Biron B

Test Microbiome Test

Your balance from the inside out

The Microbiome Test Essential identifies all bacteria present in an individual's microbiome down to the strain level. Bacterial abundances are evaluated using well-established indices such as diversity and enterotypes, and assessed for their beneficial or detrimental effects on host health. The presence of bacteria that may negatively impact both intestinal and systemic health—such as potentially harmful groups like Fusobacteria and Proteobacteria—is highlighted. Additionally, the report includes a section examining the abundance of bacteria involved in the metabolism of specific nutrients.

Biron B

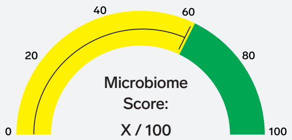
Test
Microbiome
Test

How to Read This Report

The Microbiome Test Essential report, while comprehensive, is designed for easy navigation. Page 1 provides an “at-a-glance” summary, allowing quick identification of any microbiome issues that may warrant further investigation.

Page 1

Example



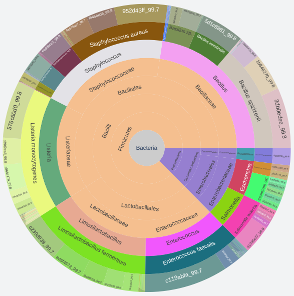
Summary: Low Microbiome Score. Focus on flagged areas.

Resistome: Poor. High load of antibiotic resistant bacteria suggests recent or historic high antibiotic use.

Pathogens: X.XX%
Proteobacteria: X.X%
Fusobacteria: X.X%

Review: X/24 areas. **Worst:** } Beta Diversity

Learn More: See “How To Use This Report” below.



Microbiome Score: A score below 60 means there are known issues with the bacterial composition of the microbiome. The score is calculated based on measures of fundamental microbiome metrics consistent across populations using our proprietary algorithm. Those include microbiome diversity, richness, evenness, Firmicutes/Bacteroidetes ratio, total percentages of pathogens, resistome and top 10 species.

Resistome: Indicates tendency to carry bacteria with antibiotic-resistant genes.

Pathogens, Proteobacteria, Fusobacteria: Percentages should be as low as possible. Some fusobacteria are associated with food poisoning and a wide range of cancers.

Review: Indicates the number of areas, out of the 24 assessed, that differ significantly from the reference population.

Worst: Highlights the metric element that is the biggest negative contributor to the overall score.

Target Plot: A visualization of the entire bacterial content of the microbiome, down to strain level. A variety of colors in the plot represents a healthier microbiome. An overabundance of a single bacterium, or a few bacteria overall, indicates improvements can be made.

Page 2 and Beyond

From more detailed sections, specific areas are flagged for your attention, along with some comments and advice.

Understanding the Flags in Your Report:

Yellow Exclamation Marks (Left Side): Indicate that your microbiome shows unusual patterns in that specific area. They help you focus on the most important parts of your report.

High **Flags in Species Tables (“High” or “Low”):** Point out specific species or groups in your microbiome that are outside the normal range. Even if the overall analysis of a section appears normal, individual species that fall out of range are flagged as a caution. These details may still be important and relevant.

1. **Microbiome Scoring Factors:** Represents overall gut health.
2. **Beneficial Bacteria:** Represents overall gut health.
3. **Gut Systems Bacterial Groups:** Information on bacteria associated with certain diseases and syndromes. i.e., This section provides a window into the microbial content to determine whether any bacteria in the sample may be associated with some GI conditions* (IBS, SIBO, IBD). Bile Acids, Trimethylamine (TMA), and Lipopolysaccharide (LPS) production can have downstream effects on wide-ranging health effects, including inflammation, metabolic syndrome, cholesterol metabolism, heart disease, atherosclerosis, and autoimmune response. Levels of these bacteria can be altered by diet.
4. **Nutrient & Dietary Component Metabolism:** This information can provide insight into food sensitivity and how diet can affect general health.

Additional Information Section: Provides context to help better understand each test result and the corresponding recommendations in greater detail.

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*IBS (Irritable Bowel Syndrome), SIBO (Small Intestinal Bacterial Overgrowth), IBD (Inflammatory Bowel Disease)

Report
Accession Number: NA
Order Number: NA
Barcode: NA
Report Generated: timestamp_test

Sample
NFN NLN
DOB: NA
Sample Collected: NA

Microbiome Test Essential

✓

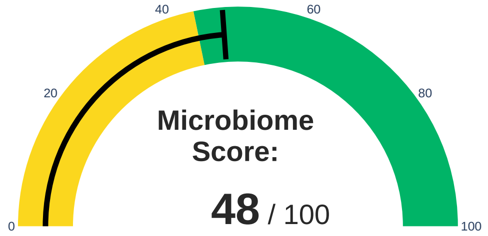
Summary: Low Microbiome Score. Focus on flagged areas.

Resistome: Good. Low load of antibiotic resistant bacteria suggests limited recent antibiotic use.

