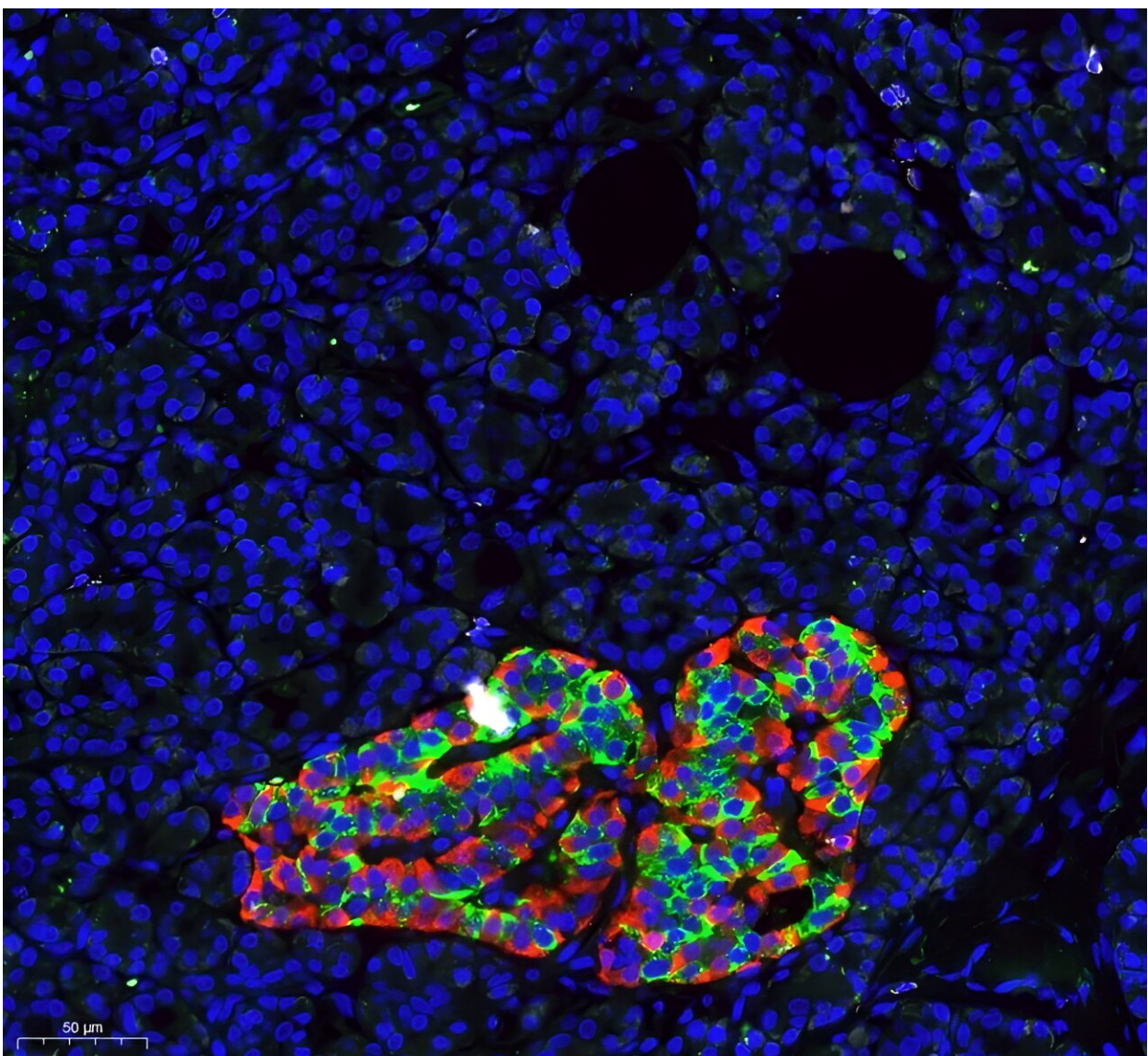


# New DNA methylation-based method for precise assessment of pancreas cell composition

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Histological image of the human pancreas, stained with antibodies against insulin (green) and glucagon (red), together marking an islet of Langerhans. Blue labels DNA, marking the nuclei of all pancreatic cells. Credit: Zeina Drawshy, Dor Lab

In a study [published](#) in *Diabetes*, Prof. Yuval Dor and his research team from Hebrew University have introduced a new approach for accurately assessing cell composition in the human pancreas and islets. The research addresses a critical need in understanding the genesis of diabetes and offers an alternative to traditional protein marker-based methods.

Current methodologies rely on detecting protein markers, such as insulin, to identify specific cell types in the [pancreas](#). However, the variability in [protein content](#) under different physiological and pathological conditions poses a significant limitation, complicating the accurate determination of cell numbers.

The study demonstrates the innovative use of cell type-specific DNA methylation markers to overcome these limitations. By identifying genomic loci uniquely demethylated in specific pancreatic cell types, the research team applied targeted PCR to assess the methylation status of these loci in human islet and pancreas specimens. This enabled a precise inference of cell type composition, offering a molecular alternative to traditional immunodetection methods.

The researchers looked at groups of [cells](#) in the pancreas called islets. They found that in people with different types of diabetes (pre-T1D, T1D, and T2D), the function of a specific type of cell called beta-cells was similar but lower than those without diabetes.

When they looked at pancreas tissues from people with recent-onset

T1D, they found that the beta-cell function was within the normal range, suggesting a problem with these cells. In people with T2D, there were more of another type of cell called alpha-cells, but the beta-cell function was normal. This helps us understand how these cells work in [diabetes](#).

Prof. Yuval Dor, the lead researcher, remarked, "The use of DNA methylation-based analysis not only provides a more accurate assessment of cell types in the human pancreas but also proves invaluable in interpreting insulin secretion assays. This method opens new avenues for understanding pancreas cell composition in both health and disease."

**More information:** Zeina Drawshy et al, DNA methylation-based assessment of cell composition in human pancreas and islets, *Diabetes* (2024). [DOI: 10.2337/db23-0704](https://doi.org/10.2337/db23-0704)

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