	NA	CD	Libioulle et al, PLOS genetics 3, 2007
rs1146	1	67.475	IL23R	NA	NA	NA	NA	NA	NA	NA	CD	Barrett, Nat Genet
rs1146	1	67.475	IL23R	NA	NA	NA	NA	NA	NA	NA	UC	Silverberg et al, Nat Genet 2009
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	CD	Libioulle, PLoS Genet
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	IBD	Duerr, Science
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	IBD	Kugathasan, Nat Genet
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	PsA	Liu et al, PLoS Genetics 4, 2008
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	UC	Barrett Nat Genet 2009
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	UC	Silverberg et al, Nat Genet 2009
rs1120	1	67.479	IL23R	NA	NA	NA	NA	NA	NA	NA	UC	Silverberg, Nat Genet
rs1343	1	67.492	IL23R	0.34	0.35	6.79E-01	add	0.94 [0.71-1.25]	0.682	0.360	CD	Duerr et al, Science 314, 2006
rs1088	1	67.498	IL23R	0.30	0.31	9.46E-01	add	0.99 [0.74-1.32]	0.659	0.242	CD	Duerr et al, Science 314, 2006
rs1088	1	67.498	IL23R	0.30	0.31	9.46E-01	add	0.99 [0.74-1.32]	0.659	0.242	UC	Silverberg, Nat Genet
rs1120	1	67.513	IL23R	0.31	0.33	7.00E-01	add	0.95 [0.71-1.25]	0.828	0.146	CD	Duerr et al, Science 314, 2006
rs1214	1	72.047	NEGR1	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1116	1	80.345	intergenic	NA	NA	NA	NA	NA	NA	NA	RA	WTCCC, Nature 447, 2007
rs6727	1	81.333	intergenic	NA	NA	NA	NA	NA	NA	NA	T1D	Hakonarson et al, Nature 448, 2007
rs1983	1	85.084	EDG7	0.08	0.12	1.79E-01	add	0.72 [0.45-1.16]	0.552	0.933	T1D	www.genome.gov/gwastudies
rs6604	1	93.076	FAM69A,RPL5	0.27	0.28	8.00E-01	add	0.96 [0.72-1.29]	0.816	0.863	MS	www.genome.gov/gwastudies
rs6604	1	93.076	FAM69A,RPL5	0.27	0.28	8.00E-01	add	0.96 [0.72-1.29]	0.816	0.863	MS	www.genome.gov/gwastudies
rs6679	1	114.105	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	RA	www.genome.gov/gwastudies
rs6679	1	114.105	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	RA	www.genome.gov/gwastudies
rs6679	1	114.105	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	www.genome.gov/gwastudies
rs6679	1	114.105	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	www.genome.gov/gwastudies
rs6679	1	114.105	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	www.genome.gov/gwastudies
rs2476	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	CD	Barrett, Nat Genet
rs2476	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	RA	Gregersen, Nat Genet

rs2476i	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	RA	Julia et al, A&R 58, 2008
rs2476i	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	RA	Plenge, N Engl J Med
rs2476i	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	Barrett, Nat Genet
rs2476i	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	Hakonarson et al, Nature 448, 2007
rs2476i	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	Hakonarson, Nature
rs2476i	1	114.179	PTPN22	0.12	0.09	2.06E-01	add	1.3 [0.87-1.94]	1.000	0.026	T1D	Todd, Nat Genet
rs1335i	1	116.902	CD58	0.13	0.13	8.29E-01	add	1.04 [0.71-1.54]	1.000	0.938	MS	www.genome.gov/gwastudies
rs2300i	1	116.906	CD58	0.13	0.13	8.29E-01	add	1.04 [0.71-1.54]	1.000	0.938	MS	www.genome.gov/gwastudies
rs2358i	1	117.513	VTCN1	NA	NA	NA	NA	NA	NA	NA	SLE	Hinks et al, A&R 60, 2009
rs1204i	1	117.553	VTCN1	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs4085i	1	150.817	LCE3D, LCE3A	0.31	0.36	1.23E-01	add	0.8 [0.6-1.06]	0.515	0.177	PS	www.genome.gov/gwastudies
rs2274i	1	159.119	ITLN1	0.33	0.31	6.75E-01	add	1.06 [0.8-1.41]	0.674	0.543	CD	www.genome.gov/gwastudies
rs1801i	1	159.746	FCGR2A	0.57	0.49	2.69E-02	add	1.36 [1.04-1.78]	1.000	0.200	UC	www.genome.gov/gwastudies
rs2343i	1	161.197	NR1I3, APOA2	NA	NA	NA	NA	NA	NA	NA	CD	Rioux et al, Nat Genet 39, 2007
rs9286i	1	171.129	FMO cluster	0.28	0.25	2.87E-01	add	1.17 [0.88-1.56]	1.000	0.616	CD	www.genome.gov/gwastudies
rs1203i	1	171.165	FMO cluster	0.41	0.38	7.41E-02	dom	1.44 [0.97-2.15]	0.082	0.419	CD	www.genome.gov/gwastudies
rs1203i	1	171.165	FMO cluster	NA	NA	NA	NA	NA	NA	NA	CD	WTCCC, Nature 447, 2007
rs2205i	1	171.458	TNFSF4	0.22	0.22	9.93E-01	add	1 [0.73-1.37]	0.592	0.454	SLE	www.genome.gov/gwastudies
rs1079i	1	171.576	Intergenic	0.34	0.36	5.83E-01	add	0.92 [0.7-1.22]	0.101	0.851	SLE in women	www.genome.gov/gwastudies
rs1204i	1	177.736	C1orf125	NA	NA	NA	NA	NA	NA	NA	MS (age of onset)	www.genome.gov/gwastudies
rs2022i	1	181.620	NMNAT2	0.34	0.42	2.19E-02	add	0.72 [0.55-0.95]	0.839	0.915	SLE	Harley, Nat Genet 40, 2008
rs1080i	1	189.826	Intergenic	0.05	0.08	1.54E-01	add	0.65 [0.36-1.17]	1.000	0.538	CD	www.genome.gov/gwastudies
rs2760i	1	190.797	RGS1	NA	NA	NA	NA	NA	NA	NA	MS	De Jager, Nat Genet 2009
rs2816i	1	190.803	RGS1	0.17	0.17	9.28E-01	add	0.98 [0.69-1.4]	0.734	0.060	CelD	www.genome.gov/gwastudies
rs7554i	1	199.144	C1orf106	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs1158i	1	199.202	Intergenic	0.36	0.29	3.36E-02	add	1.35 [1.02-1.78]	0.690	0.646	CD	www.genome.gov/gwastudies
