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Epigenetic Landscape of Adipocytes in T2DM: A Single-Cell Analysis Using sn-m3C-seq

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Type 2 diabetes mellitus (T2DM) stands as a complicated metabolic puzzle, rooted in factors such as insulin resistance and disrupted glucose metabolism. Adipocytes, essential fat cells in metabolic functions, are central to this puzzle. While their contributions to T2DM through hormone modulation and inflammation are acknowledged, there remains a gap in understanding the epigenetic alterations within these cells. Addressing this, our study employs single-nucleus methyl-3C sequencing (sn-m3C-seq), a method that profiles DNA methylation and chromosomal conformation at the single-cell level. Adipocyte samples come from three distinct groups: metabolically healthy individuals, metabolically healthy obese individuals, and obese individuals with T2DM. The research delves into the relationship between these epigenetic changes and adipocyte dysfunctions, notably diminished insulin responsiveness and increased inflammatory activity. Through sn-m3C-seq, our study aims to provide insights into the role of epigenetic modifications in adipocytes in the pathogenesis of T2DM.