

Supplementary Methods:

MAGIC (Meta-Analyses of Glucose and Insulin-related traits Consortium): HbA1C meta-analysis methods – see Supplementary Table 9 for list of investigators.

We obtained summary statistics for HbA1c associations from a meta-analysis of HbA1c levels carried out by MAGIC (unpublished data). Briefly, the meta-analysis included 23 cohorts with available HbA1c measurements and GWAS genotypes, for a total of 27,589 to 36,585 individuals depending on the SNPs analyzed. Cohorts included: B58C-WTCCC (N=1,428), BLSA (N=490), DGI (N=480), EPIC cancer cases (N=957), EPIC cohort (N=1,911), Fenland (N=1,378), FHS (N=1,996), KORA F3 (N=1,644), Lolipop (N=770), SardiNIA (N=3,346), 1958BC-T1DGC (N=2,501), ARIC (N=6,777), Croatia (N=659), deCODE (N=342), DESIR (N=731), GenomeEUtwin (N=568), HEALTH2000 (N=1,205), KORA_S4 (N=1,814), NTRNESDA (N=1,452), ORCADES (N=651), PROCARDIS (N=831), SHIP (N=3,538) and Sorbs (N=630), see (26) for details.

All participants were adults of white ancestry from Europe or the United States, and free of diabetes (define as either receiving diabetes treatment or having a fasting glucose ≥ 7 mmol/L). Local research ethic committees approved all studies and all participants gave informed consent. In each study glycated hemoglobin (HbA1c, in %) was measured from whole blood (fasting or non-fasting), with NGSP-certified methods. SNPs were either directly genotyped or imputed from the HapMap CEU phase 2 reference panel using the software MACH or IMPUTE. QC metrics were applied to genotyped (Hardy-Weinberg equilibrium $P < 10^{-4}$ or 10^{-6} and call-rate < 0.90 or 0.95) and imputed (observed-by-expected variance ratio (r^2 .hat) < 0.3 (if MACH was used for imputation), proper-info < 0.4 (if IMPUTE was used)) SNPs. In each cohort, a linear regression model was fitted using untransformed HbA1c as the dependent variable to evaluate the additive effect of genotyped and imputed SNPs, adjusting for age, sex, study-site (when applicable) and/or family structure. Regression estimates for each SNP were combined across studies in a meta-analysis using a fixed effect inverse-variance approach, as implemented in METAL software.

Supplementary Table 1. Association results for mean HbA1c in DCCT, separately by treatment group and combined, for SNPs that have previously been associated with HbA1c in non-diabetic individuals (see introduction for details and references).

chr	snp	position	Gene region	alleles	freq1	rsqr	Conventional Group p value	Intensive Group p value	Combined Groups p value
2	rs1260326	27,584,444	GCKR	C,T	0.59	1	0.34	0.15	0.76
2	rs780094	27,594,741	GCKR	C,T	0.6	1	0.33	0.15	0.77
2	rs1402837	169,465,600	G6PC2/ABCB11	C,T	0.78	1	0.93	0.36	0.49
2	rs560887	169,471,394	G6PC2/ABCB11	C,T	0.71	1	0.86	0.6	0.79
2	rs563694	169,482,317	G6PC2/ABCB11	A,C	0.66	1	0.87	0.99	0.96
2	rs552976	169,499,684	G6PC2/ABCB11	A,G	0.35	1	0.68	0.90	1.00
2	rs6709087	169,507,256	G6PC2/ABCB11	A,G	0.77	1	0.54	0.34	0.87
7	rs10244051	15,030,358	-	G,T	0.54	1	0.23	0.34	0.13
7	rs2191348	15,030,780	-	G,T	0.46	1	0.23	0.35	0.14
7	rs1799884	44,195,593	GCK	C,T	0.82	1	0.33	0.25	0.1
7	rs730497	44,263,224	GCK	A,G	0.18	1	0.32	0.25	0.10
7	rs4607517	44,275,173	GCK	A,G	0.18	1	0.36	0.24	0.10
8	rs2722425	40,603,396	ZMAT4	C,T	0.89	1	0.9	0.19	0.49
8	rs13266634	118,253,694	SLC30A8	C,T	0.69	1	0.03	0.08	0.73
9	rs4240702	136,735,680	-	C,T	0.54	1	0.84	0.65	0.58
10	rs906216	70,768,201	HK1	G,T	0.55	1	0.61	0.87	0.62
10	rs7072268	70,769,919	HK1	C,T	0.52	1	0.69	0.81	0.76
10	rs2305198	70,798,881	HK1	C,T	0.39	1	0.35	0.16	0.17
10	rs7901695	114,744,078	TCF7L2	C,T	0.32	1	0.36	0.23	0.80
11	rs1387153	92,313,476	MTNR1B	C,T	0.71	1	0.37	0.51	0.75
11	rs10765573	92,322,980	MTNR1B	A,T	0.34	0.99	0.12	0.44	0.51
11	rs7936247	92,329,680	MTNR1B	G,T	0.66	0.99	0.12	0.45	0.51
11	rs11020124	92,330,309	MTNR1B	C,T	0.29	0.97	0.37	0.55	0.74
11	rs10830963	92,348,358	MTNR1B	C,G	0.7	0.88	0.18	0.3	0.65
11	rs1447352	92,362,409	MTNR1B	A,G	0.52	1	0.15	0.24	0.68

Supplementary Table 2. Definitions of complications outcomes, statistical models, covariates included and the prevalence of outcomes separately by treatment group

System	Specific outcome	Time period	Model	Covariates	Outcome Frequency (number with event /number censored) etc.	Conventional	Intensive
Retinal ^{29, 43}							
	Mild Retinopathy: Time from DCCT baseline to mild non-proliferative diabetic retinopathy (EDTRS step 4, patient level 35/<35) *	DCCT and EDIC yr10	Cox Proportional Hazards	Stratified by DCCT year of entry, cohort as covariate	75% (807 vs 264), 1071	85% (453 vs 82), 535	66% (354 vs 182), 536
	Severe retinopathy: Time from DCCT baseline to severe non-proliferative retinopathy (ETDRS step 10, patient level at least 53/>53) or scatter laser	"	"	"	19% (246 vs 1057) = 1304	27% (178 vs 488), 666	11% (68 vs 569), 637
	Clinically Significant Macular Edema: Time from DCCT baseline to macular edema or focal laser	"	"	"	18% (240 vs 1064) = 1303	24% (162 vs 505), 667	12% (78 vs 559), 637
Renal ^{11, 29}							
	Persistent Microalbuminuria: Time from DCCT baseline to the first of two consecutive visits with Albumin Excretion Rate >30 mg/day	DCCT and EDIC yr12	"	"	22% (268 vs 976)	28% (177 vs 462), 639	15% (91 vs 514), 605
	Severe nephropathy: Time from DCCT entry to either Albumin Excretion Rate >300 mg/day or dialysis or transplant (plus two consecutive visits with Albumin Excretion Rate >30 mg/day)	"	"	"	10% (132 vs 1172)	15% (101 vs 566), 667	5% (32 vs 605), 637
Cardiac ¹⁰							
	Coronary Calcium	EDIC yr 7-9	Tobit regression with log coronary calcium	4 models with difference covariates	759 (69%) with zero values, 1102	382 with zero values, median in 176 >0 is 74	377 with zero values, median in 167 with >0 is 51
Neuropathy ¹							
	Confirmed Clinical Neuropathy	EDIC yr 13/14	Logistic regression	none	30%, 303 case, 723 control, 1026 total	34%, 171 case, 334 control, 505 total	25%, 132 case, 389 control, 521 total
System	Specific outcome	Time period	Model	Covariates	Outcome Frequency (number with event /number censored) etc.	Conventional	Intensive
Hypoglycemia ^{44, 45}							
	Requiring medical assistance (DEF2)	During DCCT	Ordinal regression	none	656 with no events, 198 with one event, 450 with >1 event	429 with no events, 100 with one event, 138 with >1 event	227 with no events, 98 with one event, 312 with >1 event
	Resulting in coma/seizure (DEF1)	"	"	none	938 with no events, 187 with one event, 179 with >1 event	540 with no events, 82 with one event, 45 with >1 event	398 with no events, 105 with one event, 134 with >1 event

*Approximately 20% of the secondary intervention cohort had Mild Retinopathy at baseline thus the smaller sample size for time-to-event.

Supplementary Table 3. Association results of top 13 SNPs for HbA1c in DCCT with renal complications in DCCT/EDIC.