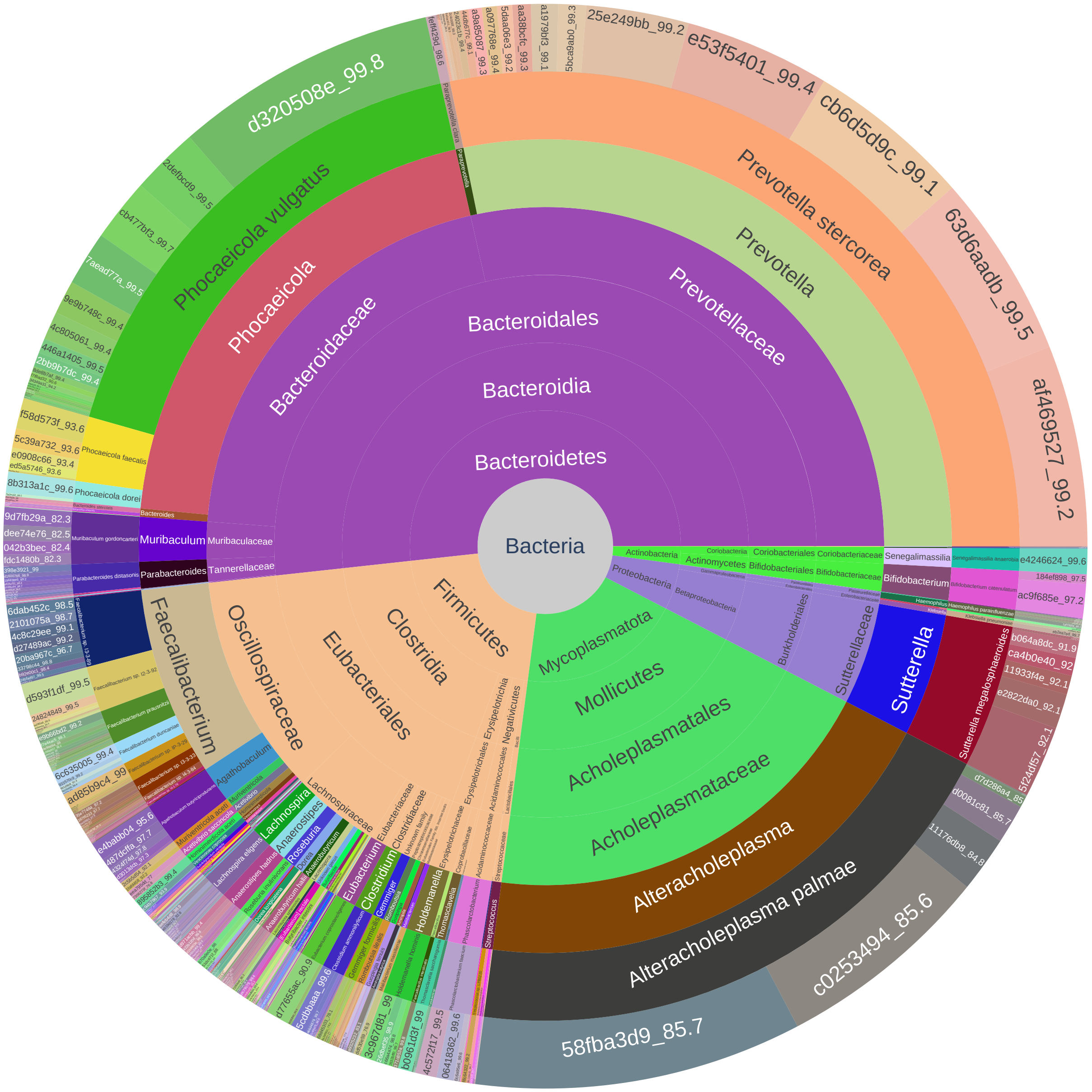
Pathogens: 0.31% **Proteobacteria:** 5.46% **Fusobacteria:** 0.03%

Review: 6 / 27 areas. **Worst: Mycoplasmatota**

Learn More: See "How To Use This Report" below.



Target Plot: Microbiome data visualization. More colors typically correlate with microbiome diversity and healthier microbiomes.



Microbiome Scoring Factors

- ☑ Resilience
- ☑ Richness
- ☑ Evenness
- ☑ Beta Diversity
- ⚠ Firmicutes/Bacteroidetes (F/B) Ratio
- ⚠ Fusobacteria
- ☑ Antibiotic Resistome Score
- ☑ Enterotype
- ☑ Pathogens
- ☑ Proteobacteria
- ☑ Top 10 Species

Summary:

Imbalance of bacterial distribution. Proteobacteria, Fusobacteria, Pathogens, or Mycoplasma out of typical range. Enterotype 2 - Prevotella.

Suggestions:

- Biodiversity: Increase consumption of dietary fiber, fermented foods, polyphenols (powerful antioxidants found in fruits, vegetables, and whole grains), nuts, and seeds. Decrease sugars, animal-derived saturated fats, and artificial sweeteners. Maintain healthy weight (Body Mass Index).
- Pathogens: Increase anti-inflammatory foods and polyphenols. Decrease sugars, saturated fat, alcohol. See Pathogens, Fusobacteria, Proteobacteria, Mycoplasma sections to check overall abundance or individual species out of range.

