



GutHealth[®]
PREMIUM

MICROBIOMA INTESTINAL DA NOVA GERAÇÃO



GERMANO DE SOUSA
CENTRO DE MEDICINA LABORATORIAL



What is measured in this test

GUT HEALTH™ Premium is a gut microbiome analysis based on a fecal sample. It enables the identification and quantification of multiple microbial groups that make up the intestinal microbiota, including bacteria, fungi and yeasts, archaea, and eukaryotic parasites. This is a comprehensive test, as shotgun metagenomics allows sequencing of all microbial DNA present in the sample (not just a target region), enabling species-level resolution and the genetic characterization of the functional potential of the community.

The test provides detailed results for a comprehensive set of gut microorganisms based on the latest scientific and clinical research. It also provides global parameters, such as diversity and evenness, contextualized against a reference database of healthy adult individuals.

This is a clinically validated test, performed in a certified and licensed clinical pathology laboratory, in the molecular pathology and genetics domain, meeting all stringent quality standards associated with this type of analysis.

Important Considerations

Gut microbiome analysis, in the context of human health, is a recent scientific and clinical development, only possible due to the current ability to analyse large quantities of DNA with the use of new generation sequencing. This area of expertise is the target of intense study by the scientific community and its results have revealed the importance of a balanced microbiota in human health, as well as the pathological consequences of its alteration.

The GUT HEALTH™ Premium report presents the frequencies of microorganisms found in the analysed sample, as well as some metrics derived from them. It is important to emphasize that this report is intended exclusively for informational purposes within the context of well-being and nutrition. The results presented are designed to support the understanding of general characteristics of the gut microbiome and should be interpreted accordingly.

This test **is not a medical device and is not intended for the diagnosis, prevention, monitoring, or treatment of any disease or medical condition**, nor does it replace clinical evaluations or other medical examinations.



User Identification

User	Sample	Requester
Name: Maria Silva	Sample identification: AA0002	Name: NA
Date of birth: 01/01/2000	Sample type: Feces	☐ Medical Doctor
Gender: Feminino	Date of reception: 25/07/2025	☐ Nutritionist
Age: 26	Date of issue: 05/05/2026	☒ Other

Results Summary

Integrity

-  The amount of human DNA in your sample was very low (<1%), indicating excellent collection quality and suggesting a stable intestinal environment.

Classification

-  The composition of your gut microbiome shows significant deviations from the healthy reference profile and has been classified as **dysbiotic**. In some cases, specific indicators may partially diverge from the overall pattern; therefore, interpretation should take into account the full set of results described in the report.

Diversity

-  The gut microbiome represented by this sample has a diversity index of 3.46, **above the range observed in our healthy reference population**. Depending on the individual context, this deviation may reflect reduced stability or resilience of the intestinal ecosystem.
-  The evenness of species distribution in this sample is consistent with the range observed in our healthy reference population, suggesting a well-balanced microbial community.
-  The species richness observed in this sample is **outside the typical range of our healthy reference population**.
-  The ratio between the bacterial phyla Firmicutes and Bacteroidetes in this sample falls within the range observed in our healthy reference population.

Composition

Your microbial profile shows a composition characterized by a greater contribution from the Entero-Signature **ES-Firm**, rich in Firmicutes and bacteria of the genus *Alistipes*.

Microbial Indicators

-  No pathogenic bacteria were identified among the species investigated in this analysis.
-  No parasitic organisms were identified among the species investigated in this analysis.



Sample Integrity

As part of our quality control process, each sample is checked for the presence of human DNA. This can naturally occur in small amounts due to the normal shedding of cells from the intestinal lining.

In your sample, the amount of human DNA was very low, **less than 1%**, which is exactly what we expect from a well-collected stool sample with a stable gut environment ^[1]. This indicates excellent sample quality and suggests no unusual levels of epithelial cell loss.

Before we begin analyzing your gut microbiome, all human DNA is carefully filtered out. This ensures that your results are based entirely on microbial data, providing a reliable foundation for both personal insights and professional nutritional or health guidance.

Microbiome Classification

Result: **Dysbiotic**

The composition of your gut microbiome shows significant deviations from healthy reference profiles and has been classified as **dysbiotic**. This finding suggests a potential imbalance in your gut microbial community.

However, it's important to note that dysbiosis is *not a diagnosis on its own*. Microbial imbalances can arise for various reasons, including diet, stress, recent illness, medications, or underlying health conditions ^[2,3]. If you are experiencing digestive symptoms or other health concerns, discussing these results with a healthcare professional may provide helpful guidance.

Important: The classification presented is based on a statistical model trained on reference populations and reflects the most likely pattern according to the microbial composition of the sample. However, individual profiles may display specific combinations of indicators that partially deviate from these patterns. For this reason, results should be interpreted in an integrated manner, taking into account the different parameters described throughout the report and the clinical and nutritional context of each individual.



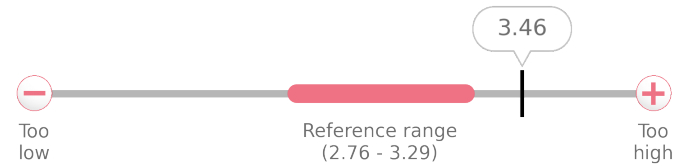
Microbial Diversity

Diversity Index

Microbial diversity reflects the richness and balance among gut species. We assess diversity using the **Shannon Index**. A higher index value suggests a more stable, resilient, and functional ecosystem. Low diversity has been associated with metabolic imbalances, inflammation, and reduced adaptive capacity in response to dietary changes or disease ^[4].

Important: diversity is a global indicator of gut health, but it should be interpreted in conjunction with microbial composition and function.

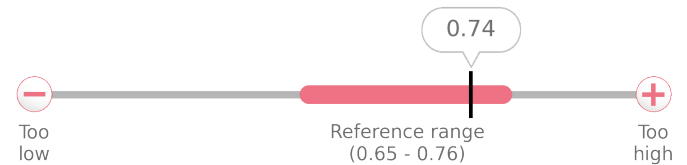
Result: **3.46** | Above Average



Species Evenness

Evenness expresses the degree of balance in the distribution of the species present. Balanced microbiomes show similar proportions among microorganisms, supporting ecological stability and the prevention of dysbiosis. Imbalances may indicate the overgrowth of certain groups and a risk of inflammation ^[5]. Higher evenness is associated with improved digestion, immune regulation, and microbial resilience ^[6].

Result: **0.74** | Normal



Microbial Richness

Richness corresponds to the total number of microbial groups detected, regardless of their abundance. Higher richness suggests an ecosystem with greater functional capacity, including the synthesis of beneficial metabolites, immune regulation, and maintenance of intestinal mucosal integrity ^[6].

It is assessed across taxonomic levels (species, genera, classes, and phyla) to provide a clearer understanding of both global and specific diversity.

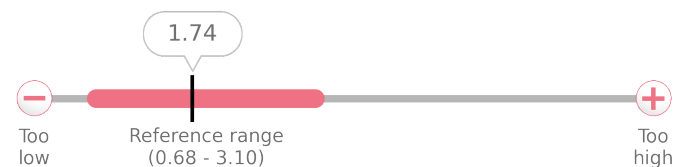
Category	Sample	Reference	Flag
Species	108	64 - 82	↑
Genera	57	35 - 44	↑
Classes	16	9 - 12	↑
Phyla	7	4 - 5	↑

The Firmicutes/Bacteroidetes Ratio

The ratio between Firmicutes and Bacteroidetes (F:B) has been used as an indirect marker of metabolic alterations. Significant deviations in this F:B ratio have been associated with obesity, insulin resistance, and intestinal inflammation ^[7,8].

Important: normal values vary between individuals; interpretations should take into account other clinical and dietary parameters, as well as lifestyle or environmental factors.