rs3024i	1	205.007	IL10	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs3024i	1	205.007	IL10	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs3024i	1	205.011	IL10	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs2639i	1	223.880	ENAH	0.34	0.27	3.32E-02	add	1.35 [1.02-1.79]	0.219	0.726	T1D	WTCCC, Nature 447, 2007
rs1109i	2	9.167	DDEF2	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1534i	2	12.558	Intergenic	0.42	0.45	3.15E-01	add	0.87 [0.67-1.14]	0.705	0.625	T1D	www.genome.gov/gwastudies
rs2165i	2	24.546	Intergenic	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1338i	2	33.555	RASGRP3	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs6544i	2	47.698	KCNK12	0.51	0.48	5.65E-01	add	1.08 [0.83-1.41]	0.140	0.890	Vitiligo	www.genome.gov/gwastudies
rs1703i	2	49.809	Intergenic	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1303i	2	60.990	REL	0.27	0.34	2.35E-02	add	0.71 [0.53-0.96]	0.816	0.107	RA	Gregersen, Nat Genet
rs1301i	2	61.018	REL	0.27	0.34	2.35E-02	add	0.71 [0.53-0.96]	0.816	0.107	RA	www.genome.gov/gwastudies
rs2164i	2	85.816	RNF181, VAMP8	0.39	0.43	4.21E-01	add	0.89 [0.68-1.17]	0.561	0.547	PS	Liu et al, PLoS Genetics 4, 2008
rs9653i	2	100.192	intergenic	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1301i	2	102.338	several	0.25	0.23	5.84E-01	add	1.09 [0.8-1.47]	0.213	0.662	CelD	www.genome.gov/gwastudies
rs6514i	2	119.112	Intergenic	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1437i	2	133.463	NAP5	0.37	0.37	9.63E-01	add	1.01 [0.77-1.32]	0.163	0.740	MS (age of onset)	www.genome.gov/gwastudies
rs8823i	2	136.693	MCM6, CXCR4	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1990i	2	162.832	IFIH1	0.41	0.41	8.14E-01	add	1.03 [0.79-1.35]	0.849	0.199	T1D	www.genome.gov/gwastudies
rs1990i	2	162.832	IFIH1	0.41	0.41	8.14E-01	add	1.03 [0.79-1.35]	0.849	0.199	T1D	www.genome.gov/gwastudies
rs3821i	2	191.611	STAT4	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs7574i	2	191.673	STAT4	0.23	0.24	7.31E-01	add	0.95 [0.69-1.29]	0.428	0.191	SLE	www.genome.gov/gwastudies
rs7574i	2	191.673	STAT4	0.23	0.24	7.31E-01	add	0.95 [0.69-1.29]	0.428	0.191	SLE	www.genome.gov/gwastudies
rs2317i	2	204.402	CTLA4	0.48	0.49	9.95E-01	add	1 [0.77-1.3]	0.713	0.836	RA	www.genome.gov/gwastudies
rs3087i	2	204.447	CTLA4	0.42	0.43	8.08E-01	add	0.97 [0.74-1.27]	0.849	0.460	T1D	www.genome.gov/gwastudies

rs3087:	2	204.447	CTLA4	0.42	0.43	8.08E-01	add	0.97 [0.74-1.27]	0.849	0.460	T1D	www.genome.gov/gwastudies
rs1261:	2	218.766	ARPC2	0.53	0.49	2.17E-01	add	1.18 [0.91-1.52]	0.198	0.189	UC	Franke et al, Nat Genet 40, 2008
rs1021:	2	233.824	ATG16L1	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs3828:	2	233.845	ATG16L1	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs2241:	2	233.848	ATG16L1	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs6441:	3	46.327	CCR1, CCR3	0.29	0.32	3.57E-01	add	0.87 [0.66-1.16]	0.372	0.812	CelD	www.genome.gov/gwastudies
rs9858:	3	49.677	BSN	0.23	0.30	1.91E-02	dom	0.63 [0.43-0.93]	0.068	0.033	CD	www.genome.gov/gwastudies
rs9858:	3	49.677	BSN	0.23	0.30	1.91E-02	dom	0.63 [0.43-0.93]	0.068	0.033	CD	www.genome.gov/gwastudies
rs9858:	3	49.677	BSN	0.23	0.30	1.91E-02	dom	0.63 [0.43-0.93]	0.068	0.033	UC	www.genome.gov/gwastudies
rs3197:	3	49.697	MST1	0.23	0.30	1.91E-02	dom	0.63 [0.43-0.93]	0.068	0.033	CD	www.genome.gov/gwastudies
rs6445:	3	58.345	PXK	0.25	0.28	2.69E-01	add	0.84 [0.62-1.14]	0.330	0.279	SLE in women	www.genome.gov/gwastudies
rs6439:	3	141.652	CLSTN2	0.23	0.18	1.78E-02	add	1.46 [1.07-1.99]	1.000	1.000	CD	Rioux et al, Nat Genet 39, 2007
rs9088:	3	142.023	SLC25A36	0.23	0.27	1.32E-01	add	0.79 [0.57-1.08]	0.611	0.569	MS	www.genome.gov/gwastudies
rs1841:	3	149.239	ZIC1	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1263:	3	158.109	FLJ16641	0.42	0.47	8.04E-02	add	0.79 [0.6-1.03]	0.340	0.755	MS (severity)	www.genome.gov/gwastudies
rs1781:	3	161.148	IL12A, SCHIP1	0.10	0.10	7.32E-01	add	0.93 [0.61-1.42]	1.000	0.092	CelD	www.genome.gov/gwastudies
rs4680:	3	161.182	IL12A	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs9834:	3	166.623	Intergenic	NA	NA	NA	NA	NA	NA	NA	Kawasaki	Burgner et al, Plos Genet 5, 2009
rs1753:	3	176.376	NAALADL2	0.43	0.46	3.16E-01	add	0.87 [0.67-1.14]	0.342	0.404	Kawasaki	www.genome.gov/gwastudies
rs6762:	3	180.495	ZNF639	0.28	0.30	7.00E-01	add	0.94 [0.7-1.27]	0.162	0.680	CelD	van Heel et al, Nat Genet 39, 2007
rs9290:	3	180.500	ZNF639	0.28	0.30	7.20E-01	add	0.95 [0.71-1.27]	0.162	0.680	CelD	van Heel et al, Nat Genet 39, 2007
rs1464:	3	189.595	LPP	0.48	0.43	1.29E-01	add	1.22 [0.94-1.59]	0.578	0.070	CelD	www.genome.gov/gwastudies
rs3816:	4	25.026	ANAPC4	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs1051:	4	25.695	SLC34A2	0.32	0.30	5.39E-01	add	1.09 [0.82-1.45]	0.669	0.161	T1D	www.genome.gov/gwastudies
rs1685:	4	41.448	PHOX2B	NA	NA	NA	NA	NA	NA	NA	CD	Rioux et al, Nat Genet 39, 2007
rs1051:	4	67.747	CENPC1	0.13	0.14	4.90E-01	add	0.87 [0.58-1.29]	0.689	0.217	MS (severity)	www.genome.gov/gwastudies
rs1051:	4	102.970	BANK1	0.27	0.31	2.10E-01	add	0.83 [0.62-1.11]	0.816	0.631	SLE	www.genome.gov/gwastudies
