

**Supplementary Table 3.** Associations of *TBR1-SLC4A10* rs117781972 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	0.806	149	811	0.313	0.193	2.26 (1.64–3.11)	$5.1 \times 10^{-7}$	-	-	--	--
	Tianjin Study	East Asian	Chinese pregnant women	Case-control	Age and PCs	0.527	229	226	0.189	0.143	1.97 (1.18–3.27)	$9.4 \times 10^{-3}$	-	-	--	--
	TGDM-NDM Study	East Asian	Cases: Chinese pregnant women; Controls: Chinese non-pregnant women	Case-control	Age and PCs	0.789	86	180	0.233	0.180	1.59 (0.90–2.81)	0.1081	-	-	--	--
	Meta-analysis of discovery cohorts	East Asian	Chinese women	-	-	-	464	1,217	-	-	2.05 (1.61–2.62)	$7.6 \times 10^{-9}$	$1.1 \times 10^{-8}$	0.5624	--	--
<i>De novo</i> replication	Guangzhou Study	East Asian	Chinese pregnant women	Case-control	None	-	564	572	0.230	0.241	0.94 (0.78–1.14)	0.5465	-	-	--	--
<i>In silico</i> replication	FinnGen Study [8]	European	Finnish pregnant women	Case-control	Age, PCs and genotyping batch	-	12,332	131,109		0.010	0.98 (0.85–1.13)	0.7850	-	-	--	--
	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	-	-	6,857			0.071	1.31 (1.07–1.60)	0.0164	-	-	0.1690	$4.5 \times 10^{-4}$

OR and 95% CI were estimated according to the GDM-related risk allele (A-allele) of *TBR1-SLC4A10* rs117781972.  $P_{additive}$  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.

TBR1, T-box brain transcription factor 1; SLC4A10, solute carrier family 4 member 10; 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.