

## Technologies for Diabetes Genomics

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### Abstract

The genetic risk for diabetes largely depends on the type of diabetes and the penetrance and severity of the effect of the contributing genes. This ranges from the high-risk mutations of neonatal diabetes and maturity-onset diabetes of the young to the lower, but still significant, risk conferred by common human leukocyte antigen alleles in type 1 diabetes to the still-lower risk conferred by the common variants associated with type 2 diabetes. There are many new molecular technologies, each with their own set of methodological issues, that have been used for genome-wide association studies and that can be used for determining the genetic risk for these various types of diabetes. These technologies include whole genome single nucleotide polymorphism microarrays, high-throughput polymorphism analyzers, next-generation sequencers, and copy-number variant technologies.

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**Abbreviations:** (BMI) body mass index, (HLA) human leukocyte antigen, (MODY) maturity-onset diabetes of the young, (PCR) polymerase chain reaction, (ROC) receiver operating characteristic, (SNP) single nucleotide polymorphism, (SURI) sulfonylurea receptor

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