



Gut Microbiome Report

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Date of Birth	20 Aug, 1985	Report Date	23 March, 2024
ID	P2020	Patient's Address	623, Gandhi Marg

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What is the gut microbiome, and why is it important for your health?

The human intestines harbor a diverse community of trillions of microorganisms, collectively forming the gut microbiome. This intricate network profoundly impacts various aspects of our lives. Beginning from birth, we initiate the assembly of this microbiome in our gut. Some of these microorganisms assist in extracting energy from indigestible components found in substances like milk.

Throughout our lives, these microbes continue to play crucial roles. They significantly contribute to our digestion, synthesize essential compounds for providing nutrients, and actively educate our immune system to distinguish between helpful and harmful bacteria. The gut microbiome's influence extends deeply into our overall health, intricately shaping the development of our brain and mental health. Moreover, it greatly influences energy extraction from our food intake, shields against harmful microbial invaders, and produces vital vitamins and metabolites that contribute to our well-being.

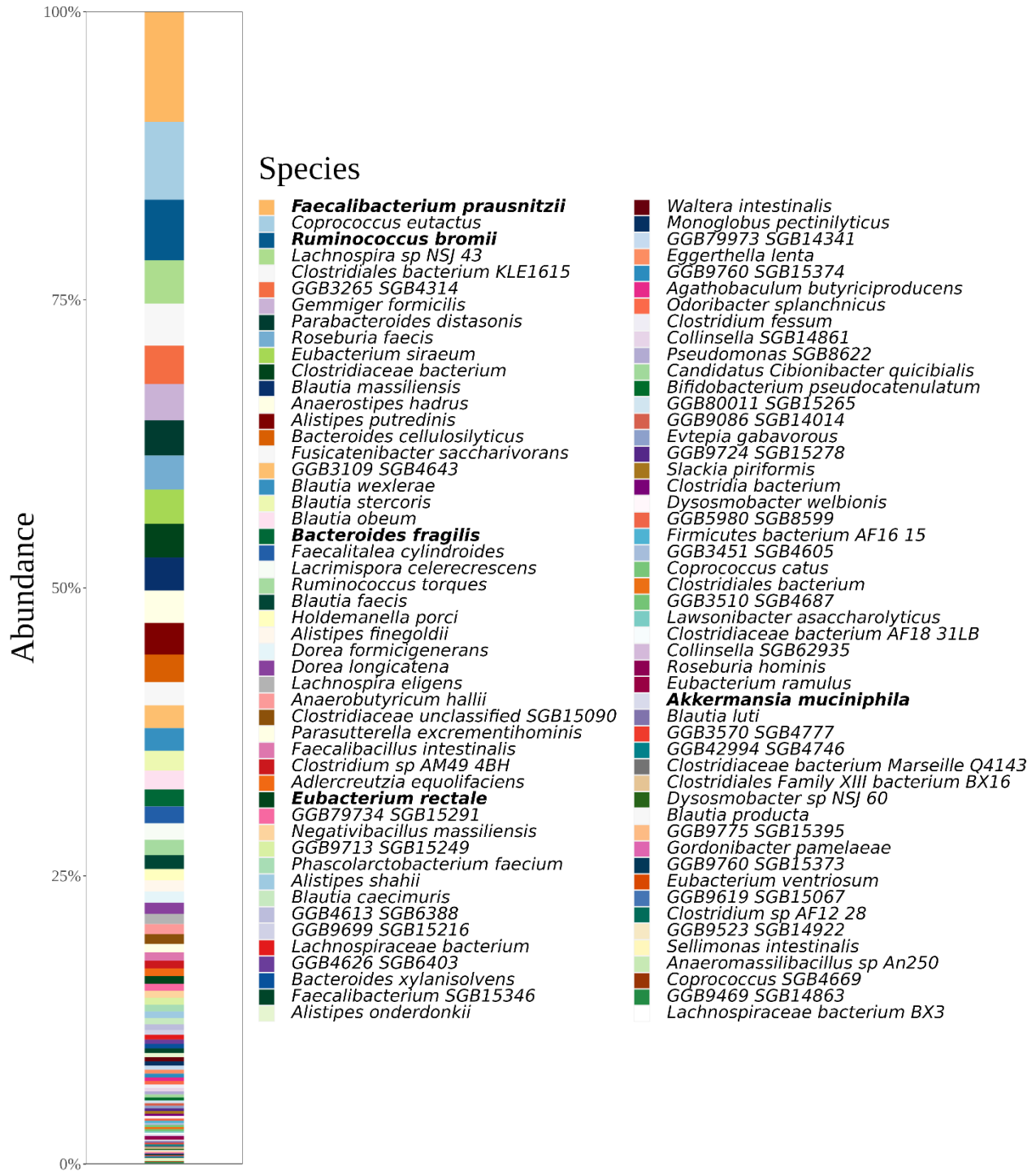
Analyzing the gut microbiome involves studying the genes of five distinct types of microorganisms: **bacteria, archaea, fungi, parasites, and viruses**. This comprehensive examination generates a detailed report outlining the microbial composition within the gut. Beyond identification, this analysis detects genes related to antibiotic resistance, aiding healthcare professionals in determining effective antibiotic treatments for infections.

