A graph of different colored lines

Description automatically generated with medium confidence

Common gut microbes of classes Firmicutes and Bacteroidetes phyla were dominant across the study participant samples. Their levels did not vary by a lot.

A colorful graph with a green background

Description automatically generated with medium confidence

Specifically, genera such as *Bacteroides* and *Faecalibacterium* appear frequently and at high relative abundances across many participants, which aligns with typical gut microbiome profiles observed in adult populations.

Notably, despite the visible variation in microbial composition between individuals, the overall taxonomic landscape remains consistent in terms of the most abundant genera. Both genuses *Faecalibacterium* and *Bacteroides* are known to be positively associated with Mediterranean diet in the gut. Mediterranean diet is rich in plant-based foods and fiber-rich ingredients that supplement growth of these gut microbes. They are considered as beneficial gut bacteria and associated with a shift in gut microbiota composition towards species that produce short-chain fatty acids (SCFAs) like butyrate.

A screenshot of a computer

Description automatically generatedA screenshot of a computer

Description automatically generated

Despite these dominant taxa, ANCOM test level did not identify any statistically significant differentially abundant features across intervention groups. ANCOM testing at the genus and family levels did not identify any significantly differentially abundant taxa between intervention groups.

A screenshot of a phone

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A screen shot of a graph

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When we compare microbial population of Mediterranean diet-based treatment to baseline (control) levels, we do not see a significant change. While there is individual variability in genus, overall trend with diet switch isn’t clearly observed.