nearest gene	chr	pos	snp	trx	hazard ratio	mild renal					severe renal					multivariate p value	
						univariate p value		multivariate p value		univariate p value		multivariate p value					
						HR lower CI	HR upper CI	HR lower CI	HR upper CI	HR lower CI	HR upper CI	HR lower CI	HR upper CI	HR lower CI	HR upper CI		
BNC2	9	16,791,850	rs2254193	intensive	0.7726	0.4215	1.4159	3.88E-1	3.97E-1	9E-08	0	8.95E-4	2.29E-3				
BNC2	9	16,791,850	rs2254193	conventional	1.9806	1.3865	2.8292	5.32E-4	1.38E-3	2.1222	1.3545	3.3248	2.51E-3	1.29E-2			
BNC2	9	16,791,850	rs2254193	combined	1.3411	0.9847	1.8266	7.28E-2	6.69E-2	1.2638	0.8192	1.9497	3.05E-1	2.13E-1			
BNC2	9	16,779,878	rs4961760	intensive	0.8045	0.4595	1.4086	4.34E-1	4.41E-1	0.3193	0.0777	1.3125	5.68E-2	8.42E-2			
BNC2	9	16,779,878	rs4961760	conventional	1.8005	1.2806	2.5315	1.57E-3	2.95E-3	1.8125	1.1659	2.8176	1.33E-2	3.85E-2			
BNC2	9	16,779,878	rs4961760	combined	1.2938	0.9666	1.7318	9.35E-2	7.61E-2	1.2338	0.8191	1.8584	3.28E-1	3.03E-1			
BNC2	9	16,779,436	rs6475082	intensive	0.8045	0.4595	1.4086	4.34E-1	4.41E-1	0.3193	0.0777	1.3125	5.68E-2	8.42E-2			
BNC2	9	16,779,436	rs6475082	conventional	1.8171	1.2923	2.555	1.35E-3	2.72E-3	1.826	1.1745	2.8387	1.23E-2	3.80E-2			
BNC2	9	16,779,436	rs6475082	combined	1.2974	0.9693	1.7365	9.01E-2	7.39E-2	1.2369	0.8212	1.8629	3.22E-1	3.01E-1			
BNC2	9	16,779,024	rs10810632	intensive	0.8045	0.4595	1.4086	4.34E-1	4.41E-1	0.3193	0.0777	1.3125	5.68E-2	8.42E-2			
BNC2	9	16,779,024	rs10810632	conventional	1.8455	1.3128	2.5943	1.02E-3	2.01E-3	1.8498	1.1899	2.8755	1.07E-2	3.41E-2			
BNC2	9	16,779,024	rs10810632	combined	1.3085	0.9777	1.7511	8.03E-2	6.74E-2	1.2438	0.826	1.8729	3.10E-1	2.94E-1			
SORCS1	10	108,113,589	rs1358030	intensive	1.2493	0.9347	1.6697	1.36E-1	6.01E-2	1.0033	0.6138	1.6399	9.90E-1	9.18E-1			
SORCS1	10	108,113,589	rs1358030	conventional	1.2564	1.0087	1.565	4.29E-2	4.22E-2	1.3942	1.0413	1.8667	2.66E-2	6.03E-2			
SORCS1	10	108,113,589	rs1358030	combined	1.2617	1.0628	1.4979	8.47E-3	1.11E-2	1.2355	0.9708	1.5723	8.81E-2	1.52E-1			
GSC	14	94,407,241	rs8007115	intensive	0.8798	0.6209	1.2468	4.66E-1	5.27E-1	0.77	0.4186	1.4162	3.88E-1	5.65E-1			
GSC	14	94,407,241	rs8007115	conventional	1.0938	0.8498	1.4078	4.89E-1	8.11E-1	1.0123	0.7223	1.4187	9.44E-1	5.17E-1			
GSC	14	94,407,241	rs8007115	combined	0.9888	0.8084	1.2095	9.13E-1	7.98E-1	0.9275	0.6931	1.2411	6.10E-1	6.79E-1			
GSC	14	94,405,244	rs11160219	intensive	0.9024	0.6387	1.275	5.57E-1	6.25E-1	0.8332	0.4601	1.5087	5.40E-1	6.67E-1			
GSC	14	94,405,244	rs11160219	conventional	1.0684	0.8315	1.3729	6.07E-1	9.20E-1	0.9866	0.7039	1.3829	9.37E-1	4.58E-1			
GSC	14	94,405,244	rs11160219	combined	0.9836	0.8048	1.2022	8.72E-1	8.18E-1	0.9219	0.6895	1.2327	5.81E-1	6.98E-1			
GSC	14	94,375,765	rs11624318	intensive	1.0109	0.7093	1.4408	9.52E-1	6.29E-1	0.7649	0.4017	1.4565	4.00E-1	6.05E-1			
GSC	14	94,375,765	rs11624318	conventional	0.9463	0.7272	1.2314	6.80E-1	2.98E-1	1.0186	0.7271	1.4269	9.15E-1	6.52E-1			
GSC	14	94,375,765	rs11624318	combined	0.9722	0.7877	1.1999	7.92E-1	6.80E-1	0.9602	0.7128	1.2935	7.89E-1	8.31E-1			
WDR72	15	51,296,486	rs482541	intensive	1.3587	0.8851	2.0858	1.76E-1	3.65E-2	1.0248	0.469	2.2389	9.51E-1	5.98E-1			
WDR72	15	51,296,486	rs482541	conventional	0.9481	0.6674	1.3468	7.64E-1	8.60E-1	0.7382	0.4407	1.2367	2.30E-1	3.45E-1			
WDR72	15	51,296,486	rs482541	combined	1.0915	0.8338	1.4288	5.28E-1	1.57E-1	0.8038	0.524	1.2329	3.02E-1	9.20E-1			
WDR72	15	51,295,884	rs566369	intensive	1.3587	0.8851	2.0858	1.76E-1	3.65E-2	1.0248	0.469	2.2389	9.51E-1	5.98E-1			
WDR72	15	51,295,884	rs566369	conventional	0.9481	0.6674	1.3468	7.64E-1	8.60E-1	0.7382	0.4407	1.2367	2.30E-1	3.45E-1			
WDR72	15	51,295,884	rs566369	combined	1.0915	0.8338	1.4288	5.28E-1	1.57E-1	0.8038	0.524	1.2329	3.02E-1	9.20E-1			
WDR72	15	51,291,964	rs690271	intensive	1.3587	0.8851	2.0858	1.76E-1	3.65E-2	1.0248	0.469	2.2389	9.51E-1	5.98E-1			
WDR72	15	51,291,964	rs690271	conventional	0.95	0.6688	1.3494	7.73E-1	8.66E-1	0.7396	0.4416	1.2388	2.32E-1	3.45E-1			
WDR72	15	51,291,964	rs690271	combined	1.0922	0.8343	1.4297	5.26E-1	1.56E-1	0.8042	0.5243	1.2336	3.03E-1	9.21E-1			
WDR72	15	51,291,924	rs572221	intensive	1.3659	0.89	2.0962	1.69E-1	3.57E-2	1.0263	0.4699	2.2415	9.48E-1	5.99E-1			
WDR72	15	51,291,924	rs572221	conventional	0.95	0.6688	1.3494	7.73E-1	8.66E-1	0.7396	0.4416	1.2388	2.32E-1	3.45E-1			
WDR72	15	51,291,924	rs572221	combined	1.0947	0.8363	1.4328	5.15E-1	1.55E-1	0.8052	0.525	1.235	3.06E-1	9.16E-1			
WDR72	15	51,277,554	rs493218	intensive	1.3587	0.8851	2.0858	1.76E-1	3.65E-2	1.0412	0.4767	2.2737	9.20E-1	5.70E-1			
WDR72	15	51,277,554	rs493218	conventional	0.9247	0.6483	1.319	6.63E-1	7.82E-1	0.6959	0.4093	1.1831	1.59E-1	2.96E-1			
WDR72	15	51,277,554	rs493218	combined	1.0748</td												

Supplementary Table 4. Association results of top 13 SNPs for HbA1c in DCCT with coronary calcium measured during EDIC.

nearest gene	CHR	pos	snp	GROUP	M1 p value	M2 p value	M3 p value	M4 p value	M1 parameter estimate	M1 SE	M2 parameter estimate	M2 SE	M3 parameter estimate	M3 SE	M4 parameter estimate	M4 SE
					0.24424	0.23373	0.37679	0.30206	0.89	0.76	0.81	0.68	0.56	0.63	0.64	0.62
BNC2	9	16,779,024	rs10810632	conventional	0.24424	0.23373	0.37679	0.30206	0.89	0.76	0.81	0.68	0.56	0.63	0.64	0.62
BNC2	9	16,779,024	rs10810632	intensive	0.13643	0.0379	0.01862	0.0186	0.99	0.66	1.25	0.6	1.34	0.57	1.34	0.57
BNC2	9	16,779,024	rs10810632	COMBINED	0.06475	0.04556	0.07268	0.04541	0.93	0.5	0.9	0.45	0.76	0.42	0.84	0.42
BNC2	9	16,779,436	rs6475082	conventional	0.2776	0.26097	0.39401	0.31815	0.83	0.76	0.76	0.67	0.54	0.63	0.62	0.62
BNC2	9	16,779,436	rs6475082	intensive	0.13643	0.0379	0.01862	0.0186	0.99	0.66	1.25	0.6	1.34	0.57	1.34	0.57
BNC2	9	16,779,436	rs6475082	COMBINED	0.07264	0.05217	0.07922	0.05034	0.9	0.5	0.87	0.45	0.74	0.42	0.82	0.42
BNC2	9	16,779,878	rs4961760	conventional	0.30866	0.30326	0.42986	0.35022	0.78	0.76	0.7	0.67	0.5	0.63	0.58	0.61
BNC2	9	16,779,878	rs4961760	intensive	0.13643	0.0379	0.01862	0.0186	0.99	0.66	1.25	0.6	1.34	0.57	1.34	0.57
BNC2	9	16,779,878	rs4961760	COMBINED	0.07986	0.05846	0.0845	0.05391	0.88	0.5	0.85	0.45	0.73	0.42	0.81	0.42
BNC2	9	16,791,850	rs2254193	conventional	0.2438	0.25557	0.37916	0.30716	0.95	0.81	0.82	0.72	0.59	0.67	0.68	0.66
BNC2	9	16,791,850	rs2254193	intensive	0.31739	0.09241	0.05748	0.05338	0.7	0.7	1.07	0.64	1.15	0.6	1.17	0.6
BNC2	9	16,791,850	rs2254193	COMBINED	0.13581	0.08898	0.15687	0.10153	0.8	0.53	0.81	0.48	0.64	0.45	0.73	0.45
SORCS1	10	108,113,589	rs1358030	conventional	0.1864	0.1295	0.0276	0.0198	0.56	0.43	0.58	0.38	0.8	0.36	0.83	0.36
SORCS1	10	108,113,589	rs1358030	intensive	0.1877	0.107	0.0761	0.0502	0.53	0.4	0.59	0.37	0.62	0.35	0.68	0.35
SORCS1	10	108,113,589	rs1358030	COMBINED	0.0608	0.0282	0.0095	0.0043	0.55	0.29	0.58	0.26	0.65	0.25	0.71	0.25
GSC	14	94,375,765	rs11624318	conventional	0.0338	0.06319	0.01727	0.01987	1.04	0.49	0.81	0.44	0.95	0.4	0.93	0.4
GSC	14	94,375,765	rs11624318	intensive	0.56384	0.24589	0.29317	0.21918	-0.28	0.48	-0.52	0.45	-0.45	0.42	-0.52	0.42
GSC	14	94,375,765	rs11624318	COMBINED	0.25733	0.49085	0.21342	0.26365	0.39	0.34	0.21	0.31	0.36	0.29	0.33	0.29
GSC	14	94,405,244	rs11160219	conventional	0.39221	0.3388	0.16105	0.21132	0.41	0.48	0.42	0.44	0.59	0.42	0.52	0.41
GSC	14	94,405,244	rs11160219	intensive	0.83883	0.71476	0.48678	0.43876	-0.09	0.46	-0.15	0.42	-0.28	0.4	-0.31	0.4
GSC	14	94,405,244	rs11160219	COMBINED	0.64742	0.76645	0.50959	0.63954	0.15	0.33	0.09	0.3	0.19	0.29	0.13	0.29
GSC	14	94,407,241	rs8007115	conventional	0.39029	0.34282	0.15165	0.19768	0.42	0.48	0.42	0.45	0.6	0.42	0.54	0.42
GSC	14	94,407,241	rs8007115	intensive	0.82192	0.69159	0.51525	0.44594	-0.1	0.46	-0.17	0.42	-0.26	0.4	-0.3	0.4
GSC	14	94,407,241	rs8007115	COMBINED	0.65577	0.78948	0.4696	0.59935	0.15	0.33	0.08	0.31	0.21	0.29	0.15	0.29
WDR72	15	51,277,554	rs493218	conventional	0.61858	0.70967	0.52761	0.52509	-0.33	0.67	-0.22	0.6	0.35	0.56	0.36	0.56
WDR72	15	51,277,554	rs493218	intensive	0.14821	0.15828	0.03032	0.09229	0.87	0.6	0.78	0.55	1.15	0.53	0.88	0.52
WDR72	15	51,277,554	rs493218	COMBINED	0.49992	0.60516	0.114	0.16924	0.3	0.45	0.21	0.41	0.61	0.39	0.53	0.38
WDR72	15	51,291,924	rs572221	conventional	0.72723	0.77537	0.54209	0.54754	-0.23	0.66	-0.17	0.6	0.34	0.56	0.34	0.56
WDR72	15	51,291,924	rs572221	intensive	0.15599	0.15476	0.02977	0.09129	0.86	0.6	0.79	0.55	1.16	0.53	0.88	0.52
WDR72	15	51,291,924	rs572221	COMBINED	0.44957	0.56355	0.11907	0.17809	0.34	0.45	0.24	0.41	0.6	0.38	0.52	0.38
WDR72	15	51,291,964	rs690271	conventional	0.72723	0.77537	0.54209	0.54754	-0.23	0.66	-0.17	0.6	0.34	0.56	0.34	0.56
WDR72	15	51,291,964	rs690271	intensive	0.16647	0.16637	0.0326	0.09809	0.83	0.6	0.77	0.55	1.14	0.53	0.86	0.52
WDR72	15	51,291,964	rs690271	COMBINED	0.46457	0.5825	0.12452	0.18581	0.33	0.45	0.22	0.41	0.59	0.38	0.51	0.38
WDR72	15	51,295,884	rs566369	conventional	0.71659	0.74533	0.56241	0.56688	-0.24	0.66	-0.19	0.6	0.32	0.56	0.32	0.56
WDR72	15	51,295,884	rs566369	intensive	0.16647	0.16637	0.0326	0.09809	0.83	0.6	0.77	0.55	1.14	0.53	0.86	0.52
WDR72	15	51,295,884	rs566369	COMBINED	0.4706	0.59601	0.1278	0.19031	0.32	0.45	0.22	0.41	0.59	0.38	0.5	0.38
WDR72	15	51,296,486	rs482541	conventional	0.71659	0.74533	0.56241	0.56688	-0.24	0.66	-0.19	0.6	0.32	0.56	0.32	0.56
WDR72	15	51,296,486	rs482541	intensive	0.16647	0.16637	0.0326	0.09809	0.83	0.6	0.77	0.55	1.14	0.53	0.86	0.52
WDR72	15	51,296,486	rs48254													