Result: **1.74** | Normal



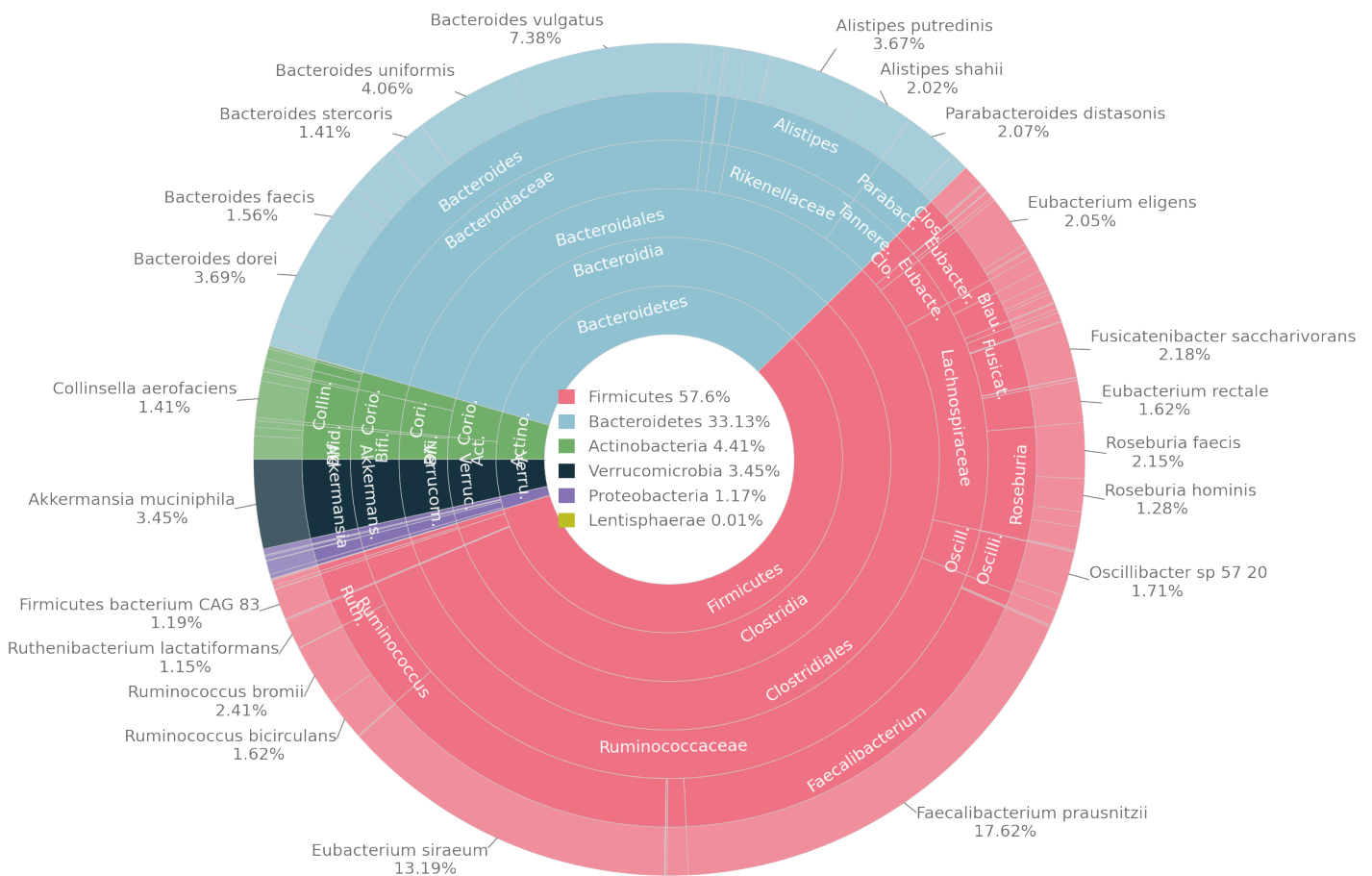
Taxonomic Composition

Overview of the bacterial taxa identified in this sample.

In total, **108 distinct bacterial species** were identified in your gut microbiome. The chart below provides a visual representation of the diversity and structure of your microbial community.

The chart is organized hierarchically, with broader groups (such as phyla or classes) at the center, and moving outward toward more specific groups, showing the most dominant species. The size of each segment reflects the relative abundance of that group in your sample: the larger the segment, the more prevalent that taxon is within your microbiome. Additionally, the greater the number of partitions within each group, the higher the diversity of your gut microbiome.

This overview helps visualize the balance between different microbial groups. It's normal for some bacteria to be more abundant than others, but the overall structure contributes to how your gut functions in areas like digestion, immune support, and metabolic health.





Phyla Distribution

In most individuals, the phyla Firmicutes and Bacteroidetes dominate, typically comprising over 90% of the bacterial community. Smaller but important contributions come from other groups. The balance between these groups can reflect key aspects and microbial trends of gut health and how the microbiome responds to lifestyle and dietary patterns.

Phylum	Sample (%)	Reference (%)	Flag
Firmicutes	57.60	34.71 - 60.77	
Bacteroidetes	33.13	19.41 - 54.41	
Actinobacteria	4.41	1.17 - 16.66	
Verrucomicrobia	3.45	0.14 - 2.36	↑
Proteobacteria	1.17	0.11 - 0.84	↑
Euryarchaeota	0.17	0.11 - 2.58	
Lentisphaerae	0.01	0.02 - 0.11	↓

Your EnteroSignature

EnteroSignatures (ES) describe the gut microbiome through five microbial guilds that consistently co-occur and interact ecologically. Although it has no standalone diagnostic value, ES reflect a **mix of tendencies**, with each person's microbiome typically showing contributions from several signatures that shift with age, diet, lifestyle, and health status ^[9-12]. The five primary ES are:

ES-Bact (*Bacteroides*-dominated): common in Western dietary patterns and often enriched after antibiotic exposure or during microbiome recovery.

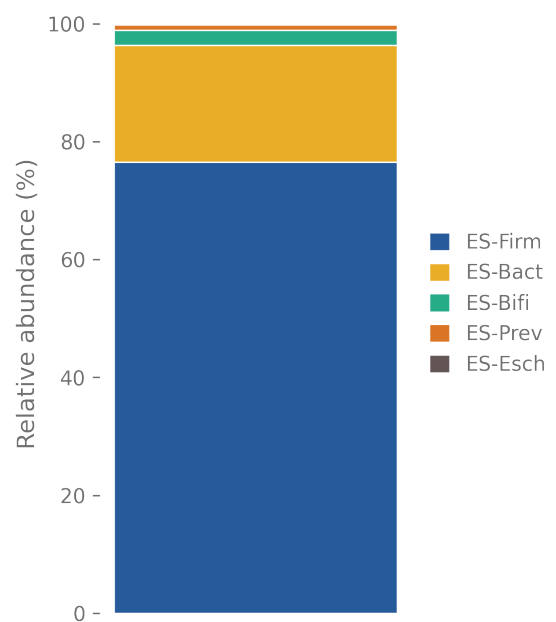
ES-Firm (rich in Firmicutes and *Alistipes*): widespread and generally associated with healthier microbiome markers.

ES-Prev (rich in *Prevotella* and related bacteria): associated with plant-rich, fiber-dense diets; tends to decrease after perturbations and typically appears later in life.

ES-Bifi (*Bifidobacterium*-dominated and certain Firmicutes): prominent in infancy and declining with age.

ES-Esch (Proteobacteria-dominated): common in early-life or perturbed microbiomes and more prevalent in older adults.

Result: predominantly of type **ES-Firm**





Dominant Bacterial Species

The gut microbiome is a highly diverse ecosystem, with each microbial species contributing uniquely to digestion, metabolism, immune function, and overall gut health. This section highlights the ten most abundant bacterial species identified in your sample. These dominant species offer a snapshot of your microbiome's current composition and may provide insights into key functions, microbial balance, or associations with certain health traits.

It's important to note that relative abundance alone does not directly indicate health or risk, some beneficial species are naturally more abundant, while others perform important functions even at low levels. However, tracking the most dominant species over time can help monitor changes in your microbiome and identify trends when compared to healthy reference populations.

Species	Sample (%)	Reference (%)	Flag
Bacteroides vulgatus	7.38	1.13 - 7.29	↑
Bacteroides uniformis	4.06	1.16 - 6.83	
Bacteroides dorei	3.69	0.31 - 3.60	↑
Alistipes putredinis	3.67	1.06 - 4.72	
Akkermansia muciniphila	3.45	0.14 - 2.36	↑
Ruminococcus bromii	2.41	1.50 - 9.63	
Fusicatenibacter saccharivorans	2.18	0.55 - 3.33	
Roseburia faecis	2.15	0.43 - 4.33	
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Eubacterium siraeum	13.19	0.09 - 1.31	↑

Unique Bacterial Species

This section presents the bacterial species detected in the sample that are absent in the healthy reference population used for comparison. Their presence may reflect individual diversity, specific dietary exposures, or geographical factors.

Interpretation note: many of these species may be common in other populations or associated with different diets.

Clinical use: these species can be useful as individualized markers to monitor microbiome changes over time.

Important: species with an abundance <0.01% should be interpreted with caution due to potential technical variability.

Result: Detected

Species	Phylum	Sample (%)
Sphingomonas sp FARSPH	Proteobacteria	0.1666
Microbacterium sp T32	Actinobacteria	0.1210
Collinsella stercoris	Actinobacteria	0.0141
Cloacibacillus evryensis	Synergistetes	0.0096
Microbacterium ginsengisoli	Actinobacteria	0.0070



Pathogenic Bacteria

Your gut microbiome consists of trillions of microorganisms, most of which play essential roles in digestion, immune regulation, and overall health. However, some bacterial species are classified as opportunistic or potentially pathogenic, meaning that while they may exist harmlessly at low levels, they have the potential to cause problems if their abundance increases or if the gut environment becomes imbalanced. While it's normal to have small amounts of some of these microbes, elevated levels may indicate imbalances that could affect your well-being, such as gut inflammation, digestive discomfort, increased intestinal permeability ("leaky gut"), or other health concerns.

