

Supplementary Table 1: Association to T2D in the Icelandic discovery group.

The upper table includes association results for all SNPs or two-marker haplotypes that have an adjusted P value less than 5×10^{-5} for either all T2D cases, non-obese T2D cases or obese T2D cases. Included in the table is the chromosome, the position of the markers (or the midpoint for two-marker haplotypes) in NCBI Build 34, the markers and alleles tested, the corresponding surrogate SNP for two-markers haplotypes selected for replication, the frequency in controls and the frequency in cases, the odds ratio (OR) and adjusted P value for the three case groups tested. The number of T2D cases in each of the three groups is included in parenthesis and the same set of 5275 controls is used in all tests. Note that information on BMI is missing for 168 of the cases. The lower table includes the corresponding values for the five most significant non-synonymous SNPs selected for replication. Included in column five are the corresponding genes and the codon changes. In both tables markers selected for further testing in the first replication group (Denmark B) are indicated with bold typesetting. Other markers / haplotypes were excluded from the replication study as they were a) highly correlated with another marker selected for replication, or b) belong to the *TCF7L2* locus that has been studied previously. The correlation (r^2) between surrogate haplotypes and the SNP they tag is estimated based on the HapMap CEU dataset.

Chr	Position	Markers	Allele	Surrogate ^a (r^2)	Con.frq	All T2D cases (1399)			NonObese T2D cases (700)			Obese T2D cases (531)		
						Case.frq	OR	P^b	Case.frq	OR	P^b	Case.frq	OR	P^b
C01	29602516	rs4949283 rs502545	TC	rs10798895 G (1)	0.149	0.117	0.76	0.00016	0.104	0.66	0.000033	0.133	0.88	0.21
C01	104461151	rs7553985	C	-	0.394	0.430	1.16	0.0023	0.419	1.11	0.11	0.466	1.34	0.000027
C01	104467009	rs2166890	T	-	0.393	0.430	1.16	0.0018	0.419	1.11	0.091	0.466	1.35	0.000024
C01	104468502	rs7552405	T	-	0.317	0.355	1.19	0.00078	0.346	1.14	0.047	0.386	1.35	0.000030
C01	151915609	rs3738028	G	-	0.360	0.407	1.22	0.000046	0.417	1.27	0.00016	0.409	1.23	0.0038
C02	40632580	rs13414307 rs1990609	AG	-	0.517	0.571	1.24	0.0000089	0.568	1.23	0.0011	0.582	1.30	0.00026
C02	40623619	rs13414307	A	-	0.543	0.593	1.22	0.000033	0.589	1.21	0.0028	0.603	1.28	0.00056
C02	55036788	rs930493 rs10173697	GT	-	0.281	0.335	1.29	0.0000017	0.325	1.23	0.0024	0.333	1.27	0.0016
C02	55040844	rs10173697	T	-	0.503	0.553	1.22	0.000040	0.545	1.18	0.0086	0.560	1.25	0.0014
C03	89162181	rs12486049	T	-	0.872	0.904	1.38	0.000035	0.907	1.43	0.00043	0.901	1.34	0.0095
C03	146863467	rs7630694	G	-	0.060	0.070	1.20	0.065	0.056	0.93	0.60	0.097	1.70	0.000033
C03	196904151	rs9858622	A	-	0.668	0.701	1.17	0.0028	0.682	1.07	0.34	0.737	1.40	0.000016
C04	140508134	rs13116075 rs6824182	AA	rs10033117 C (1)	0.741	0.763	1.13	0.036	0.734	0.96	0.60	0.804	1.43	0.000024
C04	140604420	rs2292837 rs11725721	TC	-	0.254	0.232	0.89	0.038	0.259	1.03	0.69	0.194	0.71	0.000047
C04	140621178	rs3762864 rs11725721	GC	-	0.254	0.233	0.89	0.042	0.262	1.04	0.60	0.194	0.70	0.000038
C05	76637396	rs832785 rs2859576	AA	-	0.510	0.470	0.85	0.00082	0.489	0.92	0.18	0.438	0.75	0.000043
C05	76635083	rs4704400	T	-	0.490	0.530	1.18	0.0008	0.511	1.09	0.18	0.562	1.33	0.000043
C05	87882885	rs10505855 rs12514611	GC	rs10452479 G (0.94)	0.188	0.224	1.25	0.00023	0.244	1.39	0.000015	0.200	1.08	0.38
C06	6967990	rs490213 rs814174	AG	rs12201780 A (1)	0.044	0.072	1.71	0.000016	0.080	1.89	0.000037	0.063	1.48	0.033
C06	9509965	rs214447	T	-	0.424	0.449	1.11	0.034	0.416	0.97	0.61	0.495	1.34	0.000035
C06	20779501	rs4712527 rs7756992	AG	-	0.232	0.270	1.23	0.00021	0.292	1.37	0.0000090	0.250	1.11	0.21
C06	20805960	rs7756992 rs9295478	AG	-	0.743	0.701	0.81	0.000089	0.682	0.74	0.000013	0.718	0.88	0.11