rs1315:	4	123.335	KIAA1109	NA	NA	NA	NA	NA	NA	NA	CelD	van Heel et al, Nat Genet 39, 2007
rs4505:	4	123.352	KIAA1109	0.33	0.31	7.61E-01	add	1.04 [0.79-1.38]	0.529	0.968	T1D	www.genome.gov/gwastudies
rs6534:	4	123.418	KIAA1109	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1311:	4	123.438	KIAA1109	NA	NA	NA	NA	NA	NA	NA	CelD	van Heel et al, Nat Genet 39, 2007
rs1738:	4	123.549	ADAD1	0.33	0.31	6.31E-01	add	1.07 [0.81-1.42]	0.402	0.597	T1D	www.genome.gov/gwastudies
rs1264:	4	123.728	FGF2	0.38	0.34	1.97E-01	add	1.19 [0.91-1.56]	0.244	0.939	CelD	van Heel et al, Nat Genet 39, 2007
rs6822:	4	123.729	FGF2	NA	NA	NA	NA	NA	NA	NA	CelD	www.genome.gov/gwastudies
rs6822:	4	123.729	FGF2	NA	NA	NA	NA	NA	NA	NA	CelD	www.genome.gov/gwastudies
rs1478:	4	132.010	intergenic	0.06	0.07	9.40E-01	add	0.98 [0.57-1.68]	1.000	0.109	MS (severity)	www.genome.gov/gwastudies
rs2313:	4	138.912	intergenic	0.14	0.10	2.53E-02	add	1.55 [1.06-2.27]	1.000	0.689	SLE	www.genome.gov/gwastudies
rs7672:	4	182.637	MGC45800	0.34	0.33	7.17E-01	add	1.05 [0.8-1.39]	0.532	0.844	MS	www.genome.gov/gwastudies
rs6897:	5	35.910	IL7R	0.21	0.25	4.42E-02	dom	0.67 [0.46-0.99]	0.258	0.891	MS	www.genome.gov/gwastudies
rs6897:	5	35.910	IL7R	0.21	0.25	4.42E-02	dom	0.67 [0.46-0.99]	0.258	0.891	MS	www.genome.gov/gwastudies
rs6897:	5	35.910	IL7R	0.21	0.25	4.42E-02	dom	0.67 [0.46-0.99]	0.258	0.891	T1D	www.genome.gov/gwastudies
rs1445:	5	35.946	CAPSL	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs3486:	5	40.356	Intergenic	NA	NA	NA	NA	NA	NA	NA	CD	Libioulle et al, PLOS genetics 3, 2007
rs1002:	5	40.422	Intergenic	0.28	0.32	1.98E-01	add	0.83 [0.62-1.11]	0.650	0.812	CD	Libioulle et al, PLOS genetics 3, 2007
rs4613:	5	40.428	Intergenic	0.17	0.11	1.07E-02	add	1.59 [1.11-2.27]	1.000	0.727	CD	Libioulle et al, PLOS genetics 3, 2007
rs4613:	5	40.428	Intergenic	0.17	0.11	1.07E-02	add	1.59 [1.11-2.27]	1.000	0.727	CD	Barrett, Nat Genet
rs1051:	5	40.429	Intergenic	0.28	0.32	1.98E-01	add	0.83 [0.62-1.11]	0.650	0.812	CD	Libioulle et al, PLOS genetics 3, 2007
rs1723:	5	40.437	Intergenic	0.17	0.11	1.07E-02	add	1.59 [1.11-2.27]	1.000	0.727	CD	www.genome.gov/gwastudies
rs1992:	5	40.451	Intergenic	0.38	0.40	4.78E-01	add	0.91 [0.69-1.19]	0.431	0.264	IBS	www.genome.gov/gwastudies
rs6896:	5	40.460	Intergenic	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1373:	5	40.467	Intergenic	0.38	0.40	4.78E-01	add	0.91 [0.69-1.19]	0.431	0.264	CD	www.genome.gov/gwastudies

rs9292	5	40.474	Intergenic	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs4495	5	40.513	Intergenic	NA	NA	NA	NA	NA	NA	NA	CD	Libioule et al, PLOS genetics 3, 2007
rs9792	5	42.411	GHR	0.31	0.34	5.59E-01	add	0.92 [0.69-1.22]	0.197	0.463	SLE	www.genome.gov/gwastudies
rs2544	5	86.435	Intergenic	0.24	0.23	8.36E-01	add	1.03 [0.76-1.4]	0.303	0.134	T1D	WTCCC, Nature 447, 2007
rs6596	5	131.770	Intergenic	0.18	0.16	4.13E-01	add	1.15 [0.82-1.63]	0.358	0.847	CD	www.genome.gov/gwastudies
rs2188	5	131.799	LOC441108	0.41	0.44	4.97E-01	add	0.91 [0.7-1.19]	0.849	0.400	CD	www.genome.gov/gwastudies
rs2054	5	132.024	IL13	0.15	0.19	6.81E-02	dom	0.67 [0.44-1.03]	0.134	1.000	PS	www.genome.gov/gwastudies
rs1716	5	132.657	FSTL4	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1336	5	150.204	IRGM	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1000	5	150.220	IRGM	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1174	5	150.239	IRGM	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1003	5	150.438	TNIP1	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1772	5	150.459	TNIP1	NA	NA	NA	NA	NA	NA	NA	PS	www.genome.gov/gwastudies
rs4704	5	155.434	SGCD	0.19	0.18	9.37E-01	add	0.99 [0.7-1.38]	0.760	0.817	MS (age of onset)	www.genome.gov/gwastudies
rs2082	5	158.650	IL12B	0.22	0.21	7.17E-01	add	1.06 [0.77-1.46]	0.783	0.875	PS	www.genome.gov/gwastudies
rs3213	5	158.683	IL12B	NA	NA	NA	NA	NA	NA	NA	PS	www.genome.gov/gwastudies
rs1004	5	158.747	IL12B	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs6887	5	158.755	IL12B	NA	NA	NA	NA	NA	NA	NA	CD	Parkes, Nat Genet
rs6887	5	158.755	IL212B	NA	NA	NA	NA	NA	NA	NA	PsA	Liu et al, PLoS Genetics 4, 2008
rs2431	5	159.813	intergenic	0.45	0.44	7.36E-01	add	1.05 [0.8-1.36]	1.000	0.441	SLE	Harley, Nat Genet 40, 2008
rs6941	6	15.197	JARID2	NA	NA	NA	NA	NA	NA	NA	MS (severity)	www.genome.gov/gwastudies
rs6908	6	20.837	CDKAL1	NA	NA	NA	NA	NA	NA	NA	CD	Barrett, Nat Genet
rs6908	6	20.837	CDKAL1	NA	NA	NA	NA	NA	NA	NA	CD	WTCCC, Nature 447, 2007
rs9263	6	31.219	CCHCR1	0.19	0.17	4.02E-01	add	1.16 [0.82-1.62]	0.760	0.804	UC	Asano Nat Genet 2009
rs9268	6	32.472	BTNL2	0.33	0.36	3.92E-01	add	0.89 [0.67-1.17]	0.091	0.624	UC	Asano Nat Genet 2009
rs9268	6	32.539	HLA	NA	NA	NA	NA	NA	NA	NA	UC	Barrett Nat Genet 2009
rs2395	6	32.541	HLA	NA	NA	NA	NA	NA	NA	NA	UC	Asano Nat Genet 2009
rs9271	6	32.684	HLA	NA	NA	NA	NA	NA	NA	NA	SLE	Han Nat Genet 2009
rs3757	6	91.014	BACH2	0.49	0.46	3.79E-01	add	1.13 [0.87-1.46]	0.853	0.945	T1D	www.genome.gov/gwastudies