Beneficial Bacteria

- ☑ Probiotics
- ☑ Mucosa Protection
- ☑ Short-Chain Fatty Acids (SCFAs) Production

Summary:

Within typical range. Low Lactobacillus spp. Low Akkermansia muciniphila.

Suggestions:

- Lactobacillus: Consider supplementing Lactobacillus with targeted probiotic.
- Akkermansia: Increase intake of FOS and polyphenols. Decrease animal-derived saturated fat, alcohol. Consider Akkermansia supplementation in case of metabolic disorder(s).

Gut Systems Bacterial Groups

- ⚠ Irritable Bowel Syndrome (IBS)
- ☑ Small Intestinal Bacterial Overgrowth (SIBO)
- ☑ Inflammatory Bowel Disease (IBD)
- ☑ Bile Acids (BAs) Metabolism
- ☑ Trimethylamine (TMA) Production
- ☑ Lipopolysaccharide (LPS) Production

Summary:

Imbalances detected in bacteria associated with: IBS.

Suggestions:

- IBS: Rebalance abundance of bacteria associated with IBS. Pay particular attention to pathobionts and the top 10 bacteria. BAs-metabolizing and SIBO-associated bacteria may also be out of range. Consider also the bacteria associated with serotonin and histamine production and metabolism. Check sensitivity to FODMAP. Whenever necessary, consider the use of probiotics (refer to the probiotic abundance table to better tailor the treatment to individual needs). Diarrhea-dominant IBS may be relieved by Clostridum butyricum, Bacillus coagulans, and Saccharomyces boulardii, while constipation-dominant IBS may be relieved by Bifidobacterium lactis. Lactobacillus plantarum may improve gas and bloating. Select supplements based on the area most affected (BAs metabolizers, SIBO-associated, etc.).

Nutrient and Dietary Component Metabolism

- ☑ FODMAP Sensitivity Score
- ☑ FODMAP Fermentation
- ☑ Indole Production
- ☑ Vitamin B Production

Summary:

Within typical range.

Microbiome Scoring Factors

☑ Resilience

Index of a microbiome’s resilience and diverse composition, also known as Shannon Index. Higher values are generally associated with better resilience potential.

Value:
13.73

Typical Range:
6.22 - 12.44

☑ Richness

Index referring to the number of unique species present within a sample.

Value:
90.00

Typical Range:
32.00 - 64.00

☑ Evenness

Index referring to the distribution of species identified in a microbiome sample. Values closer to 1 indicate a more desirable, even distribution.

Value:
0.58

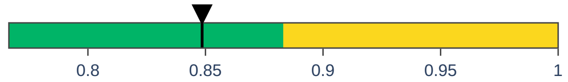
Typical Range:
0.51 - 1.00

☑ Beta Diversity

Index quantifying how different a microbial community is to the reference population, with values closer to 0 representing more similarity.

Value:
0.85

Typical Range:
0.77 - 0.88

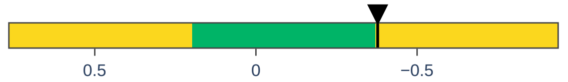


⚠ Firmicutes/Bacteroidetes (F/B) Ratio

Negative scores correspond to Bacteroidetes dominance, and positive scores correspond to Firmicutes dominance. A balanced F/B ratio is associated with intestinal homeostasis.

Value:
-0.38

Typical Range:
-0.37 - 0.20



⚠ Fusobacteria

Bacterial species that may become opportunistic pathogens, most commonly found in the mouth. If detected in the gut, they may be associated with intestinal inflammation, IBS, IBD and chronic diseases.

Value:
0.03

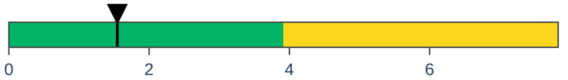
Typical Range:
0.00 - 0.02

☑ Antibiotic Resistome Score

This score includes the number and types of bacteria that are likely to contain antibiotic-resistant genes, which may play a role in spreading antibiotic resistance. It is important to note that this indicator compares the relative abundance of species associated with antibiotic-resistant genes and does not sequence these genes directly.

Value:
1.55

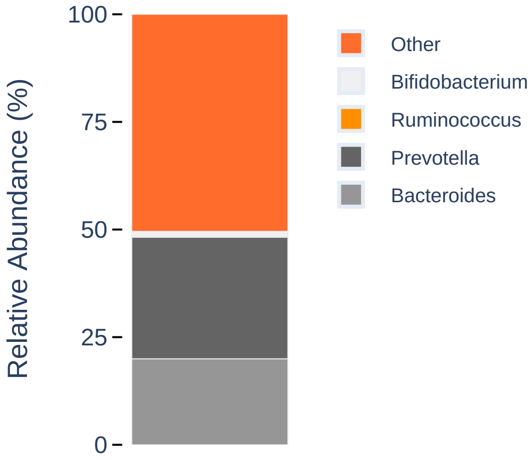
Typical Range:
0.00 - 3.92



Enterotype

In microbiome research, enterotypes serve as a classification method for identifying metabolically significant microbial species that tend to be more prevalent. Bacteroides (Type 1) is most common in diets that include significant quantities of protein and animal fat, while Prevotella (Type 2) is typically associated with plant-based diets with a lower emphasis on vegetable fiber, with more plants that are rich in carbohydrates and simple sugars. Ruminococcus (Type 3) is most common in higher fiber vegetable-based diets rich in complex carbohydrates, fruits, and vegetables. Bifidobacterium (Type 4) is more common in children, although its metabolic significance is unclear. Your enterotype usually reflects your long-term diet and may not accurately represent your current diet, especially if you have made recent changes.

