

Supplementary Online Content

Appendix S1

Anthropometric Measurements

All mother–child pairs underwent a physical examination, according to a standard protocol as previously described.^{1,2} All participants's height and weight were measured wearing light indoor clothing and without shoes by trained research doctors. Height was measured to the nearest 0.1 cm with a stadiometer, and weight was measured to the nearest 0.1 kg with a beam balance scale. Moreover, the children's physical examination also included waist circumference, hip circumference, skinfolds (triceps, subscapular, suprailiac), and body fat percentage. Waist circumference was measured midway between the 10th rib and the top of the iliac crest, and hip circumference was measured at the level of maximum extension of the hip. Both waist and hip circumference were measured to the nearest 0.1 cm. Triceps skinfold, subscapular skinfold, and suprailiac skinfold were measured with calibrated skinfold calipers to the nearest 0.5 mm. Body fat percentage was measured by a body composition analyzer (InBody J20) to the nearest 0.1%. All the measurements were conducted twice by trained medical examiner, and the averages were used. Body mass index (BMI) was calculated by dividing weight in kilograms by the square of height in meters. Weight-for-age z score, BMI-for-age z score were calculated based on the standards for the WHO growth reference.³

References:

1. Lu J, Zhang S, Li W, et al. Maternal gestational diabetes is associated with offspring's hypertension. *Am J Hypertens*. 2019;32(4):335-342.
2. Wang J, Wang L, Liu H, et al. Maternal Gestational Diabetes and Different Indicators of Childhood Obesity - A Large Study. *Endocr Connect*. 2018;7(12):1464–1471.
3. World Health Organization, The WHO Child Growth Standards, World Health Organization, Geneva, Switzerland, 2006, <http://www.who.int/childgrowth/standards/en>.

Table S1. Characteristics of included 17 SNP loci with P values $<5 \times 10^{-8}$

SNP	Chr.	Position (bp)	Nearest gene(s)	Effect Allele (1)	Other Allele (0)	EAF	Genotype (00/01/11)	HWE		Original GWAS		
								Total sample	Non-GDM group	Beta	SE	P value
rs3765467	6	39033595	<i>GLP1R</i>	G	A	0.782	50/385/679	0.624	0.717	-0.037	0.006	6.62×10^{-10}
rs60808706	11	2857233	<i>KCNQ1</i>	G	A	0.672	120/490/504	0.956	0.836	-0.051	0.005	5.10×10^{-27}
rs79105258	12	111718231	<i>CUX2</i>	C	A	0.840	34/288/792	0.215	0.825	-0.037	0.006	1.27×10^{-10}
rs1260326	2	27730940	<i>GCKR</i>	C	T	0.468	317/551/246	0.822	0.937	0.039	0.005	1.94×10^{-16}
rs12712928	2	45192080	<i>SIX3, SIX2</i>	C	G	0.365	462/491/161	0.101	0.078	0.069	0.005	7.40×10^{-46}
rs12053049	2	169767148	<i>G6PC2</i>	C	T	0.315	529/468/117	0.374	0.580	0.061	0.005	2.57×10^{-37}
rs1349497	2	173592663	<i>RAPGEF4-AS1</i>	C	G	0.491	276/583/255	0.116	0.202	0.027	0.005	7.47×10^{-9}
rs11924032	3	170735099	<i>SLC2A2</i>	G	A	0.849	30/276/808	0.275	0.838	-0.050	0.006	3.75×10^{-18}
rs11705729	3	185507299	<i>IGF2BP2</i>	T	A	0.279	567/472/75	0.078	0.063	0.029	0.005	2.71×10^{-9}
rs9358356	6	20667382	<i>CDKAL1</i>	C	T	0.465	311/570/233	0.344	0.213	0.036	0.005	9.76×10^{-14}
rs1558318	7	15065612	<i>DGKB, AGMO</i>	T	A	0.631	139/544/431	0.104	0.052	0.039	0.005	5.39×10^{-13}
rs6975024	7	44231886	<i>GCK, YKT6</i>	C	T	0.230	659/397/58	0.858	0.615	0.049	0.006	6.70×10^{-16}
rs13266634	8	118184783	<i>SLC30A8</i>	C	T	0.591	189/533/392	0.733	0.862	-0.042	0.005	1.75×10^{-19}
rs57884925	9	4285119	<i>GLIS3</i>	G	C	0.415	386/531/197	0.539	0.268	0.027	0.005	1.93×10^{-8}
rs10965246	9	22132698	<i>CDKN2B-AS1, DMRTA1</i>	T	C	0.564	219/533/362	0.367	0.533	-0.042	0.005	1.99×10^{-16}
rs4581570	13	28510712	<i>PDX1, ATP5EP2</i>	C	T	0.425	382/518/214	0.106	0.251	0.033	0.005	9.45×10^{-10}
rs1203936	20	22592430	<i>LINC01384, SSTR4</i>	T	G	0.837	22/319/773	0.096	0.349	0.041	0.006	1.53×10^{-13}