Important: the detection of these bacteria does not indicate an active infection, nor does it necessarily mean disease is present. If high levels persist or symptoms are present, consultation with a healthcare provider is recommended.

Archaea

Archaea are a distinct group of microorganisms, separate from bacteria, that form part of the gut microbiome. While typically present in much lower numbers than bacteria, certain archaeal species may play important roles in digestion and in the production of compounds, such as methane. The presence or absence of archaea is a normal variation within healthy microbiomes, and their roles are still being explored in microbiome science.

Yeast and Fungi

Yeast and fungi are a diverse group of eukaryotic organisms that are sometimes found in the gut alongside bacteria and archaea. While many fungal species are harmless, transient, or even beneficial, others may be associated with imbalances, particularly when present in higher-than-typical abundances.

These microorganisms can enter the gut through diet, environmental exposure, or as part of the natural microbiome, though their roles are less well understood compared to bacteria. For example, some species like *Saccharomyces boulardii* are considered beneficial and are used as probiotics, while others like *Candida* species may be linked to overgrowth under certain conditions.

Result: **Not detected**

Taxon	Sample (%)	Flag
Campylobacter	0.0000	
C. coli	0.0000	
C. jejuni	0.0000	
C. lari	0.0000	
C. upsaliensis	0.0000	
Clostridioides difficile	0.0000	
Helicobacter pylori	0.0000	
Klebsiella pneumoniae	0.0000	
Plesiomonas shigelloides	0.0000	
Salmonella	0.0000	
Vibrio	0.0000	
V. cholerae	0.0000	
V. parahaemolyticus	0.0000	
V. vulnificus	0.0000	
Yersinia enterocolitica	0.0000	

Result: **Detected**

Species	Sample (%)	Reference (%)	Flag
Methanobrevibacter smithii	0.17	0.11 - 2.59	

Result: **Not detected**



Parasites

Certain parasitic organisms, primarily intestinal protozoa, can occasionally be detected in the gut microbiome. The presence of these parasites may be more relevant in individuals with weakened immune systems, in those with a recent history of travel to endemic areas, or after exposure to contaminated food or water. Some protozoa detected in the gut microbiome may be considered commensal or of uncertain clinical significance, depending on the species ^[13,14].

Important: detection alone does not confirm an active infection, particularly when found at very low levels. Results should be interpreted in the context of symptoms, exposure history, and, if needed, with the guidance of a qualified healthcare professional.

Result: **Not detected**

Taxon	Sample (%)	Flag
Blastocystis	0.0000	
Cryptosporidium	0.0000	
C. andersoni	0.0000	
C. hominis	0.0000	
C. meleagridis	0.0000	
C. muris	0.0000	
C. parvum	0.0000	
C. ubiquitum	0.0000	
Entamoeba	0.0000	
E. dispar	0.0000	
E. histolytica	0.0000	
Giardia intestinalis	0.0000	



Microbial Indicators

Characterisation of Functional Potential

The gut microbiota represents a complex and dynamic ecosystem whose metabolic activities play a key role in maintaining host homeostasis. Beyond its taxonomic composition, the functional capacity of the microbiota, reflected in the metabolites it produces, largely determines its influence on health and disease.

During the metabolism of dietary components and endogenous substrates, intestinal microorganisms generate a wide range of bioactive compounds known as microbiota-derived metabolites. These include short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate, branched-chain amino-acids (BCAAs), biogenic amines, indoles, phenols, and trimethylamine (TMA, a precursor of TMAO), among others. These metabolites are not merely end-products of microbial fermentation; they act as metabolic and immunomodulatory signals, influencing crucial host physiological pathways [15-18]. Functional identification of these markers complements the taxonomic analysis of the microbiome.

Metabolic pathway	Sample (%)	Reference (%)	Flag
SCFA production	2.23	0.79 - 1.60	↑
Acetate	1.28	0.47 - 1.00	↑
Butyrate	0.41	0.16 - 0.29	↑
Propionate	0.10	0.08 - 0.16	
Lactate production	1.73	1.01 - 1.60	↑
Vitamin metabolism	7.31	7.94 - 9.07	↓
Vitamin B1	3.03	2.81 - 3.40	
Vitamin B2	0.69	1.35 - 1.72	↓
Vitamin B6	0.39	0.16 - 0.51	
Vitamin B7	0.17	0.12 - 0.25	
Vitamin B9	1.74	1.95 - 2.23	↓
Vitamin B12	0.00	0.00 - 0.01	
Vitamin K	0.09	0.04 - 0.12	
BCAA biosynthesis	4.18	5.30 - 6.19	↓
Histamine production	0.00	0.00 - 0.00	
TMA production	0.00	0.00 - 0.00	
LPS biosynthesis	0.17	0.04 - 0.16	↑
H ₂ S production	0.00	0.00 - 0.00	
Ammonia production	0.22	0.11 - 0.30	
Methane metabolism	0.15	0.07 - 0.30	

Short-Chain Fatty Acid Producers

Short-chain fatty acids (SCFAs) such as butyrate, propionate, and acetate are key microbial metabolites produced during the fermentation of dietary fibers and resistant starches in the colon. These compounds play essential roles in maintaining gut and systemic health, including supporting the intestinal barrier, modulating immune function, regulating inflammation, and contributing to energy metabolism. Certain bacterial species are particularly effective at SCFA production. For example, *Faecalibacterium prausnitzii*, *Roseburia* spp., and *Eubacterium rectale* are among the most important butyrate producers; *Bacteroides* and *Prevotella* species primarily produce propionate; while acetate, the most abundant SCFA, is commonly produced by genera like *Bifidobacterium*, *Lactobacillus*, and *Blautia*, and serves as a substrate for other beneficial microbes [19,20].

Species	Sample (%)	Reference (%)	Flag
Akkermansia muciniphila	3.45	0.14 - 2.36	↑
Bacteroides spp	22.17	7.03 - 28.33	
Bifidobacterium spp	1.50	0.75 - 12.85	
Blautia spp	1.33	0.57 - 4.18	
Coprococcus catus	0.04	0.10 - 0.46	↓
Eubacterium hallii	0.23	0.21 - 2.40	
Eubacterium rectale	1.62	0.38 - 5.88	
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Lactobacillus spp	0.01	0.03 - 0.22	↓
Prevotella spp	0.00	0.84 - 24.00	↓
Roseburia spp	4.97	1.32 - 6.72	
Ruminococcus obeum	0.00	0.02 - 0.15	↓
Veillonella spp	0.00	0.02 - 0.12	↓



Substrate Degradation Capacity

Dietary fibers are a primary energy source for many beneficial gut microbes, which ferment complex carbohydrates into short-chain fatty acids (SCFAs), notably butyrate and acetate. These metabolites help maintain the intestinal barrier, modulate immune responses, and supply energy to colonocytes, supporting metabolic balance and limiting inflammation [15,21,22].

Mucin, the main glycoprotein of the intestinal mucus layer, can also serve as a carbon source when dietary fiber is scarce. Species such as *Akkermansia muciniphila* and *Bacteroides thetaiotaomicron* specialize in mucin degradation. Controlled utilization promotes mucus renewal and epithelial integrity, whereas excessive activity, particularly from organisms like *Ruminococcus gnavus*, may erode the protective barrier and increase inflammatory risk [23,24].

Oxalates, naturally present in many plant foods, can contribute to kidney stone formation if not metabolized efficiently. Microbes including *Oxalobacter formigenes*, *Bifidobacterium animalis*, and *Lactobacillus acidophilus* convert oxalate into less harmful compounds. A healthy representation of these bacteria can help lower urinary oxalate levels, supporting renal health and reducing the risk of calcium-oxalate stone formation [25-27].

Probiotics

A healthy gut microbiota includes a variety of bacterial species that help maintain microbial balance and support overall wellbeing. Among these are probiotics, which are defined as live microorganisms that, when present in adequate amounts, confer health benefits to the host [28]. Probiotic bacteria can support gut health through various mechanisms, such as enhancing digestion, producing beneficial compounds (like short-chain fatty acids), strengthening the gut barrier, and modulating the immune system [29,30].

These microbes may be part of your resident gut community, acquired naturally through lifelong microbial exposure, or they may be introduced temporarily through diet, fermented foods, or probiotic supplements. Their presence and impact can vary depending on the specific species, their abundance, and individual health context [31].