Value:
Prevotella



Pathogens

Bacterial species that may cause severe gastrointestinal symptoms and be associated with intestinal or systemic chronic illnesses.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		0.31	0.0 - 9.92	
	Klebsiella pneumoniae	0.21	0 - 0.01	high
	Escherichia coli	0.07	0 - 3.26	
	Streptococcus parasanguinis	0.02	0	high

Proteobacteria

Bacterial species that may exhibit toxic and pathogenic mechanisms of action including lipopolysaccharide (LPS) and endotoxin synthesis and promote gastrointestinal and systemic inflammation. They are strongly associated with IBS, SIBO, IBD and immune dysregulation.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		5.46	0.26 - 15.74	
	Sutterella megalosphaeroides	4.87	0 - 0.22	high
	Haemophilus parainfluenzae	0.28	0	high
	Klebsiella pneumoniae	0.21	0 - 0.01	high
	Escherichia coli	0.07	0 - 3.26	
	Cohaesibacter haloalkalitolerans	0.03	0	high

Top 10 Species

An indication of the overall composition of your microbiome can be obtained from a list of the ten most abundant species. The F/B ratio, enterotype, and alpha diversity index alone cannot determine which species are overabundant. A review of the top 10 can very quickly reveal the presence of potential pathobionts or an overabundance of certain species.

Species	Relative Abundance (%)	Reference Range (%)	Flag
Prevotella stercorea	28.23	0.07 - 6.48	high
Alteracholeplasma palmae	19.48	0.19 - 16.51	high
Phocaeicola vulgatus	17.05	1.52 - 51.3	
Sutterella megalosphaeroides	4.87	0 - 0.22	high
Faecalibacterium sp. I3-3-89	2.37	0.06 - 2.12	high
Phocaeicola faecalis	2.20	0.3 - 12.07	
Muribaculum gordoncarteri	1.77	0.11 - 5.44	
Faecalibacterium sp. I2-3-92	1.56	0.07 - 2.47	
Agathobaculum butyriciproducens	1.42	0.02 - 0.57	high
Phascolarctobacterium faecium	1.34	0.54 - 8.91	

Beneficial Bacteria

☑ Probiotics

Well-characterized bacterial species and strains that can either be ingested via supplements and/or foods or occur naturally in the human gut.

Probiotic	Species	Relative Abundance (%)	Reference Range (%)	Flag
Other	Overall	0.0	0.01 - 8.09	low
Akkermansia	Overall	0.0	0.11 - 25.68	low
Lactobacillus	Overall	0.0	0.02 - 2.6	low
Bifidobacterium	Overall	1.31	0.27 - 52.27	
Bifidobacterium	Bifidobacterium catenulatum	1.31	0.07 - 5.02	
Akkermansia, Lactobacillus, Other	None detected			

☑ Mucosa Protection

Bacterial species that support normal gut barrier function. Abnormally low or high levels of these bacteria may lead to alterations in the intestinal mucosa and be associated with inflammation and immune dysregulation.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		1.17	0.35 - 15.77	
	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	

☑ Short-Chain Fatty Acids (SCFAs) Production

Anaerobic gut bacteria producing SCFAs such as acetate, propionate, and butyrate, which play a crucial role in maintaining gut and systemic health. A balanced presence of SCFA-producing bacteria is strongly associated with decreased inflammation, reduced risk of disease, and improved immune and metabolic function.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		2.90	1.56 - 50.15	
	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	
	Anaerostipes hadrus	0.76	0.04 - 1.25	
	Anaerobutyricum hallii	0.38	0.03 - 0.88	
	Roseburia inulinivorans	0.38	0.06 - 3.16	
	Roseburia intestinalis	0.11	0.05 - 1.42	
	Ruminococcus bromii	0.07	0.1 - 4.71	low
	Roseburia hominis	0.04	0.03 - 0.51	

Gut Systems Bacterial Groups

⚠ Irritable Bowel Syndrome (IBS)