The 17 selected SNPs were identified from a large-scale genome-wide association study (GWAS) (ref. 25, Kanai et al. 2018) conducted by BioBank Japan Project (BBJ) among 93,146 Japanese individuals. Chr., Chromosome; EAF, Effect allele frequency; GDM, gestational diabetes mellitus; HWE Hardy-Weinberg equilibrium; IFG impaired fasting glucose; SNP, single nucleotide polymorphism.

Table S2. The offspring characteristics and adiposity measures according to maternal GDM status

	Non-GDM (N=554)	GDM (N=560)	P Value
Age, years	5.9 ± 1.2	5.9 ± 1.3	0.986
Sex, boys, n (%)	290 (52.4)	294 (52.5)	0.959
Feeding pattern, n (%)			
Exclusive breast feeding	230 (41.6)	251 (44.8)	0.427
Mixed breast and formula feeding	243 (43.9)	240 (42.9)	
Exclusive formula feeding	80 (14.5)	69 (12.3)	
Vegetable intake frequency, n (%)			
≤1 time/day	75 (13.5)	15 (2.7)	<0.001
2 times/day	447 (80.7)	525 (93.8)	
≥3 times/day	32 (5.8)	20 (3.6)	
Fruit intake frequency, n (%)			
<1 time/day	18 (3.3)	20 (3.6)	0.381
1 times/day	208 (37.6)	188 (33.6)	
>3 times/day	328 (59.2)	352 (62.9)	
Sleeping time, n (%)			
≤8 hours/day	60 (10.9)	86 (15.4)	<0.001
9–10 hours/day	370 (66.9)	400 (71.4)	
≥11 hours/day	123 (22.2)	74 (13.2)	
Screen watching time, hours/day	0.9 ± 0.8	1.2 ± 0.8	<0.001
Outdoor activity, hours/day	2.1 ± 0.8	2.2 ± 0.9	0.127
Birth length, cm	50.7 ± 2	50.7 ± 1.9	0.831
Birth weight, g	3403.6 ± 452	3538.3 ± 509.6	<0.001
Height, cm	118 ± 9.2	118.4 ± 10	0.509
Weight, kg	22.2 ± 5.9	23.1 ± 7.1	0.012
BMI, kg/m ²	15.7 ± 2.3	16.2 ± 2.6	<0.001
Waist circumference, cm	54.7 ± 6	56.4 ± 6.8	<0.001
Hip circumference, cm	63.6 ± 6.8	65.3 ± 7.7	<0.001
Sum of skinfolds, mm	29.8 ± 14.2	32.5 ± 16.4	<0.001
Body fat percentage, %	19.1 ± 7.4	20.8 ± 8.1	<0.001

Abbreviations: BMI, body mass index; GDM, gestational diabetes mellitus.

Data are shown as means (SD) or n (%).

Table S3. Associations of genetically determined maternal blood glucose with offspring's obesity measures among children with and without maternal GDM (sensitivity analysis excluding SNPs associated with BMI/obesity in East Asians)

	Non-GDM (N=554)		GDM (N=560)		<i>P</i> for interaction
	OR (95% CI)	<i>P</i> Value	OR (95% CI)	<i>P</i> Value	
Overweight and obesity status					
Overweight	1.69 (1.29, 2.22)	2.63E-04	0.91 (0.73, 1.12)	0.366	0.001
Obesity	2.24 (1.45, 3.46)	2.63E-04	0.95 (0.71, 1.29)	0.763	0.002
Obesity-related quantitative traits					
	β (SE)	<i>P</i> Value	β (SE)	<i>P</i> Value	
Weight, kg	0.57 (0.20)	0.004	0.05 (0.21)	0.822	0.137
Weight-for-age z score	0.14 (0.05)	0.005	-0.02 (0.05)	0.624	0.048
BMI, kg/m ²	0.32 (0.09)	0.001	-0.02 (0.10)	0.849	0.031
BMI-for-age z score	0.16 (0.05)	0.002	-0.03 (0.05)	0.547	0.021
Waist circumference, cm	0.69 (0.23)	0.003	-0.09 (0.25)	0.705	0.044
Hip circumference, cm	0.56 (0.24)	0.017	0.10 (0.24)	0.686	0.280
Sum of skinfolds, mm	1.75 (0.60)	0.003	-0.48 (0.61)	0.432	0.022
Body fat percentage, %	1.12 (0.32)	4.70E-04	-0.23 (0.32)	0.472	0.007

Abbreviations: GDM, gestational diabetes mellitus; OR, odds ratio.