Supplementary Table 5. Association results of top 13 SNPs for HbA1c in DCCT with hypoglycemia during DCCT.

nearest gene	ch r	pos	snp	GROUP	ordinal uv def1=coma/seizure				ordinal a1c def1				ordinal uv def2=requiring assistance				ORDINAL DEF2 WITH A1c			
					ProbChisq	Odds Ratio	Lower CL	Upper CL	ProbChisq	Odds Ratio	Lower CL	Upper CL	ProbChisq	Odds Ratio	Lower CL	Upper CL	ProbChisq	Odds Ratio	Lower CL	Upper CL
BNC2	9	16,779,024	rs10810632	INTENSIVE	5.8E-01	0.89	0.60	1.33	6.1E-01	0.90	0.60	1.35	9.4E-01	1.02	0.70	1.47	9.4E-01	1.01	0.70	1.47
BNC2	9	16,779,024	rs10810632	CONVENTIONAL	9.9E-02	0.59	0.32	1.10	4.9E-01	0.80	0.42	1.51	4.4E-03	0.49	0.30	0.80	1.0E-01	0.66	0.39	1.09
BNC2	9	16,779,024	rs10810632	COMBINED	2.5E-01	0.83	0.60	1.14	3.6E-01	0.86	0.61	1.19	2.7E-01	0.86	0.65	1.13	4.2E-01	0.89	0.67	1.18
BNC2	9	16,779,436	rs6475082	INTENSIVE	5.8E-01	0.89	0.60	1.33	6.1E-01	0.90	0.60	1.35	9.4E-01	1.02	0.70	1.47	9.4E-01	1.01	0.70	1.47
BNC2	9	16,779,436	rs6475082	CONVENTIONAL	1.5E-01	0.64	0.35	1.17	6.2E-01	0.85	0.46	1.58	7.3E-03	0.51	0.32	0.84	1.4E-01	0.69	0.42	1.14
BNC2	9	16,779,436	rs6475082	COMBINED	2.9E-01	0.84	0.61	1.16	4.1E-01	0.87	0.63	1.21	3.1E-01	0.87	0.66	1.14	4.7E-01	0.90	0.68	1.20
BNC2	9	16,779,878	rs4961760	INTENSIVE	5.8E-01	0.89	0.60	1.33	6.1E-01	0.90	0.60	1.35	9.4E-01	1.02	0.70	1.47	9.4E-01	1.01	0.70	1.47
BNC2	9	16,779,878	rs4961760	CONVENTIONAL	1.4E-01	0.64	0.35	1.15	5.9E-01	0.84	0.46	1.56	1.1E-02	0.54	0.34	0.87	2.0E-01	0.73	0.44	1.18
BNC2	9	16,779,878	rs4961760	COMBINED	2.7E-01	0.84	0.60	1.15	3.9E-01	0.87	0.62	1.20	3.5E-01	0.88	0.67	1.15	5.3E-01	0.91	0.69	1.21
BNC2	9	16,791,850	rs2254193	INTENSIVE	5.4E-01	0.88	0.58	1.34	5.5E-01	0.88	0.58	1.34	5.5E-01	0.89	0.60	1.31	5.5E-01	0.89	0.60	1.31
BNC2	9	16,791,850	rs2254193	CONVENTIONAL	1.1E-01	0.58	0.30	1.14	5.2E-01	0.80	0.40	1.59	4.7E-03	0.46	0.26	0.79	9.8E-02	0.63	0.36	1.09
BNC2	9	16,791,850	rs2254193	COMBINED	2.8E-01	0.83	0.58	1.17	3.9E-01	0.86	0.60	1.22	1.3E-01	0.80	0.60	1.07	2.2E-01	0.82	0.61	1.12
SORCS1	10	108,113,589	rs1358030	INTENSIVE	6.4E-01	1.05	0.85	1.31	8.6E-01	1.02	0.82	1.27	2.8E-01	0.89	0.72	1.10	3.0E-01	0.89	0.72	1.10
SORCS1	10	108,113,589	rs1358030	CONVENTIONAL	9.7E-04	0.60	0.44	0.81	3.3E-02	0.71	0.52	0.97	1.4E-04	0.63	0.50	0.80	1.8E-02	0.75	0.58	0.95
SORCS1	10	108,113,589	rs1358030	COMBINED	7.2E-02	0.85	0.72	1.01	3.9E-01	0.93	0.78	1.10	5.5E-04	0.77	0.66	0.89	7.0E-02	0.87	0.74	1.01
GSC	14	94,375,765	rs11624318	INTENSIVE	5.1E-01	0.91	0.70	1.19	6.0E-01	0.93	0.71	1.22	5.2E-01	0.92	0.72	1.18	5.1E-01	0.92	0.71	1.18
GSC	14	94,375,765	rs11624318	CONVENTIONAL	7.3E-01	0.94	0.67	1.32	5.2E-01	0.89	0.64	1.26	5.9E-01	0.93	0.71	1.22	3.8E-01	0.88	0.67	1.16
GSC	14	94,375,765	rs11624318	COMBINED	4.3E-01	0.92	0.75	1.13	2.7E-01	0.89	0.72	1.10	3.9E-01	0.93	0.77	1.10	1.6E-01	0.88	0.73	1.05
GSC	14	94,405,244	rs11160219	INTENSIVE	9.6E-01	0.99	0.77	1.28	9.2E-01	1.01	0.79	1.31	6.5E-01	1.06	0.83	1.34	6.0E-01	1.07	0.84	1.36
GSC	14	94,405,244	rs11160219	CONVENTIONAL	7.7E-01	1.05	0.76	1.44	7.4E-01	0.95	0.68	1.31	8.8E-01	1.02	0.79	1.32	5.7E-01	0.93	0.71	1.21
GSC	14	94,405,244	rs11160219	COMBINED	7.7E-01	1.03	0.85	1.25	8.3E-01	0.98	0.80	1.19	4.1E-01	1.07	0.91	1.27	9.9E-01	1.00	0.84	1.19
GSC	14	94,407,241	rs8007115	INTENSIVE	9.6E-01	1.01	0.78	1.30	8.3E-01	1.03	0.80	1.33	5.7E-01	1.07	0.84	1.37	5.2E-01	1.08	0.85	1.38
GSC	14	94,407,241	rs8007115	CONVENTIONAL	8.9E-01	1.02	0.74	1.41	6.4E-01	0.92	0.67	1.28	8.4E-01	1.03	0.79	1.33	6.3E-01	0.94	0.72	1.22
GSC	14	94,407,241	rs8007115	COMBINED	8.1E-01	1.02	0.84	1.25	7.9E-01	0.97	0.80	1.19	3.7E-01	1.08	0.91	1.28	9.3E-01	1.01	0.84	1.20
WDR72	15	51,277,554	rs493218	INTENSIVE	7.7E-01	0.95	0.67	1.34	8.6E-01	1.03	0.73	1.47	8.7E-01	1.03	0.74	1.42	9.5E-01	1.01	0.73	1.41
WDR72	15	51,277,554	rs493218	CONVENTIONAL	5.5E-01	0.87	0.55	1.37	6.6E-01	0.90	0.57	1.43	6.6E-01	1.08	0.76	1.53	4.5E-01	1.15	0.80	1.63
WDR72	15	51,277,554	rs493218	COMBINED	6.4E-01	0.94	0.72	1.23	3.4E-01	0.87	0.66	1.15	6.2E-01	1.06	0.84	1.33	8.2E-01	0.97	0.77	1.24
WDR72	15	51,291,924	rs572221	INTENSIVE	7.4E-01	0.94	0.67	1.33	8.8E-01	1.03	0.72	1.46	8.8E-01	1.03	0.74	1.42	9.6E-01	1.01	0.73	1.40
WDR72	15	51,291,924	rs572221	CONVENTIONAL	5.0E-01	0.86	0.54	1.35	5.9E-01	0.88	0.56	1.40	7.6E-01	1.06	0.75	1.49	5.5E-01	1.11	0.78	1.59
WDR72	15	51,291,924	rs572221	COMBINED	5.9E-01	0.93	0.71	1.22	3.0E-01	0.87	0.66	1.14	6.8E-01	1.05	0.83	1.32	7.6E-01	0.96	0.76	1.22
WDR72	15	51,291,964	rs690271	INTENSIVE	7.2E-01	0.94	0.66	1.32	9.1E-01	1.02	0.72	1.45	8.9E-01	1.02	0.74	1.41	9.7E-01	1.01	0.72	1.40
WDR72	15	51,291,964	rs690271	CONVENTIONAL	5.0E-01	0.86	0.54	1.35	5.9E-01	0.88	0.56	1.40	7.6E-01	1.06	0.75	1.49	5.5E-01	1.11	0.78	1.59
WDR72																				

Supplementary Table 6. Association results of top 13 SNPs for HbA1c in DCCT with retinal complications in DCCT/EDIC.