The report not only lists the types of microbes but also provides detailed information about potentially harmful ones. It gives insights into their identity and genetic traits, helping us understand more about the different microbes living in the gut.

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For Important Terms and More Information, please refer to the Appendix.

What is the composition of your microbiome?



Note: Text in bold indicates keystone species

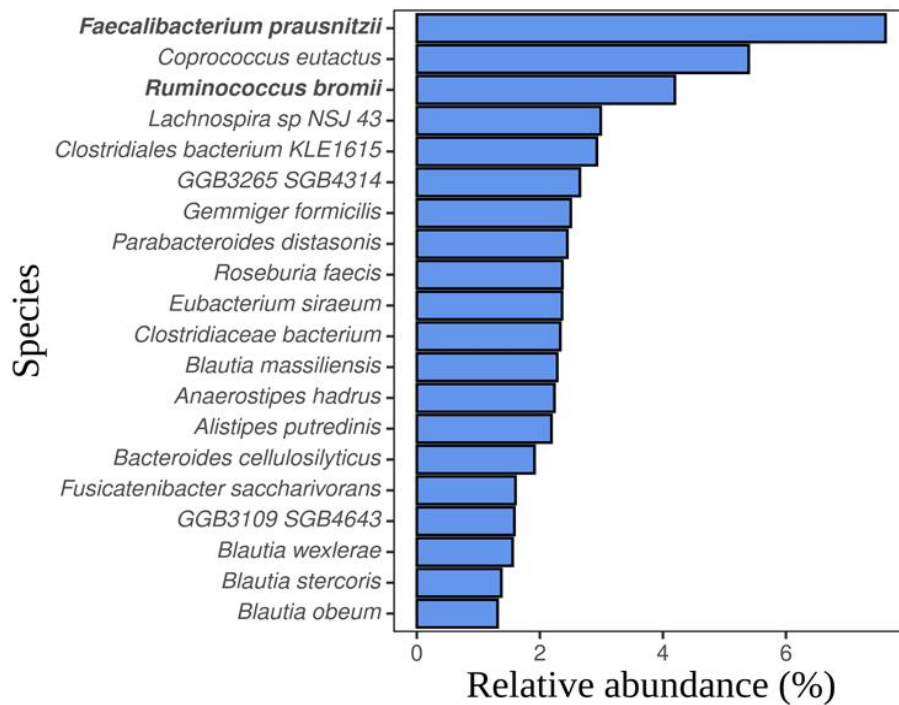
What is the diversity value for your gut microbiome and why is that important?



Gut microbiome diversity is generally considered a microbiome marker for good health. Clinical factors, such as diabetes, inflammation, liver function, and lifestyle modifications, are correlated with gut microbiome diversity. The diversity of your gut microbiome is measured through the **Shannon Diversity Index Value (SDIV)**. The SDIV for a healthy gut microbiome reference cohort is in the range of **2.34 to 3.5**. Your gut microbiome has an SDVI of **4.216**, which is indicative of a healthy microbiome diversity.

