Supplementary Material

Table S1. Mean and standard error of the genetic risk score (GRS) for T2D among all women with genetic data in the NHSII and DNBC.

Variable	Non-T2D			T2D			P-value[a]
	#	Mean	STD	#	Mean	STD	
NHSII							
GRS	1438	67.65	5.68	446	68.17	6.06	0.10
Pre-pregnancy BMI	504	25.05	5.14	149	31.18	7.15	< 0.001
AHEI after the index pregnancy[b]	894	47.27	10.54	278	45.41	9.91	0.009
DNBC							
GRS	395	67.11	5.56	155	67.82	5.60	0.50
Pre-pregnancy BMI	395	26.15	4.93	155	30.26	6.33	< 0.001
AHEI after the index pregnancy[c]	395	51.94	9.44	155	50.68	9.32	0.14

[a]*P*-values were obtained from t-test between the two groups.
[b]Derived from the earliest dietary assessment after the index pregnancy.
[c]Derived from the dietary assessment at the follow-up clinical exam in DNBC.

Table S2. Candidate single nuclear polymorphisms (SNPs) and their associations with the risk of type 2 diabetes among women who had gestational diabetes in the Nurses' Health Study II (NHSII, N = 1,884) and the Danish National Birth Cohort (DNBC, N = 550).

