Supplementary Table 6. Associations of *KCNQ1* rs2237897 with gestational diabetes in all discovery and replication cohorts

Stage	Study	Ethnicity	Population	Study design	Covariates	Imputation quality, Rsq	Number		Risk allele frequency		Association for gestational diabetes					
							GDM case	Non-GDM control	GDM case	Non-GDM control	OR (95% CI)	$P_{additive}$	P_{GC}	P_{Q}	$P_{ancestry}$	$P_{residual}$
Discovery	HAPO-HK Study	East Asian	Chinese pregnant women	Population-based	Age and PCs	0.968	149	811	0.741	0.634	1.76 (1.31–2.36)	1.7×10^{-4}	-	-	-	-
	Tianjin Study	East Asian	Chinese pregnant women	Case-control	Age and PCs	0.995	229	226	0.715	0.661	1.29 (0.97–1.72)	0.0806	-	-	-	-
	TGDM-NDM Study	East Asian	Cases: Chinese pregnant women; Controls: Chinese non-pregnant women	Case-control	Age and PCs	0.963	86	180	0.695	0.644	1.40 (0.88–2.25)	0.1582	-	-	-	-
	Meta-analysis of discovery cohorts	East Asian	Chinese women	-	-	-	464	1,217	-	-	1.48 (1.23–1.79)	3.8×10^{-5}	4.7×10^{-5}	0.3238	-	-
De novo replication	Guangzhou Study	East Asian	Chinese pregnant women	Case-control	None	-	564	572	0.717	0.660	1.33 (1.10–1.60)	2.7×10^{-3}	-	-	-	-
In silico replication I	FinnGen Study [8]	European	Finnish pregnant women	Case-control	Age, PCs and genotyping batch	-	12,332	131,109	0.919		1.13 (1.07–1.19)	8.0×10^{-6}	-	-	-	-
	GenDIP Consortium [9]	Multi-ethnicities	72.2% European, 13.4% East Asian, 9.9% South Asian, 2.8% Hispanic/Latino, and 1.7% African	Meta-analysis	-	-	345,656		0.951		1.19 (1.10–1.28)	2.2×10^{-4}	-	-	0.6109	0.1958
In silico replication II	Mexican Study [15]	Hispanic	Mexican pregnant women	Case-control	Age, pregestational BMI, dummy reference hospital and PCs	-	408	342	0.753	0.656	1.85 (1.39–2.50)	4.5×10^{-5}	-	-	-	-
Lookup from literatures	Overall meta-analysis	Multi-ethnicities	1.9% Chinese, 0.5% Mexican, and 97.6% Finnish	-	-	-	13,768	133,240	-	-	1.16 (1.10–1.22)	2.4×10^{-9}	-	0.0405	-	-

A total of three studies (i.e., the HAPO-HK Study, the Tianjin Study, and the TGDM-NDM Study) were included in the "meta-analysis of discovery cohorts." A total of six studies (i.e., the HAPO-HK Study, the Tianjin Study, the TGDM-NDM Study, the Guangzhou Study, the FinnGen Study, and the Mexican Study) were included in the "overall meta-analysis." OR and 95% CI were reported according to the type 2 diabetes mellitus-related risk allele (C-allele) of *KCNQ1* rs2237897. $P_{additive}$ was obtained from either logistic regression model with the adjustments of covariates, or meta-analysis under a fixed effect model. P_{GC} was obtained from meta-analysis under a fixed effect model after genomic control. P_{Q} was obtained from heterogeneity test (Cochran's Q test). For the GenDIP analysis, $P_{additive}$, $P_{ancestry}$, and $P_{residual}$ were obtained from meta-regression implement in Meta-Regression of Multi-AncEstry Genetic Association (MR-MEGA). The combined OR and 95% CI was estimated by meta-analysis under a fixed effect model.

KCNQ1, potassium voltage-gated channel subfamily Q member 1; GDM, gestational diabetes mellitus; OR, odds ratio; CI, confidence interval; HAPO-HK, Hyperglycemia and Adverse Pregnancy Outcome-Hong Kong; PC, principal component; TGDM-NDM, Treated GDM Cases vs. Non-diabetes Controls; GenDIP, GENetics of Diabetes In Pregnancy; BMI, body mass index.