Various types of bacteria and their metabolites may alter intestinal motility and affect the perception of visceral pain. It is possible that IBS symptoms are positively affected by adjusting the abundance and distribution of these bacteria. The composition of the intestinal bacterial population is critically important in cases of post-infectious IBS. Note that IBS is not always caused by gastrointestinal or systemic infection, it is possible to experience IBS symptoms without unusual microbiome composition.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		45.17	6.71 - 61.16	
	Prevotella stercorea	28.23	0.07 - 6.48	high
	Sutterella megalosphaeroides	4.87	0 - 0.22	high
	Faecalibacterium sp. I3-3-89	2.37	0.06 - 2.12	high
	Faecalibacterium sp. I2-3-92	1.56	0.07 - 2.47	
	Bifidobacterium catenulatum	1.31	0.07 - 5.02	
	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	
	Holdemanella hominis	0.99	0.3 - 18.4	
	Anaerostipes hadrus	0.76	0.04 - 1.25	
	Faecalibacterium duncaniae	0.75	0.06 - 1.47	
	Faecalibacterium sp. IP-3-29	0.65	0.09 - 2.32	
	Faecalibacterium sp. I3-3-33	0.63	0.07 - 3.07	
	Anaerobutyricum hallii	0.38	0.03 - 0.88	
	Paraprevotella clara	0.32	0.12 - 3.56	
	Dorea longicatena	0.23	0.02 - 0.48	
	Faecalibacterium sp. I4-3-84	0.22	0.1 - 3.95	
	Faecalibacillus intestinalis	0.17	0.04 - 5.17	
	Subdoligranulum variabile	0.14	0.08 - 2.46	
	Faecalibacterium sp. I4-1-79	0.13	0.06 - 2.78	
	Dorea phocaeensis	0.10	0.03 - 1.53	
	Ruminococcus bromii	0.07	0.1 - 4.71	low
	Dorea formicigenerans	0.06	0.02 - 0.32	
	Blautia obeum	0.03	0.02 - 0.57	
	Faecalibacterium sp. IP-1-18	0.03	0.06 - 2.69	low
	Faecalibacterium sp. HTF-F	0.02	0.04 - 1.32	low
Detrimental species		0.07	0.03 - 11.92	
	Escherichia coli	0.07	0 - 3.26	
Overall species balance		45.09	5.05 - 59.0	

☑ Small Intestinal Bacterial Overgrowth (SIBO)

This test identifies specific bacteria that are typically observed in the aspirates obtained from the duodenum or jejunum of patients suffering from SIBO. It is important to note that this test does not diagnose SIBO. An abnormal abundance of these bacteria in the colon and in the stool may suggest SIBO and warrant follow-up testing to confirm. Archaea causing Intestinal Methanogen Overgrowth (IMO) are not included.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		1.03	0.38 - 16.63	
	Klebsiella pneumoniae	0.21	0 - 0.01	high
	Bacteroides stercoris	0.19	0.05 - 2.35	
	Streptococcus sp. LPB0220	0.16	0.02 - 1.22	
	Streptococcus thermophilus	0.10	0.02 - 2.0	
	Bacteroides uniformis	0.10	0.07 - 2.19	
	Streptococcus salivarius	0.08	0.03 - 4.54	
	Escherichia coli	0.07	0 - 3.26	
	Streptococcus viridans	0.05	0.03 - 0.32	
	Streptococcus parasanguinis	0.02	0	high
	Bacteroides ovatus	0.02	0.03 - 1.15	
	Bacteroides xylanisolvens	0.02	0.03 - 0.87	

☑ Inflammatory Bowel Disease (IBD)

There is evidence that changes to the gut microbiome can occur before the onset of an IBD flare-up, and may be correlated with the severity and duration of symptoms during all phases of the disease. Intestinal bacteria and their metabolites may affect the intestinal epithelial barrier and mucosa health, inducing immune activation and inflammation. The subsequent increased intestinal permeability (IP) sustains the inflammatory responses and favors pathogens invasion.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		21.13	6.67 - 58.11	
	Sutterella megalosphaeroides	4.87	0 - 0.22	high
	Faecalibacterium sp. I3-3-89	2.37	0.06 - 2.12	high
	Faecalibacterium sp. I2-3-92	1.56	0.07 - 2.47	
	Agathobaculum butyriciproducens	1.42	0.02 - 0.57	high
	Bifidobacterium catenulatum	1.31	0.07 - 5.02	
	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	
	Lachnospira eligens	0.84	0.04 - 0.88	
	Anaerostipes hadrus	0.76	0.04 - 1.25	
	Faecalibacterium duncaniae	0.75	0.06 - 1.47	
	Faecalibacterium sp. IP-3-29	0.65	0.09 - 2.32	
	Faecalibacterium sp. I3-3-33	0.63	0.07 - 3.07	
	Anaerobutyricum hallii	0.38	0.03 - 0.88	
	Roseburia inulinivorans	0.38	0.06 - 3.16	
	Muriventricola aceti	0.35	0.02 - 0.18	high
	Acetivibrio saccincola	0.31	0.04 - 2.88	
	Hominimerdicola aceti	0.28	0.06 - 9.02	
	Butyribacter intestini	0.23	0.02 - 0.19	high
	Dorea longicatena	0.23	0.02 - 0.48	
	[Eubacterium] rectale	0.23	0.03 - 0.56	
	Faecalibacterium sp. I4-3-84	0.22	0.1 - 3.95	
	Vescimonas coprocola	0.19	0.06 - 1.46	
	Bacteroides stercoris	0.19	0.05 - 2.35	
	Lacrimispora sphenoides	0.18	0.01 - 0.07	high
	Subdoligranulum variabile	0.14	0.08 - 2.46	
	[Ruminococcus] lactaris	0.13	0.02 - 0.65	
	Faecalibacterium sp. I4-1-79	0.13	0.06 - 2.78	
	Lachnoclostridium edouardi	0.11	0.01 - 0.05	high
	Roseburia intestinalis	0.11	0.05 - 1.42	
	Dorea phocaeensis	0.10	0.03 - 1.53	
	Bacteroides uniformis	0.10	0.07 - 2.19	
	Anaerotignum faecicola	0.09	0.02 - 0.14	
	Dysosmobacter sp. Marseille-Q4140	0.09	0.03 - 0.56	
	Lacrimispora xylanolytica	0.08	0.01 - 0.12	
	Dorea formicigenerans	0.06	0.02 - 0.32	
	Pusillibacter faecalis	0.06	0.02 - 0.65	
	Laedolimicola ammoniilytica	0.05	0.01 - 0.06	
	Neglectibacter timonensis	0.05	0.03 - 0.72	
	Coprococcus comes	0.04	0.02 - 0.18	
	Roseburia hominis	0.04	0.03 - 0.51	
	Blautia obeum	0.03	0.02 - 0.57	
	[Clostridium] symbiosum	0.03	0.01 - 0.13	
	Faecalibacterium sp. IP-1-18	0.03	0.06 - 2.69	low
	Fournierella massiliensis	0.03	0.05 - 0.55	low
	[Eubacterium] siraeum	0.03	0.04 - 2.23	low
	Anaerocolumna cellulosilytica	0.02	0.03 - 2.99	low
	Anaeromicropila herbilytica	0.02	0.02 - 0.27	
	Faecalibacterium sp. HTF-F	0.02	0.04 - 1.32	low
	Oscillibacter acetigenes	0.02	0.03 - 0.66	low
	Bacteroides ovatus	0.02	0.03 - 1.15	low
	Bacteroides xylanisolvens	0.02	0.03 - 0.87	low
Detrimental species		0.72	0.89 - 26.73	
	Haemophilus parainfluenzae	0.28	0	high
	Klebsiella pneumoniae	0.21	0 - 0.01	high
	Ruminococcus bromii	0.07	0.1 - 4.71	
	Escherichia coli	0.07	0 - 3.26	
	Veillonella nakazawae	0.04	0.02 - 0.52	
	Fusobacterium pseudoperiodonticum	0.03	0	high