Logistic regression models or general linear models were performed to explore the associations of genetically determined maternal blood glucose with offspring's obesity measures. Interactions were also tested, adjusted for children's age, sex, birth weight, feeding patterns, outdoor physical activity time, screen watching time, sleeping time, vegetable intake frequency, fruit intake frequency, illness within the last three months, and maternal age at pregnancy, gestational weight gain, gestational age at delivery, smoking status, drinking status, marital status, education, family monthly income, hypertensive disorders of pregnancy, treatment of GDM, any family history of diabetes, and maternal pre-pregnancy BMI. For weight-for-age z score and BMI-for-age z score, which were calculated based on sex- and age-specific standards, children's age, and sex were excluded in the adjustment. BMI, body mass index; GDM, gestational diabetes mellitus.

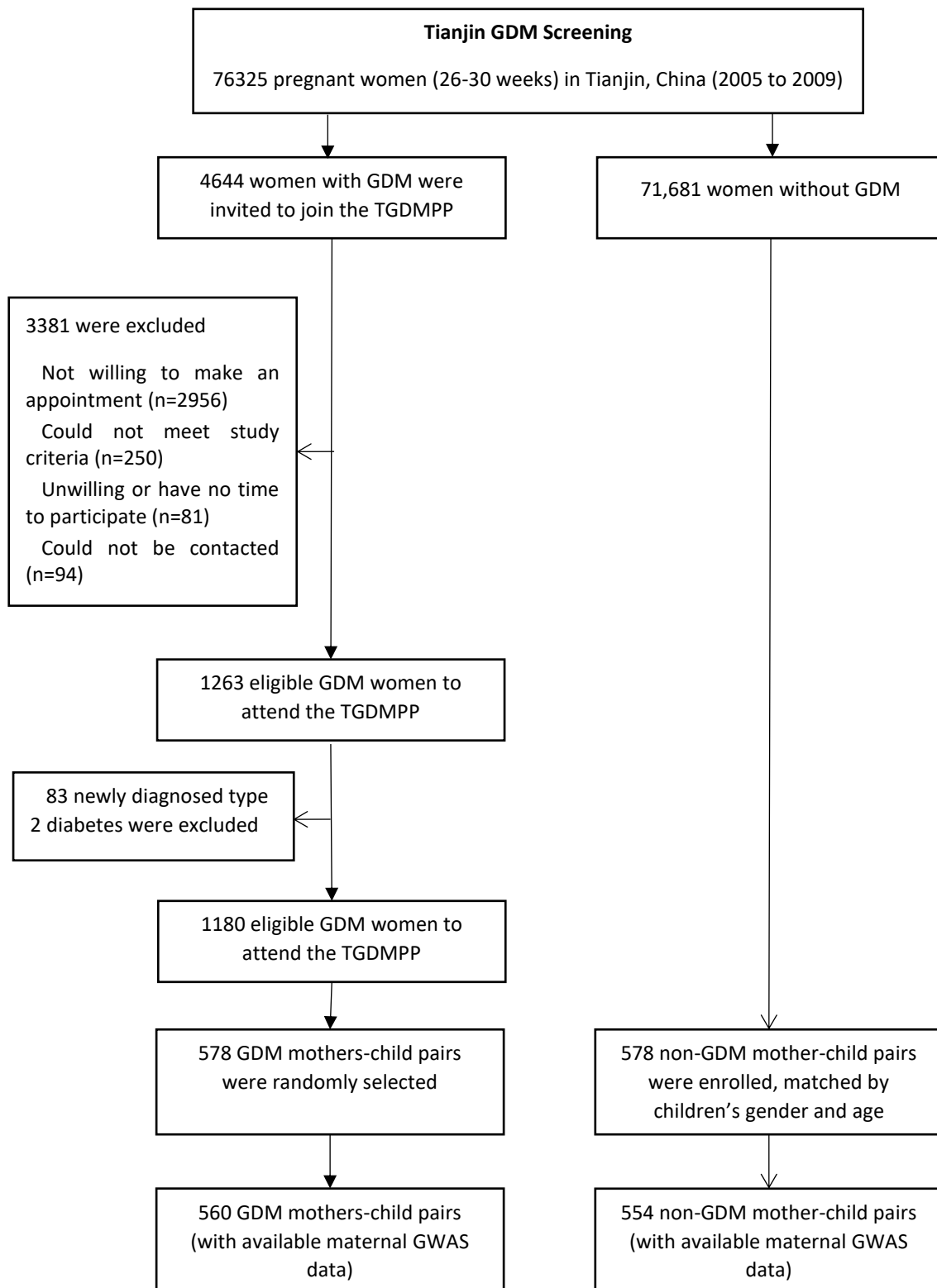


Figure S1. Flow chart.

From 2005 to 2009, a total of 76,325 pregnant women were screened, with a screening rate >91%, among whom 4,644 pregnant women were diagnosed with GDM. We invited all the 4,644 women to join the Tianjin Gestational Diabetes Mellitus Prevention Program (TGDMPP), a large randomized controlled trial conducted at the Tianjin Women's and Children's Health Centre, Tianjin, China. The study design of TGDMPP, including recruitment, screening