rs1175	6	91.015	BACH2	0.49	0.46	3.79E-01	add	1.13 [0.87-1.46]	0.853	0.945	T1D	www.genome.gov/gwastudies
rs1175	6	91.015	BACH2	0.49	0.46	3.79E-01	add	1.13 [0.87-1.46]	0.853	0.945	T1D	www.genome.gov/gwastudies
rs7746	6	106.542	PRDM1, ATG5	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs5482	6	106.675	PRDM1, ATG5	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs6568	6	106.695	PRDM1, ATG5	NA	NA	NA	NA	NA	NA	NA	SLE	Harley, Nat Genet 40, 2008
rs5737	6	106.872	ATG5	NA	NA	NA	NA	NA	NA	NA	SLE	Harley, Nat Genet 40, 2008
rs9388	6	126.740	C6orf173	0.50	0.48	6.89E-01	add	1.05 [0.81-1.37]	0.457	0.350	T1D	www.genome.gov/gwastudies
rs1049	6	138.044	TNFAIP3	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs6920	6	138.048	TNFAIP3	0.18	0.20	5.27E-01	add	0.89 [0.63-1.26]	0.761	0.956	RA	Plenge, Nat Genet
rs6920	6	138.048	TNFAIP3	0.18	0.20	5.27E-01	add	0.89 [0.63-1.26]	0.761	0.956	RA	Raychaudhuri, Nat Genet
rs6920	6	138.048	TNFAIP3	0.18	0.20	5.27E-01	add	0.89 [0.63-1.26]	0.761	0.956	RA	WTCCC, Nature 447, 2007
rs7753	6	138.127	TNFAIP3	NA	NA	NA	NA	NA	NA	NA	CD	WTCCC, Nature 447, 2007
rs5029	6	138.237	TNFAIP3	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs2230	6	138.238	TNFAIP3	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs6106	6	138.241	TNFAIP3	NA	NA	NA	NA	NA	NA	NA	PS	www.genome.gov/gwastudies
rs1738	6	159.386	TAGAP	NA	NA	NA	NA	NA	NA	NA	CeID	www.genome.gov/gwastudies
rs2301	6	167.358	FGFR1OP	0.46	0.46	2.11E-01	dom	0.78 [0.53-1.15]	0.024	0.164	CD	www.genome.gov/gwastudies
rs1320	6	168.684	SMOC2	NA	NA	NA	NA	NA	NA	NA	Vitiligo	www.genome.gov/gwastudies
rs1025	7	7.235	C1GALT1	NA	NA	NA	NA	NA	NA	NA	MS (severity)	www.genome.gov/gwastudies
rs1177	7	7.781	RPA3	NA	NA	NA	NA	NA	NA	NA	RA	WTCCC, Nature 447, 2007
rs1015	7	8.154	ICA1	0.12	0.09	1.89E-01	add	1.3 [0.88-1.94]	0.667	0.062	SLE	Harley, Nat Genet 40, 2008
rs7804	7	26.858	SKAP2	0.22	0.24	5.37E-01	add	0.91 [0.66-1.24]	1.000	0.397	T1D	www.genome.gov/gwastudies

rs3177	7	29.069	CPVL	NA	NA	NA	NA	NA	NA	NA	BD	Fei, Arthritis Res Ther
rs1456:	7	50.240	Intergenic	0.29	0.31	5.21E-01	add	0.91 [0.68-1.21]	0.656	0.746	CD	www.genome.gov/gwastudies
rs4917:	7	50.276	IKZF1	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs4948:	7	50.995	COBL	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1167:	7	75.011	HIP1	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs4204	7	92.085	CDK6	0.27	0.29	6.46E-01	add	0.93 [0.69-1.25]	0.157	0.704	RA	www.genome.gov/gwastudies
rs1025:	7	93.870	COL1A2	NA	NA	NA	NA	NA	NA	NA	T1D	Hakonarson et al, Nature 448, 2007
rs1715	7	103.415	RELN	NA	NA	NA	NA	NA	NA	NA	MS (age of onset)	www.genome.gov/gwastudies
rs2108:	7	107.240	SLC26A3	0.44	0.43	7.61E-01	add	1.04 [0.8-1.36]	1.000	0.052	UC	www.genome.gov/gwastudies
rs4730:	7	107.267	SLC26A4	0.28	0.30	6.35E-01	add	0.93 [0.7-1.25]	0.820	0.934	UC	www.genome.gov/gwastudies
rs4730:	7	107.272	SLC26A4	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs8867	7	107.283	SLC26A4	0.43	0.41	4.80E-01	add	1.1 [0.84-1.44]	0.704	0.694	UC	www.genome.gov/gwastudies
rs4598	7	107.291	SLC26A4	0.40	0.42	3.87E-01	add	0.89 [0.68-1.16]	0.442	0.357	UC	www.genome.gov/gwastudies
rs2158:	7	107.368	LAMB1	0.42	0.38	2.67E-01	add	1.16 [0.89-1.52]	0.340	0.912	UC	www.genome.gov/gwastudies
rs1024:	7	116.134	MET	0.25	0.24	7.42E-01	add	1.05 [0.78-1.42]	0.326	0.814	MS (severity)	www.genome.gov/gwastudies
rs7293:	7	128.356	IRF5, TNPO3	0.24	0.31	6.95E-03	dom	0.59 [0.41-0.87]	0.203	0.903	SLE	Harley, Nat Genet 40, 2008
rs4728	7	128.361	IRF5, TNPO3	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1048:	7	128.381	IRF5, TNPO3	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1023:	7	128.456	IRF5, TNPO3	0.28	0.37	2.40E-03	add	0.64 [0.48-0.85]	0.489	0.319	SLE	Harley, Nat Genet 40, 2008
rs1027:	7	128.471	IRF5, TNPO3	0.28	0.37	2.40E-03	add	0.64 [0.48-0.85]	0.489	0.319	SLE	Harley, Nat Genet 40, 2008
rs1253:	7	128.505	IRF5, TNPO3	0.18	0.13	3.24E-02	add	1.45 [1.03-2.05]	1.000	0.821	SLE in women	www.genome.gov/gwastudies
rs1176:	7	131.021	Intergenic	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs7807:	7	147.889	Intergenic	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1529:	8	3.816	CSMD1	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs6601:	8	9.433	Intergenic	0.37	0.35	6.64E-01	add	1.06 [0.81-1.39]	0.229	0.733	SLE	Harley, Nat Genet 40, 2008
rs6985	8	10.799	XKR6	NA	NA	NA	NA	NA	NA	NA	SLE	Harley, Nat Genet 40, 2008
rs4240:	8	10.805	XKR6	0.49	0.50	7.38E-01	add	0.96 [0.74-1.24]	0.854	0.756	SLE	Harley, Nat Genet 40, 2008
rs1178:	8	10.826	XKR6	NA	NA	NA	NA	NA	NA	NA	SLE	Harley, Nat Genet 40, 2008
rs6984	8	10.834	XKR6	NA	NA	NA	NA	NA	NA	NA	SLE	Harley, Nat Genet 40, 2008
rs7836:	8	11.310	C8orf12	0.48	0.50	4.14E-01	add	0.89 [0.68-1.17]	0.851	0.835	SLE	Harley, Nat Genet 40, 2008
rs7812:	8	11.378	BLK	0.16	0.18	3.33E-01	add	0.84 [0.58-1.2]	0.735	0.454	SLE	www.genome.gov/gwastudies
rs2736:	8	11.381	BLK	0.26	0.23	3.46E-01	add	1.15 [0.86-1.56]	0.634	0.961	RA	www.genome.gov/gwastudies