SNP	BP	Chr	Gene	Func	type 2 diabetes risk allele	Reference allele	Confirmation in Scott et. al., 2017[1]		Confirmation in Mahajan et. al., 2014[2]		NHSI			DNBC			Pooled[a]		P, FDR corrected
							Relevant SNP	R²	Relevant SNP	R²	EAF	RR (95% CI)[b]	P	EAF	RR (95% CI)[b]	P	RR (95% CI)	P	
rs10923931	119975336	1	NOTCH2	-	T	G			rs10923931	Same	0.11	1.03 (0.85, 1.23)	0.79	0.11	0.77 (0.55, 1.07)	0.12	0.96 (0.82, 1.12)	0.59	0.75
rs243021	60357684	2	BCL11A	-	A	G			rs243088	0.88	0.47	0.99 (0.89, 1.11)	0.91	0.49	1.06 (0.87, 1.29)	0.56	1.01 (0.91, 1.12)	0.85	0.88
rs2943641	226229029	2	LOC64673, IRS1	IR	C	T	rs2972156	0.91	rs2943640	0.94	0.65	1.07 (0.95, 1.20)	0.30	0.65	1.10 (0.89, 1.34)	*0.38*	1.07 (0.97, 1.19)	0.18	0.59
rs3923113	164645339	2	GRB14	IR	A	C			rs3923113	Same	0.64	1.06 (0.94, 1.20)	0.34	0.63	1.19 (0.97, 1.47)	0.10	1.09 (0.98, 1.21)	0.10	0.39
rs7578326	226155937	2	IRS1	IR	A	G					0.66	1.08 (0.96, 1.22)	0.20	0.77	1.06 (0.87, 1.30)	0.56	1.08 (0.97, 1.20)	0.16	0.56
rs7578597	43505684	2	THADA	BC	T	C	rs6757251	0.97	rs10203174	0.91	0.90	1.07 (0.87, 1.31)	0.53	0.92	1.21 (0.83, 1.76)	0.33	1.10 (0.92, 1.32)	0.30	0.65
rs7593730	160314943	2	ITGB6/RBMS1	IR	C	T			rs7593730	Same	0.78	1.06 (0.92, 1.22)	0.43	0.81	0.93 (0.74, 1.17)	0.54	1.02 (0.90, 1.15)	0.73	0.84
rs7607980	164694691	2	COBLL1	-	T	C					0.86	1.10 (0.92, 1.30)	0.29	0.85	1.32 (0.97, 1.79)	0.08	1.15 (0.99, 1.33)	0.07	0.34
rs16861329	186948673	3	ST6GAL1	-	C	T			rs16861329	Same	0.87	1.13 (0.94, 1.36)	0.19	0.87	1.21 (0.91, 1.60)	0.18	1.03 (0.88, 1.20)	0.71	0.84
rs1801282	12351626	3	PPARG	IR	C	G	rs11712037	0.94	rs1801282	Same	0.88	1.00 (0.84, 1.20)	0.96	0.86	1.00 (0.76, 1.31)	0.99	1.00 (0.86, 1.16)	0.97	0.97
rs4402960	185793899	3	IGF2BP2	BC	T	G	rs4402960	Same	rs4402960	Same	0.33	1.07 (0.95, 1.20)	0.29	0.32	1.06 (0.87, 1.30)	0.55	1.07 (0.96, 1.18)	0.22	0.59
rs4607103	64726228	3	ADAMTS9	IR	C	T					0.77	0.94 (0.82, 1.07)	0.34	0.78	0.96 (0.77, 1.19)	0.70	0.94 (0.84, 1.06)	0.31	0.65
rs1801214	**6301295**	**4**	**WFS1**	**BC**	**T**	**C**			**rs4458523**	**0.96**	**0.60**	**1.15 (1.02, 1.30)**	**0.03**	**0.60**	**1.02 (0.85, 1.24)**	**0.81**	**1.11 (1.00, 1.23)**	**0.04**	**0.24**
rs4689388	**6268329**	**4**	**WFS1**	**BC**	**A**	**G**			**rs4458523**	**0.85**	**0.59**	**1.16 (1.03, 1.31)**	**0.02**	**0.58**	**1.04 (0.86, 1.26)**	**0.68**	**1.12 (1.02, 1.25)**	**0.02**	**0.24**
rs6815464	1316113	4	MAEA	BC	C	G					0.97	1.05 (0.73, 1.51)	0.78	0.98	1.24 (0.72, 2.16)	0.44	0.97 (0.72, 1.31)	0.85	0.88
rs4457053	77129124	5	ZBED3	-	G	A			rs6878122	0.93	0.31	1.06 (0.94, 1.20)	0.37	0.30	1.20 (0.96, 1.50)	0.12	1.00 (0.90, 1.12)	0.97	0.97
rs1535500	39316274	6	KCNK16	-	T	G					0.50	0.95 (0.85, 1.06)	0.37	0.49	1.00 (0.83, 1.20)	0.97	0.96 (0.87, 1.06)	0.44	0.72
rs7754840	20661019	6	CDKAL1	BC	C	G					0.33	0.97 (0.86, 1.10)	0.64	0.37	1.33 (1.10, 1.60)	0.00	1.06 (0.96, 1.18)	0.24	0.62
rs7766070	**20686342**	**6**	**CDKAL1**	**BC**	**A**	**C**	**rs7451008**	**0.97**	**rs7756992**	**0.98**	**0.28**	**1.05 (0.93, 1.19)**	**0.45**	**0.32**	**1.28 (1.06, 1.54)**	**0.01**	**1.11 (1.00, 1.24)**	**0.04**	**0.24**
rs10229583	**127606849**	**7**	**ARF5, PAX4, SND1**	**-**	**G**	**A**			**rs10229583**	**Same**	**0.78**	**1.06 (0.92, 1.23)**	**0.39**	**0.77**	**1.31 (1.04, 1.65)**	**0.02**	**1.13 (1.00, 1.27)**	**0.05**	**0.27**
rs849134	28156603	7	JAZF1	BC	A	G	rs1635852	0.95	rs849135	0.95	0.51	1.04 (0.93, 1.16)	0.53	0.45	0.99 (0.82, 1.20)	0.94	1.03 (0.93, 1.13)	0.62	0.75
rs972283	130782095	7	KLF14	IR	G	A	rs10954284	0.98	rs13233731	0.95	0.54	1.05 (0.93, 1.18)	0.43	0.51	0.97 (0.80, 1.17)	0.74	1.03 (0.93, 1.13)	0.62	0.75
rs13266634	117172544	8	SLC30A8	BC	C	T	rs3802177	Same	rs3802177	Same	0.72	0.96 (0.84, 1.09)	0.51	0.72	1.00 (0.82, 1.22)	1.00	0.97 (0.87, 1.08)	0.57	0.75
rs896854	94948283	8	TP53INP1	-	T	C			rs7845219	0.92	0.49	0.96 (0.86, 1.08)	0.54	0.45	1.07 (0.88, 1.29)	0.52	0.99 (0.90, 1.09)	0.84	0.88
rs10811661	**22134095**	**9**	**CDKN2A/B**	**BC**	**T**	**C**	**rs10965248**	**0.97**	**rs10811661**	**Same**	**0.83**	**0.90 (0.78, 1.05)**	**0.19**	**0.85**	**0.75 (0.59, 0.95)**	**0.02**	**0.86 (0.76, 0.97)**	**0.02**	**0.24**
rs11787792	**136357696**	**9**	**GPSM1**	**-**	**A**	**G**	**rs11787792**	**Same**			**0.64**	**1.18 (1.04, 1.33)**	**0.01**	**0.66**	**0.99 (0.81, 1.22)**	**0.95**	**1.12 (1.01, 1.25)**	**0.03**	**0.24**
rs13292136	79337213	9	CHCHD9	-	C	T					0.94	0.96 (0.76, 1.21)	0.72	0.94	1.47 (0.88, 2.47)	0.15	1.03 (0.83, 1.27)	0.80	0.88