nearest gene	chr	pos	snp	trx	mild retinal						csme						severe retinal					
								mild		retinal_mv					csme_uv		csme_mv					
					snp	trx	hr0	hr_lowci0	hr_uppc0	mild	retinal_uv	mild	retinal_mv	hr1	hr_lowci1	hr_uppc1	csme_uv	csme_mv	hr2	hr_lowci2	hr_uppc2	sev ret_uv
BNC2	9	16,779,024	rs10810632	intensive	1.02	0.77	1.35	9.01E-01	8.05E-01	0.97	0.56	1.69	9.19E-01	9.82E-01	0.61	0.3	1.25	1.49E-01	1.89E-01			
BNC2	9	16,779,024	rs10810632	conventional	1.73	1.31	2.27	1.99E-04	6.79E-06	1.87	1.31	2.67	1.36E-03	1.54E-03	1.83	1.28	2.62	1.69E-03	2.04E-03			
BNC2	9	16,779,024	rs10810632	combined	1.15	0.95	1.4	1.52E-01	2.83E-01	1.36	1.01	1.83	4.81E-02	3.93E-02	1.19	0.88	1.62	2.72E-01	1.99E-01			
BNC2	9	16,779,436	rs6475082	combined	1.15	0.95	1.39	1.63E-01	2.71E-01	1.35	1.01	1.82	5.36E-02	4.11E-02	1.18	0.87	1.61	2.99E-01	2.08E-01			
BNC2	9	16,779,436	rs6475082	conventional	1.68	1.28	2.2	3.82E-04	8.28E-06	1.83	1.28	2.62	1.89E-03	1.95E-03	1.79	1.25	2.56	2.51E-03	2.67E-03			
BNC2	9	16,779,436	rs6475082	intensive	1.02	0.77	1.35	9.01E-01	8.05E-01	0.97	0.56	1.69	9.19E-01	9.82E-01	0.61	0.3	1.25	1.49E-01	1.89E-01			
BNC2	9	16,779,878	rs4961760	intensive	1.02	0.77	1.35	9.01E-01	8.05E-01	0.97	0.56	1.69	9.19E-01	9.82E-01	0.61	0.3	1.25	1.49E-01	1.89E-01			
BNC2	9	16,779,878	rs4961760	conventional	1.63	1.24	2.14	7.45E-04	2.23E-05	1.81	1.27	2.59	2.22E-03	2.35E-03	1.78	1.25	2.54	2.72E-03	2.84E-03			
BNC2	9	16,779,878	rs4961760	combined	1.14	0.94	1.38	1.82E-01	3.02E-01	1.35	1	1.82	5.59E-02	4.29E-02	1.18	0.87	1.61	3.03E-01	2.10E-01			
BNC2	9	16,791,850	rs2254193	intensive	1.06	0.79	1.42	7.03E-01	9.70E-01	1.02	0.57	1.82	9.41E-01	9.15E-01	0.8	0.4	1.58	5.04E-01	5.35E-01			
BNC2	9	16,791,850	rs2254193	conventional	1.54	1.15	2.06	5.93E-03	2.26E-04	1.85	1.26	2.72	3.59E-03	6.53E-03	1.89	1.29	2.75	2.01E-03	2.84E-03			
BNC2	9	16,791,850	rs2254193	combined	1.13	0.92	1.39	2.41E-01	4.04E-01	1.35	0.99	1.86	7.14E-02	7.53E-02	1.28	0.93	1.76	1.44E-01	1.27E-01			
SORCS1	10	108,113,589	rs1358030	combined	1.14	1.02	1.27	1.66E-02	2.29E-02	1.12	0.93	1.34	2.43E-01	3.67E-01	1.22	1.02	1.46	3.02E-02	3.83E-02			
SORCS1	10	108,113,589	rs1358030	conventional	1.15	0.99	1.34	7.49E-02	1.11E-01	1.16	0.92	1.46	2.23E-01	2.20E-01	1.3	1.04	1.63	2.19E-02	2.81E-02			
SORCS1	10	108,113,589	rs1358030	intensive	1.16	0.99	1.35	7.34E-02	3.32E-02	1.1	0.8	1.5	5.68E-01	4.49E-01	1.27	0.92	1.77	1.53E-01	8.40E-02			
GSC	14	94,375,765	rs11624318	intensive	1.09	0.9	1.32	3.88E-01	1.95E-01	0.9	0.6	1.33	5.79E-01	9.26E-01	0.69	0.44	1.1	1.04E-01	2.88E-01			
GSC	14	94,375,765	rs11624318	combined	0.98	0.86	1.11	7.19E-01	5.32E-01	1.02	0.82	1.26	8.92E-01	9.57E-01	0.93	0.74	1.16	5.07E-01	5.66E-01			
GSC	14	94,375,765	rs11624318	conventional	0.87	0.73	1.04	1.21E-01	7.86E-02	1.11	0.85	1.45	4.54E-01	4.26E-01	1.08	0.83	1.4	5.62E-01	6.00E-01			
GSC	14	94,405,244	rs11160219	combined	0.96	0.86	1.09	5.55E-01	6.31E-01	0.88	0.71	1.09	2.42E-01	1.72E-01	1.01	0.82	1.25	9.26E-01	9.09E-01			
GSC	14	94,405,244	rs11160219	intensive	1.13	0.94	1.35	1.91E-01	8.70E-02	1.12	0.78	1.59	5.46E-01	3.80E-01	1.01	0.69	1.49	9.56E-01	5.66E-01			
GSC	14	94,405,244	rs11160219	conventional	0.81	0.68	0.96	1.14E-02	4.77E-03	0.8	0.6	1.06	1.11E-01	6.05E-02	1.1	0.85	1.42	4.61E-01	7.60E-01			
GSC	14	94,407,241	rs8007115	combined	0.96	0.85	1.09	5.29E-01	5.46E-01	0.87	0.7	1.08	2.10E-01	1.24E-01	1.01	0.82	1.25	9.13E-01	9.36E-01			
GSC	14	94,407,241	rs8007115	conventional	0.82	0.69	0.97	1.86E-02	6.88E-03	0.79	0.59	1.05	9.16E-02	4.78E-02	1.1	0.86	1.42	4.50E-01	7.46E-01			
GSC	14	94,407,241	rs8007115	intensive	1.12	0.94	1.34	2.21E-01	8.54E-02	1.09	0.76	1.56	6.36E-01	4.28E-01	0.98	0.66	1.45	9.30E-01	6.54E-01			
WDR72	15	51,277,554	rs493218	intensive	0.75	0.57	0.97	2.47E-02	1.09E-02	0.62	0.35	1.12	9.18E-02	7.88E-02	0.36	0.16	0.82	4.30E-03	5.70E-03			
WDR72	15	51,277,554	rs493218	combined	0.92	0.78	1.09	3.52E-01	2.96E-01	0.76	0.55	1.04	7.67E-02	1.20E-01	0.71	0.51	0.99	3.38E-02	7.30E-02			
WDR72	15	51,277,554	rs493218	conventional	1.19	0.95	1.5	1.41E-01	1.11E-01	0.83	0.57	1.23	3.47E-01	4.62E-01	0.9	0.62	1.31	5.70E-01	8.59E-01			
WDR72	15	51,291,924	rs572221	intensive	0.76	0.58	0.98	3.14E-02	1.27E-02	0.62	0.34	1.11	8.53E-02	6.85E-02	0.36	0.16	0.81	3.80E-03	4.58E-03			
WDR72	15	51,291,924	rs572221	conventional	1.2	0.96	1.51	1.18E-01	9.01E-02	0.83	0.56	1.22	3.24E-01	4.39E-01	0.87	0.6	1.27	4.56E-01	7.54E-01			
WDR72	15	51,291,924	rs572221	combined	0.94	0.79	1															

Supplementary Table 7. Association of top 13 SNPs for HbA1c identified in DCCT, tested for association with HbA1c in GoKinD, cases and controls separately.

TRAIT	group	chr	pos	nearest gene	MARKER	ALLELES	FREQ1	RSQR	EFFECT1_add	STDERR_add	CHISQ_add	PVALUE_add
hba1c	cases	9	16,779,024	BNC2	rs10810632	T,C	0.9296	0.9388	0.164	0.127	1.6612	0.1974
hba1c	controls	9	16,779,024	BNC2	rs10810632	T,C	0.9296	0.9388	0.082	0.097	0.7044	0.4013
hba1c	cases	9	16,779,436	BNC2	rs6475082	A,G	0.9278	0.9962	0.153	0.123	1.5495	0.2132
hba1c	controls	9	16,779,436	BNC2	rs6475082	A,G	0.9278	0.9962	0.068	0.093	0.5317	0.4659
hba1c	cases	9	16,779,878	BNC2	rs4961760	T,C	0.9278	0.9977	0.153	0.123	1.5473	0.2135
hba1c	controls	9	16,779,878	BNC2	rs4961760	T,C	0.9278	0.9977	0.068	0.093	0.5281	0.4674
hba1c	cases	9	16,791,850	BNC2	rs2254193	A,C	0.931	0.9998	0.141	0.12	1.3778	0.2405
hba1c	controls	9	16,791,850	BNC2	rs2254193	A,C	0.931	0.9998	0.082	0.098	0.7089	0.3998
hba1c	cases	10	108,113,589	SORCS1	rs1358030	G,A	0.3561	0.8017	-0.019	0.074	0.0626	0.8024
hba1c	controls	10	108,113,589	SORCS1	rs1358030	G,A	0.356	0.8017	0.146	0.057	6.635	0.01
hba1c	cases	14	94,375,765	GSC	rs11624318	C,A	0.8051	0.8483	-0.078	0.086	0.8315	0.3618
hba1c	controls	14	94,375,765	GSC	rs11624318	C,A	0.8051	0.8483	-0.045	0.067	0.4401	0.5071
hba1c	cases	14	94,405,244	GSC	rs11160219	G,A	0.7613	0.4048	-0.209	0.114	3.3627	0.06669
hba1c	controls	14	94,405,244	GSC	rs11160219	G,A	0.7613	0.4048	0	0.09	0	0.9992
hba1c	cases	14	94,407,241	GSC	rs8007115	C,T	0.7721	0.3254	-0.178	0.128	1.9201	0.1658
hba1c	controls	14	94,407,241	GSC	rs8007115	C,T	0.7721	0.3254	-0.016	0.101	0.0251	0.8742
hba1c	cases	15	51,277,554	WDR72	rs493218	T,C	0.9016	0.989	0.087	0.115	0.5628	0.4531
hba1c	controls	15	51,277,554	WDR72	rs493218	T,C	0.9016	0.989	0.058	0.08	0.5174	0.472
hba1c	cases	15	51,291,924	WDR72	rs572221	G,A	0.9025	1	0.083	0.115	0.5207	0.4705
hba1c	controls	15	51,291,924	WDR72	rs572221	G,A	0.9025	1	0.059	0.08	0.5446	0.4605
hba1c	cases	15	51,291,964	WDR72	rs690271	G,A	0.9025	1	0.083	0.115	0.5207	0.4705
hba1c	controls	15	51,291,964	WDR72	rs690271	G,A	0.9025	1	0.059	0.08	0.5446	0.4605
hba1c	cases	15	51,295,884	WDR72	rs566369	G,A	0.9025	1	0.083	0.115	0.5207	0.4705
hba1c	controls	15	51,295,884	WDR72	rs566369	G,A	0.9025	1	0.059	0.08	0.5446	0.4605
hba1c	cases	15	51,296,486	WDR72	rs482541	G,A	0.9024	0.999	0.083	0.115	0.5199	0.4709
hba1c	controls	15	51,296,486	WDR72	rs482541	G,A	0.9024	0.999	0.059	0.08	0.5473	0.4594

Supplementary Table 8. Association of top 13 SNPs for HbA1c identified in DCCT, tested for association with renal disease case-control status in GoKinD.