C06	20787688	rs7756992	G	-	0.232	0.270	1.23	0.00021	0.292	1.37	0.0000090	0.250	1.11	0.20
C06	31552682	rs2516424	C	-	0.325	0.372	1.23	0.000039	0.375	1.25	0.00080	0.376	1.25	0.0020
C06	31592562	rs2516424 rs4947324	CC	-	0.320	0.368	1.24	0.000027	0.370	1.25	0.00074	0.373	1.26	0.0016
C06	41130207	rs10456499	A	-	0.563	0.597	1.15	0.0040	0.575	1.05	0.43	0.637	1.36	0.000018
C06	132387934	rs9483377 rs997607	GC	-	0.234	0.278	1.26	0.000040	0.272	1.22	0.0067	0.276	1.25	0.0065
C06	132379686	rs9483377 rs7745875	GG	-	0.233	0.276	1.25	0.000048	0.271	1.22	0.0052	0.273	1.23	0.0087
C06	132361238	rs9483377	G	-	0.307	0.356	1.25	0.000013	0.348	1.20	0.0052	0.354	1.24	0.0040
C06	150399255	rs11155700	A	-	0.749	0.794	1.29	0.0000095	0.786	1.23	0.0049	0.801	1.35	0.00039
C06	150399954	rs12213837	C	-	0.749	0.794	1.29	0.0000097	0.786	1.23	0.0049	0.801	1.35	0.00040
C06	164421443	rs206732 rs933251	TC	rs10085202 A (1)	0.531	0.479	0.81	0.000037	0.469	0.78	0.00015	0.497	0.87	0.058
C08	124084183	rs952656	G	-	0.673	0.721	1.25	0.000019	0.706	1.17	0.021	0.725	1.28	0.0012
C08	124092339	rs13252935 rs7824293	TG	-	0.143	0.108	0.72	0.000010	0.116	0.78	0.0099	0.104	0.69	0.00067
C08	128249239	rs283710 rs412835	CC	-	0.254	0.222	0.84	0.0024	0.245	0.95	0.51	0.190	0.69	0.000025
C08	128250055	rs185852	G	-	0.755	0.791	1.22	0.000050	0.764	1.05	0.49	0.822	1.49	0.0000046
C08	128265112	rs283718 rs283720	CA	-	0.255	0.223	0.84	0.0026	0.256	1.01	0.94	0.189	0.68	0.0000092
C09	88426790	rs10993008	A	-	0.154	0.192	1.30	0.000027	0.181	1.21	0.019	0.194	1.32	0.0020
C09	93768899	rs10818991 rs10990303	CC	rs10985640 A (0.85)	0.537	0.490	0.83	0.00019	0.469	0.76	0.000037	0.513	0.91	0.18
C09	93802193	rs10990568 rs4743148	GG	-	0.263	0.309	1.25	0.000032	0.314	1.28	0.00038	0.306	1.23	0.0076
C09	93810412	rs4743148	G	-	0.315	0.365	1.25	0.000010	0.371	1.28	0.00013	0.358	1.21	0.0092
C09	124790974	rs3814120	T	-	0.093	0.113	1.25	0.0046	0.094	1.01	0.91	0.140	1.59	0.000014
C10	52735263	rs7915186 rs3829170	TT	-	0.328	0.377	1.24	0.000021	0.374	1.22	0.0021	0.375	1.23	0.0049
C10	52746400	rs3829170 rs7922112	TG	rs12247188 T (0.9)	0.336	0.386	1.24	0.000021	0.381	1.22	0.0027	0.387	1.24	0.0027
C10	93976392	rs2421943	G	-	0.555	0.614	1.28	9.1×10^{-7}	0.600	1.20	0.0043	0.621	1.31	0.00017
C10	94022896	rs2421943 rs7917359	GC	-	0.521	0.585	1.30	1.3×10^{-8}	0.565	1.19	0.0052	0.602	1.39	0.0000041
C10	94068337	rs7908111 rs2497304	GG	-	0.499	0.443	0.80	0.0000034	0.456	0.84	0.0072	0.427	0.75	0.000039
C10	94011761	rs1999763 rs10882091	GT	-	0.517	0.455	0.78	2.9×10^{-7}	0.472	0.83	0.0038	0.442	0.74	0.000019
C10	94023632	rs1999763 rs6583830	GG	-	0.517	0.455	0.78	2.9×10^{-7}	0.472	0.83	0.0038	0.442	0.74	0.000019
C10	94012407	rs6583826	G	-	0.467	0.518	1.23	0.000020	0.508	1.18	0.0080	0.527	1.28	0.00048
C10	94025680	rs6583826 rs10882091	GC	-	0.393	0.449	1.26	0.0000021	0.435	1.19	0.0062	0.469	1.36	0.000012
C10	94092724	rs10882091 rs7923837	CG	-	0.410	0.466	1.26	0.0000022	0.452	1.19	0.0063	0.486	1.36	0.000011
C10	94038954	rs10882091	C	-	0.415	0.472	1.26	0.0000024	0.456	1.18	0.0079	0.491	1.36	0.000014
C10	94047527	rs7914814	T	-	0.416	0.472	1.26	0.0000025	0.456	1.18	0.0081	0.491	1.35	0.000014
C10	94062695	rs6583830	A	-	0.415	0.472	1.26	0.0000024	0.456	1.18	0.0079	0.491	1.36	0.000014
C10	94122233	rs2275729 rs1111875	AG	-	0.470	0.527	1.26	0.0000023	0.519	1.22	0.0018	0.534	1.29	0.00025
C10	94157293	rs2497304	A	-	0.530	0.473	0.80	0.0000	0.481	0.82	0.00	0.466	0.77	0.000251

