

**Online supplemental Table S1. Characteristics and quality criteria for tagging SNPs in/around the *CNR1* gene<sup>a</sup>.**

SNP	SNP position	Callrate	HWE P	Allele 1 (%)	Allele 2 (%)	Genotype 1	Genotype 2	Genotype 3	Genotype 1 count (%)	Genotype 2 count (%)	Genotype 3 count (%)
<b>rs10485171</b>	88900109	0.97	0.559	T (56.7)	C (43.3)	C/C	T/C	T/T	529 (19.5)	1306 (48.2)	872 (32.2)
<b>rs806365</b>	88902668	0.99	1.000	C (57.4)	T (42.6)	C/C	C/T	T/T	896 (32.3)	1335 (48.2)	537 (19.4)
<b>rs7766029</b>	88904154	0.99	0.143	C (52.9)	T (47.1)	C/C	C/T	T/T	758 (27.5)	1378 (50)	617 (22.4)
<b>rs806366</b>	88904308	0.98	0.876	C (50.0)	T (50.0)	C/C	C/T	T/T	742 (27.0)	1375 (50.1)	623 (22.7)
<b>rs806368</b>	88906819	0.99	0.350	T (76.4)	C (23.6)	C/C	T/C	T/T	136 (4.8)	953 (34.3)	1688 (60.7)
<b>rs12720071</b>	88907900	0.94	0.327	A (89.3)	G (10.7)	A/A	A/G	G/G	2136 (81.2)	472 (17.9)	21 (0.01)
<b>rs1049353</b>	88910354	0.98	0.269	G (74.8)	A (25.2)	A/A	G/A	G/G	172 (6.2)	1021 (37.1)	1556 (56.6)
<b>rs806369</b>	88912897	0.99	0.899	C (71.0)	T (29.0)	C/C	C/T	T/T	1400 (50.5)	1108 (40)	261 (9.4)
<b>rs806371</b>	88913082	1.00	0.750	T (85.8)	G (14.2)	G/G	T/G	T/T	48 (1.7)	646 (23.1)	2095 (75.1)
<b>rs806374</b>	88914039	0.99	0.575	T (63.7)	C (36.3)	C/C	T/C	T/T	347 (12.4)	1236 (44.5)	1194 (43)
<b>rs806375</b>	88915240	0.99	0.750	A (57.0)	T (43.0)	A/A	A/T	T/T	882 (31.9)	1345 (48.6)	535 (19.3)
<b>rs806376</b>	88915367	0.98	0.601	T (51.7)	C (48.3)	C/C	T/C	T/T	653 (23.8)	1386 (50.5)	703 (25.6)
<b>*rs6928813</b>	88918417	0.96	0.000	A (83.8)	G (16.2)	A/A	A/G	G/G	1948 (72.4)	623 (23.1)	118 (4.3)
<b>rs806380</b>	88921372	0.98	0.954	A (65.4)	G (34.6)	A/A	A/G	G/G	1143 (41.6)	1235 (45)	364 (13.2)
<b>rs7752758</b>	88923095	0.99	0.128	A (89.5)	G (10.5)	A/A	A/G	G/G	2221 (80.0)	517 (18.6)	37 (1.3)
<b>rs12528858</b>	88924207	0.98	0.807	A (94.3)	G (5.7)	A/A	A/G	G/G	2434 (88.9)	291 (10.6)	11 (0.01)
<b>rs12205430</b>	88924644	0.95	0.131	T (79.0)	C (21.0)	C/C	T/C	T/T	143 (5.4)	854 (32.2)	1651 (62.3)

<b>rs6454673</b>	88927768	0.99	0.319	G (70.4)	A (29.6)	A/A	G/A	G/G	280 (10.0)	1158 (41.6)	1339 (48.2)
<b>rs6914429</b>	88928435	0.97	0.027	A (88.6)	C (11.4)	A/A	A/C	C/C	2192 (80.5)	482 (17.7)	47 (1.7)

<sup>a</sup>Abbreviations: SNP = single nucleotide polymorphism. HWE *P* = *P* value for departure of Hardy–Weinberg equilibrium.

SNP rs6928813 was not included in the statistical analysis, as its observed genotype frequencies deviated from Hardy–Weinberg equilibrium (HWE) (*P*<0.001).

All minor allele frequencies (MAF) are > 5% (percentage in the allele 2 column).