CHR	SNP	BP	nearest gene	A1	F_A	F_U	A2	CHISQ	P	OR
9	rs10810632	16,779,024	BNC2	C	0.0717	0.07301	T	0.02126	0.8841	0.9806
9	rs6475082	16,779,436	BNC2	G	0.0717	0.07301	A	0.02126	0.8841	0.9806
9	rs4961760	16,779,878	BNC2	C	0.0717	0.07301	T	0.02126	0.8841	0.9806
9	rs2254193	16,791,850	BNC2	C	0.0717	0.06659	A	0.3348	0.5629	1.083
9	rs2254468	16,794,197	BNC2	G	0.06981	0.06484	A	0.3253	0.5684	1.082
10	rs1358030	108,113,589	SORCS1	G	0.3314	0.3405	A	0.3053	0.5806	0.9601
14	rs11624318	94,375,765	GSC	A	0.1943	0.1846	C	0.5118	0.4744	1.066
14	rs11160219	94,405,244	GSC	A	0.2019	0.212	G	0.5167	0.4723	0.94
14	rs8007115	94,407,241	GSC	T	0.1761	0.1904	C	1.128	0.2882	0.9087
15	rs493218	51,277,554	WDR72	C	0.08868	0.1057	T	2.721	0.09901	0.8231
15	rs572221	51,291,924	WDR72	A	0.08868	0.1057	G	2.721	0.09901	0.8231
15	rs690271	51,291,964	WDR72	A	0.08868	0.1057	G	2.721	0.09901	0.8231
15	rs566369	51,295,884	WDR72	A	0.08868	0.1057	G	2.721	0.09901	0.8231
15	rs482541	51,296,486	WDR72	A	0.08868	0.1057	G	2.721	0.09901	0.8231

Supplementary Table 9. Effect on SNP association with mean HbA1c in DCCT when either no covariates, mean BMI, or mean insulin dose during DCCT were used as covariates.

chr	SNP	Treatment group	Covariate	SNP effect	
				β (SE)	P value
10	rs1358030	CONVENTIONAL	none	0.329 (0.055)	3.5 E-9
10	rs1358030	CONVENTIONAL	BMI	0.328 (0.055)	3.6 E-9
10	rs1358030	CONVENTIONAL	Insulin dose	0.334 (0.055)	2.0E-9
9	rs10810632	CONVENTIONAL	none	0.568 (0.102)	3.7E-8
9	rs10810632	CONVENTIONAL	BMI	0.578 (0.102)	3.8E-8
9	rs10810632	CONVENTIONAL	Insulin dose	0.562 (0.102)	4.8E-8
14	rs11624318	CONVENTIONAL	none	0.554 (0.193)* 0.560 (0.198)†	4.2E-3* 4.9E-3†
14	rs11624318	CONVENTIONAL	BMI	0.550 (0.193)* 0.556 (0.198)†	4.5E-3* 5.3 E-3†
14	rs11624318	CONVENTIONAL	Insulin dose	0.560 (0.192)* 0.564 (0.198)†	3.8 E-3* 4.5 E-3†
14	rs11624318	INTENSIVE	none	0.600 (0.192) * 0.521 (0.200) †	1.9 E-3* 9.2 E-3†
14	rs11624318	INTENSIVE	BMI	0.564 (0.190) * 0.481 (0.197) †	3.1 E-3* 1.5 E-2†
14	rs11624318	INTENSIVE	Insulin dose	0.592 (0.182) * 0.524 (0.189) †	1.2 E-3* 5.8 E-3†
15	rs482541	INTENSIVE	none	-0.434 (0.084)	3.5 E-7
15	rs482541	INTENSIVE	BMI	-0.419 (0.083)	6.1 E-7
15	rs482541	INTENSIVE	Insulin dose	-0.413 (0.080)	3.7 E-7

Results for all SNPs, apart from rs11624318, are from an additive coding of genotypes. For rs11624318, since there is evidence for deviation from an additive model (Table 2), we used a 2df test, and report genotype specific parameter estimates and p values, with the following coded: * = common homozygote compared to rare homozygote, † = heterozygote compared to rare homozygote.

Supplementary Table 10. List of MAGIC investigators.

AUTHORSHIP FOR MAGIC HbA1C

DATA

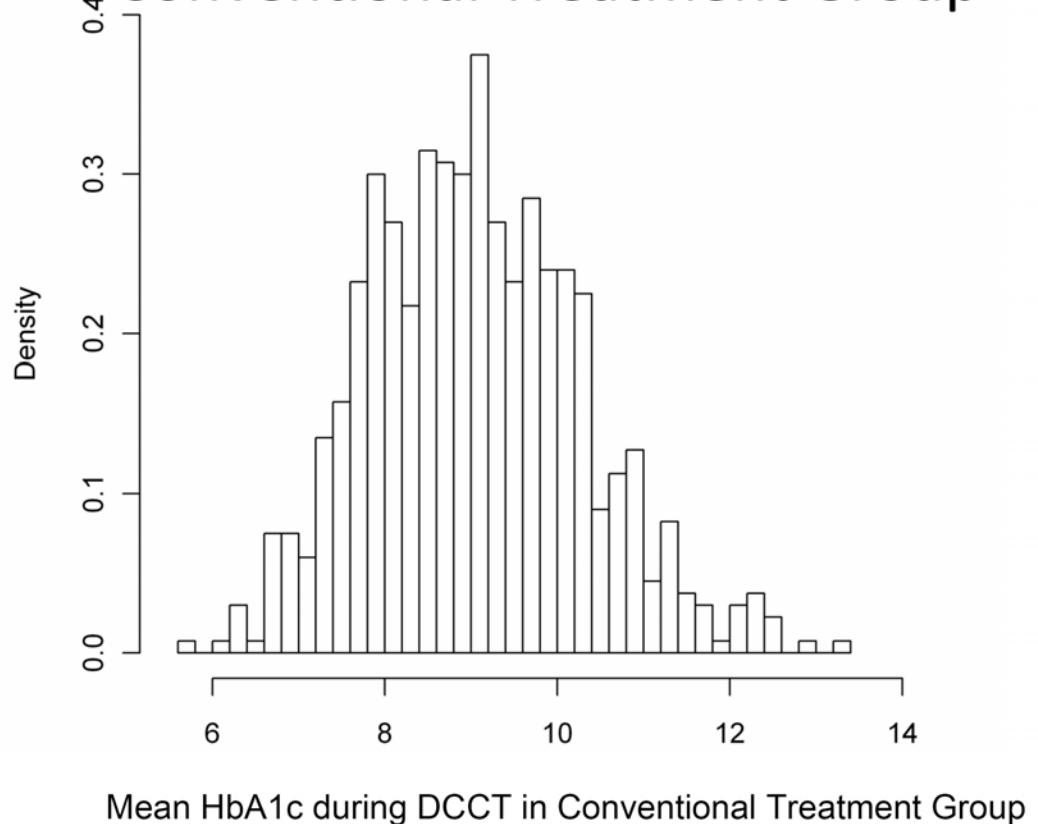
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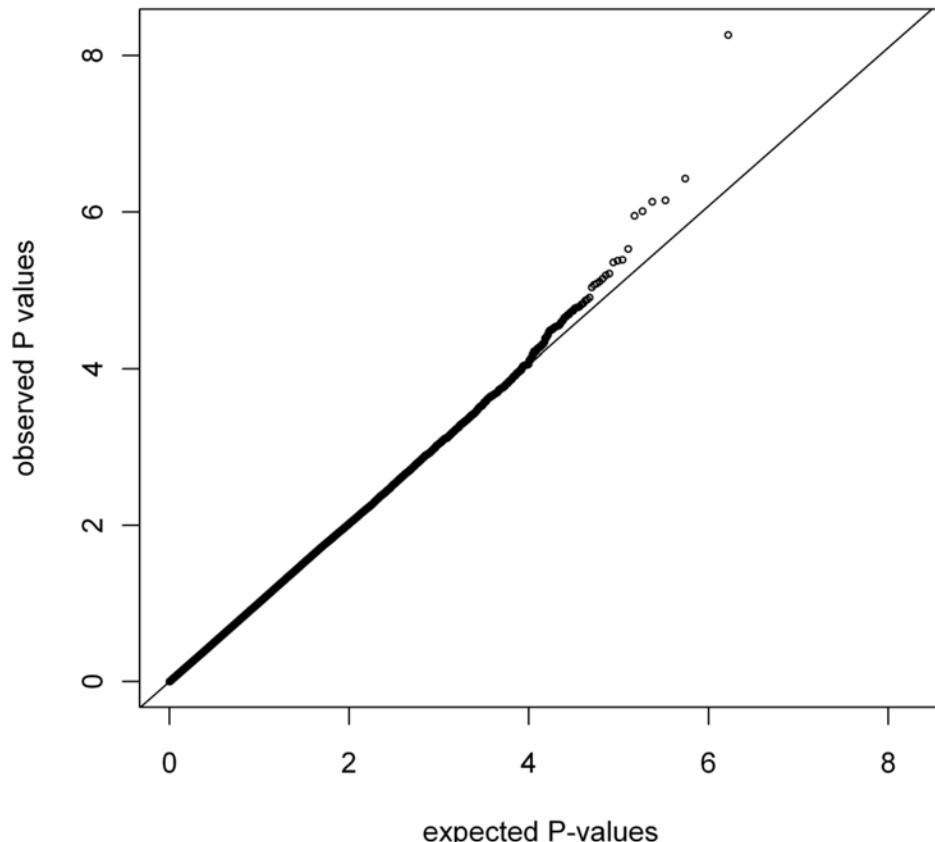
Supplementary Figure 1. Histogram of Mean HbA1c during DCCT in the conventional treatment group.

Supplementary Figure 1: mean HbA1c in Conventional Treatment Group



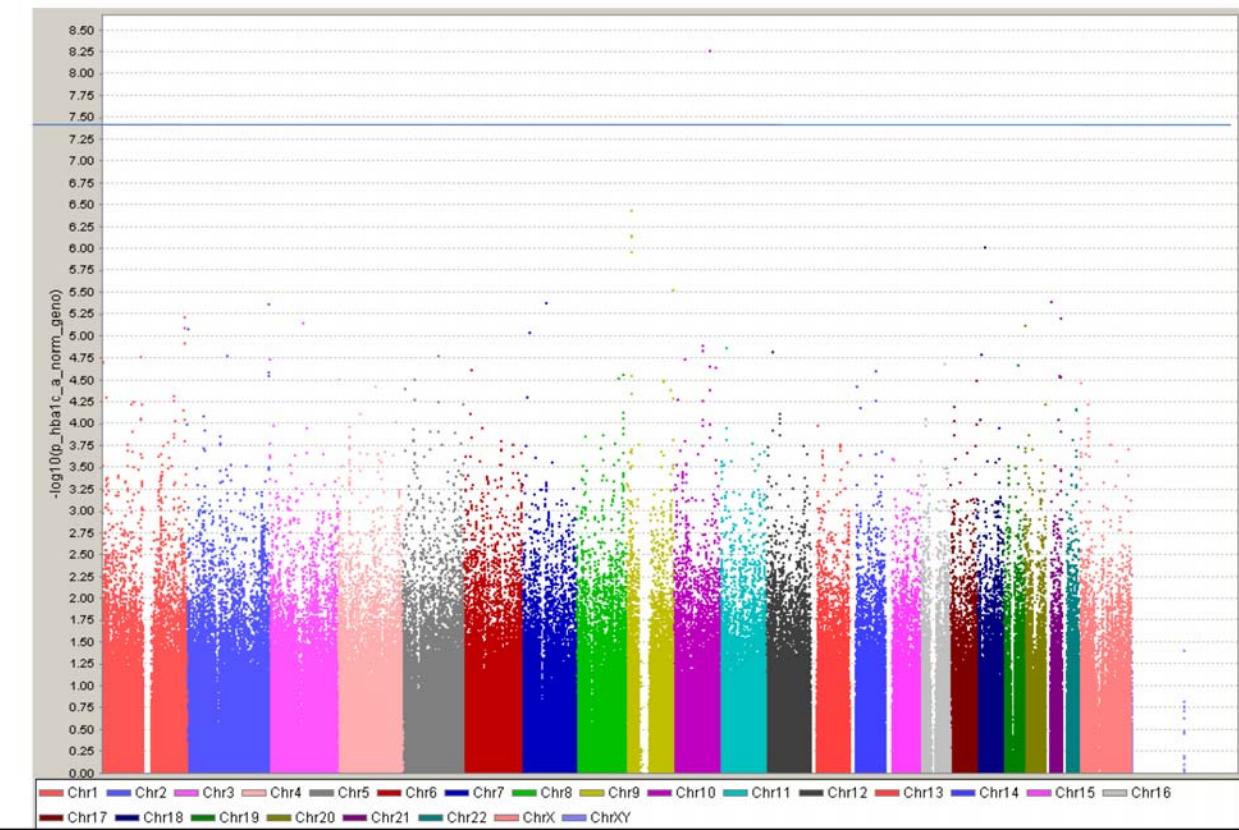
Supplementary Figure 2. Q-Q plot of the observed and expected distribution of $-\log_{10}(p \text{ values})$ from the normal score 2df genotype test comparing the 841K SNPs for Stage 1 (association with mean HbA1c during DCCT in the conventional treatment group).