SNP	BP	Chr	Gene	Func	type 2 diabetes risk allele	Reference allele	Confirmation in Scott et. al., 2017[1]		Confirmation in Mahajan et. al., 2014[2]		NHSI			DNBC			Pooled[a]		P, FDR corrected
							Relevant SNP	R²	Relevant SNP	R²	EAF	RR (95% CI)[b]	P	EAF	RR (95% CI)[b]	P	RR (95% CI)	P	
rs7018475	22137686	9	CDKN2B	BC	T	G					0.73	1.11 (0.97, 1.27)	0.13	0.72	1.09 (0.88, 1.34)	0.42	1.10 (0.99, 1.24)	0.09	0.38
rs7020996	**22129580**	**9**	**CDKN2A/B**	**BC**	**C**	**T**					**0.87**	**0.88 (0.75, 1.03)**	**0.12**	**0.89**	**0.83 (0.64, 1.09)**	**0.18**	**0.87 (0.76, 1.00)**	**0.04**	**0.24**
rs7041847	**4287466**	**9**	**GLIS3**	**BC**	**A**	**G**			**rs7041847**	**Same**	**0.54**	**0.91 (0.81, 1.02)**	**0.10**	**0.52**	**0.87 (0.72, 1.04)**	**0.12**	**0.89 (0.81, 0.99)**	**0.03**	**0.24**
rs10906115	12272998	10	CDC123-CAMK1D	BC	A	G					0.61	1.01 (0.90, 1.15)	0.82	0.61	0.89 (0.74, 1.07)	0.22	0.97 (0.88, 1.08)	0.62	0.75
rs1111875	92703125	10	HHEX	BC	C	T			rs1111875	Same	0.61	0.97 (0.86, 1.09)	0.57	0.64	0.87 (0.71, 1.05)	0.15	0.94 (0.85, 1.04)	0.22	0.59
rs11257655	12265895	10	CDC123	BC	T	C	rs11257659	0.94	rs11257655	Same	0.21	0.97 (0.84, 1.12)	0.66	0.77	0.95 (0.76, 1.18)	0.61	0.96 (0.85, 1.08)	0.52	0.75
rs4506565	112996282	10	TCF7L2	BC	T	A	rs7903146	0.92	rs7903146	0.92	0.35	1.08 (0.96, 1.22)	0.21	0.33	0.99 (0.81, 1.20)	0.89	1.05 (0.95, 1.17)	0.31	0.65
rs10830963	92975544	11	MTNR1B	BC	G	C	rs10830963	Same	rs10830963	Same	0.32	0.95 (0.83, 1.09)	0.47	0.33	0.92 (0.75, 1.12)	0.41	0.94 (0.84, 1.05)	0.29	0.65
rs1387153	92940662	11	MTNR1B	BC	T	C					0.33	0.95 (0.84, 1.08)	0.47	0.33	1.00 (0.82, 1.23)	0.98	0.97 (0.87, 1.08)	0.54	0.75
rs1552224	72722053	11	ARAP1/CENTD2	BC	A	C	rs76550717	0.99	rs1552224	Same	0.86	1.11 (0.93, 1.31)	0.25	0.83	1.09 (0.84, 1.43)	0.52	1.10 (0.95, 1.27)	0.19	0.59
rs2237892	2818521	11	KCNQ1	BC	C	T					0.93	0.98 (0.78, 1.23)	0.87	0.96	0.76 (0.52, 1.12)	0.17	0.92 (0.75, 1.12)	0.40	0.69
rs2237897	2837316	11	KCNQ1	BC	C	T	rs2237897	Same			0.96	0.90 (0.69, 1.18)	0.44	0.97	0.78 (0.50, 1.22)	0.27	0.87 (0.69, 1.09)	0.22	0.59
rs231356	**2684113**	**11**	**KCNQ1**	**BC**	**T**	**A**					**0.28**	**1.09 (0.96, 1.24)**	**0.18**	**0.32**	**1.23 (1.02, 1.48)**	**0.03**	**1.13 (1.02, 1.26)**	**0.02**	**0.24**