Substrate / Species	Sample (%)	Reference (%)	Flag
Fiber			
Bifidobacterium spp	1.50	0.75 - 12.85	
Roseburia spp	4.97	1.32 - 6.72	
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Ruminococcus bromii	2.41	1.50 - 9.63	
Mucin			
Akkermansia muciniphila	3.45	0.14 - 2.36	↑
Bacteroides thetaiotaomicron	0.03	0.12 - 0.82	↓
Ruminococcus gnavus	0.14	0.03 - 0.50	
Oxalates			
Bifidobacterium animalis	0.00	0.03 - 0.29	↓
Lactobacillus acidophilus	0.00	0.03 - 0.24	↓
Oxalobacter formigenes	0.00	0.08 - 0.21	↓

Taxon	Sample (%)	Reference (%)	Flag
Akkermansia muciniphila	3.45	0.14 - 2.36	↑
Bifidobacterium	1.50	0.75 - 12.85	
B. adolescentis	0.00	0.48 - 7.70	↓
B. bifidum	0.90	0.27 - 2.92	
B. breve	0.00	0.06 - 0.24	↓
B. longum	0.34	0.29 - 3.80	
Lactobacillus	0.01	0.03 - 0.22	↓
L. acidophilus	0.00	0.03 - 0.24	↓
L. casei group	0.00	0.00 - 0.00	
L. plantarum	0.00	0.03 - 0.10	↓
L. reuteri	0.00	0.16 - 0.32	↓
L. rhamnosus	0.00	0.04 - 0.13	↓
L. salivarius	0.00	0.01 - 0.04	↓
Lactococcus lactis	0.00	0.02 - 0.13	↓
Streptococcus thermophilus	0.00	0.04 - 0.48	↓



Health Indicators



Gastrointestinal Symptoms

The gut microbiota plays a key role in the pathophysiology of both functional and organic gastrointestinal symptoms. Changes in the presence, relative abundance, or metabolic activity of certain species can contribute to manifestations such as abdominal pain, diarrhea, constipation, flatulence, and food intolerances or sensitivities [32-36].

These effects arise largely from the production of bioactive metabolites (gases, short-chain fatty acids, toxins, and biogenic amines) that act directly on intestinal motility, epithelial barrier integrity, immune responses, and neuroendocrine signaling. Recognizing these associations provides a foundation for diagnostic and nutritional intervention strategies, while always considering that symptoms result from complex interactions among the microbiota, diet, and host.

Symptom / Species	Sample (%)	Reference (%)	Flag
Stomach pains			
Escherichia coli	0.05	0.04 - 0.27	
Campylobacter spp	0.00	0.01 - 0.02	↓
Clostridium spp	1.20	0.06 - 0.71	↑
Diarrhea			
Escherichia coli	0.05	0.04 - 0.27	
Clostridioides difficile	0.00	0.00 - 0.00	
Campylobacter spp	0.00	0.01 - 0.02	↓
Constipation			
Methanobrevibacter smithii	0.17	0.11 - 2.59	
Clostridium spp	1.20	0.06 - 0.71	↑
Flatulence and bloating			
Prevotella spp	0.00	0.84 - 24.00	↓
Desulfovibrio spp	0.00	0.09 - 0.42	↓
Bacteroides spp	22.17	7.03 - 28.33	
Non-celiac gluten sensitivity			
Prevotella spp	0.00	0.84 - 24.00	↓
Lactobacillus spp	0.01	0.03 - 0.22	↓
Lactose intolerance			
Bifidobacterium spp	1.50	0.75 - 12.85	
Lactobacillus spp	0.01	0.03 - 0.22	↓
Histamine intolerance			
Morganella morganii	0.00	0.00 - 0.00	
Enterobacter cloacae	0.00	0.03 - 0.15	↓
Lactobacillus reuteri	0.00	0.16 - 0.32	↓



Obesity

The gut microbiome plays an important role in how the body manages energy balance, processes nutrients, and regulates fat storage, all of which can influence weight regulation. Certain bacterial species and microbial pathways have been consistently linked to patterns associated with weight gain or, conversely, to mechanisms that support a healthier body weight ^[37-42].

Some microbial activities are considered detrimental in the context of weight management. Elevated pathways for glutamine and glutamate biosynthesis have been associated with shifts in appetite regulation and fat storage ^[43]. Similarly, higher microbial aromatic amino acid (AAA) biosynthesis has been linked to greater energy harvest from the diet and biochemical patterns associated with obesity ^[44,45].

On the protective side, pathways such as branched-chain amino acid (BCAA) degradation are beneficial, as inefficient BCAA breakdown is often observed in obesity ^[46]. Additionally, glycosaminoglycan degradation supports the production of beneficial compounds like short-chain fatty acids (SCFA), which contribute to appetite regulation, gut barrier function, and reduced fat accumulation ^[47].

It is important to keep in mind that while the microbiome plays a meaningful role, it is just one part of a complex system that includes diet, physical activity, sleep, stress, hormonal regulation, and host genetics.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
Akkermansia muciniphila	3.45	0.14 - 2.36	↑
Bacteroides thetaiotaomicron	0.03	0.12 - 0.82	↓
Blautia coccooides	0.00	0.02 - 0.11	↓
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Methanobrevibacter smithii	0.17	0.11 - 2.59	
Oscillibacter spp	2.32	0.18 - 0.97	↑
Detrimental species			
Dorea longicatena	0.34	0.37 - 2.49	↓
Eubacterium ventriosum	0.00	0.07 - 0.44	↓
Prevotella copri	0.00	1.04 - 26.56	↓
Roseburia intestinalis	0.59	0.10 - 1.46	
Ruminococcus gnavus	0.14	0.03 - 0.50	
Ruminococcus torques	0.36	0.25 - 2.04	
Protective pathways			
BCAA degradation	0.00	0.00 - 0.00	
Glycosaminoglycan degradation	0.02	0.01 - 0.03	
Detrimental pathways			
Glutamine and glutamate biosynthesis	0.27	0.09 - 0.19	↑
AAA biosynthesis	3.12	1.49 - 1.82	↑



Type 2 Diabetes

The gut microbiome plays a crucial role in glucose regulation, insulin sensitivity, and inflammation, all of which are key factors in the development and progression of Type 2 Diabetes (T2D). Several bacterial species have been linked to T2D-related metabolic patterns, including *Akkermansia muciniphila*, often associated with improved glucose homeostasis, while others are frequently enriched in individuals with impaired glucose control ^[42,48-53].

Certain microbial functions are considered detrimental in the context of T2D. These include branched-chain amino acid (BCAA) biosynthesis, which has been consistently linked to insulin resistance and glucose intolerance ^[44], and microbial activity related to glucose metabolism, which may contribute to altered nutrient handling. Additionally, increased methane metabolism has been associated with slower intestinal transit, a factor that may negatively influence glucose metabolism and energy balance ^[54].

On the protective side, microbial pathways that support the production of short-chain fatty acids (SCFA) are beneficial, as SCFAs help improve insulin sensitivity, reduce inflammation, and support gut barrier integrity ^[47]. The microbiome's ability to synthesize essential cofactors and vitamins also plays a supportive role in maintaining glucose homeostasis and metabolic resilience. Together, the balance between these protective and detrimental microbial activities offers insights into how the gut microbiome may influence the risk or progression of T2D.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
<i>Akkermansia muciniphila</i>	3.45	0.14 - 2.36	↑
<i>Blautia obeum</i>	0.49	0.12 - 1.08	
<i>Eubacterium eligens</i>	2.05	0.23 - 1.83	↑
<i>Faecalibacterium prausnitzii</i>	17.62	3.37 - 8.84	↑
Detrimental species			
<i>Bacteroides vulgatus</i>	7.38	1.13 - 7.29	↑
<i>Clostridium clostridioforme</i>	0.00	0.02 - 0.12	↓
<i>Hungatella hathewayi</i>	0.00	0.01 - 0.08	↓
<i>Prevotella copri</i>	0.00	1.04 - 26.56	↓
<i>Ruminococcus torques</i>	0.36	0.25 - 2.04	
Protective pathways			
SCFA production	2.23	0.79 - 1.60	↑
Cofactors and vitamins biosynthesis	9.37	10.05 - 11.19	↓
Detrimental pathways			
Glucose regulation	5.69	2.55 - 3.30	↑
BCAA biosynthesis	4.18	5.30 - 6.19	↓
Methane metabolism	0.15	0.07 - 0.30	



Inflammatory Bowel Disease

Inflammatory Bowel Disease (IBD), which includes Crohn's disease and ulcerative colitis, is a chronic condition characterized by persistent inflammation of the digestive tract. While the exact causes are multifactorial, research consistently shows that imbalances in the gut microbiome play a central role in the development and maintenance of intestinal inflammation [6,55-60].