Supplementary Figure 2: Q-Q plot for mean HbA1c in Conventional



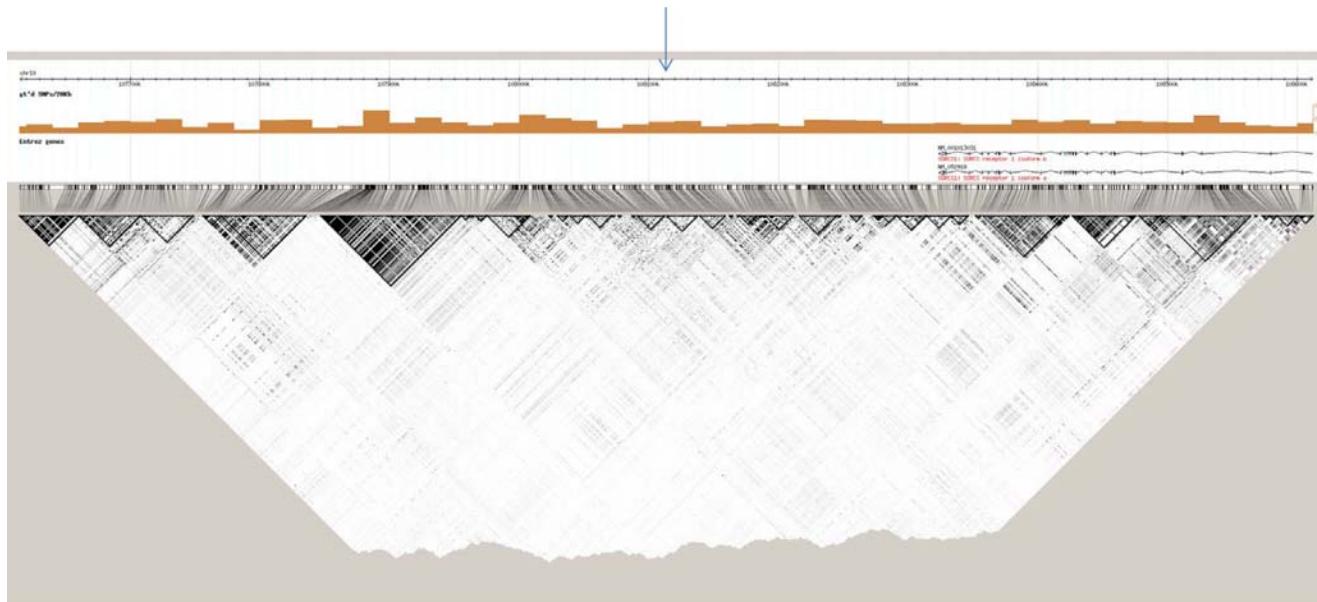
Supplementary Figure 3. Genome-wide association analysis of mean Hba1c in the Conventional group (Stage 1). The X axis is the genome (chromosomes 1-22 and X and Y chromosomes in different colors) and SNPs ordered along chromosomes by nucleotide position. The gaps in the middle of some chromosomes are due to the low SNP density around the centromeres. The Y axis is the $-\log_{10}(P$ value), so a value of 8 denotes a p value of 10^{-8} . The blue horizontal line at 7.3 is the criterion for genome-wide significance ($p=5\times 10^{-8}$).

Supplementary Figure 3: GWAS of mean Hba1c in the Conventional



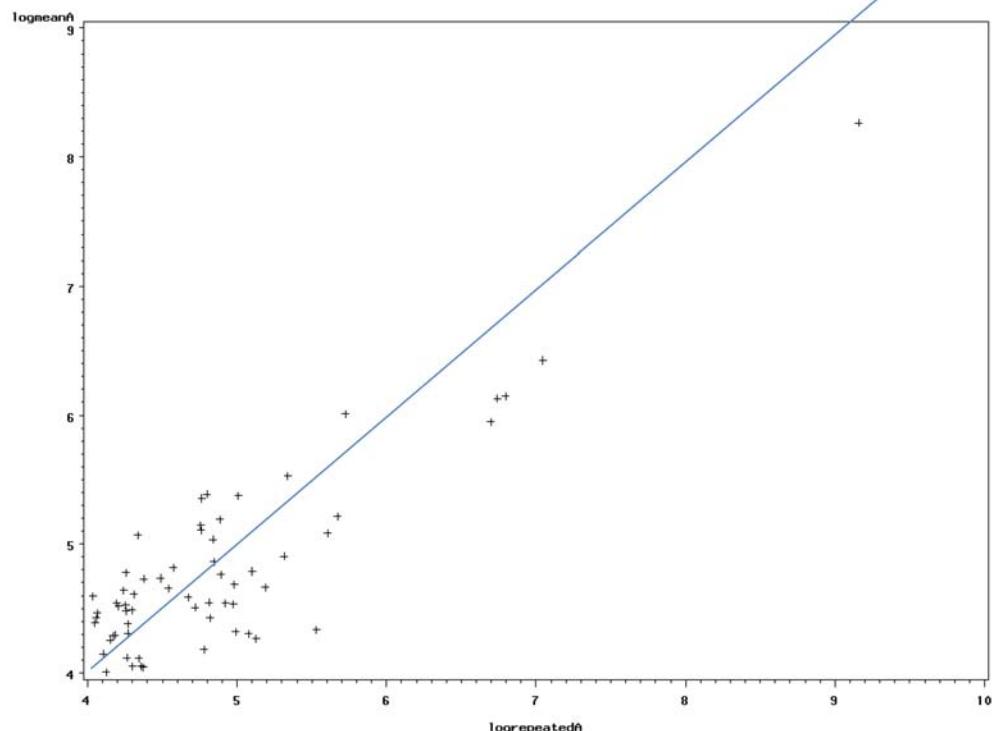
Supplementary Figure 4. Linkage disequilibrium between SNPs in a 1Mb region centered around rs1358030 in the *SORCS1* genomic region from chromosome 10 in CEU HapMap phase II data (release 23a). Linkage disequilibrium between SNPs is indicated by pairwise r^2 value. The grey scale indicates the relative strength of linkage disequilibrium (darker, higher r^2 value). *SORCS1* gene is annotated. The blue arrow indicates the location of rs1358030.

Supplementary Figure 4: Linkage disequilibrium in a 1Mb region centered around rs1358030 in the SORCS1



Supplementary Figure 5. Comparison of p values from the conventional treatment group for the top 62 SNPs with $p < 10^{-4}$ from Stage 1 using mean HbA1c to the results from the mixed models using longitudinal repeated measures from Stage 2. For each SNP, the mean DCCT HbA1c $-\log_{10}(p \text{ value})$ is plotted on the Y axis, while the repeated measures $-\log_{10}(p \text{ value})$ is on the X axis, with a line indicating unity plotted. As can be seen, the evidence for association as assessed by the p value was smaller (i.e. more significant) using the longitudinal mixed model compared to the analysis of the mean, especially for the SNPs with the smallest p values from the mean results.

Supplementary Figure 5: p values from conventional for the top 62 SNPs with $p < 10^{-4}$ from mean (Y axis) and repeated (X axis)



Supplementary Figure 6. Flow-chart describing the multi-stage analysis of the DCCT data. CON=Conventional Treatment Group, INT=Intensive Treatment Group.

Supplementary Figure 6: Flowchart of DCCT analysis plan

Stage 1

ANALYSIS: Genome-wide association of 841K SNPs with mean DCCT HbA1c in CON, INT and COMB. Similar analysis of 1.7M un-genotyped imputed SNPs

RESULTS: 12 SNPs with $p < 10^{-6}$ of which 1 SNP at genome-wide significance (Table 2). A total of 233 genotyped SNPs with $p < 10^{-4}$

Stage 2

ANALYSIS: Mixed model for 233 SNPs from Stage 1 using quarterly repeated HbA1c measures in CON, monthly HbA1c in INT, or quarterly in COMB

RESULTS: 13 genotyped SNPs from 4 regions with $p < 10^{-7}$ (Table 3)

These 13 SNPs were also tested for association with mean glucose during DCCT (Table 3)

Stage 3

ANALYSIS: Mixed models for 13 SNPs from Stage 2 using quarterly glucose measures and c-peptide

RESULTS: 5 SNPs with $p < 10^{-2}$ for glucose (Table 4)

Stage 4

ANALYSIS: 13 SNPs from Stage 2 were tested for association with HbA1c in both treatment groups together, and specifically evidence for SNP * treatment interaction

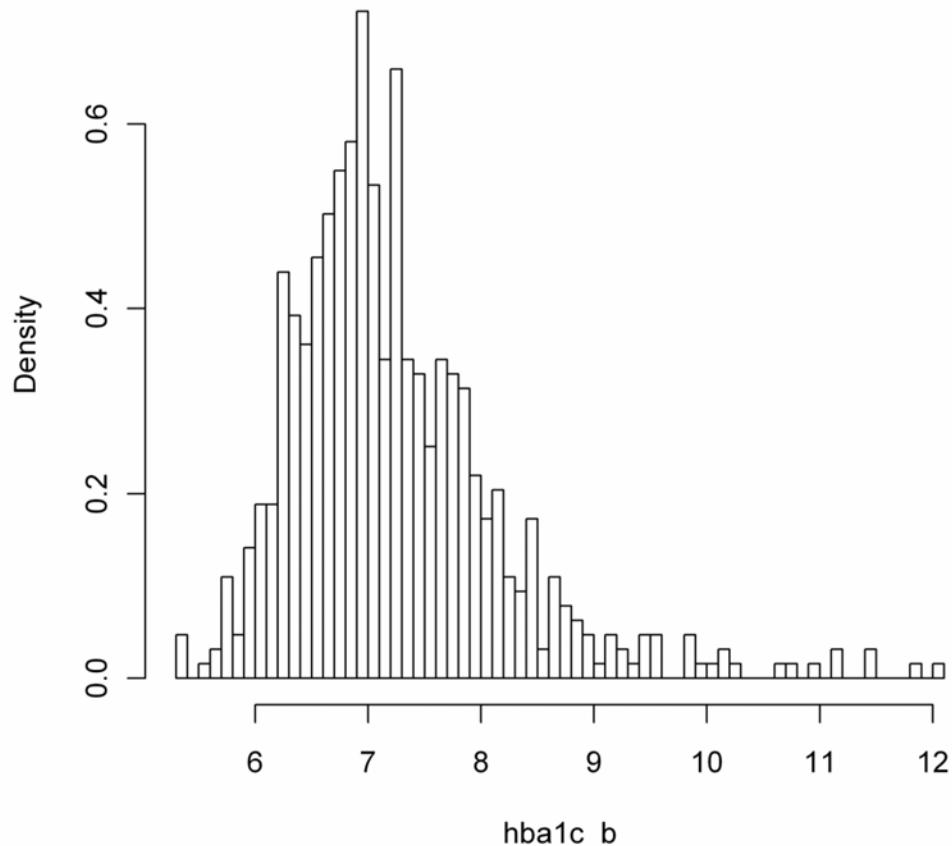
RESULTS: 10 SNPs with evidence for SNP * treatment interaction (Table 4)

Stage 5

ANALYSIS: 13 SNPs from Stage 2 were tested for association with time-to-event- renal, retinal, and neuropathy complications, as well as coronary calcium, and prevalence of hypoglycemia during DCCT/EDIC. RESULTS: rs1358030 (SORCS1) associated with renal and hypoglycemia. BNC2 SNPs are associated with retinal, renal and hypoglycemia.