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
	Cohaesibacter haloalkalitolerans	0.03	0	high
Overall species balance		20.41	-11.85 - 49.18	

☑ Bile Acids (BAs) Metabolism

The abundance of BAs-metabolizing bacteria can negatively affect symptoms in IBS and IBD, particularly when increasing intestinal motility in patients with IBS-D. Clostridium spp and their metabolites can upregulate BAs secretion. Secondary BAs, however, usually exert an anti-inflammatory effect. Therefore, balancing the abundance and type of BAs-metabolizing bacteria may help address motility, mucosal, and inflammatory issues. Note: the abundance of BAs-metabolizing bacteria should also be considered in several other conditions such as obesity, metabolic syndrome and neurodegenerative disorders.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Overall		21.89	6.33 - 66.16	
	Phocaeicola vulgatus	17.05	1.52 - 51.3	
	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	
	Parabacteroides distasonis	0.99	0.08 - 3.17	
	Lachnospira eligens	0.84	0.04 - 0.88	
	Phocaeicola dorei	0.72	0.08 - 42.48	
	Dorea longicatena	0.23	0.02 - 0.48	
	Bacteroides stercoris	0.19	0.05 - 2.35	
	Subdoligranulum variabile	0.14	0.08 - 2.46	
	[Ruminococcus] lactaris	0.13	0.02 - 0.65	
	Roseburia intestinalis	0.11	0.05 - 1.42	
	Bacteroides uniformis	0.10	0.07 - 2.19	
	Dorea formicigenerans	0.06	0.02 - 0.32	
	Parabacteroides merdae	0.06	0.05 - 0.7	
	Coprococcus comes	0.04	0.02 - 0.18	
	[Clostridium] symbiosum	0.03	0.01 - 0.13	
	Bacteroides ovatus	0.02	0.03 - 1.15	low
	Bacteroides xylanisolvens	0.02	0.03 - 0.87	low

☑ Trimethylamine (TMA) Production

Trimethylamine (TMA) is synthesized by gut bacteria such as Desulfovibrio, Proteobacteria, Clostridium etc. This molecule is produced by the intestinal bacterial transformation of dietary choline, L-carnitine and betaine. When formed in the gut, TMA is transported to the liver through the portal vein and oxidized into TMAO. The level of TMAO is considered an independent risk factor and predictor of cardiovascular diseases. TMAO can alter cholesterol metabolism and induce inflammation, platelet activation and endothelial dysfunction.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		1.01	0.08 - 9.76	
	Clostridium ammoniilyticum	0.77	0.08 - 8.99	
	Klebsiella pneumoniae	0.21	0 - 0.01	high
	Clostridium nigeriense	0.03	0.03 - 1.22	

