

# THE MICROBIOME AND EPIGENOME PROFILE IN PEDIATRIC TYPE 1 DIABETES IN QATAR

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## ABSTRACT

This study focused on Qatar's pediatric population that has witnessed a steep increase in the incidence of the disease. In order to understand this, we analyzed the blood and stool samples of a pilot group of 21 T1D subjects (age 6-12 yrs. old) for the microbiome composition, Short Chain Fatty Acid (SCFA) levels and methylation profiles using 16s rDNA sequencing, gas Chromatography and Infinium methylation assay respectively.

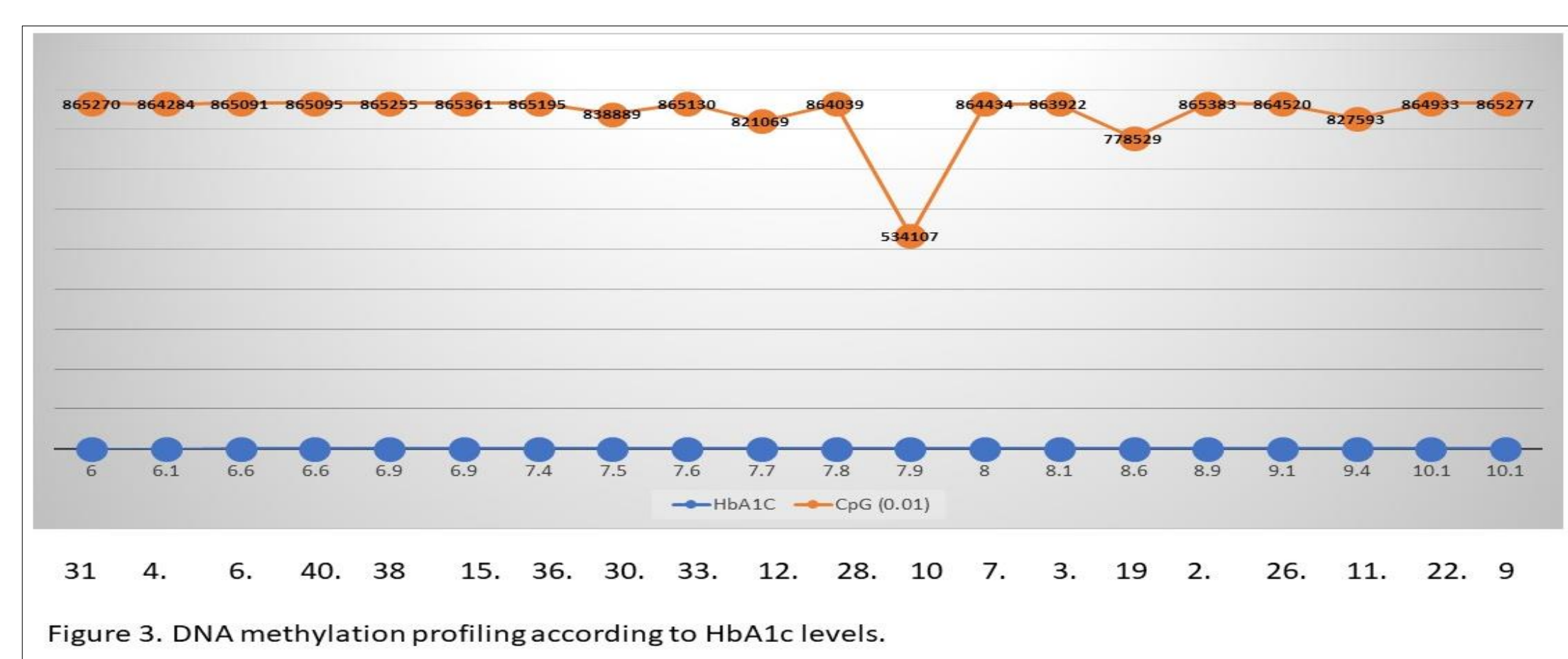
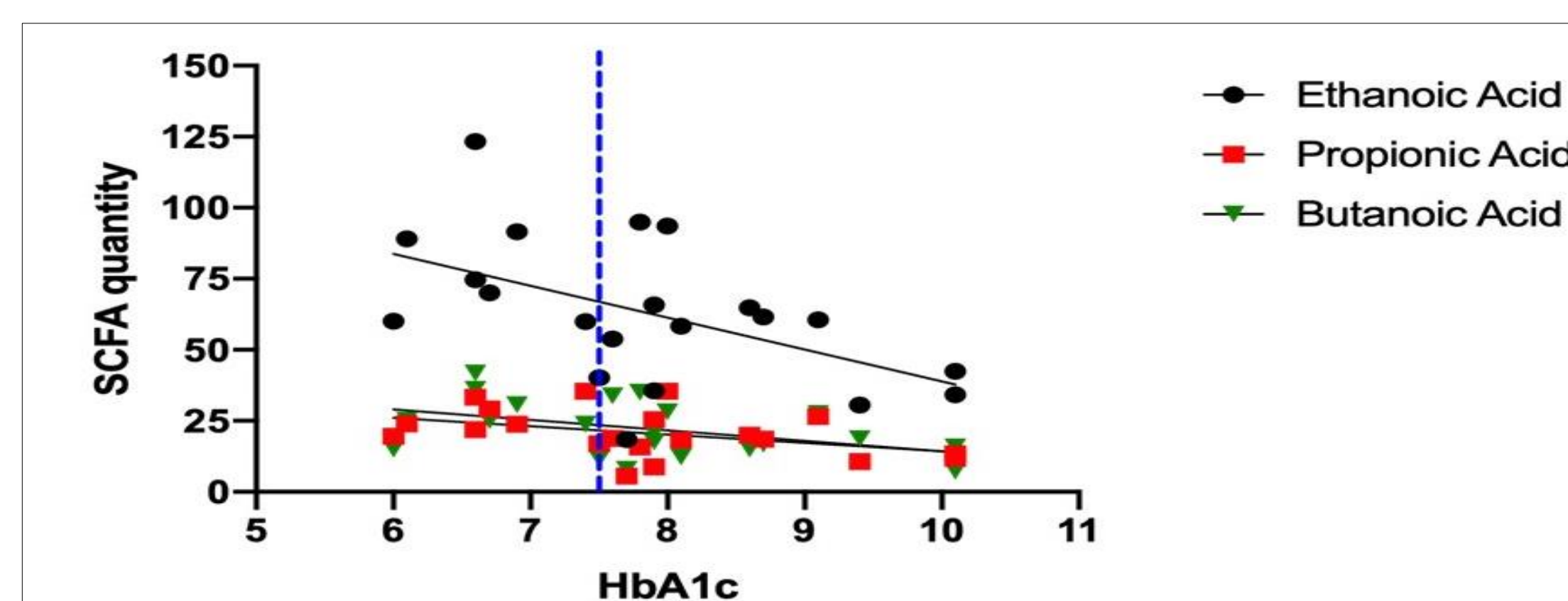
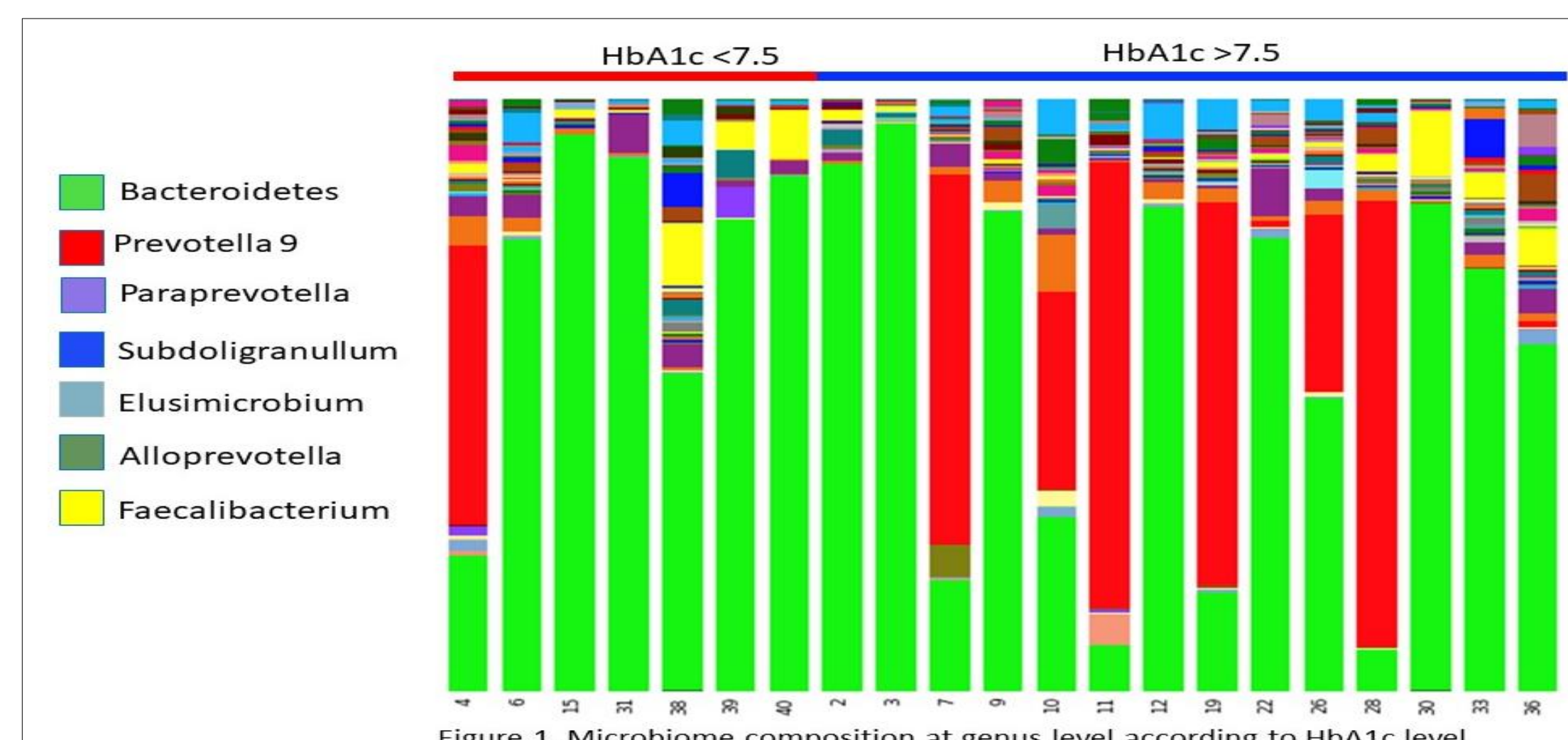
## INTRODUCTION