**Online supplemental Table S2. Association of tagging SNPs in/around the *CNR1* gene with glucose-related traits at exam 7<sup>a</sup>.**

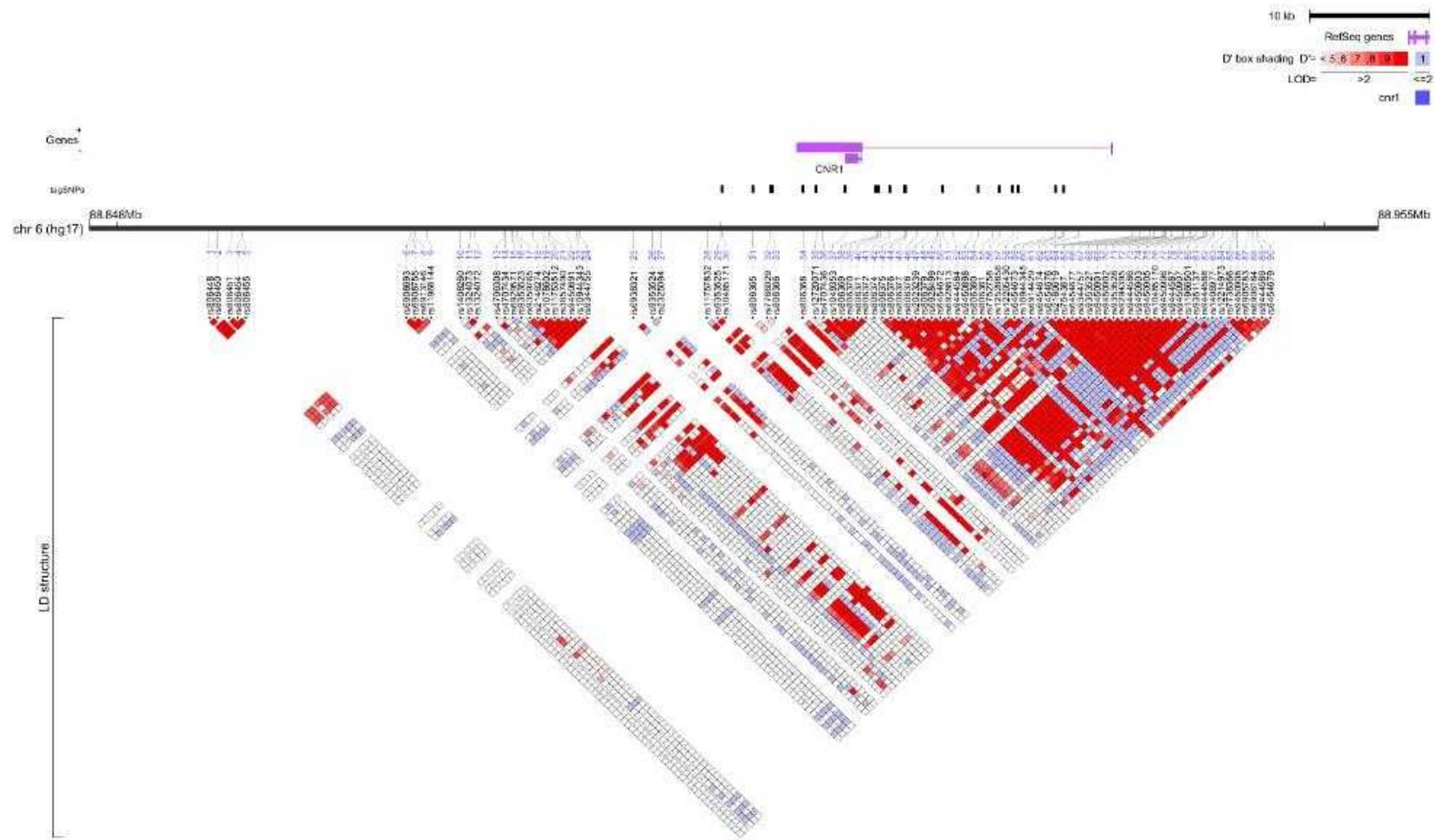
SNP	SNP position	Risk allele (% frequency) / other (%)	Trait	$\beta$ estimate (standard error)	Nominal <i>P</i> value	Empirical <i>P</i> value
rs10485171	88900109	C (43.3) / T (56.7)	Fasting glucose	0.01 (0.0054)	0.066	0.55
rs806365	88902668	C (57.4) / T (42.6)	Fasting glucose	0.014 (0.0054)	0.0084	0.11
rs7766029	88904154	C (52.9) / T (47.1)	Fasting glucose	0.0053 (0.0054)	0.32	0.98
rs806366	88904308	T (50.0) / C (50.0)	Fasting glucose	0.0031 (0.0053)	0.56	1
rs806368	88906819	C (23.6) / T (76.4)	Fasting glucose	0.0049 (0.0064)	0.44	1
rs12720071	88907900	A (89.3) / G (10.7)	Fasting glucose	0.0023 (0.0094)	0.8	1
rs1049353	88910354	A (25.2) / G (74.8)	Fasting glucose	0.00083 (0.0061)	0.89	1
rs806369	88912897	C (71.0) / T (29.0)	Fasting glucose	0.013 (0.0058)	0.028	0.3
rs806371	88913082	G (14.2) / T (85.8)	Fasting glucose	0.0091 (0.0077)	0.23	0.95
rs806374	88914039	T (63.7) / C (36.3)	Fasting glucose	0.0038 (0.0055)	0.49	1
rs806375	88915240	T (43.0) / A (57.0)	Fasting glucose	0.01 (0.0053)	0.057	0.5
rs806376	88915367	C (48.3) / T (51.7)	Fasting glucose	0.0071 (0.0054)	0.19	0.91
rs806380	88921372	G (34.6) / A (65.4)	Fasting glucose	0.0051 (0.0055)	0.36	0.99
rs7752758	88923095	G (10.5) / A (89.5)	Fasting glucose	0.0057 (0.0085)	0.5	1
rs12528858	88924207	A (94.3) / G (5.7)	Fasting glucose	0.0054 (0.011)	0.63	1
rs12205430	88924644	C (21.0) / T (79.0)	Fasting glucose	0.0039 (0.0065)	0.55	1
rs6454673	88927768	A (29.6) / G (70.4)	Fasting glucose	0.0051 (0.0057)	0.37	0.99