Microbial patterns associated with IBD typically involve a reduction in beneficial bacteria that help regulate inflammation and protect the gut barrier, such as butyrate producers, alongside an increase in pro-inflammatory species like certain members of Enterobacteriaceae [6]. Detrimental microbial functions in this context include elevated lipopolysaccharide (LPS) biosynthesis, which can drive immune activation, mucin degradation, contributing to erosion of the gut's protective lining, and increased tryptophan degradation, which reduces production of anti-inflammatory metabolites [45,61]. Additionally, pathways linked to oxidative stress are often enriched in IBD, further sustaining inflammation [59].

Conversely, certain microbial activities are considered protective. These include butyrate production, which supports gut barrier integrity and immune regulation, along with the synthesis of essential vitamins like B12 and K, both of which are implicated in modulating inflammation and maintaining mucosal health [59,62]. Interestingly, branched-chain amino acid (BCAA) biosynthesis, which is generally seen as detrimental in metabolic diseases, may have a protective role in IBD, likely supporting mucosal healing and immune modulation [59]. Understanding the balance between these microbial features can inform targeted dietary and lifestyle strategies.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
Akkermansia muciniphila	3.45	0.14 - 2.36	⬆️
Bifidobacterium adolescentis	0.00	0.48 - 7.70	⬇️
Coprococcus comes	0.23	0.31 - 1.62	⬇️
Dorea formicigenerans	0.15	0.17 - 0.84	⬇️
Eubacterium spp	2.59	1.91 - 6.46	
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	⬆️
Roseburia hominis	1.28	0.07 - 0.58	⬆️
Ruminococcus obeum	0.00	0.02 - 0.15	⬇️
Detrimental species			
Bacteroides vulgatus	7.38	1.13 - 7.29	⬆️
Clostridium clostridioforme	0.00	0.02 - 0.12	⬇️
Eggerthella lenta	0.10	0.04 - 0.26	
Escherichia coli	0.05	0.04 - 0.27	
Ruminococcus gnavus	0.14	0.03 - 0.50	
Ruminococcus torques	0.36	0.25 - 2.04	
Protective pathways			
BCAA biosynthesis	4.18	5.30 - 6.19	⬇️
Butyrate production	0.41	0.16 - 0.29	⬆️
Vitamin B12 metabolism	0.00	0.00 - 0.01	
Vitamin K metabolism	0.09	0.04 - 0.12	
Detrimental pathways			
LPS biosynthesis	0.17	0.04 - 0.16	⬆️
Mucine degradation	1.49	0.85 - 1.25	⬆️
Tryptophan degradation	0.00	0.00 - 0.00	
Oxidative damage	0.00	0.00 - 0.00	



Gut-Heart Axis

Growing evidence supports a strong link between the gut microbiome and cardiovascular health, often referred to as the gut-heart axis. The composition and metabolic activity of gut bacteria can influence key factors such as inflammation, cholesterol metabolism, and blood pressure regulation, all of which are closely tied to heart health [42,63-68]. Imbalances in the gut microbiome may contribute to increased cardiometabolic risk, while a balanced microbial community can offer protective benefits.

Some microbial pathways are considered detrimental in this context. A prominent example is the production of trimethylamine (TMA), which is converted in the liver to trimethylamine-N-oxide (TMAO), a compound strongly linked to atherosclerosis and cardiovascular disease risk [69]. Additionally, elevated lipopolysaccharide (LPS) biosynthesis contributes to systemic low-grade inflammation, a key driver of vascular damage [70]. An increase in tryptophan biosynthesis may also influence inflammatory pathways and metabolic disturbances associated with cardiovascular risk [45].

On the protective side, microbial pathways involved in the production of short-chain fatty acids (SCFA), particularly butyrate, are beneficial. SCFAs help regulate inflammation, improve lipid metabolism, and support vascular health [67,69]. Likewise, the microbial synthesis of certain vitamins, such as B vitamins and vitamin K, contributes to anti-inflammatory effects and cardiovascular protection [71,72]. The balance between these beneficial and harmful microbial activities can provide meaningful insights into how the gut microbiome supports or challenges heart health.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
Bacteroides spp	22.17	7.03 - 28.33	
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Detrimental species			
Clostridium spp	1.20	0.06 - 0.71	↑
Desulfovibrio spp	0.00	0.09 - 0.42	↓
Escherichia coli	0.05	0.04 - 0.27	
Klebsiella spp	0.01	0.02 - 0.71	↓
Klebsiella aerogenes	0.00	0.23 - 8.07	↓
Ruminococcus gnavus	0.14	0.03 - 0.50	
Streptococcus spp	0.00	0.08 - 0.71	↓
Protective pathways			
SCFA production	2.23	0.79 - 1.60	↑
Vitamin metabolism	7.31	7.94 - 9.07	↓
Butyrate production	0.41	0.16 - 0.29	↑
Detrimental pathways			
TMA production	0.00	0.00 - 0.00	
LPS biosynthesis	0.17	0.04 - 0.16	↑
Tryptophan biosynthesis	0.99	0.52 - 0.70	↑



Gut-Brain Axis

The gut-brain axis describes the two-way communication system between the gut microbiome and the brain, involving neural, immune, endocrine, and metabolic pathways. Mounting research shows that gut microbes influence mood, stress response, sleep quality, and cognitive function through the production of neuroactive compounds and modulation of inflammation ^[73-77].

Protective microbial functions within this axis include the biosynthesis of neurotransmitters such as serotonin and melatonin, along with tryptophan biosynthesis, which is a precursor for serotonin production ^[71,78]. Pathways like glutamate degradation may help regulate excitatory signals in the nervous system, supporting emotional balance and mental clarity. Some bacteria also produce histamine, which plays roles in modulating wakefulness, appetite, and cognitive function ^[79,80].

Conversely, certain microbial activities are potentially detrimental. For example, trimethylamine (TMA) production, while primarily linked to cardiovascular risk, also appears to influence neuroinflammation ^[65,81]. Elevated microbial GABA production, though beneficial in some contexts, may disrupt the balance of excitatory and inhibitory neurotransmission when poorly regulated ^[80]. Additionally, excess propionate production, especially when disproportionate, has been associated with altered cognition, stress response, and even behavioral disturbances in animal models ^[82,83]. The balance of these microbial functions offers valuable insight into how gut health may influence mental resilience and emotional well-being.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
Alistipes putredinis	3.67	1.06 - 4.72	
Blautia obeum	0.49	0.12 - 1.08	
Blautia wexlerae	0.33	0.07 - 0.67	
Clostridium sporogenes	0.00	0.00 - 0.00	
Coprococcus spp	0.26	0.61 - 3.56	↓
Eubacterium hallii	0.23	0.21 - 2.40	
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Detrimental species			
Bacteroides spp	22.17	7.03 - 28.33	
Bifidobacterium spp	1.50	0.75 - 12.85	
Escherichia coli	0.05	0.04 - 0.27	
Odoribacter spp	0.78	0.15 - 0.70	↑
Protective pathways			
Histamine production	0.00	0.00 - 0.00	
Tryptophan biosynthesis	0.99	0.52 - 0.70	↑
Neurotransmitter biosynthesis	0.10	0.02 - 0.06	↑
Glutamate degradation	0.04	0.01 - 0.02	↑
Detrimental pathways			
TMA production	0.00	0.00 - 0.00	
GABA production	0.10	0.02 - 0.06	↑
Propionate production	0.10	0.08 - 0.16	



Gut-Liver Axis

The gut-liver axis refers to the bidirectional communication between the gut microbiome and the liver, primarily mediated through the portal vein, which delivers gut-derived metabolites, microbial components, and immune signals directly to the liver [42,84-86]. This connection means that changes in the gut microbiome can have direct and significant effects on liver function, detoxification processes, metabolic balance, and inflammation.

Several microbial pathways are considered detrimental for liver health. Increased lipopolysaccharide (LPS) and peptidoglycan biosynthesis can promote systemic inflammation and hepatic immune activation, contributing to conditions like non-alcoholic fatty liver disease (NAFLD) [87]. Elevated ethanol production by gut fermentation has also been implicated in liver steatosis and inflammation, even in individuals who do not consume alcohol [88,89]. Other detrimental activities include oxidative damage pathways, GABA production, and denitrification processes, all of which may disrupt metabolic and immune homeostasis [90-92]. Furthermore, excess branched-chain amino acid (BCAA) and aromatic amino acid (AAA) biosynthesis has been associated with metabolic dysregulation and liver dysfunction [93].