C10	94160330	rs947591	A	-	0.475	0.526	1.23	0.000023	0.521	1.21	0.0028	0.545	1.33	0.000053
C10	114441018	rs7895307 rs12255372	GT	-	0.257	0.308	1.29	0.0000049	0.330	1.42	4.5×10 ⁻⁷	0.269	1.06	0.45
C10	114422936	rs7903146	T	-	0.300	0.372	1.38	1.8×10 ⁻¹⁰	0.396	1.53	2.4×10 ⁻¹¹	0.342	1.21	0.010
C10	114434905	rs7903146 rs11196192	TT	-	0.220	0.282	1.39	3.4×10 ⁻⁹	0.298	1.51	9.4×10 ⁻⁹	0.263	1.27	0.0042
C10	114438514	rs7904519	G	-	0.480	0.522	1.18	0.00045	0.553	1.34	0.0000026	0.483	1.01	0.84
C10	114455586	rs7904519 rs10885409	GC	-	0.474	0.516	1.18	0.00055	0.549	1.35	0.0000018	0.476	1.01	0.90
C10	114455586	rs7904519 rs10885409	AT	-	0.510	0.471	0.86	0.0013	0.441	0.76	0.000011	0.510	1.00	0.99
C10	114472659	rs10885409	C	-	0.484	0.523	1.17	0.0014	0.555	1.33	0.0000060	0.483	0.99	0.94
C10	114473489	rs12255372	T	-	0.294	0.351	1.29	4.9×10 ⁻⁷	0.371	1.41	1.6×10 ⁻⁷	0.317	1.11	0.15
C10	118261345	rs1681748 rs2170862	TT	-	0.238	0.265	1.15	0.013	0.245	1.04	0.59	0.302	1.38	0.000041
C10	118285583	rs2170862	T	-	0.256	0.281	1.13	0.020	0.259	1.02	0.82	0.320	1.37	0.000043
C10	118555280	rs10787760	G	-	0.278	0.300	1.12	0.037	0.269	0.96	0.53	0.347	1.38	0.000017
C11	23946882	rs1879230	T	-	0.088	0.111	1.30	0.00097	0.128	1.53	0.000021	0.093	1.07	0.57
C11	106474406	rs1455593	T	-	0.097	0.114	1.20	0.021	0.087	0.89	0.29	0.142	1.54	0.000040
C12	30390375	rs1429622 rs1506382	AG	rs794598 C (0.9)	0.368	0.321	0.82	0.000083	0.341	0.89	0.092	0.296	0.72	0.000023
C12	33373479	rs1905421	T	-	0.082	0.110	1.39	0.000044	0.116	1.47	0.00020	0.107	1.35	0.011
C13	25558690	rs565707 rs6491198	AA	-	0.281	0.249	0.85	0.0039	0.220	0.72	0.000016	0.274	0.97	0.69
C13	25478564	rs565707	C	-	0.700	0.734	1.19	0.0016	0.763	1.38	0.0000073	0.710	1.05	0.53
C13	25535031	rs7984685	C	-	0.540	0.582	1.19	0.00043	0.606	1.31	0.000022	0.568	1.12	0.11
C13	25537643	rs7998347	C	-	0.540	0.582	1.19	0.00046	0.606	1.31	0.000024	0.568	1.12	0.11
C13	25715179	rs1333350 rs7987436	GT	-	0.254	0.216	0.81	0.00030	0.195	0.71	0.000010	0.251	0.98	0.82
C14	80759910	rs799099 rs4899801	AG	-	0.365	0.390	1.11	0.037	0.359	0.97	0.64	0.439	1.36	0.000022
C14	80763881	rs2066041	G	-	0.367	0.394	1.12	0.021	0.368	1.01	0.92	0.437	1.34	0.000038
C14	80820260	rs10483957	A	-	0.459	0.493	1.15	0.0042	0.476	1.07	0.28	0.530	1.33	0.000042
C15	98094991	rs9920347 rs11635811	AG	rs2045107 C (0.9)	0.521	0.469	0.81	0.000044	0.475	0.84	0.0056	0.468	0.81	0.0041
C16	12811478	rs6498353 rs9941146	CG	-	0.105	0.080	0.74	0.00054	0.068	0.62	0.000047	0.082	0.75	0.026
C16	22764405	rs724466	T	-	0.738	0.781	1.26	0.000038	0.781	1.27	0.0012	0.783	1.29	0.0025
C16	24353768	rs11074618 rs985729	AC	rs11644596 G (1)	0.299	0.342	1.21	0.00044	0.332	1.16	0.040	0.372	1.39	0.000032
C16	73296557	rs1862773 rs825842	CT	-	0.059	0.038	0.63	0.000048	0.041	0.67	0.0075	0.039	0.64	0.0072
C16	73311680	rs2432543 rs4887826	TG	-	0.069	0.043	0.61	0.000010	0.042	0.60	0.00046	0.049	0.69	0.019
C17	69180675	rs17763769 rs1860316	GA	-	0.511	0.564	1.24	0.000013	0.585	1.35	0.0000023	0.543	1.14	0.069
C17	69203439	rs1860316	A	-	0.653	0.707	1.28	0.0000020	0.734	1.46	3.2×10 ⁻⁸	0.687	1.17	0.039
C17	69242752	rs1860316 rs17763811	GC	-	0.335	0.282	0.78	0.0000028	0.254	0.68	2.6×10 ⁻⁸	0.301	0.86	0.039
C17	69218316	rs1981647	C	-	0.513	0.563	1.23	0.000026	0.583	1.33	0.0000065	0.544	1.14	0.071
C17	69234630	rs1843622	T	-	0.615	0.665	1.24	0.000021	0.684	1.35	0.0000043	0.640	1.11	0.14