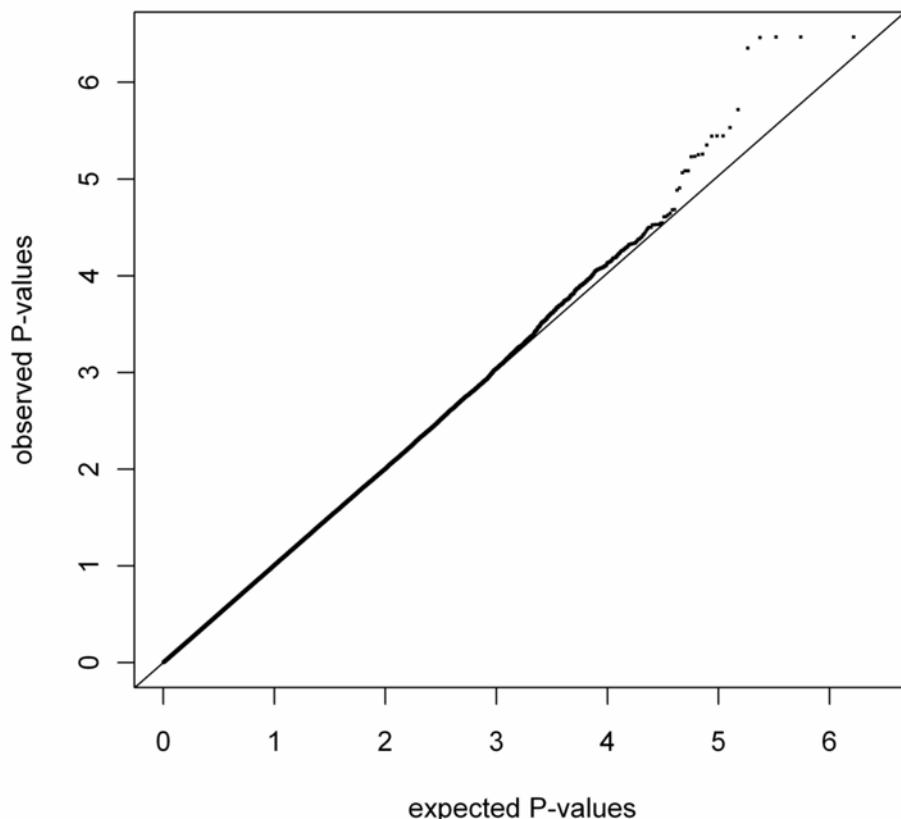
Supplementary Figure 7. Histogram of Mean HbA1c during DCCT in the intensive treatment group.

Supplementary Figure 7: Mean HbA1c in Intensive treatment group



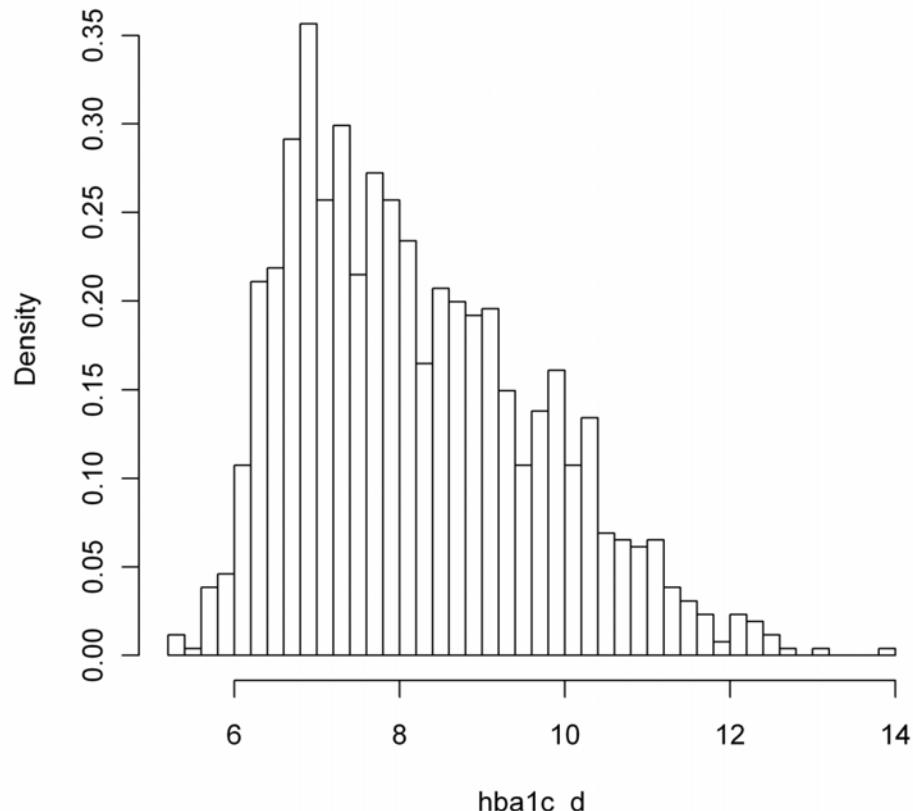
Supplementary Figure 8. QQ plot of SNP p value test statistics for INT group.

Supplementary Figure 8: INT mean HbA1c qq plot



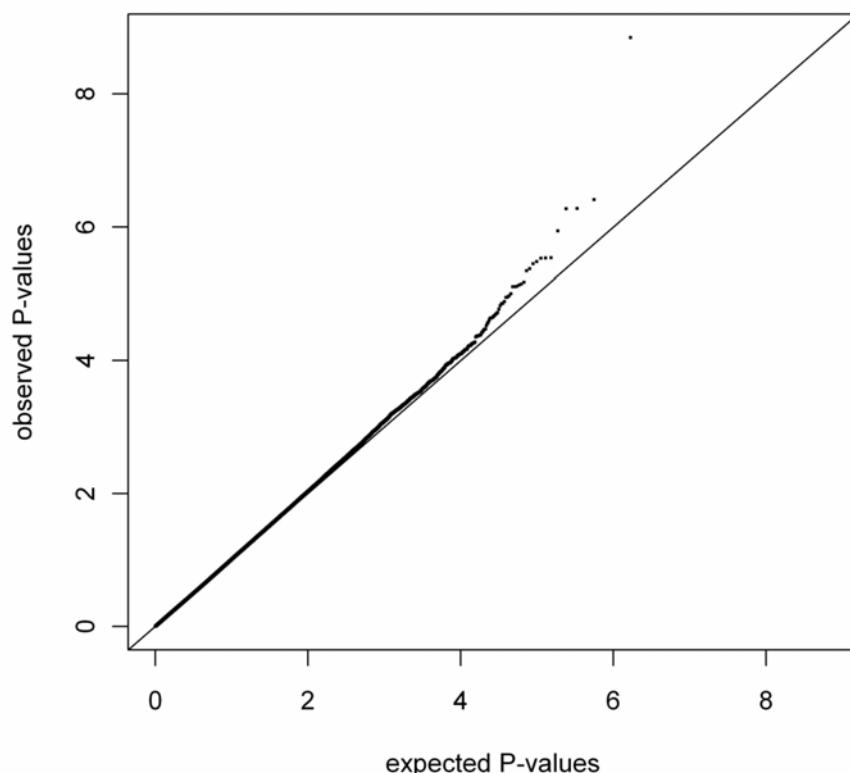
Supplementary Figure 9. Histogram of Mean HbA1c during DCCT in the combined treatment groups.

Supplementary Figure 9: Mean HbA1c in both treatment groups



Supplementary Figure 10. QQ plot of SNP p value test statistics for the combined treatment groups.

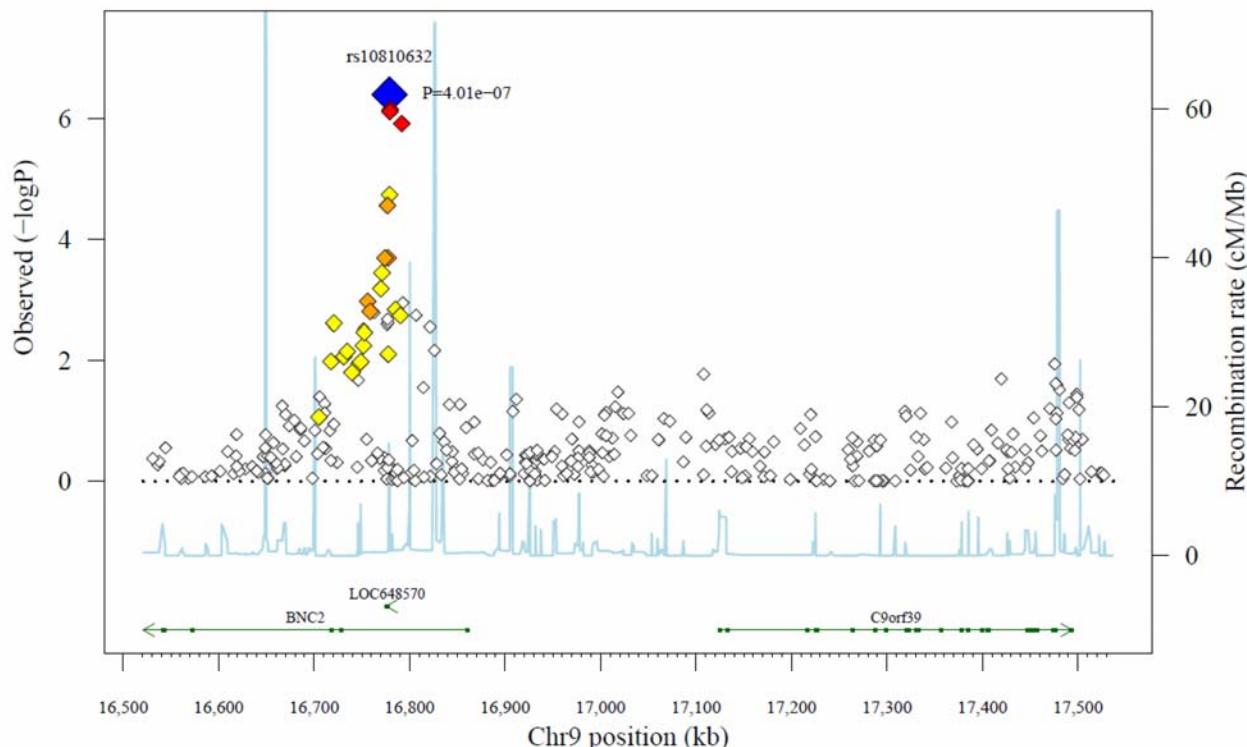
Supplementary Figure 10: QQ plot for Mean HbA1c in both treatment groups



Supplementary Figure 11. Association results for mean HbA1c levels in the conventional treatment group at a region of 500kb surrounding the BNC2 locus (chromosome 9). On the left Y axis is the- $\log_{10}(P)$ value for each SNP genotyped. On the right Y axis and plotted in the blue line is the recombination rate estimated from our data. The annotated genes in the region are indicated along the bottom of the figure. SNPs are colored based on their linkage disequilibrium with the most significant SNP, i.e. rs10810632, where blue indicates the index SNP, red $r^2 \geq 0.8$, orange $0.8 > r^2 > 0.5$, yellow $0.5 > r^2 > 0.2$, and white $r^2 < 0.2$.