rs6914429	88928435	C (11.4) / A (88.6)	Fasting glucose	0.0068 (0.0085)	0.42	1	
rs10485171	88900109	C (43.3) / T (56.7)	HbA1C	0.0014 (0.0044)	0.74	1	
rs806365	88902668	C (57.4) / T (42.6)	HbA1C	0.0041 (0.0043)	0.35	0.99	
rs7766029	88904154	C (52.9) / T (47.1)	HbA1C	0.0031 (0.0044)	0.47	1	
rs806366	88904308	T (50.0) / C (50.0)	HbA1C	0.0028 (0.0043)	0.51	1	
rs806368	88906819	C (23.6) / T (76.4)	HbA1C	0.0083 (0.0052)	0.11	0.72	
rs12720071	88907900	G (10.7) / A (89.3)	HbA1C	0.0057 (0.0076)	0.45	1	
rs1049353	88910354	G (74.8) / A (25.2)	HbA1C	0.0055 (0.0049)	0.27	0.97	
rs806369	88912897	C (71.0) / T (29.0)	HbA1C	0.0066 (0.0047)	0.16	0.87	
rs806371	88913082	G (14.2) / T (85.8)	HbA1C	0.0064 (0.0063)	0.31	0.98	
rs806374	88914039	C (36.3) / T (63.7)	HbA1C	0.0044 (0.0044)	0.32	0.98	
rs806375	88915240	T (43.0) / A (57.0)	HbA1C	0.0048 (0.0043)	0.27	0.97	
rs806376	88915367	C (48.3) / T (51.7)	HbA1C	0.0045 (0.0044)	0.3	0.98	
rs806380	88921372	A (65.4) / G (34.6)	HbA1C	0.0041 (0.0045)	0.36	0.99	
rs7752758	88923095	G (10.5) / A (89.5)	HbA1C	0.00043 (0.0068)	0.95	1	
rs12528858	88924207	A (94.3) / G (5.7)	HbA1C	0.011 (0.0091)	0.24	0.95	
rs12205430	88924644	C (21.0) / T (79.0)	HbA1C	0.00095 (0.0052)	0.86	1	
rs6454673	88927768	A (29.6) / G (70.4)	HbA1C	0.00038 (0.0046)	0.93	1	
rs6914429	88928435	C (11.4) / A (88.6)	HbA1C	0.01 (0.0067)	0.13	0.82	

<sup>a</sup>Abbreviations: SNP = single nucleotide polymorphism. HbA1C: Hemoglobin A1C at exam 7. Results are derived from age-, sex-, BMI-adjusted models.

The  $\beta$  estimates reflect the additive effect of the risk allele on the log-transformed outcome. Nominal and empirical  $P$  values: To determine the distribution of the minimum  $P$  value across all SNPs under the null hypothesis of no association, we simulated 1,000 traits for our sample, as an approach to correct for the multiple SNPs tested. The empirical  $P$  values correspond to the proportion of simulated minimum  $P$  values smaller or equal to the observed nominal  $P$  values in our data. An empirical value  $<0.05$  denotes statistical significance.

SNP rs6928813 was not included in the statistical analysis, as its observed genotype frequencies deviated from Hardy–Weinberg equilibrium (HWE) ( $P<0.001$ ).



Online supplemental FIGURE S1