rs231362	2670241	11	KCNQ1	BC	G	A			rs231362	Same	0.52	1.02 (0.91, 1.15)	0.76	0.52	1.11 (0.92, 1.34)	0.27	1.04 (0.95, 1.15)	0.40	0.69
rs5215	17387083	11	KCNJ11	BC	C	T	rs5219	Same	rs5215	Same	0.37	0.98 (0.87, 1.10)	0.73	0.41	1.18 (0.98, 1.41)	0.08	1.03 (0.94, 1.14)	0.51	0.75
rs1531343	65781114	12	HMGA2	IR	C	G			rs2261181	0.81	0.12	0.96 (0.80, 1.14)	0.62	0.12	0.96 (0.73, 1.26)	0.76	0.96 (0.82, 1.11)	0.55	0.75
rs7305618	120965129	12	HNF1A	BC	C	T					0.78	0.91 (0.79, 1.05)	0.20	0.79	1.06 (0.85, 1.33)	0.60	0.95 (0.85, 1.07)	0.42	0.71
rs7957197	121022883	12	HNF1A	BC	T	A			rs12427353	0.82	0.82	0.89 (0.77, 1.02)	0.10	0.16	1.17 (0.90, 1.50)	0.24	0.95 (0.84, 1.07)	0.39	0.69
rs1359790	80143021	13	SPRY2	BC	G	A	rs11616380	0.97	rs1359790	Same	0.74	1.00 (0.88, 1.14)	0.97	0.74	0.86 (0.70, 1.05)	0.13	0.95 (0.85, 1.06)	0.40	0.69
rs7961581	71269322	13	TSPAN8	BC	C	T	rs6581998	0.96	rs7955901	0.99	0.30	0.97 (0.85, 1.11)	0.67	0.27	0.96 (0.77, 1.19)	0.69	0.97 (0.87, 1.08)	0.58	0.75
rs11634397	80139880	15	ZFAND6	-	G	A			rs11634397	Same	0.65	0.99 (0.88, 1.13)	0.93	0.62	1.06 (0.87, 1.31)	0.55	1.01 (0.91, 1.13)	0.82	0.88
rs1436955	62112183	15	C2CD4B (NLF2, FAM148B)	-	C	T					0.74	0.99 (0.87, 1.13)	0.89	0.72	1.09 (0.87, 1.36)	0.44	1.02 (0.91, 1.14)	0.79	0.88
rs2028299	**89831025**	**15**	**AP3S2**	**BC**	**C**	**A**			**rs2028299**	**Same**	**0.29**	**1.18 (1.05, 1.34)**	**0.01**	**0.28**	**0.98 (0.79, 1.20)**	**0.82**	**1.12 (1.01, 1.25)**	**0.03**	**0.24**
rs7172432	62104190	15	C2CD4A, C2CD4B	BC	A	G			rs7163757	0.99	0.58	1.00 (0.89, 1.13)	0.97	0.55	1.15 (0.94, 1.42)	0.17	1.04 (0.94, 1.15)	0.47	0.73
rs7178572	77454848	15	HMG20A	-	G	A	rs952471	0.96	rs7178572	Same	0.71	1.01 (0.89, 1.16)	0.84	0.71	0.87 (0.71, 1.07)	0.18	0.97 (0.87, 1.08)	0.59	0.75
rs11642841	53811575	16	FTO	IR	A	C					0.39	1.08 (0.96, 1.22)	0.19	0.38	1.01 (0.82, 1.25)	0.91	1.06 (0.95, 1.17)	0.28	0.65
rs8042680	90978107	16	PRC1	BC	A	C					0.34	0.98 (0.86, 1.10)	0.69	0.70	0.89 (0.71, 1.10)	0.28	0.95 (0.86, 1.06)	0.38	0.69
rs4430796	**37738049**	**17**	**HNF1B**	**BC**	**G**	**A**			**rs4430796**	**Same**	**0.49**	**1.10 (0.98, 1.23)**	**0.12**	**0.47**	**1.17 (0.97, 1.41)**	**0.10**	**1.12 (1.01, 1.23)**	**0.03**	**0.24**