rs1327	8	11.387	BLK	0.26	0.23	3.46E-01	add	1.15 [0.86-1.56]	0.634	0.961	SLE	www.genome.gov/gwastudies
rs2618:	8	11.390	BLK	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs2248:	8	11.429	BLK	0.37	0.33	2.63E-01	add	1.17 [0.89-1.54]	0.844	0.697	SLE	Harley, Nat Genet 40, 2008
rs1090:	8	11.488	BLK	NA	NA	NA	NA	NA	NA	NA	SLE	Harley, Nat Genet 40, 2008
rs7829:	8	57.012	LYN	0.23	0.21	3.86E-01	add	1.15 [0.84-1.57]	0.792	0.959	SLE	Harley, Nat Genet 40, 2008
rs2667:	8	57.061	LYN	0.22	0.23	9.52E-01	add	1.01 [0.74-1.38]	1.000	0.061	SLE	Harley, Nat Genet 40, 2008
rs2116:	8	73.527	Intergenic	0.45	0.48	4.81E-01	add	0.91 [0.7-1.19]	0.352	0.628	MS (age of onset)	www.genome.gov/gwastudies
rs1551:	8	126.609	Intergenic	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1050:	8	134.097	TG	0.23	0.26	3.70E-01	add	0.87 [0.63-1.19]	1.000	0.928	CelD	van Heel et al, Nat Genet 39, 2007
rs4469:	9	1.329	Intergenic	0.43	0.40	2.92E-01	add	1.15 [0.89-1.5]	0.851	0.351	CelD	van Heel et al, Nat Genet 39, 2007
rs7020:	9	4.282	GLIS3	0.44	0.49	1.53E-01	add	0.82 [0.63-1.07]	0.348	0.511	T1D	www.genome.gov/gwastudies
rs1075:	9	4.282	GLIS3	0.47	0.44	3.27E-01	add	1.14 [0.88-1.49]	1.000	0.362	T1D	www.genome.gov/gwastudies
rs1075:	9	4.972	JAK2	0.36	0.36	7.93E-01	add	1.04 [0.79-1.36]	1.000	0.163	CD	www.genome.gov/gwastudies
rs1097:	9	5.204	INSL4, INSL6	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs1755:	9	17.928	in	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs2812:	9	34.700	CCL21	0.28	0.29	6.98E-01	add	0.94 [0.71-1.26]	0.489	0.046	RA	www.genome.gov/gwastudies
rs2842:	9	78.096	RFK	0.28	0.27	6.34E-01	add	1.07 [0.8-1.44]	0.489	1.000	MS (age of onset)	www.genome.gov/gwastudies
rs6688:	9	84.501	in	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs2061:	9	99.146	KIAA1529	0.23	0.29	1.07E-01	add	0.77 [0.57-1.06]	1.000	0.704	BD	Fei, Arthritis Res Ther

rs4263:	9	116.606	TNFSF15	0.34	0.31	3.05E-01	add	1.15 [0.88-1.52]	0.839	0.516	CD	www.genome.gov/gwastudies
rs6478	9	116.609	TNFSF15	0.34	0.31	3.05E-01	add	1.15 [0.88-1.52]	0.839	0.516	IBD	www.genome.gov/gwastudies
rs1098:	9	121.024	DBC1	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs8813	9	122.693	TRAF1-C5	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs3761:	9	122.730	TRAF1	0.38	0.40	3.40E-01	add	0.88 [0.67-1.15]	0.552	0.429	RA	www.genome.gov/gwastudies
rs1124:	9	134.087	NTNG2	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1076	9	134.766	TSC1	0.43	0.47	2.37E-01	add	0.85 [0.66-1.11]	0.342	0.365	PS	www.genome.gov/gwastudies
rs1078	9	138.389	CARD9	0.38	0.40	3.52E-01	add	0.88 [0.67-1.15]	0.693	0.220	UC	www.genome.gov/gwastudies
rs6601	10	3.853	KLF6	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs2104:	10	6.139	IL2RA	NA	NA	NA	NA	NA	NA	NA	MS	Bahlo, Nat Genet 2009
rs2104:	10	6.139	IL2RA	NA	NA	NA	NA	NA	NA	NA	MS	De Jager, Nat Genet 2009
rs2104:	10	6.139	IL2RA	NA	NA	NA	NA	NA	NA	NA	MS	Hafler, N Engl J Med 357, 2007
rs2104:	10	6.139	IL2RA	NA	NA	NA	NA	NA	NA	NA	RA	WTCCC, Nature 447, 2007
rs2104:	10	6.139	IL2RA	NA	NA	NA	NA	NA	NA	NA	RA+T1D	WTCCC, Nature 447, 2007
rs2104:	10	6.139	IL2RA	NA	NA	NA	NA	NA	NA	NA	T1D	WTCCC, Nature 447, 2007
rs1272:	10	6.142	IL2RA	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1225	10	6.164	IL2RA	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1225	10	6.164	IL2RA	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1064:	10	6.317	PFKFB3	0.46	0.42	2.61E-01	add	1.16 [0.89-1.52]	0.135	0.215	CelD	van Heel et al, Nat Genet 39, 2007
rs1539:	10	6.317	PFKFB3	0.46	0.42	2.61E-01	add	1.16 [0.89-1.52]	0.135	0.215	CelD	van Heel et al, Nat Genet 39, 2007
rs9474	10	6.430	PRKCQ	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs4750:	10	6.433	PRKCQ	0.23	0.19	1.38E-01	add	1.27 [0.93-1.73]	0.792	0.778	RA	www.genome.gov/gwastudies
rs1125:	10	6.513	PRKCQ	0.27	0.21	3.80E-02	add	1.37 [1.02-1.84]	0.009	0.916	T1D	www.genome.gov/gwastudies
rs1398:	10	23.705	C10orf67	0.22	0.24	7.71E-01	add	0.95 [0.7-1.3]	0.027	0.084	CD+Sarc	www.genome.gov/gwastudies
rs1758:	10	35.328	Intergenic	0.38	0.35	5.01E-02	dom	1.48 [1-2.19]	0.031	0.878	CD	www.genome.gov/gwastudies
rs1110:	10	49.606	C10orf64	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs1913:	10	49.789	LRRRC18	0.53	0.50	7.00E-01	add	1.05 [0.81-1.37]	0.852	0.468	SLE	www.genome.gov/gwastudies
rs1099:	10	64.108	ZNF365	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1076	10	64.116	ZNF365	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs2241:	10	64.141	Intergenic	0.14	0.15	6.10E-01	add	0.91 [0.62-1.32]	0.226	0.256	CD	www.genome.gov/gwastudies
rs1250:	10	80.706	ZMIZ1	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1250:	10	80.730	ZMIZ1	0.32	0.32	9.00E-02	dom	0.72 [0.49-1.05]	0.005	0.905	IBD (early onset)	www.genome.gov/gwastudies
rs1050:	10	90.013	RNLS	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1088:	10	101.278	NKX2-3	0.54	0.49	2.03E-01	add	1.19 [0.91-1.54]	0.580	0.534	CD	www.genome.gov/gwastudies
rs1088:	10	101.278	NKX2-3	0.54	0.49	2.03E-01	add	1.19 [0.91-1.54]	0.580	0.534	CD	www.genome.gov/gwastudies
