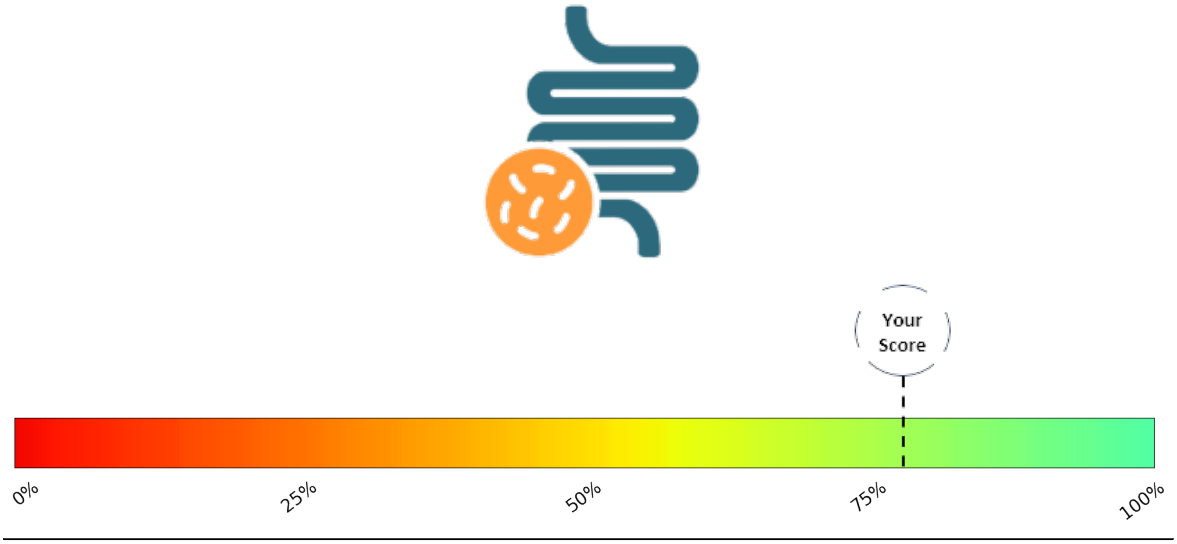
Name:
Sample ID: 1223263

Email:

## Gut Health Overview




The overall score is a combinational grading of predictive factors including presence and abundance ranges of common species in the gut, relative abundances and ratios at the phylum level, alpha diversity and species richness, and the presence of keystone species or pathogens in the host. These factors are assigned weighted values and summated, then divided by the maximum possible score to generate a percentage outcome. Most healthy individuals score between 70-100%.

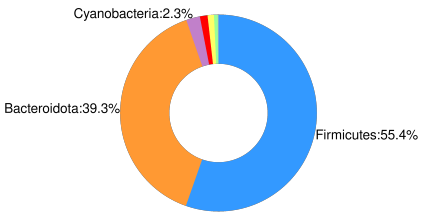
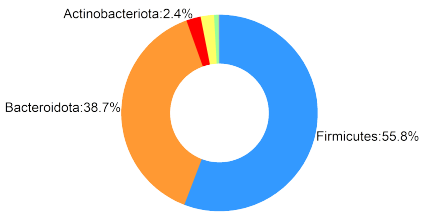
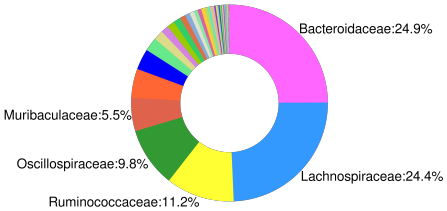
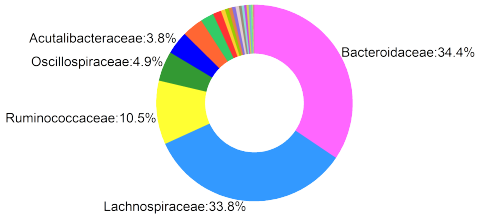
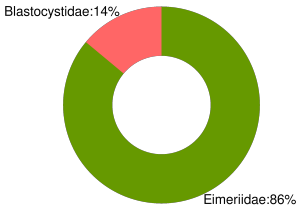
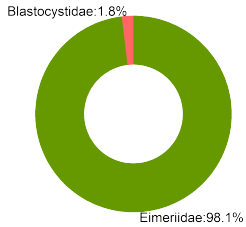
Your overall score is calculated by comparing user values for predictive factors of digestive function to a healthy reference group. These factors include presence of foundational organisms, ratios of macronutrient digestive groups, species richness and diversity. While low scores with these predictors generally correlate to poor digestive health, gut health can vary widely among individuals and low scores do not always correlate to poor gut function. More detailed sections for each category will be highlighted throughout the following report.