SNP	BP	Chr	Gene	Func	type 2 diabetes risk allele	Reference allele	Confirmation in Scott et. al., 2017[1]		Confirmation in Mahajan et. al., 2014[2]		NHSI			DNBC			Pooled[a]		*P*, FDR corrected
							Relevant SNP	R²	Relevant SNP	R²	EAF	RR (95% CI)[b]	P	EAF	RR (95% CI)[b]	P	RR (95% CI)	*P*	
rs8050136	53782363	17	FTO	IR	A	C	rs1558902	0.92	rs9936385	0.99	0.39	1.11 (0.99, 1.25)	0.08	0.39	1.01 (0.83, 1.25)	0.89	1.09 (0.98, 1.20)	0.11	0.41
rs3786897	33402102	19	PEPD	IR	A	G			rs3786897	Same	0.59	1.10 (0.98, 1.24)	0.12	0.59	1.07 (0.89, 1.30)	0.47	1.05 (0.95, 1.16)	0.34	0.69
rs8090011	7068463	19	LAMA1	-	G	C	rs7234111	0.90			0.38	1.01 (0.89, 1.14)	0.90	0.38	1.34 (1.11, 1.61)	0.00	1.09 (0.99, 1.21)	0.08	0.36
rs4812829	44360627	20	HNF4A	BC	A	G			rs4812829	Same	0.17	0.92 (0.79, 1.07)	0.29	0.21	1.03 (0.81, 1.30)	0.82	0.95 (0.83, 1.08)	0.45	0.72