Conversely, the microbiome can also support liver health through protective pathways. Choline biosynthesis helps prevent fat accumulation in the liver [94], while heme biosynthesis plays a role in oxidative stress control and cellular energy metabolism [95]. Monitoring the balance between these protective and detrimental microbial functions offers valuable insights into how the gut microbiome may be influencing liver health and metabolic resilience.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
Coprococcus comes	0.23	0.31 - 1.62	↓
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Detrimental species			
Bilophila wadsworthia	0.15	0.02 - 0.09	↑
Desulfovibrio piger	0.00	0.09 - 0.43	↓
Hungatella hathewayi	0.00	0.01 - 0.08	↓
Klebsiella pneumoniae	0.00	0.03 - 0.65	↓
Streptococcus anginosus	0.00	0.02 - 0.07	↓
Veillonella atypica	0.00	0.02 - 0.06	↓
Protective pathways			
Choline biosynthesis	0.00	0.00 - 0.00	
Heme biosynthesis	0.04	0.02 - 0.06	
Detrimental pathways			
Oxidative damage	0.00	0.00 - 0.00	
GABA production	0.10	0.02 - 0.06	↑
Denitrification	0.00	0.00 - 0.00	
Ethanol production	0.65	0.11 - 0.34	↑
LPS and peptidoglycan biosynthesis	3.25	3.49 - 3.88	↓
BCAA and AAA biosynthesis	7.30	6.88 - 7.97	



Gut-Autoimmunity Axis

The association between the gut and immunity is an emerging clinical field of increasing relevance in the context of autoimmune diseases (AID). Alterations in microbial composition, such as a reduction in beneficial species and an increase in potentially pro-inflammatory microorganisms, may contribute to heightened immune activation and a breakdown of immune tolerance ^[96-105]. These patterns have been linked to various AID, although with notable differences between conditions.

At a functional level, the production of short-chain fatty acids (SCFAs), essential for immune regulation and maintenance of the intestinal barrier, tends to be reduced, while metabolic pathways such as fatty acid biosynthesis, excessive succinate production, and mucin degradation are frequently increased ^[96,101,105-110]. The modulation of the immune system by tryptophan-derived metabolites, particularly indoles, may also be impaired, contributing to a dysregulated immune response ^[111]. Together, these mechanisms may promote systemic inflammatory states associated with the development or worsening of AID.

Important Note: the relationship between the gut microbiome and AID remains a developing scientific field, and some reported associations are still preliminary. The patterns presented in this section therefore reflect general observations. In specific conditions, opposite associations may occur. Interpretation of these results should therefore be integrated and cautious.

Species / Pathway	Sample (%)	Reference (%)	Flag
Protective species			
Bifidobacterium bifidum	0.90	0.27 - 2.92	
Coprococcus spp	0.26	0.61 - 3.56	↓
Faecalibacterium prausnitzii	17.62	3.37 - 8.84	↑
Detrimental species			
Bifidobacterium dentium	0.00	0.02 - 0.13	↓
Collinsella spp	1.78	0.47 - 4.43	
Eggerthella spp	0.10	0.04 - 0.26	
Enterococcus gallinarum	0.00	0.01 - 0.05	↓
Escherichia coli	0.05	0.04 - 0.27	
Fusobacterium spp	0.00	0.05 - 0.46	↓
Klebsiella spp	0.01	0.02 - 0.71	↓
Prevotella spp	0.00	0.84 - 24.00	↓
Prevotella copri	0.00	1.04 - 26.56	↓
Protective pathways			
SCFA production	2.23	0.79 - 1.60	↑
Tryptophan degradation	0.00	0.00 - 0.00	
Succinate degradation	0.00	0.00 - 0.01	
Detrimental pathways			
Fatty acids biosynthesis	0.40	0.29 - 0.72	
Mucine degradation	1.49	0.85 - 1.25	↑



Detected Microbial Species

Below is a list of the microbial species identified in your sample through shotgun metagenomic sequencing. For each **genus** and **species**, we show its relative abundance in your gut and how it compares to a reference population, a group of healthy individuals used as a baseline. This comparison helps highlight which microbes are more or less prevalent in your gut in comparison to this healthy population.

Note that species detected at very low abundances (below 0.01%), while they may reflect true biological presence, could also represent background noise or technical variation, and should be interpreted with caution.

Domain*	Phylum	Genus	Species	Sample (%)	Reference (%)	Flag
A	Euryarchaeota	Methanobrevibacter		0.1737	0.1146 - 2.5855	
A	Euryarchaeota	Methanobrevibacter	smithii	0.1737	0.1146 - 2.5855	
B	Actinobacteria	Actinomyces		0.0006	0.0159 - 0.0651	↓
B	Actinobacteria	Actinomyces	sp HMSC035G02	0.0006	0.0128 - 0.0264	↓
B	Actinobacteria	Adlercreutzia		0.3644	0.0268 - 0.1248	↑
B	Actinobacteria	Adlercreutzia	equolifaciens	0.3644	0.0268 - 0.1248	↑
B	Actinobacteria	Asaccharobacter		0.4076	0.0395 - 0.1896	↑
B	Actinobacteria	Asaccharobacter	celatus	0.4076	0.0395 - 0.1896	↑
B	Actinobacteria	Bifidobacterium		1.4954	0.7483 - 12.8529	
B	Actinobacteria	Bifidobacterium	bifidum	0.9017	0.2658 - 2.9222	
B	Actinobacteria	Bifidobacterium	longum	0.3393	0.2898 - 3.8017	
B	Actinobacteria	Bifidobacterium	pseudocatenulatum	0.2544	0.0812 - 1.2792	
B	Actinobacteria	Collinsella		1.7838	0.4668 - 4.4340	
B	Actinobacteria	Collinsella	aerofaciens	1.4054	0.4706 - 4.4019	
B	Actinobacteria	Collinsella	intestinalis	0.3644	0.0140 - 0.0336	↑
B	Actinobacteria	Collinsella	massiliensis	0.0004	0.0133 - 0.0569	↓
B	Actinobacteria	Collinsella	stercoris	0.0141	0.0000 - 0.0000	↑
B	Actinobacteria	Eggerthella		0.1005	0.0396 - 0.2634	
B	Actinobacteria	Eggerthella	lenta	0.1005	0.0396 - 0.2634	
B	Actinobacteria	Enorma		0.1114	0.0141 - 0.0414	↑
B	Actinobacteria	Enorma	massiliensis	0.1110	0.0141 - 0.0357	↑
B	Actinobacteria	Enterorhabdus		0.0009	0.0121 - 0.0266	↓
B	Actinobacteria	Enterorhabdus	caecimuris	0.0009	0.0121 - 0.0266	↓
B	Actinobacteria	Gordonibacter		0.0225	0.0324 - 0.1968	↓
B	Actinobacteria	Gordonibacter	pamelaeae	0.0225	0.0324 - 0.1968	↓
B	Actinobacteria	Microbacterium		0.1280	0.0000 - 0.0000	↑
B	Actinobacteria	Microbacterium	ginsengisoli	0.0070	0.0000 - 0.0000	↑
B	Actinobacteria	Microbacterium	sp T32	0.1210	0.0000 - 0.0000	↑
B	Bacteroidetes	Alistipes		6.8725	1.4341 - 6.2207	↑
B	Bacteroidetes	Alistipes	finegoldii	0.9594	0.0847 - 0.7928	↑
B	Bacteroidetes	Alistipes	indistinctus	0.0359	0.0303 - 0.2191	
B	Bacteroidetes	Alistipes	inops	0.1408	0.0843 - 0.8554	
B	Bacteroidetes	Alistipes	putredinis	3.6654	1.0604 - 4.7182	
B	Bacteroidetes	Alistipes	shahii	2.0155	0.0556 - 0.3013	↑
B	Bacteroidetes	Alistipes	timonensis	0.0556	0.0257 - 0.1386	
B	Bacteroidetes	Bacteroides		22.1700	7.0292 - 28.3328	
B	Bacteroidetes	Bacteroides	caccae	0.2205	0.2410 - 1.2155	↓
B	Bacteroidetes	Bacteroides	cellulosilyticus	0.7914	0.0616 - 1.3364	
B	Bacteroidetes	Bacteroides	dorei	3.6910	0.3070 - 3.5983	↑