| Keystone Species | Dysbiosis Risk | Enterotype |
|---|---|---|
| 7 | low | Type A (Bacteroides) |

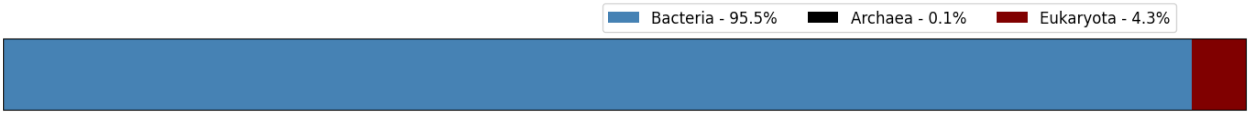
# Microbial Composition Overview

## Commensal Balance

Commensal abundance, the measure of “good” microorganisms in our body, is one of the primary indicators for overall gut health. Commensal organisms interact with our gut in a symbiotic relationship. You supply these microbes with a constant source of nutrients while in exchange they break down complex molecules into more basic forms that our bodies can readily use. Specie profiles can vary greatly from person to person, but most individuals conform more broadly to a consensus profile at higher levels of taxonomy such as phylum and family.

| | Your Sample | Healthy Sample |
|---|---|---|
| Bacterial Phyla |   |   |
| Bacterial Family |   |   |
| Fungal Family |   |   |

## Super-Kingdom Profile




The Super Kingdom taxonomy level provides the broadest view of your gut microbiome. This graph above breaks down your microbiome profile into four main groups at the Super-Kingdom level: Bacteria, Archaea, Eukaryotes, and Viruses. This broader view is typically dominated by bacteria and is less informative for functional health, but drastic profile shifts at this level can provide insight into dysbiosis drivers that would typically be overlooked by analyzing the microbiome with only bacteria in mind. Gut microbiome research continues to find more and more significance surrounding the Virome - viruses -and the Mycobiome - Eukaryotic Fungi - and their involvement in stabilizing the microbiome.

# Phyla and Diversity

Commensal profiles are typically assembled as a ratio of seven main bacterial phyla. You can consider each phylum as one of seven major bacterial groups that are distinct in their basic metabolic function. Each phylum contains a wide variety of species that perform key digestive processes. Like most things in life, these phyla are good to have in moderation but require balance. Falling outside of this normal functional balance is known as 'dysbiosis'. Studies have found that not only can dysbiosis impact your digestive health, but also play a role in immune system function and mental health as well.

## Relative Commensal Abundance by Phyla

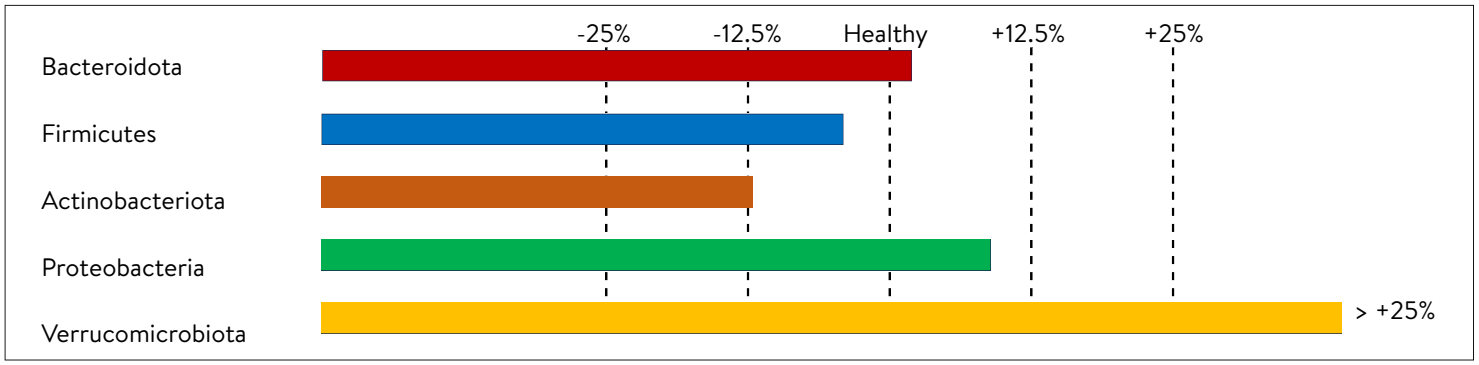
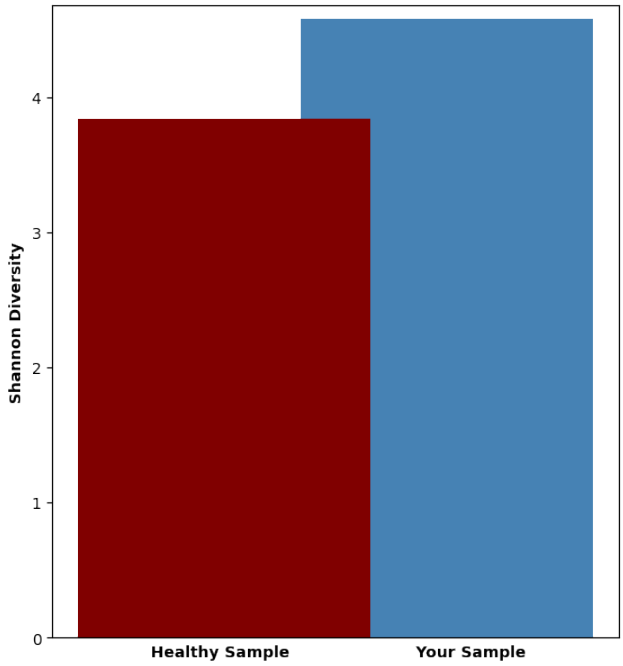