rs6584:	10	101.280	NKX2, NKX3	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs1119:	10	101.282	NKX2-3	0.54	0.49	2.03E-01	add	1.19 [0.91-1.54]	0.580	0.534	CD	www.genome.gov/gwastudies
rs4963	11	0.580	KIAA1542	NA	NA	NA	NA	NA	NA	NA	SLE in women	www.genome.gov/gwastudies
rs3741:	11	2.126	INS	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1004	11	2.127	INS	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs6356	11	2.148	INS	0.39	0.37	5.25E-01	add	1.09 [0.83-1.44]	1.000	0.192	T1D	Hakonarson et al, Nature 448, 2007
rs1077:	11	2.150	INS	NA	NA	NA	NA	NA	NA	NA	T1D	Hakonarson et al, Nature 448, 2007
rs1074:	11	2.153	INS	NA	NA	NA	NA	NA	NA	NA	T1D	Hakonarson et al, Nature 448, 2007
rs7111:	11	2.170	INS	0.31	0.25	4.76E-02	add	1.32 [1-1.75]	0.019	0.254	T1D	Barrett, Nat Genet 2009
rs7111:	11	2.170	INS	0.31	0.25	4.76E-02	add	1.32 [1-1.75]	0.019	0.254	T1D	Hakonarson et al, Nature 448, 2007
rs1793:	11	20.656	NELL1	NA	NA	NA	NA	NA	NA	NA	IBS	www.genome.gov/gwastudies
rs1782:	11	60.517	CD6	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs7927:	11	75.979	Intergenic	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1386:	11	87.459	Intergenic	NA	NA	NA	NA	NA	NA	NA	MS (age of onset)	www.genome.gov/gwastudies
rs1803:	11	116.105	Intergenic	0.28	0.26	6.66E-01	add	1.07 [0.8-1.43]	1.000	0.167	MS (severity)	www.genome.gov/gwastudies
rs4639:	11	118.079	Intergenic	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies

rs6590:	11	127.816	Intergenic	0.11	0.10	6.88E-01	add	1.09 [0.71-1.69]	1.000	0.008	SLE	www.genome.gov/gwastudies
rs8868:	12	2.352	CACNA1C	NA	NA	NA	NA	NA	NA	NA	CD	Rioux et al, Nat Genet 39, 2007
rs1800:	12	6.310	TNFRSF1A	0.44	0.42	6.69E-01	add	1.06 [0.81-1.38]	0.708	0.523	MS	www.genome.gov/gwastudies
rs4149:	12	6.313	TNFRSF1A	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs3764:	12	9.725	CLEC2D	0.44	0.49	2.59E-01	add	0.86 [0.66-1.12]	0.348	0.299	T1D	www.genome.gov/gwastudies
rs1105:	12	9.747	KLRB1	0.46	0.50	3.48E-01	add	0.88 [0.68-1.15]	0.354	0.253	T1D	www.genome.gov/gwastudies
rs4763:	12	9.801	CD69	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1117:	12	38.888	LRRK2, MUC19	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1458:	12	40.252	PDZRN4	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs7731:	12	54.656	RAB5B	0.30	0.32	5.15E-01	add	0.91 [0.69-1.21]	0.276	0.063	T1D	Hakonarson et al, Diabetes 57, 2008
rs1087:	12	54.687	RAB5B	0.37	0.41	2.57E-01	add	0.86 [0.65-1.12]	0.428	0.410	T1D	Hakonarson et al, Diabetes 57, 2008
rs1701:	12	54.699	RAB5B	0.32	0.33	7.48E-01	add	0.96 [0.72-1.26]	1.000	0.158	T1D	www.genome.gov/gwastudies
rs1117:	12	54.757	RAB5B	0.37	0.41	2.57E-01	add	0.86 [0.65-1.12]	0.428	0.410	T1D	www.genome.gov/gwastudies
rs2292:	12	54.768	ERBB3	0.30	0.32	5.15E-01	add	0.91 [0.69-1.21]	0.276	0.063	T1D	www.genome.gov/gwastudies
rs2292:	12	54.768	ERBB3	0.30	0.32	5.15E-01	add	0.91 [0.69-1.21]	0.276	0.063	T1D	www.genome.gov/gwastudies
rs2292:	12	54.768	ERBB3	0.30	0.32	5.15E-01	add	0.91 [0.69-1.21]	0.276	0.063	T1D	www.genome.gov/gwastudies
rs2066:	12	55.024	STAT2	0.05	0.07	2.97E-01	add	0.73 [0.4-1.32]	1.000	0.679	PS	www.genome.gov/gwastudies
rs1678:	12	56.255	KIF5A	0.34	0.38	2.47E-01	add	0.85 [0.64-1.12]	0.537	0.580	RA	www.genome.gov/gwastudies
rs1087:	12	56.351	multiple	NA	NA	NA	NA	NA	NA	NA	MS	Bahlo, Nat Genet 2009
rs1236:	12	56.420	CENTG1	0.49	0.49	6.96E-01	add	0.95 [0.73-1.24]	0.138	0.557	MS	Bahlo, Nat Genet 2009
rs7038:	12	56.449	CYP27B1, METTL	0.28	0.30	3.32E-01	add	0.86 [0.64-1.16]	1.000	0.805	MS	www.genome.gov/gwastudies
rs7134:	12	66.786	IL26	NA	NA	NA	NA	NA	NA	NA	UC	Silverberg et al, Nat Genet 2009
rs1558:	12	66.791	IL26	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs2870:	12	66.883	IL26	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs9398:	12	90.192	Intergenic	0.18	0.17	5.18E-01	add	1.12 [0.8-1.57]	0.762	0.377	SLE	Hinks et al, A&R 60, 2009
rs3184:	12	110.369	SH2B3	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs6531:	12	110.492	ATXN2	NA	NA	NA	NA	NA	NA	NA	CelD	www.genome.gov/gwastudies
rs1769:	12	110.971	C12orf30	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1769:	12	110.971	C12orf30	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1769:	12	110.971	C12orf30	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1790:	12	122.223	MPHOSPH9	0.24	0.22	3.38E-01	add	1.16 [0.86-1.58]	1.000	0.683	MS	www.genome.gov/gwastudies
rs1385:	12	127.867	SLC15A4	0.14	0.11	1.25E-01	add	1.34 [0.92-1.95]	1.000	0.186	SLE	www.genome.gov/gwastudies
rs9550:	13	19.848	Intergenic	NA	NA	NA	NA	NA	NA	NA	RA	WTCCC, Nature 447, 2007
rs1708:	13	26.429	Intergenic	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs3812:	13	39.128	COG6	NA	NA	NA	NA	NA	NA	NA	PS	Liu et al, PLoS Genetics 4, 2008
rs7993:	13	39.249	COG6	NA	NA	NA	NA	NA	NA	NA	PS	www.genome.gov/gwastudies
rs9548:	13	39.404	Intergenic	0.47	0.49	2.47E-01	add	0.86 [0.66-1.11]	0.262	0.120	UC	www.genome.gov/gwastudies
rs3764:	13	43.356	C13orf31	0.26	0.25	4.74E-01	add	1.11 [0.83-1.5]	0.634	0.130	CD	www.genome.gov/gwastudies