Domain*	Phylum	Genus	Species	Sample (%)	Reference (%)	Flag
B	Bacteroidetes	Bacteroides	faecis	1.5603	0.1476 - 1.0359	↑
B	Bacteroidetes	Bacteroides	faecis CAG 32	0.1078	0.0451 - 0.6776	
B	Bacteroidetes	Bacteroides	finegoldii	0.5083	0.0703 - 0.7211	
B	Bacteroidetes	Bacteroides	fragilis	0.0915	0.0932 - 0.8336	↓
B	Bacteroidetes	Bacteroides	massiliensis	0.7646	0.1319 - 0.8693	
B	Bacteroidetes	Bacteroides	ovatus	0.6681	0.1117 - 0.9361	
B	Bacteroidetes	Bacteroides	salyersiae	0.4810	0.0617 - 0.6777	
B	Bacteroidetes	Bacteroides	sp CAG 144	0.0596	0.0707 - 0.5264	↓
B	Bacteroidetes	Bacteroides	stercoris	1.4132	0.1956 - 2.6056	
B	Bacteroidetes	Bacteroides	thetaiotaomicron	0.0316	0.1182 - 0.8215	↓
B	Bacteroidetes	Bacteroides	uniformis	4.0591	1.1579 - 6.8263	
B	Bacteroidetes	Bacteroides	vulgatus	7.3788	1.1305 - 7.2923	↑
B	Bacteroidetes	Bacteroides	xylanisolvens	0.3433	0.0641 - 0.5294	
B	Bacteroidetes	Barnesiella		0.4805	0.2858 - 1.6570	
B	Bacteroidetes	Barnesiella	intestinihominis	0.4805	0.2870 - 1.6450	
B	Bacteroidetes	Butyrivibrio		0.0588	0.0385 - 0.2413	
B	Bacteroidetes	Butyrivibrio	synergistica	0.0018	0.0249 - 0.1364	↓
B	Bacteroidetes	Butyrivibrio	virosa	0.0571	0.0311 - 0.1764	
B	Bacteroidetes	Odoribacter		0.7751	0.1471 - 0.6983	↑
B	Bacteroidetes	Odoribacter	laneus	0.1396	0.0439 - 0.4745	
B	Bacteroidetes	Odoribacter	splanchnicus	0.6355	0.1470 - 0.6859	
B	Bacteroidetes	Parabacteroides		2.7778	0.8372 - 2.9345	
B	Bacteroidetes	Parabacteroides	distasonis	2.0694	0.3907 - 1.4434	↑
B	Bacteroidetes	Parabacteroides	goldsteinii	0.0427	0.0328 - 0.3027	
B	Bacteroidetes	Parabacteroides	johnsonii	0.2772	0.0916 - 0.6852	
B	Bacteroidetes	Parabacteroides	merdae	0.3886	0.3806 - 1.5101	
B	Firmicutes	Agathobaculum		0.6226	0.0934 - 0.4683	↑
B	Firmicutes	Agathobaculum	butyriciproducens	0.6226	0.0934 - 0.4683	↑
B	Firmicutes	Anaeromassilibacillus		0.0113	0.0186 - 0.0685	↓
B	Firmicutes	Anaeromassilibacillus	sp An250	0.0113	0.0186 - 0.0672	↓
B	Firmicutes	Anaerostipes		0.6195	0.3720 - 2.6811	
B	Firmicutes	Anaerostipes	hadrus	0.6195	0.3719 - 2.6889	
B	Firmicutes	Anaerotruncus		0.0613	0.0192 - 0.3279	
B	Firmicutes	Anaerotruncus	colihominis	0.0613	0.0162 - 0.0669	
B	Firmicutes	Blautia		1.3286	0.5705 - 4.1811	
B	Firmicutes	Blautia	obeum	0.4939	0.1207 - 1.0842	
B	Firmicutes	Blautia	wexlerae	0.3343	0.0677 - 0.6737	
B	Firmicutes	Clostridium		1.2042	0.0618 - 0.7108	↑
B	Firmicutes	Clostridium	bolteae	0.0082	0.0197 - 0.1020	↓
B	Firmicutes	Clostridium	citroniae	0.0044	0.0153 - 0.0447	↓
B	Firmicutes	Clostridium	lavalense	0.0172	0.0195 - 0.0532	↓
B	Firmicutes	Clostridium	leptum	0.0294	0.0192 - 0.0714	
B	Firmicutes	Clostridium	sp CAG 167	0.8583	0.0589 - 0.3597	↑
B	Firmicutes	Clostridium	sp CAG 242	0.0499	0.0350 - 0.1804	
B	Firmicutes	Clostridium	sp CAG 253	0.0189	0.0275 - 0.2387	↓
B	Firmicutes	Clostridium	sp CAG 58	0.2771	0.0287 - 0.1674	↑
B	Firmicutes	Clostridium	symbiosum	0.0025	0.0223 - 0.0907	↓
B	Firmicutes	Coprococcus		0.2649	0.6074 - 3.5558	↓
B	Firmicutes	Coprococcus	catus	0.0352	0.1031 - 0.4601	↓
B	Firmicutes	Coprococcus	comes	0.2297	0.3056 - 1.6179	↓



Domain*	Phylum	Genus	Species	Sample (%)	Reference (%)	Flag
B	Firmicutes	Dialister		0.0214	0.1267 - 1.3267	↓
B	Firmicutes	Dialister	invisus	0.0214	0.1024 - 0.6068	↓
B	Firmicutes	Dorea		0.4924	0.5224 - 3.3231	↓
B	Firmicutes	Dorea	formicigenerans	0.1498	0.1731 - 0.8417	↓
B	Firmicutes	Dorea	longicatena	0.3426	0.3710 - 2.4928	↓
B	Firmicutes	Eisenbergiella		0.0379	0.0226 - 0.1423	
B	Firmicutes	Eisenbergiella	massiliensis	0.0379	0.0215 - 0.0974	
B	Firmicutes	Eubacterium		2.5926	1.9064 - 6.4597	
B	Firmicutes	Eubacterium	eligens	2.0495	0.2300 - 1.8284	↑
B	Firmicutes	Eubacterium	hallii	0.2273	0.2130 - 2.4048	
B	Firmicutes	Eubacterium	ramulus	0.0600	0.0559 - 0.2704	
B	Firmicutes	Eubacterium	rectale	1.6196	0.3793 - 5.8801	
B	Firmicutes	Eubacterium	siraeum	13.1917	0.0874 - 1.3055	↑
B	Firmicutes	Eubacterium	sp CAG 38	0.2535	0.0581 - 0.4677	
B	Firmicutes	Eubacterium	ventriosum	0.0023	0.0734 - 0.4357	↓
B	Firmicutes	Faecalibacterium		17.6193	3.3656 - 8.8356	↑
B	Firmicutes	Faecalibacterium	prausnitzii	17.6193	3.3656 - 8.8356	↑
B	Firmicutes	Firmicutes	bacterium CAG 110	0.0208	0.0763 - 0.6543	↓
B	Firmicutes	Firmicutes	bacterium CAG 145	0.0003	0.0263 - 0.1425	↓
B	Firmicutes	Firmicutes	bacterium CAG 83	1.1856	0.0469 - 0.3310	↑
B	Firmicutes	Firmicutes	bacterium CAG 94	0.0197	0.0270 - 0.1453	↓
B	Firmicutes	Firmicutes	bacterium CAG 95	0.0066	0.0302 - 0.2830	↓
B	Firmicutes	Firmicutes unclassified		1.2331	0.1489 - 1.1911	↑
B	Firmicutes	Flavonifractor		0.8153	0.0335 - 0.2218	↑
B	Firmicutes	Flavonifractor	plautii	0.8093	0.0321 - 0.2171	↑
B	Firmicutes	Flavonifractor	sp An100	0.0060	0.0146 - 0.0241	↓
B	Firmicutes	Fusicatenibacter		2.1797	0.5475 - 3.3271	
B	Firmicutes	Fusicatenibacter	saccharivorans	2.1797	0.5475 - 3.3271	
B	Firmicutes	Gemmiger		0.0708	0.0878 - 0.3559	↓
B	Firmicutes	Gemmiger	formicilis	0.0708	0.0885 - 0.3562	↓
B	Firmicutes	Harryflintia		0.0049	0.0157 - 0.0250	↓
B	Firmicutes	Harryflintia	acetispora	0.0049	0.0157 - 0.0250	↓
B	Firmicutes	Holdemania		0.0563	0.0178 - 0.0619	
B	Firmicutes	Holdemania	filiformis	0.0563	0.0178 - 0.0619	
B	Firmicutes	Intestinibacter		0.0008	0.0320 - 0.1620	↓
B	Firmicutes	Intestinibacter	bartlettii	0.0008	0.0320 - 0.1620	↓
B	Firmicutes	Intestinimonas		0.0331	0.0210 - 0.0797	
B	Firmicutes	Intestinimonas	butyriciproducens	0.0331	0.0210 - 0.0797	
B	Firmicutes	Lachnoclostridium		0.0330	0.0253 - 0.2120	
B	Firmicutes	Lachnoclostridium	sp An138	0.0007	0.0130 - 0.0405	↓
B	Firmicutes	Lachnospira		0.1199	0.2061 - 1.8269	↓
B	Firmicutes	Lachnospira	pectinoschiza	0.1199	0.2061 - 1.8269	↓
B	Firmicutes	Lachnospiraceae unclassified		1.6196	0.3756 - 5.8761	
B	Firmicutes	Lactobacillus		0.0137	0.0325 - 0.2220	↓
B	Firmicutes	Lactobacillus	rogosae	0.0137	0.0248 - 0.1462	↓
B	Firmicutes	Lawsonibacter		0.2673	0.0211 - 0.1051	↑
B	Firmicutes	Lawsonibacter	asaccharolyticus	0.2673	0.0211 - 0.1051	↑
B	Firmicutes	Megamonas		0.2651	0.0556 - 0.8596	
B	Firmicutes	Megamonas	funiformis	0.2128	0.0303 - 0.5352	