*Table 1:* The table above shows the five most common phyla that are used to grade commensal health in individuals. The bars represent the relative abundance of each phylum in the user sample compared to the relative abundance in the average healthy sample. Bars are scaled accordingly based on the ratio of values to reflect a percentage range of over or underabundance compared to the healthy range.

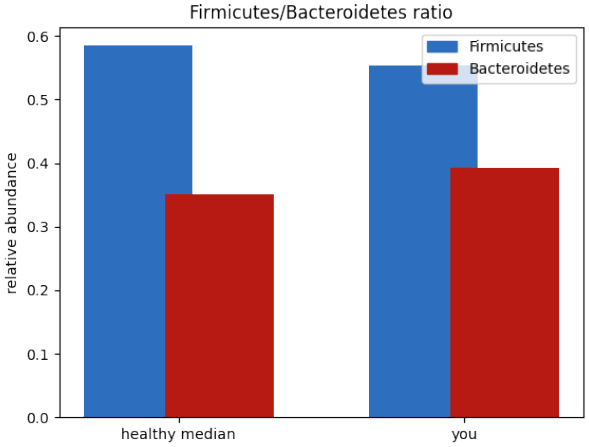
## Alpha Diversity



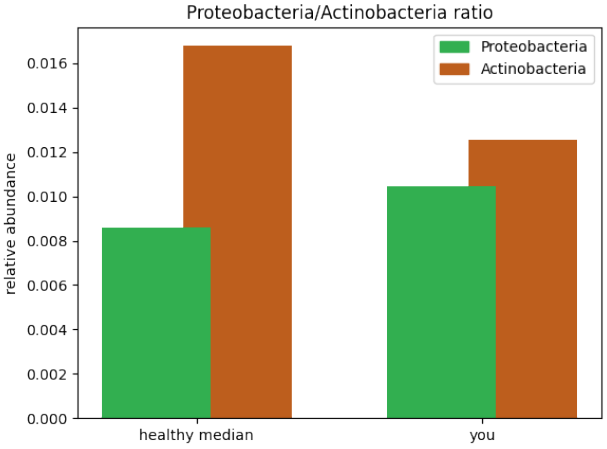

Alpha Diversity refers to the richness of different species identified within the microbiome. A low alpha diversity score indicates a lack of diversity and may be evidence of recent damage incurred to the microbiome via environmental toxins, stress, pathogens, or antibiotic use. High alpha diversity scores can suggest overabundance, and a microbiome that is struggling to stabilize. Percentages out of range will be cut off and its value will be provided next to the bar.

# Key Metabolic Ratios

Key abundance ratios between specific phyla have been identified in literature as important indicators of marked gut health. These key ratios are a measure between two groups and may serve to identify dietary trends or function as precursors for predicting dysbiosis. Select interactions between compared phyla can correlate highly with macronutrient consumption and reflect dietary/ metabolite deficiencies. Overly skewed ratios between phyla can further serve as indicators of commensal imbalance driven by external factors or other pre-existing conditions present in the host.