[a]Meta-analyzed results from the two cohorts using fixed effects models weighted by inverse variance of the estimates.

[b]Estimated in log-binomial models adjusting for women's age.

Abbreviates: SNP – single nuclear polymorphism; Chr – chromosome; Func – functional annotation; GWAS – genome-wide association studies; EAF – effective allele frequency; RR – relative risk; CI – confidence interval; FDR – false discovery rate.
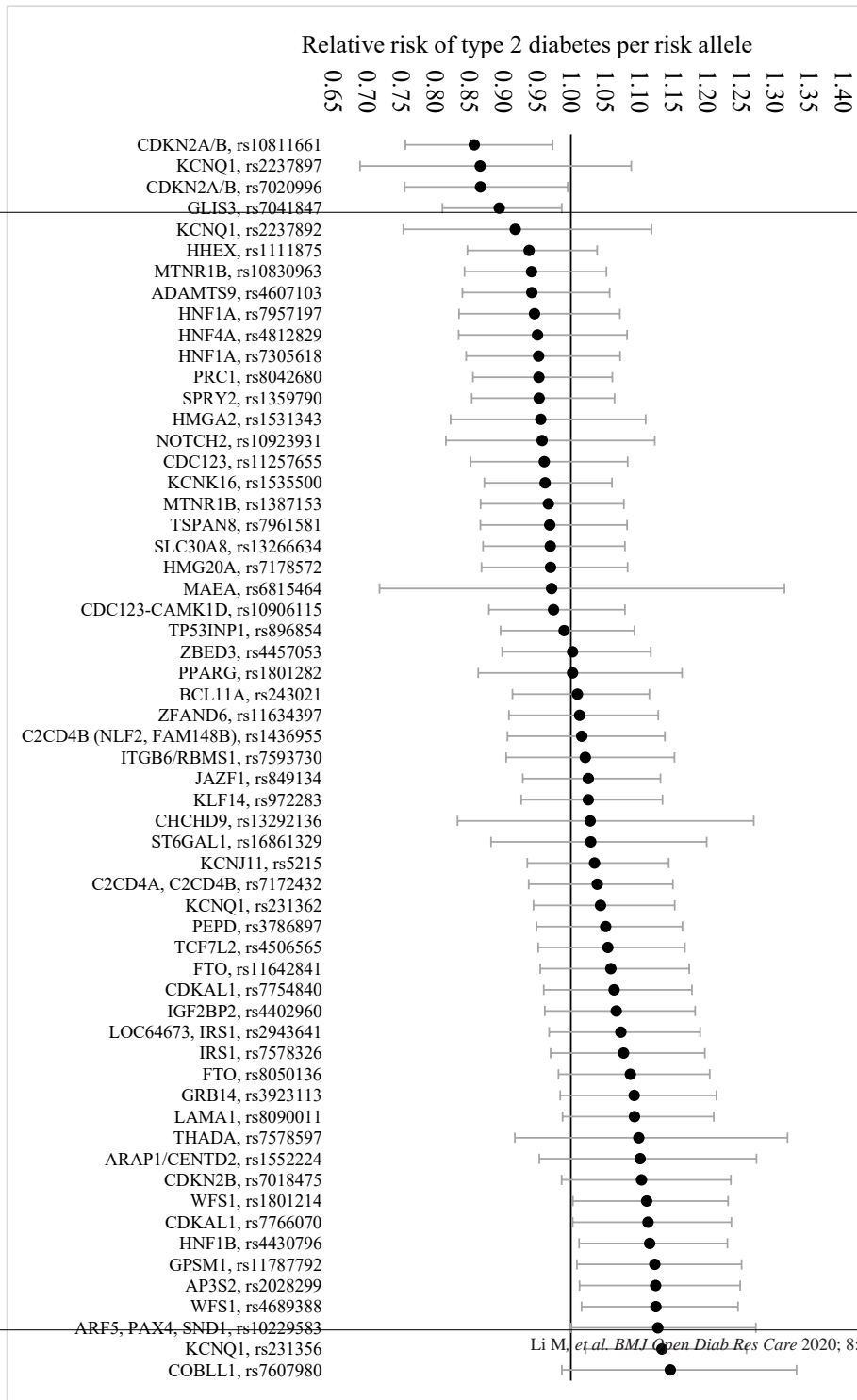
Relative risk of type 2 diabetes per risk allele

0.65 0.70 0.75 0.80 0.85 0.90 0.95 1.00 1.05 1.10 1.15 1.20 1.25 1.30 1.35 1.40

CDKN2A/B, rs10811661
KCNQ1, rs2237897
CDKN2A/B, rs7020996
GLIS3, rs7041847
KCNQ1, rs2237892
HHEX, rs1111875
MTNR1B, rs10830963
ADAMTS9, rs4607103
HNF1A, rs7957197
HNF4A, rs4812829
HNF1A, rs7305618
PRC1, rs8042680
SPRY2, rs1359790
HMGA2, rs1531343
NOTCH2, rs10923931
CDC123, rs11257655
KCNK16, rs1535500
MTNR1B, rs1387153
TSPAN8, rs7961581
SLC30A8, rs13266634
HMG20A, rs7178572
MAEA, rs6815464
CDC123-CAMK1D, rs10906115
TP53INP1, rs896854
ZBED3, rs4457053
PPARG, rs1801282
BCL11A, rs243021
ZFAND6, rs11634397
C2CD4B (NLF2, FAM148B), rs1436955
ITGB6/RBMS1, rs7593730
JAZF1, rs849134
KLF14, rs972283
CHCHD9, rs13292136
ST6GAL1, rs16861329
KCNJ11, rs5215
C2CD4A, C2CD4B, rs7172432
KCNQ1, rs231362
PEPD, rs3786897
TCF7L2, rs4506565
FTO, rs11642841
CDKAL1, rs7754840
IGF2BP2, rs4402960
LOC64673, IRS1, rs2943641
IRS1, rs7578326
FTO, rs8050136
GRB14, rs3923113
LAMA1, rs8090011
THADA, rs7578597
ARAP1/CENTD2, rs1552224
CDKN2B, rs7018475
WFS1, rs1801214
CDKAL1, rs7766070
HNF1B, rs4430796
GPSM1, rs11787792
AP3S2, rs2028299
WFS1, rs4689388
ARF5, PAX4, SND1, rs10229583
KCNQ1, rs231356
COBLL1, rs7607980