What are the most abundant members of your gut microbiome

The following graph depicts the top 20 organisms in your gut and their relative abundance:



The table provides important details about the **top 10 organisms and keystone species** in your gut, including their roles, impact on health, and suggestions for lifestyle change

Keystone bacteria are pivotal players among the multitude of microorganisms residing in our gut. Think of them as essential leaders responsible for maintaining a healthy balance within our gut community. These particular bacteria wield significant influence over how other microbes interact, contributing to tasks such as efficient digestion and overall gut well-being. A decline in these crucial bacteria can upset the gut’s equilibrium, potentially leading to health concerns. Hence, they hold immense importance in sustaining a harmonious and functional gut environment. When your gut is out of balance (**dysbiosis**), these key species are found to be lower than normal.

Scientific Name	Abundance in your profile	Reference IQR (%)	Significance
<i>Ruminococcus bicirculans</i>	6.958%	<0.915%	Ruminococcus bicirculans, a firmicutes helps in the digestion of certain components of plant fiber. However, literature also suggests an association with negative health outcomes such as colorectal cancer. More research is required to understand the role of this bacteria in health and disease.
<i>Eubacterium rectale</i>	3.590%	0.220%-1.840%	This bacterium produces the short chain fatty acid butyrate as a primary fermentation end-product. Butyrate-producing organisms in the intestinal tract of special interest in the prevention and treatment of inflammatory bowel diseases as well as colorectal cancers.
<i>Faecalibacterium prausnitzii</i>	3.467%	0.220%-2.640%	This bacterium is known for its ability to produce short chain fatty acid (SCFA), specifically butyrate. This important bacteria in your gut, belonging to Firmicutes phylum, is protective against inflammatory bowel diseases, irritable bowel syndrome, colorectal cancer, and obesity. This bacterium is a consumer of acetate that generates butyrate and bioactive anti-inflammatory compounds like salicylic and shikimic acids.
<i>Blautia wexlerae</i>	2.642%	0.032%-0.195%	The gram-positive, anaerobic bacteria Blautia wexlerae is found in the human gut and produces SCFA. Oral administration of B. wexlerae to mice induce metabolic changes and anti-inflammatory effects that decrease both high-fat diet–induced obesity and diabetes.
<i>Gemmiger formicilis</i>	2.298%	<0.217%	This bacterium is gram-negative, anaerobic and involved in fermenting carbohydrates, producing butyric and formic acids. Higher abundance of G. formicilis linked to an increased risk of colitis.
<i>Lachnospira eligens</i>	2.200%	<0.211%	Lachnospira eligens is known to build and breakdown complex carbohydrates and glycoconjugates. L. eligens utilizes pectin and polygalacturonic acid, with acetate, formate, ethanol, and CO2 as major end products.

Scientific Name	Abundance in your profile	Reference IQR (%)	Significance
<i>Ruminococcus bromii</i>	2.101%	<0.716%	R. bromii as a 'keystone' species in degradation of resistant starch.
<i>Clostridium sp AM49 4BH</i>	1.988%	<0.041%	This is unclassified clostridium species. As the predominant commensal bacterial cluster in our gut, Clostridium species has numerous beneficial effects on intestinal homeostasis. Because of their unique biological properties, Clostridium species have been shown to effectively reduce inflammation and allergic diseases thus far.
<i>GGB51647 SGB4348</i>	1.923%	<0.001%	This unclassified species belongs to Firmicutes phylum. Many species in this phylum break down in the stomach substances like resistant starch and dietary fiber that the body's enzymes are unable to digest.
<i>Oscillospiraceae bacterium</i>	1.886%	<0.001%	A common bacteria of the human gut microbiota, Oscillospiraceae bacteria are understudied anaerobic bacterial genera from the Clostridial cluster and have been frequently linked to health.
<i>Akkermansia muciniphila</i>	1.669%	<0.499%	<i>A. muciniphila</i> is known for its probiotic properties and association with other beneficial microbes, leading to a stable mucosal colonization throughout life. The bacterium is more abundant in the gut of healthy individuals in comparison to diabetic, obese patients, patients with bowel diseases and metabolic disorders.
<i>Bacteroides stercoris</i>	0.426%	<3.220%	Species in the genus Bacteroides perform degradation of complex plant polysaccharides, proteolytic activities, mucosal barrier integrity, short chain fatty acid production, and glucose metabolism. <i>B. stercoris</i> is associated with higher risk of colon cancer.
<i>Bacteroides fragilis</i>	0.087%	<0.852%	This bacterium alters the immune response and control health and illness through a variety of mechanisms, such as Polysaccharide A (PSA) synthesis and the release of multiple antimicrobial proteins. <i>B. fragilis</i> has been reported to be a pathobiont and as an opportunistic pathogen outside the colon.