rs1324:	13	73.534	KLF12	0.29	0.33	2.26E-01	add	0.84 [0.63-1.12]	0.656	0.559	RA	Julia et al, A&R 58, 2008
rs1327:	13	89.201	Intergenic	0.44	0.43	5.67E-01	add	1.08 [0.83-1.41]	0.577	0.778	MS	Comabella et al, PLoS ONE 3, 2008
rs9523:	13	92.130	GPC5	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1465:	14	68.333	C14orf181	0.28	0.27	8.39E-01	add	1.03 [0.77-1.38]	0.650	0.295	T1D	www.genome.gov/gwastudies
rs7159:	14	81.135	Intergenic	NA	NA	NA	NA	NA	NA	NA	CelD	van Heel et al, Nat Genet 39, 2007
rs4900:	14	97.569	Intergenic	0.31	0.28	2.44E-01	add	1.19 [0.89-1.58]	0.134	0.148	T1D	www.genome.gov/gwastudies
rs8035:	15	36.626	RASGRP1	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs3825:	15	77.023	CTSH	0.33	0.30	3.27E-01	add	1.15 [0.87-1.52]	0.529	0.967	T1D	www.genome.gov/gwastudies
rs3825:	15	77.023	CTSH	0.33	0.30	3.27E-01	add	1.15 [0.87-1.52]	0.529	0.967	T1D	www.genome.gov/gwastudies
rs1186:	16	11.074	CLEC16A	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs7256:	16	11.077	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	Hakonarson et al, Nature 448, 2007
rs1270:	16	11.087	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1270:	16	11.087	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies

rs1270:	16	11.087	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1270:	16	11.087	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs2903:	16	11.146	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1767:	16	11.149	CLEC16A	NA	NA	NA	NA	NA	NA	NA	T1D	Hakonarson et al, Nature 448, 2007
rs6498	16	11.157	CLEC16A	0.37	0.35	5.61E-01	add	1.08 [0.82-1.43]	0.423	1.000	MS	www.genome.gov/gwastudies
rs4166:	16	11.272	TNP2	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1244:	16	20.250	Intergenic	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs4788:	16	28.447	IL27	0.34	0.39	6.07E-02	add	0.76 [0.58-1.01]	0.835	0.146	T1D	www.genome.gov/gwastudies
rs8049:	16	28.745	ATXN2L	0.31	0.38	3.02E-02	add	0.73 [0.55-0.97]	0.521	0.151	IBD (early onset)	www.genome.gov/gwastudies
rs7186:	16	30.543	ZNF768	0.41	0.37	1.61E-01	add	1.21 [0.93-1.58]	0.702	0.882	SLE	www.genome.gov/gwastudies
rs7197:	16	30.550	ZNF768	0.41	0.37	1.61E-01	add	1.21 [0.93-1.58]	0.702	0.882	SLE	www.genome.gov/gwastudies
rs9888:	16	31.221	ITGAM	0.12	0.13	8.26E-01	add	0.96 [0.64-1.43]	0.670	0.939	SLE in women	www.genome.gov/gwastudies
rs1115:	16	31.242	ITGAM	0.40	0.43	5.84E-01	add	0.93 [0.71-1.21]	1.000	0.245	SLE	www.genome.gov/gwastudies
rs1143:	16	31.251	ITGAM	0.16	0.18	6.32E-01	add	0.92 [0.64-1.31]	0.733	0.812	SLE	Harley, Nat Genet 40, 2008
rs4548:	16	31.272	ITGAM	0.20	0.21	6.97E-01	add	0.94 [0.67-1.3]	1.000	0.644	SLE	Harley, Nat Genet 40, 2008
rs1157:	16	31.276	ITGAX	0.16	0.18	6.32E-01	add	0.92 [0.64-1.31]	0.733	0.812	SLE	www.genome.gov/gwastudies
rs1722:	16	49.297	NOD2	0.27	0.28	9.44E-01	add	0.99 [0.74-1.33]	1.000	0.762	CD	www.genome.gov/gwastudies
rs2066:	16	49.303	NOD2	0.27	0.28	9.44E-01	add	0.99 [0.74-1.33]	1.000	0.762	CD	Duerr et al, Science 314, 2006
rs5743:	16	49.314	NOD2	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs5743:	16	49.314	NOD2	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs5743:	16	49.314	NOD2	NA	NA	NA	NA	NA	NA	NA	IBD	www.genome.gov/gwastudies
rs2076:	16	49.314	NOD2	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs2076:	16	49.314	NOD2	NA	NA	NA	NA	NA	NA	NA	IBD	www.genome.gov/gwastudies
rs2076:	16	49.314	NOD2	NA	NA	NA	NA	NA	NA	NA	IBS	www.genome.gov/gwastudies
rs2066:	16	49.321	NOD2	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1728:	16	67.149	ZFP90	0.19	0.23	1.89E-01	add	0.8 [0.58-1.11]	1.000	0.074	UC	www.genome.gov/gwastudies
rs7199:	16	71.567	ZFH3	0.27	0.34	1.87E-02	add	0.7 [0.52-0.94]	0.641	0.877	Kawasaki	www.genome.gov/gwastudies
rs7191:	16	72.139	TXNL4B	NA	NA	NA	NA	NA	NA	NA	MS (severity)	www.genome.gov/gwastudies
rs7202:	16	73.805	Intergenic	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1744:	16	84.575	IRF8	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs1695:	17	7.574	DNAH2	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs1294:	17	13.675	Intergenic	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs2872:	17	35.294	ORMDL3	0.50	0.49	6.03E-01	add	1.07 [0.82-1.4]	0.459	0.268	CD	www.genome.gov/gwastudies
rs2290:	17	35.320	GSDML	0.49	0.48	8.41E-01	add	1.03 [0.79-1.34]	0.710	0.579	T1D	www.genome.gov/gwastudies
rs7221:	17	36.024	HNF1B, DDX52	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs7441:	17	37.768	STAT3	0.42	0.42	8.09E-01	add	0.97 [0.74-1.27]	0.340	0.119	CD	www.genome.gov/gwastudies
rs2542:	18	12.770	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	CD	Barrett, Nat Genet
rs2542:	18	12.770	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	CD	Parkes, Nat Genet
rs2542:	18	12.770	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	CD	WTCCC, Nature 447, 2007
rs2542:	18	12.770	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	T1D	Cooper, Nat Genet