☑ Lipopolysaccharide (LPS) Production

The cell surface of most Gram-negative bacteria, such as Proteobacteria, contains LPS. In some cases, this glycolipid can even lead to a toxic reaction from the host due to its strong ability to elicit an immune response. Therefore, LPS is also referred to as an "endotoxin". Although the immune system must recognize LPS and mount a prompt response, a chronic or excessive immune activation is detrimental to the host. LPS-induced inflammation may increase intestinal and blood-brain-barrier permeability and trigger significant inflammatory and pro-oxidative reactions.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		5.15	0.11 - 15.33	
	Sutterella megalosphaeroides	4.87	0 - 0.22	high
	Klebsiella pneumoniae	0.21	0 - 0.01	high
	Escherichia coli	0.07	0 - 3.26	

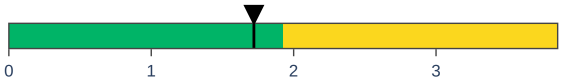
Nutrient and Dietary Component Metabolism

☑ FODMAP Sensitivity Score

This score assesses the potential response to foods high in FODMAP (fermentable oligosaccharides, disaccharides, monosaccharides, and polyols) such as high fructose corn syrup, fruit juices, and some dairy products. An excessive representation of certain bacterial taxa and altered population dynamics may cause an increased sensitivity to foods high in FODMAPs as compared to the general population.

Value:
1.72

Typical Range:
0.00 - 1.93



☑ FODMAP Fermentation

This list includes bacteria fermenting FODMAPs that create common undesirable symptoms. It is possible for the same species to ferment more than one type of FODMAP. Use this list to identify foods that are more likely to be problematic, but don't exclude entire categories of foods based on it.

Type of FODMAP	Species	Relative Abundance (%)	Reference Range (%)	Flag
FOS	Overall	3.21	1.81 - 50.61	
GOS	Overall	1.39	0.21 - 49.61	
Inulin	Overall	4.09	1.58 - 47.51	
Isomalt	Overall	1.79	0.22 - 49.88	
Lactose	Overall	1.31	0.25 - 50.59	
Xylitol	Overall	0.0	0.02 - 0.1	
Fructose	Overall	2.47	0.69 - 47.38	
Maltitol	Overall	1.31	0.25 - 50.59	
Mannitol	Overall	0.42	0.04 - 5.47	
Sorbitol	Overall	0.07	0.04 - 11.91	
FOS	Bacteroides stercoris	0.19	0.05 - 2.35	
	Bacteroides xylanisolvens	0.02	0.03 - 0.87	low
	Bacteroides ovatus	0.02	0.03 - 1.15	low
Inulin	Anaerostipes hadrus	0.76	0.04 - 1.25	
	Roseburia inulinivorans	0.38	0.06 - 3.16	
	Roseburia hominis	0.04	0.03 - 0.51	
FOS, Inulin	Dorea longicatena	0.23	0.02 - 0.48	
	Roseburia intestinalis	0.11	0.05 - 1.42	
	Bacteroides uniformis	0.1	0.07 - 2.19	
Isomalt, Mannitol	Streptococcus sp. LPB0220	0.16	0.02 - 1.22	
	Streptococcus thermophilus	0.1	0.02 - 2.0	
	Streptococcus viridans	0.05	0.03 - 0.32	
	Streptococcus parasanguinis	0.02	0	high
FOS, Fructose, Inulin	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	
FOS, Isomalt, Sorbitol	Escherichia coli	0.07	0 - 3.26	
GOS, Isomalt, Mannitol	Streptococcus salivarius	0.08	0.03 - 4.54	
FOS, Fructose, GOS, Inulin, Isomalt, Lactose, Maltitol	Bifidobacterium catenulatum	1.31	0.07 - 5.02	
Xylitol	None detected			

☑ Indole Production

Indole produced by the bacterial metabolism of dietary tryptophan may have beneficial effects on intestinal mucosa and barrier functions. However, an excess of some indole-derived compounds (especially indoxyl sulfate) may have detrimental effects on kidney and intestinal cells. Additionally, indole and its metabolites may negatively affect behavior and brain function.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		2.24	0.6 - 46.15	
	Parabacteroides distasonis	0.99	0.08 - 3.17	
	Clostridium ammoniilyticum	0.77	0.08 - 8.99	
	Anaerobutyricum hallii	0.38	0.03 - 0.88	
	Escherichia coli	0.07	0 - 3.26	
	Clostridium nigeriense	0.03	0.03 - 1.22	

☑ Vitamin B Production

Although vitamins produced in the gut are not a significant contributor to the host’s nutritional needs, they can affect colon health and immune function. This list is not intended to identify vitamin deficiencies or suboptimal intake, but to rebalance bacteria associated with their metabolism.

Type of Vitamin B	Species	Relative Abundance (%)	Reference Range (%)	Flag
1	Overall	0.13	0.04 - 26.9	
2	Overall	0.13	0.04 - 24.74	
3	Overall	0.13	0.04 - 28.1	
5	Overall	0.13	0.04 - 24.64	
6	Overall	0.0	0.21 - 57.14	low
7	Overall	0.0	0.04 - 14.38	low
9	Overall	0.1	0.07 - 24.42	
12	Overall	1.29	0.58 - 51.99	
9	Streptococcus thermophilus	0.1	0.02 - 2.0	
12	Faecalibacterium prausnitzii	1.17	0.21 - 6.49	
1, 2, 3, 5, 12	[Ruminococcus] lactaris	0.13	0.02 - 0.65	
6, 7	None detected			

Quality Metrics

☑ **Sequencing Quality Control**

This sample exceeds the minimum quality control standard of 10,000 sequencing reads per sample.