Figure S1. Relative risks and 95% confidence intervals[a] of type 2 diabetes associated with single nuclear polymorphism (SNP) among women who had gestational diabetes in the Nurses' Health Study II (NHSII, N=1,884) and the Danish National Birth Cohort (DNBC, N=550).

[a]The RRs were estimated using log-binomial models adjusting for women's age in each cohort, and then meta-analyzed using fixed effects models weighted by inverse variance of the estimates.

Table S3. Relative risks (95% confidence interval)[a] of type 2 diabetes associated with the genetic risk scores for beta-cell function (GRS$_{BC}$) and insulin resistance (GRS$_{IR}$) among women who had gestational diabetes in the Nurses' Health Study II (NHSII, N = 1,884) and the Danish National Birth Cohort (DNBC, N = 550).

| | | Quartiles of GRS | | | | | Per five allele |
		Quartile 1	Quartile 2	Quartile 3	Quartile 4	*P*-trend	incremenet
				GRS$_{BC}$			
NHSII	Range	17.0-35.0	35.0-38.0	38.0-41.0	41.0-51.0		
	Case/total	120/477 (25.2)	103/502 (20.5)	93/380 (24.5)	130/525 (24.8)		
	RR (95% CI)	1.00	0.82 (0.65, 1.03)	0.99 (0.78, 1.25)	1.01 (0.82, 1.26)	0.65	1.03 (0.94, 1.14)
DNBC	Range	24.0-35.0	35.0-38.0	38.1-41.0	41.2-52.6		
	Case/total	42/165 (25.5)	45/156 (28.8)	36/119 (30.3)	32/110 (29.1)		
	RR (95% CI)	1.00	1.14 (0.80, 1.63)	1.18 (0.82, 1.72)	1.15 (0.78, 1.70)	0.43	1.07 (0.91, 1.25)
Pooled[b]	RR (95% CI)	1.00	0.90 (0.75, 1.10)	1.04 (0.85, 1.27)	1.04 (0.86, 1.26)	0.44	1.04 (0.96, 1.13)
				GRS$_{IR}$			
NHSII	Range	0.0-11.0	11.0-13.0	13.0-14.3	14.4-22.0		
	Case/total	98/543 (18.1)	86/319 (27.0)	150/563 (26.6)	112/459 (24.4)		
	RR (95% CI)	1.00	1.46 (1.14, 1.89)	1.48 (1.18, 1.85)	1.35 (1.06, 1.72)	0.01	1.23 (1.06, 1.42)
DNBC	Range	5.5-11.0	12.0-13.0	13.2-14.7	15.0-22.0		
	Case/total	47/173 (27.2)	46/162 (28.4)	19/78 (24.4)	43/137 (31.4)		
	RR (95% CI)	1.00	1.06 (0.75, 1.50)	0.90 (0.57, 1.42)	1.18 (0.84, 1.67)	0.47	1.03 (0.78, 1.35)
Pooled[b]	RR (95% CI)	1.00	1.31 (1.07, 1.60)	1.34 (1.10, 1.64)	1.29 (1.06, 1.58)	0.01	1.18 (1.03, 1.34)

[a]Estimated in log-binomial models adjusting for women's age.
[b]Meta-analyzed results from the two cohorts using fixed effects models weighted by inverse variance of the estimates.

References

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