visits, inclusion and exclusion criteria, randomization and intervention, has been described in detail in previous publications. In brief, after exclusion of those who were not available to make an appointment due to different reasons, could not meet study criteria, unwilling or had no time to participate, could not be contacted, 1263 GDM women at their postpartum 1-5 years completed the baseline survey between August 1, 2009 and July 31, 2011. Among them, 83 were newly diagnosed as having type 2 diabetes during the baseline survey, leaving the rest of 1180 GDM women to attend the TGDMPP. Subsequently, we randomly selected 578 GDM mother-child pairs who finished the year 1 or 2 follow-up survey of TGDMPP. Simultaneously, we also enrolled 578 non-GDM mother-child pairs, with age and sex frequency matched to the 578 children of GDM mothers. Among them, 1114 mothers had available GWAS data (560 GDM and 554 non-GDM mother-child pairs), forming the present trans-generation observational study.

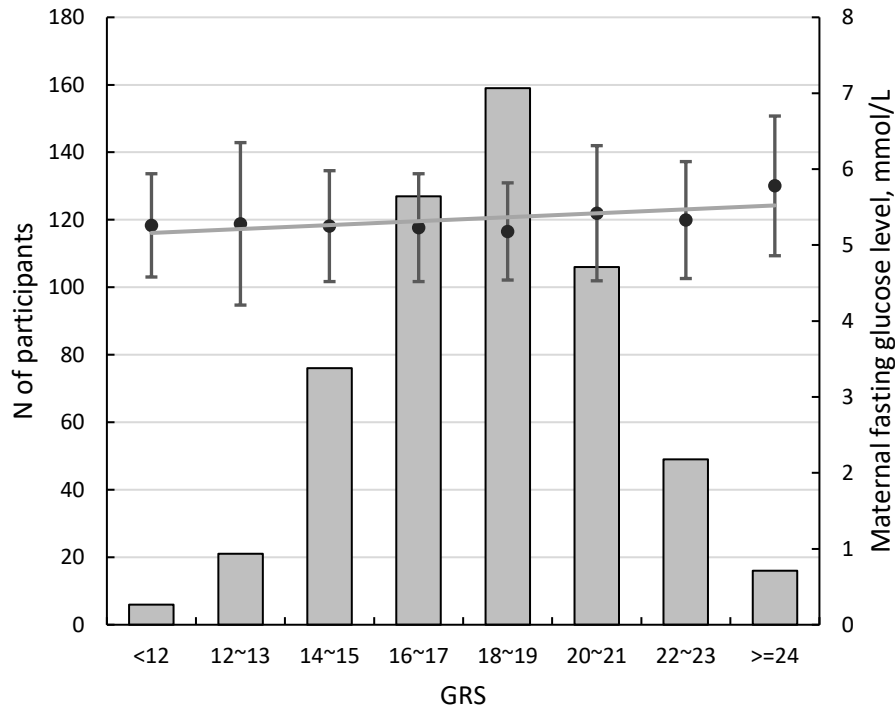


Figure S2. Maternal genetic risk score distribution and its association with maternal fasting glucose among women with GDM

The histograms represent the number of participants, and the mean (\pm SD) maternal glucose levels are plotted with the trend lines across the GRS. The slope of the trend lines represents the effects of GRS on maternal glucose among women with GDM (β (SE) = 0.05 (0.02), $P=0.015$).