Note: Grey color highlighted species are Keystone specie

Firmicutes/Bacteroidetes (F/B) ratio and why that is important for your health?

The F/B for your gut profile is higher (8.293%) when compared with healthy reference cohort (0.14% - 0.76%). Your gut has more firmicutes than bacteroidetes. Increased inter-individual variance and decreased species diversity are characteristics of age-related gut dysbiosis. Increased or decreased F/B is associated with various diseases.

Condition-specific microbial markers

What is a biomarker?

The FDA defines a biomarker as a measurable characteristic to tell how the body is doing and overall health. It is a measurable indicator or characteristic that can be objectively assessed and used as a signpost for biological processes, conditions, or diseases in the body. In the context of the gut microbiome analysis, biomarkers are specific molecules, genes, or organisms found in the microbiome that can signal various aspects of gut health, disease risk, or treatment response.

Biomarkers in the gut microbiome analysis can serve several purposes:

- **Health Assessment:** Help indicate the overall health status of the gut. For instance, the presence or absence of certain bacteria or microbial metabolites can be indicative of a healthy or diseased gut environment.
- **Disease Identification:** Specific biomarkers might be linked to certain diseases or conditions. Changes in the abundance or diversity of certain microbial species could signal conditions like inflammatory bowel disease, irritable bowel syndrome, or metabolic disorders.
- **Treatment Efficacy:** Can be used to assess how the gut microbiome responds to treatments or interventions.
- **Predictive Indicators:** Serve as predictive markers, indicating an individual's susceptibility to certain diseases or response to particular treatments based on their unique gut microbial profile.

Identifying and understanding these biomarkers can provide valuable insights into gut health, disease mechanisms, and personalized approaches for improving gut-related conditions.

Microbial markers for Irritable Bowel Syndrome (IBS)

Reduced levels in these microbial markers are linked to symptoms of Irritable Bowel Syndrome (IBS).

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Faecalibacterium prausnitzii</i>	3.467%	0.003%-2.161%
<i>Bacteroides thetaiotaomicron</i>	ND	0.217%-2.636%

Increased levels in these microbial markers are linked to symptoms of Irritable Bowel Syndrome (IBS).

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Alistipes ihumii</i>	ND	<0.070%
<i>Intestinibacter bartlettii</i>	0.03%	<0.001%

Microbial markers for Inflammatory Bowel Disease (IBD)

Reduced levels in these microbial markers are linked to symptoms of Inflammatory Bowel Disease (IBD).

