dmj

Supplementary Table 14. Sensitivity analysis for the association of identified variants with the risk of gestational diabetes in Chinese women from the HAPO-HK Study, with different covariates adjustments

SNP	Nearest gene(s)	Chr	Position (Build 37)	Risk/non-risk allele	Adjustment	Number	Risk allele frequency	OR (95% CI)	P value
rs117781972	TBR1-SLC4A10	2	162,332,226	A/G	PCs, age	960	0.212	2.26 (1.64–3.11)	5.1×10^{-7}
					PCs, age, BMI	959	0.211	2.25 (1.63–3.10)	7.4×10^{-7}
					PCs, age, BMI, GWG	952	0.211	2.28 (1.65–3.16)	5.3×10^{-7}
					PCs, age, BMI, GWG, SBP, DBP	952	0.211	2.30 (1.66–3.19)	5.1×10^{-7}
					PCs, age, BMI, GWG, SBP, DBP, smoking status	952	0.211	2.30 (1.66–3.18)	5.9×10^{-7}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year	927	0.212	2.32 (1.67–3.22)	5.6×10^{-7}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity	927	0.212	2.32 (1.67–3.22)	5.8×10^{-7}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes	921	0.212	2.33 (1.67–3.24)	5.4×10^{-7}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes and hypertension	921	0.212	2.29 (1.64–3.18)	9.4×10^{-7}
rs7754840	CDKAL1	6	20,661,250	C/G	PCs, age	960	0.375	1.47 (1.14–1.90)	3.4×10^{-3}
					PCs, age, BMI	959	0.375	1.47 (1.13–1.91)	3.6×10^{-3}
					PCs, age, BMI, GWG	952	0.375	1.47 (1.13–1.91)	4.2×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP	952	0.375	1.47 (1.13–1.92)	4.2×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status	952	0.375	1.47 (1.12–1.91)	4.7×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year	927	0.373	1.49 (1.14–1.95)	3.2×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity	927	0.373	1.51 (1.16–1.97)	2.6×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes	921	0.374	1.50 (1.15–1.96)	3.2×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes and hypertension	921	0.374	1.50 (1.15–1.97)	3.1×10^{-3}
rs2237897	INS-IGF2-KCNQ1	11	2,858,546	C/T	PCs, age	960	0.349	1.76 (1.31–2.36)	1.7×10^{-4}
					PCs, age, BMI	959	0.349	1.77 (1.31–2.37)	1.7×10^{-4}
					PCs, age, BMI, GWG	952	0.349	1.76 (1.31–2.37)	2.1×10^{-4}
					PCs, age, BMI, GWG, SBP, DBP	952	0.349	1.76 (1.30–2.37)	2.4×10^{-4}
					PCs, age, BMI, GWG, SBP, DBP, smoking status	952	0.349	1.77 (1.31–2.39)	2.0×10^{-4}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year	927	0.347	1.79 (1.32–2.42)	1.7×10^{-4}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity	927	0.347	1.80 (1.33–2.43)	1.5×10^{-4}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes	921	0.348	1.79 (1.32–2.42)	1.8×10^{-4}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes and hypertension	921	0.348	1.80 (1.33–2.44)	1.6×10^{-4}
rs7945617	MTNR1B	11	92,700,287	C/T	PCs, age	960	0.490	1.61 (1.23–2.12)	6.0×10^{-4}
					PCs, age, BMI	959	0.490	1.59 (1.21–2.09)	9.0×10^{-4}
					PCs, age, BMI, GWG	952	0.490	1.59 (1.21–2.09)	1.0×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP	952	0.490	1.56 (1.18–2.07)	1.6×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status	952	0.490	1.56 (1.18–2.07)	1.6×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year	927	0.488	1.58 (1.19–2.09)	1.5×10^{-3}

(*Continued to the next page*)

Supplementary Table 14. Continued

SNP	Nearest gene(s)	Chr	Position (Build 37)	Risk/non-risk allele	Adjustment	Number	Risk allele frequency	OR (95% CI)	P value
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity	927	0.488	1.58 (1.19–2.09)	1.5×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes	921	0.489	1.58 (1.20–2.10)	1.4×10^{-3}
					PCs, age, BMI, GWG, SBP, DBP, smoking status, education year, parity, family history of diabetes and hypertension	921	0.489	1.56 (1.18–2.07)	2.0×10^{-3}

OR and 95% CI were reported according to the GDM-related risk allele. *P* value was obtained from logistic regression model with the adjustments of covariates.

HAPO-HK, Hyperglycemia and Adverse Pregnancy Outcome-Hong Kong; SNP, single nucleotide polymorphism; Chr, chromosome; OR, odds ratio; CI, confidence interval; *TBR1*, T-box brain transcription factor 1; *SLC4A10*, solute carrier family 4 member 10; PC, principal component; BMI, body mass index; GWG, gestational weight gain; SBP, systolic blood pressure; DBP, diastolic blood pressure; *CDKAL1*, CDK5 regulatory subunit-associated protein 1-like 1; *INS-IGF2*, insulin-insulin-like growth factor 2; *KCNQ1*, potassium voltage-gated channel subfamily Q member 1; *MTNR1B*, melatonin receptor 1B.