Supplementary Figure 11: Region plot for Conventional BNC2

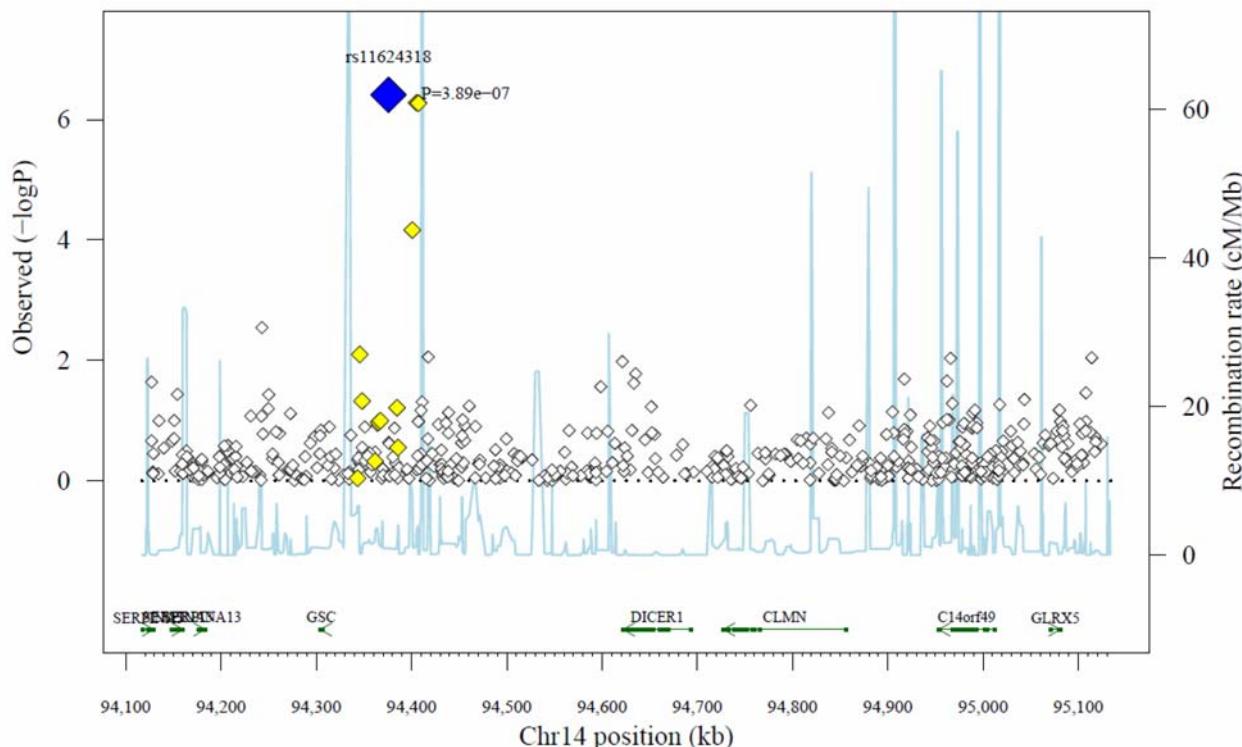
1M pval_hba1c_a_norm_genotype : rs10810632



Supplementary Figure 12. Association results for mean HbA1c levels at a region of 500kb surrounding the WDR72 locus (chromosome 14) in the combined treatment groups. On the left Y axis is the- $\log_{10}(P)$ value for each SNP genotyped. On the right Y axis and plotted in the blue line is the recombination rate estimated from our data. The annotated genes in the region are indicated along the bottom of the figure. SNPs are colored based on their linkage disequilibrium with the most significant SNP, i.e. rs111624318, where blue indicates the index SNP, red $r^2 \geq 0.8$, orange $0.8 > r^2 > 0.5$, yellow $0.5 > r^2 > 0.2$, and white $r^2 < 0.2$.

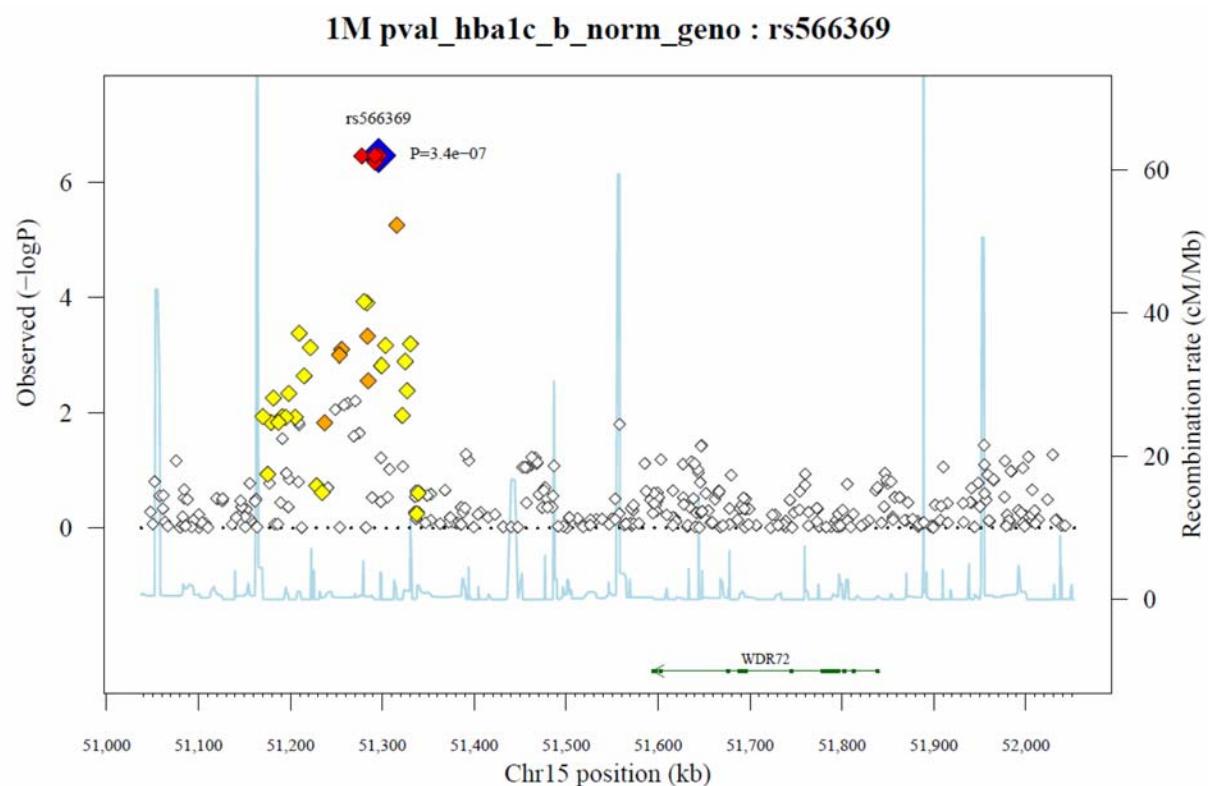
Supplementary Figure 12: Region plot for Combined chr 14 (WDR72)

1M pval_hba1c_d_norm_genotype : rs111624318



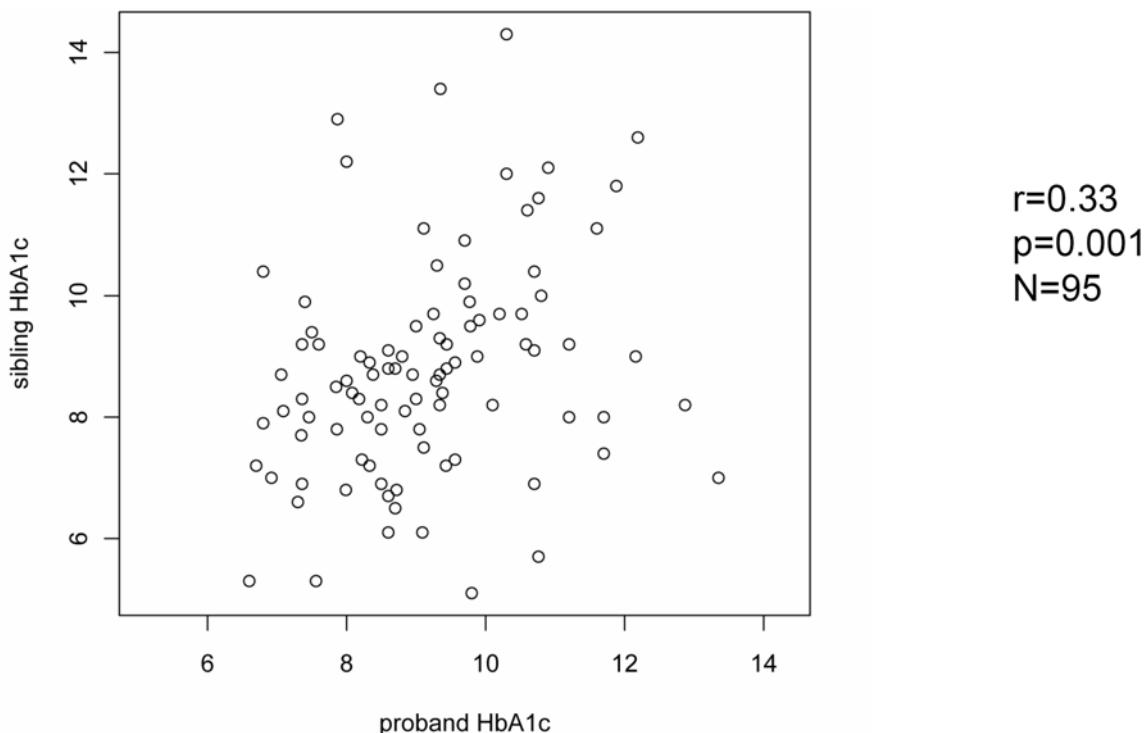
Supplementary Figure 13. Association results for mean HbA1c levels at a region of 500kb surrounding the GSC locus (chromosome 15) in the intensive treatment group. On the left Y axis is the- $\log_{10}(P)$ value for each SNP genotyped. On the right Y axis and plotted in the blue line is the recombination rate estimated from our data. The annotated genes in the region are indicated along the bottom of the figure. SNPs are colored based on their linkage disequilibrium with the most significant SNP, i.e. rs566369, where blue indicates the index SNP, red $r^2 \geq 0.8$, orange $0.8 > r^2 > 0.5$, yellow $0.5 > r^2 > 0.2$, and white $r^2 < 0.2$.

Supplementary Figure 13: Region plot for Intensive chr 15 (GSC)



Supplementary Figure 14. Correlation of HbA1c measured at eligibility for DCCT probands and HbA1c measured either during the DCCT family study, or the EDIC genetics study in their sibling with type 1 diabetes.

Supplementary Figure 14: Correlation of DCCT proband's eligibility HbA1c with type 1 diabetic sibs HbA1c



Supplementary Figure 15. Cluster-plot of called genotypes by theta and R for rs1358030 from the Illumina 1M data, plotted using polar co-ordinates. This shows that there is good separation of the 3 genotype groups at this SNP, consistent with high quality genotype data. Red are called TT, purple are called TC, and blue are called CC. No calls are in black.

Supplementary Figure 15: Cluster-plot for rs1358030