T1D is characterized by immune destruction of pancreatic  $\beta$ -cells directed by autoantibodies against islet cells autoantigens. The genetic factors are the key factors in the development of the etiology and pathogenicity of the disease. Other factors are contributing strongly for the onset of the disease including complex interactions among genes, immune response, environmental factors, gut microbiota and diet.

## RESULTS

T1D patients have higher fraction of Bacteroidetes followed by Firmicutes. In the uncontrolled ( $>7.5\%$  HbA1c) T1D patients there is an abundance of Prevotella 9 strain in genus level (figure 1), SCFA analysis indicated a dramatic decrease in ethanoic, propionic and butanoic acids (figure 2) and considerable fluctuation in DNA methylation levels (figure 3).

## IMAGES



## CONCLUSION

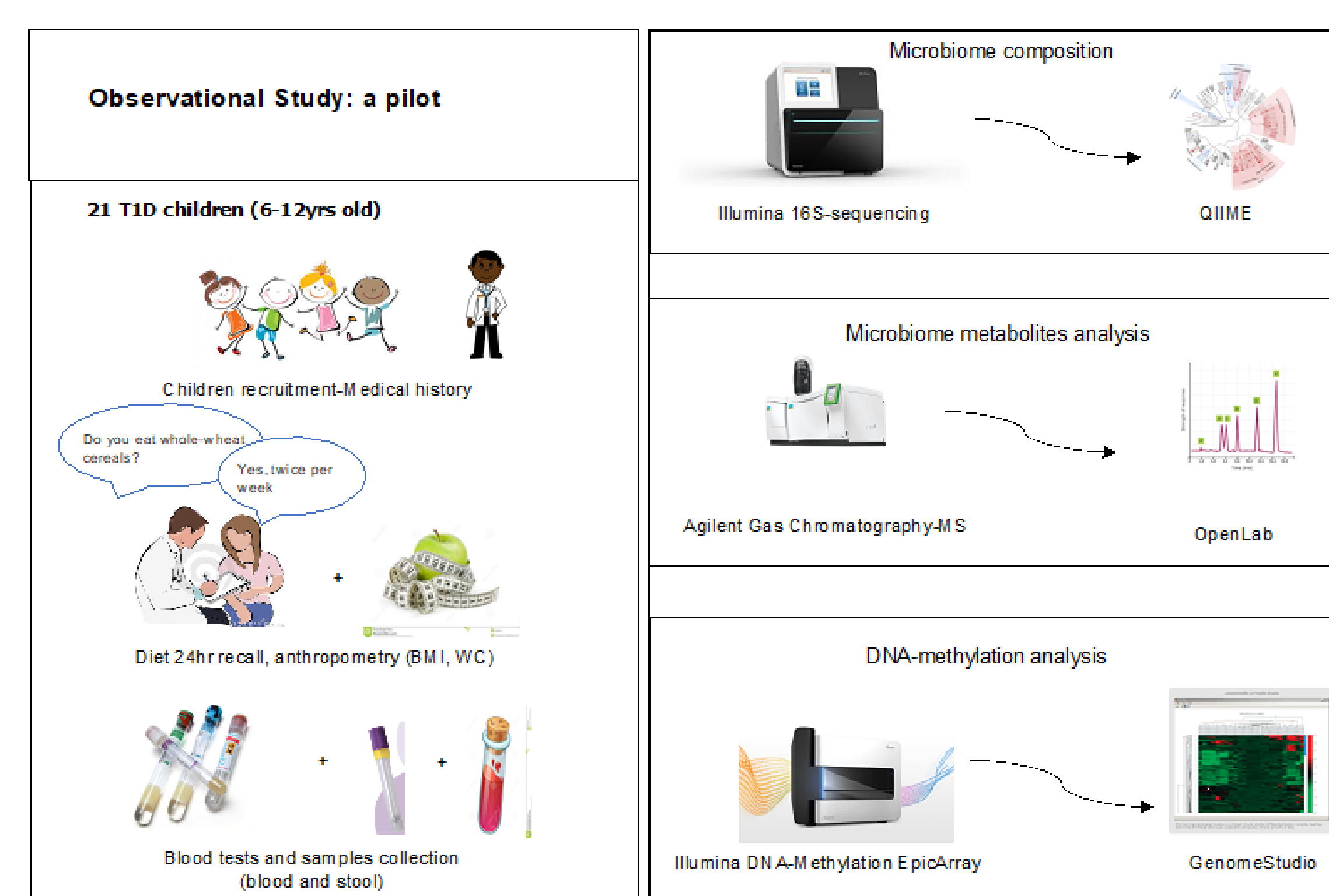
We can hypothesize that changes in gut microbiota, through its metabolites like SCFA, can modulate epigenetic patterns with an impact on T1D reducing the effect of the treatment. We will continue the DNA methylation data analysis to identify the locus and genes the impact on the gene expression and use the result as a clinical biomarker for T1D.

## REFERENCES

- 1- Agilent-Technologies. OpenLAB Software Suite. Retrieved from <http://www.agilent.com/en-us/products/software-informatics/openlab-software-suite>
- 2- Alkanani, A. K., Hara, N., Gottlieb, P. A., Ir, D., Robertson, C. E., Wagner, B. D., . . . Zipris, D. (2015). Alterations in Intestinal Microbiota Correlate With Susceptibility to Type 1 Diabetes. *Diabetes*, 64(10), 3510-3520. doi:10.2337/db14-1847

## METHODOLOGY

Diet-Microbiome-Epigenome interaction in type 1 diabetes



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