

**Supplementary Table 1 The transcriptome datasets related to gestational diabetes mellitus**

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**Supplementary Table 2 Glossary of major transcriptomic technologies**

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<b>Terms</b>	<b>Brief descriptions</b>	<b>Reference</b>
Microarray	Hybridization-based platform using predefined probes to quantify relative	[1]

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	gene expression across thousands of genes in parallel.
Bulk RNA-seq	High-throughput sequencing approach that measures average transcript abundance from mixed cell populations within a tissue or sample. [2]
ncRNA-seq	RNA-sequencing strategies optimized to capture non-coding RNAs, including microRNAs, long non-coding RNAs, and circular RNAs. [3]
Single-cell RNA-seq (scRNA-seq)	Sequencing of individual cells to resolve cellular heterogeneity and identify distinct cell types and transcriptional states. [4]
MeRIP-seq (m6A-seq)	Antibody-based immunoprecipitation of N6-methyladenosine (m6A)-modified RNA followed by sequencing to map RNA methylation patterns transcriptome-wide. [5]
Spatial transcriptomics	Technologies that profile gene expression while preserving spatial context within intact tissue sections. [6]

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2 **Wang Z**, Gerstein M, Snyder M. RNA-Seq: a revolutionary tool for transcriptomics. *Nat Rev Genet* 2009; **10**: 57-63 [PMID: 19015660 DOI: 10.1038/nrg2484]

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