rs2542:	18	12.770	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	T1D	Todd, Nat Genet
rs2542:	18	12.770	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	T1D	WTCCC, Nature 447, 2007
rs1893:	18	12.799	PTPN2	0.19	0.16	2.64E-01	add	1.21 [0.86-1.7]	0.761	0.516	T1D	www.genome.gov/gwastudies
rs1557:	18	52.903	Intergenic	0.25	0.23	3.28E-01	add	1.16 [0.86-1.58]	0.452	0.377	MS (age of onset)	www.genome.gov/gwastudies
rs1050:	18	53.605	ATP8B1	0.22	0.21	7.74E-01	add	1.05 [0.76-1.44]	0.408	0.464	Vitiligo	www.genome.gov/gwastudies
rs3809:	18	54.354	ALPK2	NA	NA	NA	NA	NA	NA	NA	CelD	van Heel et al, Nat Genet 39, 2007
rs3809:	18	54.354	ALPK2	0.46	0.48	7.03E-01	add	0.95 [0.73-1.23]	0.851	0.101	CelD	van Heel et al, Nat Genet 39, 2007
rs9378:	18	54.719	ZNF532	0.11	0.09	5.73E-01	add	1.13 [0.74-1.74]	1.000	0.467	CD	Rioux et al, Nat Genet 39, 2007
rs7633:	18	65.683	CD226	0.46	0.50	1.20E-01	add	0.81 [0.62-1.06]	0.189	0.890	T1D	www.genome.gov/gwastudies
rs1708:	18	66.993	SOCS6	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs3377:	18	67.925	SOCS6	0.30	0.30	8.41E-01	add	1.03 [0.77-1.37]	0.377	0.836	MS (severity)	www.genome.gov/gwastudies

rs2002:	18	74.511	SALL3	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs7253:	19	11.543	PRKCSH	NA	NA	NA	NA	NA	NA	NA	MS (severity)	www.genome.gov/gwastudies
rs1050:	19	38.442	CEBPA, SLC7A10	0.16	0.17	8.88E-01	add	0.98 [0.69-1.39]	0.492	0.027	IBD (early onset)	www.genome.gov/gwastudies
rs8111:	19	50.999	RSHL1	0.07	0.11	1.51E-01	add	0.69 [0.42-1.14]	1.000	0.586	CD	WTCCC, Nature 447, 2007
rs4251:	19	51.900	PRKD2	0.15	0.16	6.84E-01	add	0.93 [0.64-1.34]	0.721	0.650	T1D	www.genome.gov/gwastudies
rs2991:	19	61.005	NLRP11	0.49	0.45	2.32E-01	add	1.17 [0.9-1.52]	1.000	0.124	MS (severity)	www.genome.gov/gwastudies
rs3970:	20	1.154	PSMF1	NA	NA	NA	NA	NA	NA	NA	MS	www.genome.gov/gwastudies
rs2281:	20	1.559	SIRPG	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs6017:	20	42.498	HNF4A	NA	NA	NA	NA	NA	NA	NA	UC	www.genome.gov/gwastudies
rs6131:	20	44.158	CD40	NA	NA	NA	NA	NA	NA	NA	MS	Bahlo, Nat Genet 2009
rs6074:	20	44.174	CD40	0.28	0.27	5.00E-01	add	1.11 [0.82-1.49]	0.647	0.691	MS	www.genome.gov/gwastudies
rs1569:	20	44.175	CD40	0.28	0.27	5.00E-01	add	1.11 [0.82-1.49]	0.647	0.691	MS	Bahlo, Nat Genet 2009
rs4810:	20	44.181	CD40	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs4953:	20	47.956	SPATA2	0.35	0.39	1.58E-01	add	0.82 [0.62-1.08]	0.838	0.884	PS	www.genome.gov/gwastudies
rs2315:	20	61.814	ZGPAT	0.32	0.30	6.24E-01	add	1.07 [0.81-1.42]	1.000	0.902	IBD	www.genome.gov/gwastudies
rs1736:	21	15.727	TNFRSF6B	0.40	0.43	2.68E-01	add	0.86 [0.66-1.12]	0.438	0.943	CD	www.genome.gov/gwastudies
rs2833:	21	32.303	Intergenic	0.19	0.23	1.21E-01	add	0.77 [0.55-1.07]	1.000	0.772	Vitiligo	www.genome.gov/gwastudies
rs2836:	21	39.214	FLJ45139	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs2836:	21	39.387	PSMG1	0.29	0.27	3.38E-01	add	1.15 [0.86-1.53]	0.262	0.825	IBD	www.genome.gov/gwastudies
rs2837:	21	41.434	Intergenic	NA	NA	NA	NA	NA	NA	NA	RA	www.genome.gov/gwastudies
rs1120:	21	42.709	UBASH3A	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs9976:	21	42.709	UBASH3A	0.43	0.45	6.34E-01	add	0.94 [0.72-1.22]	0.705	1.000	T1D	www.genome.gov/gwastudies
rs7624:	21	44.440	ICOSLG	NA	NA	NA	NA	NA	NA	NA	CD	www.genome.gov/gwastudies
rs1316:	22	20.247	UBE2L3	NA	NA	NA	NA	NA	NA	NA	SLE	www.genome.gov/gwastudies
rs5754:	22	20.270	UBE2L3	0.21	0.18	2.20E-01	add	1.22 [0.89-1.69]	0.047	0.773	SLE	Harley, Nat Genet 40, 2008
rs2412:	22	28.860	HORMAD2	0.50	0.47	3.86E-01	add	1.12 [0.86-1.47]	0.265	0.282	IBD (early onset)	www.genome.gov/gwastudies
rs5753:	22	28.912	LOC729980	0.32	0.37	7.67E-02	add	0.77 [0.58-1.03]	0.669	0.003	T1D	www.genome.gov/gwastudies
rs7437:	22	35.882	RASD2, MCM5	0.31	0.31	9.78E-01	add	1 [0.75-1.34]	0.200	0.291	RA	www.genome.gov/gwastudies
rs2295:	22	35.921	RASD2, MCM5	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs2295:	22	35.921	RASD2, MCM5	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies
rs2071:	22	41.940	SCUBE1	0.12	0.14	3.40E-01	add	0.82 [0.54-1.23]	1.000	0.389	SLE	Harley, Nat Genet 40, 2008
rs2664:	X	153.599	GAB3	NA	NA	NA	NA	NA	NA	NA	T1D	www.genome.gov/gwastudies

* Association results reported for proxy ($r^2 > 0.8$ and < 500 kb distance) for the autoimmune disease SNP listed. Chr – chromosome, Pos – position, MAF – Minor Allele Frequency, genetic transmission model: add – additive, rec - recessive, dom – dominant, OR – odds ratio, CI – 95% confidence interval, HWE – Hardy Weinberg Equilibrium, Ref – reference, NA – not available (SNP not genotyped or failed quality control criteria defined in the Methods, RA – rheumatoid arthritis, SLE – systemic lupus erythematosus, T1D – type 1 diabetes, MS – multiple sclerosis, IBD - inflammatory bowel disease, IBS - inflammatory bowel syndrome, CD – Crohn's disease, UC – ulcerative colitis, CeID – celiac disease, PS – psoriasis, PsA – psoriatic arthritis, JIA – juvenile idiopathic arthritis, BD – Behcet's disease, Sarc – sarcoidosis.