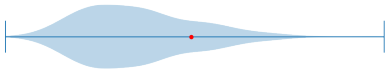
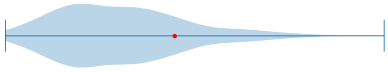
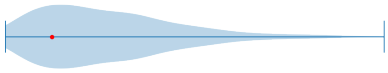



| Description | Healthy | Sample |
|---|---|---|
| The Firmicutes to Bacteroidetes ratio is shown to shift continually throughout an individual's life, leaning heavily towards Firmicutes in both infants and the elderly, but being more balanced with Bacteroidetes throughout Adulthood. High F/B ratios tend to correlate with carbohydrate rich diets with reduced protein intake, which drives the abundance of Firmicutes, the guts primary metabolizers of complex carbohydrates. | 1.67 | 1.41 |




| | | |
|---|---|---|
| Actinobacteria metabolize organic carbohydrates and starches into secondary metabolites that have antibiotic, antifungal, and anticancer properties. Proteobacteria are known for reducing oxidative stresses within the gut by consuming oxygen. This also plays an important role in providing a suitable oxygen-free environment for essential anaerobes - microbes that prefer to grow in environments without oxygen. A balanced 1:2 ratio of these two phyla is generally associated with good microbiome health and healthy cell turnover. | 0.511 | 0.83 |

# Metabolites

| Metabolite | Sample | Result | Healthy Range |
|---|---|---|---|
| **Fatty Acid Production** | | | |
| Short Chain Fatty Acid Total | 0.16 |  | 0.07-0.14 |
| N-butyrate | 0.08 |  | 0.04 - 0.10 |
| Acetate | Not Detected |  | < 0.01 |
| Propionate | < 0.01 |  | 0.0 - 0.02 |
| **Inflammation and Immune Response** | | | |
| Inflammation | < 0.01 |  | 0.0 - 0.01 |
| **Vitamin Synthesis Capacity** | | | |
| Vitamin Synthesis Total | < 0.01 |  | 0.07-0.20 |
| Folate | < 0.01 |  | 0.0 - 0.01 |
| Riboflavin | Not Detected |  | < 0.01 |
| B12 | Not Detected |  | < 0.01 |
| **Bile Production** | | | |
| Bile Acid Production Total | 0.02 |  | 0.08 - 0.21 |

This table represents the metabolite production capacity of an individual to that of the healthy range. This is the ability for a person to produce a substance, based on the presence of certain bacteria with a known capacity to produce the metabolite. Generative capacity is inferred by the relative abundance of reference species within the sample. The violin plots above show the user capacity value as a red dot. The blue background represents the range of outcomes from the reference set of healthy individuals.

# Potential Clinically Relevant Species

The bacteria that populate the gut can be broken down into three main groups: Commensal, Pathogenic, and Keystone species. Commensal species are organisms that contribute to the diversity and balance of the gut and are the largest class of microbe identities. A healthy gut should contain several hundred commensal species in low abundances. Pathogenic species are organisms that can cause disease. Some commensal organisms can become pathogenic if they are over-abundant in the gut. Keystone species are organisms that are recognized to form the foundation of the microbial ecosystem that makes our microbiome. These species perform key metabolic conversions that drive and stabilize the abundance of many different commensal organisms.

| | Average Healthy Keystone | Keystone Present |
|---|---|---|
| Keystone Species | 7 | 7 |

| Species | Healthy Range | Abundance |
|---|---|---|
| Akkermansia muciniphila | 0 - 2.33% | 0.21% |
| Bacteroides thetaiotaomicron | 0 - 4.36% | 2.00% |
| Bifidobacterium longum | 0 - 1.86% | 0.02% |
| Christensenella minuta | 0 - 0.01% | Not Detected |
| Faecalibacterium prausnitzii | 0 - 10.02% | 4.26% |
| Ruminococcus bromii | 0 - 4.09% | 1.09% |
| Bacteroides fragilis | 0 - 1.90% | Not Detected |
| Bacteroides stercoris | 0 - 9.92% | 0.09% |
| Methanobrevibacter smithii | 0 - 0.58% | 0.12% |
| Bifidobacterium pseudolongum | 0 - 1.02% | Not Detected |