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Akermansia muciniphila</i>	1.669%	<0.499%
<i>Bifidobacterium longum</i>	ND	<0.039%
<i>Eubacterium rectale</i>	3.590%	0.222%-1.839%
<i>Faecalibacterium prausnitzii</i>	3.467%	0.217%-2.636%
<i>Roseburia intestinalis</i>	0.206%	<0.186%

Increased levels in these microbial markers are linked to symptoms of Inflammatory Bowel Disease (IBD)

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Bacteroides fragilis</i>	0.087%	<0.852%
<i>Escherichia coli</i>	0.001%	<0.007%
<i>Malassezia restricta</i>	ND	<0.001%
<i>Ruminococcus gnavus</i>	ND	<0.048%
<i>Ruminococcus torques</i>	0.392%	0.044%-0.452%

Microbial markers for Obesity

Reduced levels or depletion of the following microbial biomarkers have been linked to obesity.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Methanobrevibacter smithii</i>	ND	<0.001%
<i>Parabacteroides merdae</i>	1.338%	<3.145%

Increased levels of the following microbial biomarkers have been linked to obesity.

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Clostridium hylemonae</i>	ND	<0.001%
<i>Clostridium scindens</i>	ND	<0.001%

Microbial markers for cardiovascular disease

Reduced abundance in *Eubacterium rectale* and higher levels in these microbial markers are associated with cardiovascular diseases (CVD).

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Clostridioides difficile</i>	ND	<0.001%
<i>Bilophila wadsworthia</i>	0.023%	<0.047%
<i>Eubacterium rectale</i>	3.590%	0.222%-1.839%
<i>Helicobacter pylori</i>	ND	<0.001%

Microbial biomarkers for colorectal cancer (CRC)

Higher levels in these microbial markers are associated with colorectal cancer (CRC).

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Clostridium symbiosum</i>	ND	<0.001%
<i>Solobacterium moorei</i>	ND	<0.001%
<i>Fusobacterium nucleatum</i>	<0.001%	<0.001%
<i>Lachnospira eligens</i>	2.200%	<0.211%
<i>Peptostreptococcus anaerobius</i>	ND	<0.001%

Microbial markers for Acid-Reflux

Higher abundance in these microbial markers are associated with Acid reflux symptoms.

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Roseburia spp.</i>	2.295%	0.207%-1.453%
<i>Clostridium spp.</i>	3.417%	0.163%-1.353%
<i>Desulfovibrio spp.</i>	0.001%	<0.076%
<i>Eubacterium spp.</i>	0.89%	<0.001%

<i>Methanobrevibacter spp.</i>	ND	0.062%-2.531%
<i>Ruminococcus spp.</i>	9.059%	0.207%-1.453%

Microbial Markers for Mental health

Higher levels in these microbial markers are associated with mental health.

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Lactobacillaceae</i>	2.353%	<0.533%
<i>Eubacterium ventriosum</i>	0.141%	<0.076%
<i>Prevotella spp.</i>	ND	<0.067%
<i>Ruminococcus spp.</i>	9.059%	0.062%-2.531%

Microbial markers for Depression

Reduced levels or depletion of the following microbial biomarkers have been linked to depression.

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Butyricoccus spp.</i>	0.622%	0.00%-0.17%
<i>Coprococcus spp.</i>	0.35%	0.00%-3.54%
<i>Faecalibacterium spp.</i>	4.14%	0.22%-2.64%
<i>Eubacterium spp.</i>	0.89%	0.06%-0.30%
<i>Fusicatenibacter spp.</i>	1.46%	0.00%-1.15%

Higher abundance in these microbial markers is associated with depression.

Microbial marker	Relative abundance (%)	Reference IQR (%)
<i>Eggerthella spp.</i>	0.013%	0.00%-0.11%
<i>Enterococcus spp.</i>	ND	0.00%-0.01%
<i>Escherichia spp.</i>	0.001%	0.00%-0.01%
<i>Holdemania spp.</i>	0.01%	0.00%-0.08%
<i>Paraprevotella spp.</i>	ND	0.00%-3.05%
<i>Streptococcus spp.</i>	0.03%	0.00%-0.003%

Microbial markers for Lactose intolerance

Reduced levels or depletion of the following microbial biomarkers have been linked to lactose intolerance.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Lactobacillus spp.</i>	ND	<0.001%
<i>Bifidobacterium spp.</i>	1.345%	0.003%-0.157%
<i>Faecalibacterium spp.</i>	4.146%	0.317%-2.818%
<i>Roseburia Spp.</i>	2.295%	0.207%-1.453%

