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Methylated gene

A methylated gene refers to a gene whose DNA has undergone a chemical modification known as DNA methylation.

Elucidating the interplay between DNA methylation and intracranial aneurysm pathogenesis is paramount to identifying potential biomarkers and therapeutic interventions.

Maimaiti et al. employed a comprehensive bioinformatics investigation of DNA methylation in IA, utilizing a transcriptomics-based methodology that encompassed 100 machine learning algorithms, genome-wide association study (GWAS), Mendelian randomization (MR), and summary-data-based Mendelian randomization (SMR). The sophisticated analytical strategy allowed for a systematic assessment of differentially methylated genes and their implications on the onset, progression, and rupture of IA.

They identified DNA methylation-related genes (MRGs) and associated molecular pathways, and the MR and SMR analyses provided evidence for potential causal links between the observed DNA methylation events and IA predisposition.

These insights not only augment our understanding of the molecular underpinnings of IA but also underscore potential novel biomarkers and therapeutic avenues. Although the study faces inherent limitations and hurdles, it represents a groundbreaking initiative in deciphering the intricate relationship between genetic, epigenetic, and environmental factors implicated in IA pathogenesis ¹⁾.

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Maimaiti A, Turhon M, Abulaiti A, Dilixiati Y, Zhang F, Axieer A, Kadeer K, Zhang Y, Maimaitili A, Yang X. DNA methylation regulator-mediated modification patterns and risk of intracranial aneurysm: a multi-omics and epigenome-wide association study integrating machine learning, Mendelian randomization, eQTL and mQTL data. J Transl Med. 2023 Sep 23;21(1):660. doi: 10.1186/s12967-023-04512-w. PMID: 37742034.

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