Supplementary Table 7. Conditional analysis for gestational diabetes at the *CDKAL1* and *MTNR1B* loci in Chinese women

SNP	Chr	Position (Build 37)	Nearest gene(s)	Risk/ other alleles	Conditional SNP	Cohort	LD r^2	Number		Risk allele frequency		Unconditional analysis			Conditional analysis		
								Case	Control	Case	Control	OR (95% CI)	P value	P_Q	OR (95% CI)	P value	P_Q
rs7754840	6	20661250	CDKAL1	C/G	rs9348441	HAPO-HK Study	0.809	149	811	0.451	0.361	1.47 (1.14–1.90)	3.4E-03	-	0.82 (0.43–1.55)	0.5415	-
						Tianjin Study	0.812	229	226	0.465	0.381	1.41 (1.08–1.84)	0.0110	-	1.61 (0.86–3.01)	0.1390	-
						TGDM-NDM Study	0.807	86	180	0.353	0.346	0.92 (0.61–1.38)	0.6836	-	0.33 (0.13–0.86)	0.0232	-
						Meta-analysis	-	464	1,217	-	-	1.33 (1.13–1.58)	7.9E-04	0.1400	0.92 (0.61–1.39)	0.6981	0.0228
rs9348441	6	20661250	CDKAL1	C/G	rs7754840	HAPO-HK Study	0.809	149	811	0.445	0.341	1.59 (1.22–2.06)	4.9E-04	-	1.91 (1.00–3.64)	0.0500	-
						Tianjin Study	0.812	229	226	0.445	0.376	1.34 (1.02–1.75)	0.0340	-	0.87 (0.46–1.63)	0.6567	-
						TGDM-NDM Study	0.807	86	180	0.403	0.341	1.16 (0.79–1.71)	0.4565	-	3.01 (1.20–7.53)	0.0187	-
						Meta-analysis	-	464	1,217	-	-	1.40 (1.18–1.65)	9.4E-05	0.3808	1.51 (1.01–2.27)	0.0469	0.0603
rs10830962	11	92698427	MTNR1B	G/C	rs7945617	HAPO-HK Study	0.899	149	811	0.522	0.439	1.52 (1.16–2.00)	2.4E-03	-	0.69 (0.29–1.61)	0.3899	-
						Tianjin Study	0.928	229	226	0.505	0.421	1.36 (1.05–1.76)	0.0180	-	0.26 (0.07–0.97)	0.0445	-
						TGDM-NDM Study	0.877	86	180	0.504	0.384	2.01 (1.28–3.16)	2.6E-03	-	0.26 (0.06–1.10)	0.0677	-
						Meta-analysis	-	464	1,217	-	-	1.51 (1.27–1.79)	3.1E-06	0.3381	0.45 (0.24–0.86)	0.0148	0.3373
rs7945617	11	92700287	MTNR1B	C/T	rs10830962	HAPO-HK Study	0.899	149	811	0.572	0.476	1.61 (1.23–2.12)	6.0E-04	-	2.30 (0.98–5.36)	0.0548	-
						Tianjin Study	0.928	229	226	0.535	0.434	1.48 (1.14–1.93)	3.7E-03	-	5.75 (1.48–22.3)	0.0115	-
						TGDM-NDM Study	0.877	86	180	0.557	0.411	2.40 (1.52–3.79)	1.9E-04	-	8.42 (1.99–35.6)	3.8E-03	-
						Meta-analysis	-	464	1,217	-	-	1.64 (1.38–1.96)	2.6E-08	0.1988	3.66 (1.92–6.96)	7.9E-05	0.2383
rs7945617	11	92700287	MTNR1B	C/T	rs10830963	HAPO-HK Study	0.827	149	811	0.572	0.476	1.61 (1.23–2.12)	6.0E-04	-	2.21 (1.14–4.29)	0.0188	-
						Tianjin Study	0.879	229	226	0.535	0.434	1.48 (1.14–1.93)	3.7E-03	-	1.67 (0.74–3.79)	0.2179	-
						TGDM-NDM Study	0.776	86	180	0.557	0.411	2.40 (1.52–3.79)	1.9E-04	-	3.40 (1.07–10.8)	0.0378	-
						Meta-analysis	-	464	1,217	-	-	1.64 (1.38–1.96)	2.6E-08	0.1988	2.17 (1.35–3.47)	1.3E-03	0.6150
rs10830963	11	92708710	MTNR1B	G/C	rs7945617	HAPO-HK Study	0.827	149	811	0.498	0.426	1.51 (1.13–2.01)	5.3E-03	-	0.69 (0.34–1.40)	0.3063	-
						Tianjin Study	0.879	229	226	0.478	0.393	1.47 (1.11–1.96)	7.9E-03	-	0.87 (0.36–2.11)	0.7550	-
						TGDM-NDM Study	0.776	86	180	0.486	0.357	2.22 (1.37–3.60)	1.2E-03	-	0.67 (0.20–2.27)	0.5156	-
						Meta-analysis	-	464	1,217	-	-	1.58 (1.31–1.91)	1.5E-06	0.3257	0.74 (0.45–1.22)	0.2403	0.9103

Association was assessed by logistic regression with adjustments for age and principal components. Results obtained from the individual cohorts were meta-analyzed under a fixed effect model. OR and 95% CI were reported according to the gestational diabetes mellitus-related risk allele. P_Q was obtained from the heterogeneity test (Cochran's Q test).

CDKAL1, CDK5 regulatory subunit-associated protein 1-like 1; *MTNR1B*, melatonin receptor 1B; SNP, single nucleotide polymorphism; Chr, chromosome; LD, linkage disequilibrium; 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.