C17	69244944	rs2191113	A	-	0.696	0.744	1.27	0.000013	0.771	1.47	9.5×10 ⁻⁸	0.713	1.08	0.30
C17	69259003	rs9890889	A	-	0.839	0.869	1.27	0.00053	0.885	1.47	0.000032	0.857	1.14	0.17
C18	41051796	rs10502860	G	-	0.167	0.194	1.20	0.0035	0.218	1.39	0.000028	0.174	1.05	0.61
C18	63451377	rs764133 rs7237209	TT	-	0.167	0.132	0.76	0.00010	0.121	0.69	0.000048	0.135	0.78	0.014
C18	63463071	rs7237209	C	-	0.819	0.852	1.27	0.00028	0.867	1.44	0.000029	0.847	1.22	0.037
C19	3316583	rs3810420	A	-	0.176	0.189	1.09	0.16	0.227	1.37	0.000045	0.146	0.80	0.021
C20	37651862	rs4592915 rs2232580	GC	rs6127771 C (1)	0.495	0.550	1.25	0.0000048	0.558	1.29	0.000051	0.543	1.21	0.0060
C21	13769165	rs468601	A	-	0.888	0.908	1.25	0.0054	0.927	1.60	0.000026	0.895	1.08	0.48
C21	33296778	rs2834061	G	-	0.249	0.291	1.24	0.000076	0.311	1.36	0.0000094	0.271	1.12	0.15
C21	39373432	rs369906	T	-	0.566	0.613	1.21	0.00010	0.631	1.31	0.000028	0.587	1.09	0.24

Gene														
C03	69453958	rs10510980	A	ENST00000343145 (K211R)	0.808	0.840	1.25	0.00065	0.836	1.22	0.019	0.845	1.30	0.0061
C08	118141371	rs13266634	C	SLC30A8 (R325W)	0.646	0.685	1.19	0.00060	0.678	1.16	0.030	0.697	1.26	0.0020
C10	124472418	rs2495774	G	LOC390009 (Q27H)	0.547	0.594	1.21	0.00011	0.592	1.20	0.0039	0.597	1.22	0.0043
C11	3624302	rs2271586	T	ART5 (T284K)	0.176	0.208	1.23	0.00059	0.212	1.26	0.0033	0.203	1.20	0.042
C19	8669900	rs10410943	G	MGC33407 (A51V)	0.674	0.714	1.20	0.00043	0.713	1.20	0.0076	0.708	1.17	0.035

^aA surrogate of the corresponding two marker haplotype with a correlation coefficient r^2 . ^b P values adjusted for relatedness and population stratification using genomic control (see **Methods**).