

# Preliminary Data Summary

**Project Title:** The Interplay of Circulating MicroRNAs and Gut Microbiome Diversity in Predicting Early-Onset Type 2 Diabetes Mellitus Risk

**Date:** October 2025

## 1. Pilot Cohort Description

A pilot study was conducted on a small, retrospectively collected cohort ( ) to assess the feasibility of simultaneous microRNA and microbiome analysis in our lab setting.

- **EO-T2DM ( ):** Mean age 35.5 years; mean HbA1c 8.1%.
- **High-Risk Pre-Diabetic ( ):** Mean age 38.2 years; mean HbA1c 6.1%.
- **Healthy Controls ( ):** Mean age 37.0 years; mean HbA1c 5.3%.

## 2. Key Preliminary Findings

### 2.1 MicroRNA Feasibility and Differentially Expressed microRNAs (DE-miRs)

- **Feasibility:** RNA isolation from of stored plasma yielded high-quality small RNA libraries suitable for sequencing.
- **Finding:** Comparing the EO-T2DM group to controls, three circulating microRNAs were found to be significantly dysregulated (FDR ):
  - **miR-29a:** Downregulated by -fold in EO-T2DM. Known to target insulin signaling pathways.
  - **miR-143:** Upregulated by -fold in EO-T2DM. Associated with adipogenesis and inflammation.

### 2.2 Microbiome Diversity and Composition

- **Feasibility:** High-quality DNA was successfully extracted from all stored fecal samples.
- **Finding (Alpha Diversity):** The High-Risk group showed significantly reduced microbial -diversity (Shannon Index mean ) compared to the Healthy Controls (Shannon Index mean ). The EO-T2DM group had the lowest diversity (Shannon Index mean ).
- **Finding (Taxa):** Significant depletion of the **genus *Faecalibacterium*** and enrichment of the **genus *Bacteroides*** was observed in both the EO-T2DM and High-Risk groups compared to Controls ( ).

## 3. Conclusion and Project Justification

These preliminary data demonstrate the technical feasibility of simultaneous molecular and microbial profiling and, more importantly, provide strong evidence for the dysregulation of key biomarkers (miR-29a, miR-143, *Faecalibacterium*) in the high-risk and EO-T2DM populations.

These findings strongly justify the proposed comprehensive, integrated analysis in a larger, prospectively recruited cohort.