## Potentially Pathogenic Species

| Species | Abundance |
|---|---|
| | |
| | |
| | |
| | |
| | |
| | |
| | |

# Total Species Level Microbial Compositions

## Bacterial Species*

| Species | Role | Abundance |
|---|---|---|
| Phocaeicola dorei | Commensal | 10.5% |
| Faecalibacterium prausnitzii | Keystone | 4.26% |
| UBA7173 sp900546835 | Commensal | 3.75% |
| Phocaeicola vulgatus | Commensal | 3.7% |
| Dysosmobacter sp001916835 | Commensal | 2.83% |
| Blautia faecis | Commensal | 2.56% |
| Stercorousia sp900761225 | Commensal | 2.21% |
| Alistipes putredinis | Commensal | 2.05% |
| Phocaeicola plebeius | Commensal | 2.04% |
| Bacteroides thetaiotaomicron | Keystone | 2.0% |

Keystone Pathogen Commensal

## Eukaryotic Species*

| Species | Abundance |
|---|---|
| Blastocystis sp. | 13.96% |

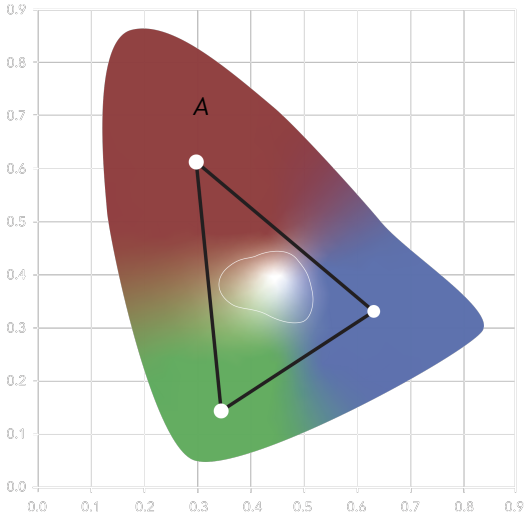
*Our bioinformatics pipeline uses the Genome Taxonomy Database (GTDB) for taxonomy analysis. Some of the bacterial species shown in this section may not have the more common NCBI IDs. Please refer to the GTDB website (https://gtdb.ecogenomic.org/) for more information regarding the species with GTDB IDs.

# Enterotype

Studies on a variety of populations have suggested that the human gut microbiota is classified under the following three distinct categories or "enterotypes": Type A - Bacteroides, Type B - Prevotella, and Type C - Ruminococcus. Enterotypes help classify molecular function beyond species abundance by measuring the interactions between key expression pathways in the microbiome. The use/disuse of these pathways can help predict metabolic and gut health (i.e. if a pathway associated with gut inflammation is being heavily expressed). Enterotypes can help to illuminate these enriched pathways influenced by microbiome composition, dietary influence, and patient metabolism. Read more about enterotypes here:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3728647/

Your Enterotype: A




Enterotype A is the most frequent one and is enriched in Bacteroidetes. It is also enriched in membrane transporters, mostly of sugars, suggesting the efficient binding of mucin and its subsequent hydrolysis as well as uptake of the resulting simple sugars by these genera. The enriched genera suggest that enterotypes employ different routes to generate energy from fermentable substrates.

# Additional Information

## References

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Thursby, Elizabeth, and Nathalie Juge. "Introduction to the human gut microbiota." Biochemical journal 474, no. 11 (2017): 1823-1836.

## Methods

The ZymoBIOMICS®-96 MagBead DNA Kit (Zymo Research, Irvine, CA) was used to extract DNA using the automated KingFisher platform. Genomic DNA samples were profiled with shotgun metagenomic sequencing. Illumina DNA Prep Kit™ (Illumina, San Diego, CA). All libraries were pooled in equal abundance. The final pool was quantified using TapeStation® (Agilent Technologies, Santa Clara, CA) and Invitrogen Qubit 1X DSDNA High-Sensitivity Assay Kits® (Thermo Fisher Scientific, Waltham, MA). The final library was sequenced on either the Illumina NovaSeq®, or the Illumina Nextseq®.

## Disclaimer

The information contained in this report is intended only to be factor for use in a diagnosis and treatment regime for the patient or client. As with any diagnosis or treatment regime, you should use clinical discretion with each patient based on a complete evaluation of the patient's condition, including history, physical presentation, and complete laboratory data, including confirmatory tests. All test results should be evaluated in the context of the patient's individual clinical presentation. The information in the report has not been evaluated by the FDA.

Customer Support

Tel:
Email:
microbiome@kefirlab.com