

Abundant Bacterial Species in YOUR Beyond Bacteria Sample

All four Beyond Bacteria participants had very different microbiome profiles when looking at the top ten genera detected in each participant. The microbiome composition of each participant provided intriguing bits

of food for thought. Disclaimer: science is not at the stage to confidently assess human health status based on the microbiome, and the American Gut is not a medical diagnostic. The microbiome could also follow the old adage that too much of a good thing is a bad thing, and not enough studies have been done to determine whether certain abundance thresholds of "good" bacteria become harmful. Only time and well-designed, peer-reviewed research will tell us how useful microbiome composition can be as a proxy for predicting human health status.



You can find the specific top taxa in your sample [here](#).

An archaeon, *Methanobrevibacter smithii*, was the most abundant taxon (20.40% abundance) in your sample (000004607), followed by *Akkermansia muciniphila* (16.6% abundance). Both of these taxa have been negatively associated with obesity, as described in the top taxon document, indicating that your microbiome may be enriched for microbial taxa that are efficient at effectively utilizing food energy. *A. muciniphila* has also been described to exert anti-inflammatory effects, as has butyrate-producing *F. prausnitzii*, which was also present in your sample (6.19%). In general, the composition of your microbiome is suggestive of a healthy microbiome that is not only efficient at utilizing nutrients from food but is also actively involved in promoting intestinal health. Indeed, based on the data you provided, you appear to be relatively healthy, at a normal weight, with only occasional alcohol consumption and no smoking or antibiotic use; however, other lifestyle habits are not traditionally associated with the "golden standard" for health: you eat few vegetables but a lot of meat and seldom exercise. Therefore, you represent a good example of the difficulty in predicting health status and lifestyle habits solely via the microbiome, and you underscore the fact that the relationship between the microbiome and lifestyle is quite complex.

Notable Metabolic Pathways in YOUR Beyond Bacteria Sample

The most abundant pathways were similar across the four individuals, despite taxonomic differences. This is not unprecedented; the Human Microbiome Project also large variations in taxonomy, while pathway abundance remained relatively stable ([ref](#)). Unsurprisingly, we find common housekeeping genes, like DNA biosynthesis and carbon metabolism, across all four samples. We also find less common pathways. Again, we must issue a disclaimer: metagenomics is still in its infancy. Few samples have been analyzed in this way.

Therefore, making health inferences based on metagenomic findings would be very premature at this time.

You can find the specific top pathways in your sample [here](#).

We found several unique pathways within your metagenome (000004607). One of the most notable differences was the presence of genes associated with the degradation of the aromatic compounds toluene, xylene, catechols, and benzoate. Toluene and xylene are industrial solvents with potentially neurotoxic effects. Catechols are found in many plants, and are responsible for browning. Catechols may also be found in perfumes. Benzoate is naturally occurring in many foods, as well as being used as a preservative. Benzoate can react with vitamin C to form the carcinogen, benzene. Most aromatic compounds are broken down by cytochrome P450 enzymes in the liver. Bacterial degradation of aromatics has been used in bioremediation of oil spills ([ref](#)); such potential within the human gut is poorly characterized. Your sample was also unique in that your metagenome encodes for the biosynthesis of vitamin C and the neurotransmitter GABA, pathways which were not found in the other three individuals. You also had more pathways for methanogenesis than the other samples. This is likely due to your high levels of *M. smithii*. Methanogenesis is associated with constipation in some individuals ([ref](#)).