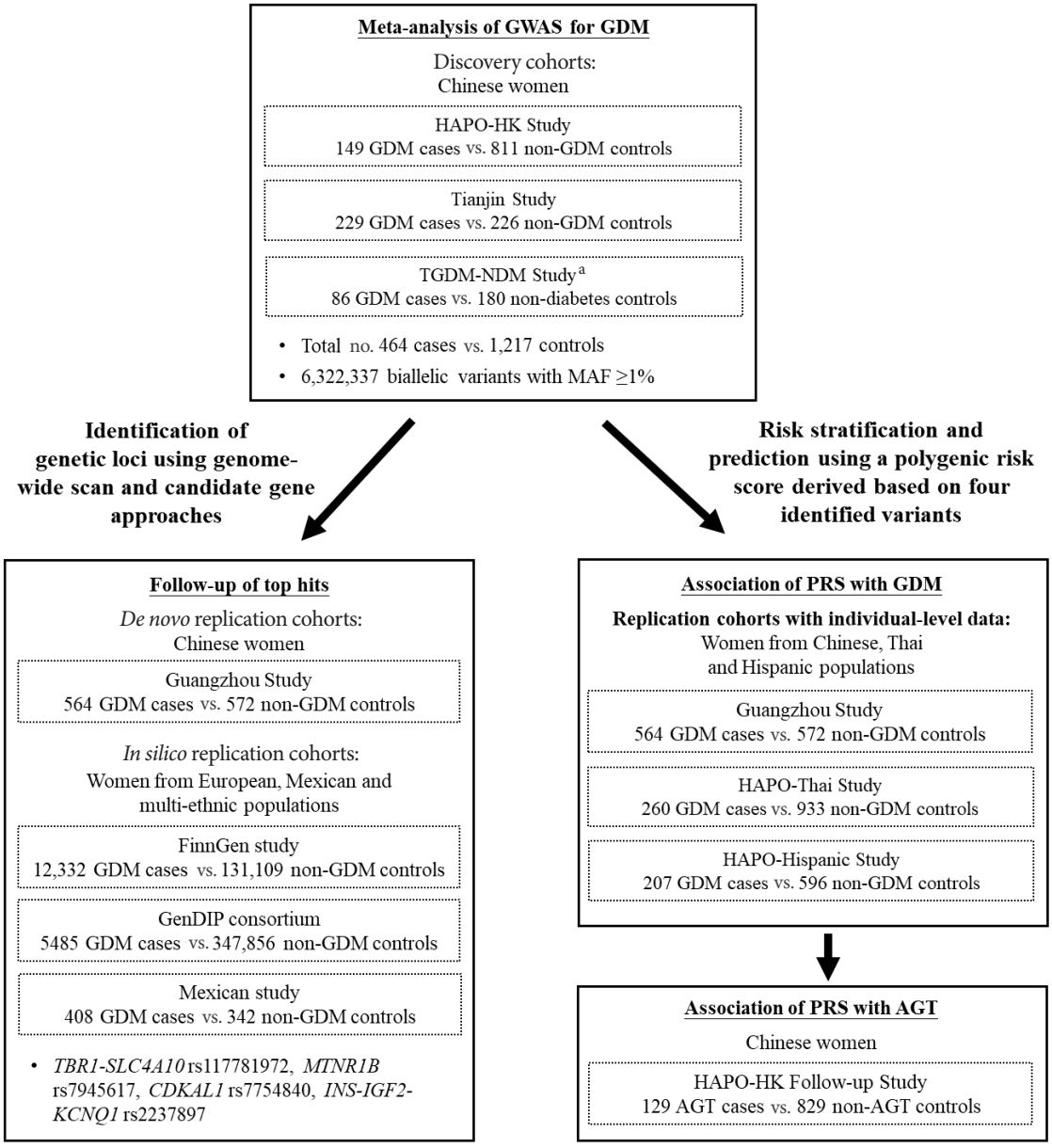

Supplementary Fig. 1. Study design and workflow. Step 1: To identify novel loci associated with an increased risk of gestational diabetes mellitus (GDM), we conducted a meta-analysis of three genome-wide association studies in Chinese women. This was followed by *de novo* replication in an independent Chinese cohort and *in silico* replications in European, Mexican and multi-ethnic populations. Through a combination of genome-wide scan and candidate gene approaches, we identified four loci associated with GDM. Step 2: In order to explore the potential clinical utility of personal genetic information, we derived a polygenic risk score (PRS) for GDM based on the four identified variants from step 1. We evaluated the predictive value of this PRS for GDM in Chinese, Thai and Hispanic populations. Additionally, we assessed its predictive value for abnormal glucose tolerance (AGT) at 7-year postpartum in a Chinese population. GWAS, genome-wide association studies; HAPO-HK, Hyperglycemia and Adverse Pregnancy Outcome-Hong Kong; MAF, minor allele frequency; GenDIP, GENetics of Diabetes In Pregnancy; *TBR1*, T-box brain transcription factor 1; *SLC4A10,* solute carrier family 4 member 10; *MTNR1B*, melatonin receptor 1B; *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. [a]Women in the control group of the Treated GDM Cases vs. Non-diabetes Controls (TGDM-NDM) Study were non-diabetic and non-pregnant, and their glucose tolerance status was not assessed during pregnancy.