Domain*	Phylum	Genus	Species	Sample (%)	Reference (%)	Flag
B	Firmicutes	Megamonas	hypermegale	0.0524	0.0374 - 0.2881	
B	Firmicutes	Monoglobus		0.1434	0.0449 - 0.2618	
B	Firmicutes	Monoglobus	pectinilyticus	0.1434	0.0449 - 0.2618	
B	Firmicutes	Oscillibacter		2.3243	0.1774 - 0.9719	↑
B	Firmicutes	Oscillibacter	sp 57 20	1.7113	0.1368 - 0.7587	↑
B	Firmicutes	Oscillibacter	sp CAG 241	0.6130	0.0497 - 0.3420	↑
B	Firmicutes	Phascolarctobacterium		0.1232	0.2413 - 1.6040	↓
B	Firmicutes	Phascolarctobacterium	faecium	0.1232	0.1012 - 0.6399	
B	Firmicutes	Pseudoflavonifractor		0.0114	0.0163 - 0.0973	↓
B	Firmicutes	Pseudoflavonifractor	capillosus	0.0114	0.0173 - 0.0339	↓
B	Firmicutes	Roseburia		4.9676	1.3231 - 6.7232	
B	Firmicutes	Roseburia	faecis	2.1521	0.4261 - 4.3320	
B	Firmicutes	Roseburia	hominis	1.2760	0.0742 - 0.5770	↑
B	Firmicutes	Roseburia	intestinalis	0.5857	0.1014 - 1.4591	
B	Firmicutes	Roseburia	inulinivorans	0.8902	0.1442 - 1.1515	
B	Firmicutes	Roseburia	sp CAG 182	0.0625	0.0400 - 0.2975	
B	Firmicutes	Roseburia	sp CAG 309	0.0010	0.0227 - 0.1054	↓
B	Firmicutes	Ruminococcaceae	bacterium D16	0.0003	0.0186 - 0.0505	↓
B	Firmicutes	Ruminococcaceae	bacterium D5	0.0393	0.0193 - 0.0527	
B	Firmicutes	Ruminococcaceae unclassified		13.2608	0.0673 - 1.0485	↑
B	Firmicutes	Ruminococcus		4.0497	1.3250 - 9.3596	
B	Firmicutes	Ruminococcus	bicirculans	1.6188	0.1882 - 1.8581	
B	Firmicutes	Ruminococcus	bromii	2.4080	1.4968 - 9.6325	
B	Firmicutes	Ruminococcus	gnavus	0.1397	0.0328 - 0.5024	
B	Firmicutes	Ruminococcus	lactaris	0.0229	0.1878 - 1.2325	↓
B	Firmicutes	Ruminococcus	torques	0.3608	0.2497 - 2.0418	
B	Firmicutes	Ruthenibacterium		1.1479	0.0315 - 0.1722	↑
B	Firmicutes	Ruthenibacterium	lactatiformans	1.1479	0.0315 - 0.1722	↑
B	Firmicutes	Streptococcus		0.0020	0.0850 - 0.7114	↓
B	Firmicutes	Streptococcus	salivarius	0.0005	0.0425 - 0.3841	↓
B	Firmicutes	Streptococcus	thermophilus	0.0015	0.0440 - 0.4782	↓
B	Firmicutes	Tyzzereella		0.0169	0.0210 - 0.2159	↓
B	Firmicutes	Tyzzereella	nexilis	0.0169	0.0210 - 0.2159	↓
B	Lentisphaerae	Victivallis		0.0117	0.0201 - 0.1130	↓
B	Lentisphaerae	Victivallis	vadensis	0.0117	0.0201 - 0.1130	↓
B	Proteobacteria	Bilophila		0.1526	0.0208 - 0.0860	↑
B	Proteobacteria	Bilophila	wadsworthia	0.1526	0.0208 - 0.0860	↑
B	Proteobacteria	Escherichia		0.0488	0.0436 - 0.2812	
B	Proteobacteria	Escherichia	coli	0.0488	0.0434 - 0.2714	
B	Proteobacteria	Haemophilus		0.0025	0.0207 - 0.1165	↓
B	Proteobacteria	Haemophilus	parainfluenzae	0.0025	0.0181 - 0.0948	↓
B	Proteobacteria	Klebsiella		0.0146	0.0220 - 0.7074	↓
B	Proteobacteria	Klebsiella	oxytoca	0.0146	0.0175 - 0.0456	↓
B	Proteobacteria	Parasutterella		0.5261	0.0412 - 0.3534	↑
B	Proteobacteria	Parasutterella	excrementihominis	0.5261	0.0412 - 0.3534	↑
B	Proteobacteria	Proteobacteria	bacterium CAG 139	0.2376	0.0329 - 0.4513	
B	Proteobacteria	Proteobacteria unclassified		0.2376	0.0329 - 0.4513	
B	Proteobacteria	Sphingomonas		0.1666	0.0000 - 0.0000	↑



Domain*	Phylum	Genus	Species	Sample (%)	Reference (%)	Flag
B	Proteobacteria	Sphingomonas	sp FARSPH	0.1666	0.0000 - 0.0000	⬆
B	Proteobacteria	Turicimonas		0.0245	0.0196 - 0.0833	
B	Proteobacteria	Turicimonas	muris	0.0245	0.0196 - 0.0833	
B	Synergistetes	Cloacibacillus		0.0096	0.0239 - 0.0904	⬇
B	Synergistetes	Cloacibacillus	evryensis	0.0096	0.0000 - 0.0000	⬆
B	Verrucomicrobia	Akkermansia		3.4462	0.1392 - 2.3631	⬆
B	Verrucomicrobia	Akkermansia	muciniphila	3.4462	0.1392 - 2.3631	⬆

* (A): Archaea; (B): Bacteria; (E): Eukarya



Methodology and Limitations

Gut microbiome analysis was performed using shotgun metagenomic sequencing, a comprehensive approach that captures the entire microbial DNA content of a stool sample. Sequencing was conducted using Illumina technology, which provides high-throughput and accurate short-read data. Raw sequencing reads were first processed to remove low-quality bases and adapter sequences, followed by the removal of human DNA by mapping against the human reference genome to ensure that only microbial-derived sequences were retained for analysis.

Taxonomic profiling of the microbial community was carried out using MetaPhlAn3 v3.1.0^[112], a tool that identifies microbial species based on clade-specific marker genes. For clarity and robustness of reporting, we only include taxa with a relative abundance equal to or greater than 0.01%, unless otherwise noted, to reduce potential technical variability. Functional profiling of the microbiome was performed using HUMAnN3 v3.9^[113], which quantifies the presence and abundance of microbial metabolic pathways based on known gene families and reference databases.

To assess overall microbiome health, we apply a Random Forests machine learning model trained on gut microbiome profiles from over 1,300 adult individuals sourced from the publicly available curatedMetagenomicData v3.20 repository^[114,115]. This dataset includes a reference group of healthy adults and a group with known digestive imbalances. The healthy samples were selected to ensure they had a normal Body Mass Index (BMI) and no reported diagnoses of conditions such as Inflammatory Bowel Disease (IBD), diabetes, adenomas, colorectal cancer, or cardiovascular disease. During validation, the model achieved an accuracy of 83% and a receiver operating characteristic area under the curve (ROC-AUC) of 0.82, indicating robust performance in distinguishing between healthy and altered gut microbiomes.

The identification of organisms in this sample is based on the detection of specific taxonomic markers. The absence of detection of a given organism should not be interpreted as absolute absence, as it may be present below the detection limits of the technique, not represented in the reference databases, or genetically similar to other species, making it difficult to distinguish based on the available markers.

Functional predictions are genetic inferences based on microbial DNA profiles of the identified microorganisms, and therefore represent potential metabolic capacities rather than direct measurements of metabolites or metabolic fluxes.

The GUT HEALTH™ Premium report is intended for informational purposes related to wellbeing and nutrition, and is not designed to diagnose, prevent, or treat any medical condition. While the gut microbiome can provide valuable insights into overall health, the results presented here should not be interpreted as a clinical diagnosis. You are advised to discuss the significance of these results with your primary care physician, nutritionist, or the healthcare professional who requested this test.



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