Higher abundance in these microbial markers is associated with lactose intolerance.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Methanobrevibacter smithii</i>	ND	<0.001%
<i>Parabacteroides merdae</i>	1.33%	0.00%-3.15%

Microbial markers for Bloating

Reduced levels or depletion of the following microbial biomarkers have been linked to bloating.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Bacteroides uniformis</i>	0.323%	1.096%-7.354%
<i>Bifidobacterium adolescentis</i>	<0.001%	<0.053%

Higher abundance in these microbial markers is associated with bloating.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Faecalibacterium prausnitzii</i>	3.467%	0.217%-2.636%
<i>Prevotella copri</i>	ND	<0.001%

Microbial markers for Gas

Reduced levels or depletion Bifidobacterium spp. and higher abundance in these microbial markers is associated with gas.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Bifidobacterium spp.</i>	1.344%	0.3%-2.24%
<i>Ruminococcus spp.</i>	9.05%	0.06%-2.53%
<i>Clostridium spp.</i>	3.14%	0.02%-1.33%
<i>Roseburias spp.</i>	2.29%	0.21%-1.45%
<i>Eubacterium spp.</i>	0.89%	0.06%-0.30%
<i>Desulfovibrio spp.</i>	0.0006%	0.00%-0.08%
<i>Methanobrevibacter spp.</i>	ND	0.00%-0.00%

Did you find any pathogens in my gut profile?

In our study of the microbiome, we looked into checking for harmful or pathogenic bacteria. These kinds of bacteria can make you sick, leading to stomach problems like gastroenteritis or other sudden digestive issues.

<i>Microbial marker</i>	<i>Relative abundance (%)</i>	<i>Reference IQR (%)</i>
<i>Salmonella</i>	ND	ND
<i>Vibrio cholerae</i>	ND	ND
<i>Campylobacter</i>	ND	0.00%-0.00%
<i>Clostridioides difficile</i>	ND	0.00%-0.00%
<i>Cryptosporidium</i>	ND	ND
<i>Entamoeba histolytica</i>	ND	ND
<i>Giardia</i>	ND	ND
<i>Yersinia enterocolitica</i>	ND	ND

Overall lifestyle recommendations

Taking care of our gut involves fostering an environment where beneficial bacteria thrive while keeping harmful ones in check. Making small but impactful lifestyle changes can significantly enhance the diversity and health of our gut microbiome. Here are some recommendations along with practical tips to help improve your gut health.

Lifestyle Recommendations:

- **Diverse Diet:** Enjoy a range of foods rich in fiber like fruits, veggies, whole grains, legumes, and nuts. Try to include various colors on your plate to get a mix of nutrients.
- **Prebiotic Foods:** Eat foods such as onions, garlic, leeks, bananas, and oats that contain prebiotics, fuel for good gut bacteria.
- **Probiotic Foods:** Incorporate yogurt, kefir, kimchi, sauerkraut, and miso into your meals for live bacteria that promote a healthy gut.
- **Limit Sugar and Processed Foods:** Reduce intake of sugary and highly processed foods to avoid feeding harmful bacteria in your gut.
- **Stay Hydrated:** Drink plenty of water throughout the day to support overall gut function.
- **Manage Stress:** Practice stress-reduction techniques like meditation or deep breathing to positively impact gut health.
- **Adequate Sleep:** Ensure you get enough quality sleep each night for a healthy gut and well-being.
- **Regular Exercise:** Engage in physical activity regularly to promote gut health and diversity of gut bacteria.
- **Limit Antibiotics Use:** Only take antibiotics as prescribed by a healthcare professional to avoid disturbing the balance of gut bacteria.
- **Avoid Smoking and Excessive Alcohol:** Minimize smoking and excessive alcohol consumption to protect and nurture your gut microbiome.

By embracing these simple yet effective lifestyle adjustments, you can cultivate an environment in your gut that encourages the growth of beneficial bacteria, ultimately supporting a healthier gut and overall well-being.

References