Processing Lab Director

Report Authorized By:

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Additional Information

Drug and Supplement Impact Table

Drug/Supplement	Main effects
Metformin hydrochloride	**Gut microbiota modulation:** increased abundance of *Akkermansia*, *Bacteroides* (especially *B. intestinalis*, *B. vulgatus*, and *B. acidifaciens), Parabacteroides*, *Escherichia coli*, *Bifidobacterium adolescentis*, Subdoligranulum.
Proton Pump Inhibitors	**Altered microbiota:** increased abundance of *Bifidobacterium dentium*, *Streptococcus* (especially *S.mutans*, *S. salivarius*, *S. parasanguinis*, *S. vestibularis*), *Veillonella parvula*. Increased risk of SIBO (increased abundance of *Streptococcus*, *Clostridium*, *Escherichia*, *Klebsiella* in small intestine). Increased risk of *C.difficile*, *Salmonella*, *Shigella* and *Campylobacter* infection. Increased abundance of oral bacteria in stool (i.e., *Fusobacterium nucleatum*).
Rifaximin	**Gut microbiota modulation:** overall eubiotic effect, increased abundance of *Bifidobacterium*, *Faecalibacterium prausnitzii and Lactobacillus,* decreased *C. difficile*
Statins	**Altered microbiota:** likely decreased diversity. They may cause increased abundance of *Akkermansia* and *F. prausnitzii*. Possible disturbances in SCFAs producing and BAs metabolizing bacteria. More human studies are needed.
L-thyroxine	**Altered microbiota:** likely contributor to SIBO. Possible alterations in abundance of *Odoribacter* and *Enterococcus* species (dose-dependent effect: higher abundance with medium dose, lower abundance with high dose of medication). *Alistipes*, *Ruminococcus* and *Anaerotruncus* species may result out of typical ranges.
Metronidazole	**Altered microbiota:** likely increased abundance of *Bifidobacterium* (especially *B. pseudolongum*) and *Enterobacteria*.
Selective Serotonin Reuptake Inhibitors	**Altered microbiota:** increased abundance of *Eubacterium ramulus*. SSRIs in general have an antimicrobial effect. Long-term use may cause dysbiosis.
Fructooligosaccharides	**Gut microbiota modulation:** increased abundance of *Bifidobacterium* and *F. prausnitzii*, decreased Proteobacteria.
Resveratrol	**Gut microbiota modulation:** inhibition of *E. coli* growth, *Enterococcus faecalis*. Increased abundance of *Bifidobacterium* and *Lactobacillus*.
Berberine chloride	**Gut microbiota modulation:** possible increased abundance of *Akkermansia* and SCFAs-producing bacteria in general. Decreased *Clostridium* spp*,* inhibition of *E. coli* growth. Microbiota conversion into dihydroberberine.

Food and Nutrient Impact Table

Foods, nutrients, diets	Main effects
Fibers	**Gut microbiota modulation:** in general, microbiota accessible carbohydrates (MAC) may increase microbial diversity and distribution as well as improve short chain fatty acid (SCFA) production by bacterial fermentation. Low abundance of beneficial species such as *Akkermansia* and/or *Bifidobacterium* may indicate an inadequate fiber intake. However, excess fiber intake, especially those high in FODMAPs may cause microbiota imbalances and exacerbate gastrointestinal symptoms such as gas, bloating, and abdominal pain. Extremely high fiber intake may decrease the absorption of key nutrients. Additionally, different types of fiber may promote specific modifications to intestinal bacterial composition: **-Inulin** (ex: dandelion greens, asparagus, onions, leeks, bananas, whole wheat) may increase *Bifidobacterium* spp, especially *B. bifidum* and *F. prausnitzii* **-Beta-glucans** (ex: oats, barley) may increase *Bifidobacterium*, *Ruminococcus*, *Prevotella*, *Roseburia* hominis, and other butyrate-producing bacteria as well as decrease *Fusobacteria* and *Clostridium* spp **-Resistant Starch** (ex: green banana, legumes, and potatoes, rice, and pasta that has been cooked and then cooled) may increase *Bifidobacterium* spp, *Ruminococcus bromii*, and *F. prausnitzii*
Polyphenols	**Gut microbiota modulation:** Polyphenols are metabolized by gut bacteria to positively affect microbiota composition, diversity, and distribution. Sources of polyphenols include berries, dark chocolate and pure cocoa powder, olives, extra virgin olive oil, green tea, black coffee, nuts, peanuts, seeds, and red wine. Adequate polyphenol intake may decrease the abundance of potential pathogens such as *Clostridium* spp and *E. coli*, promote LPS-induced inflammation, restore *Lactobacillus* and *Bifidobacterium* population, rebalance the F/B ratio, and increase mucosa protective bacteria such as *Akkermansia* and *F. prausnitzii*.
Nuts and seeds	**Gut microbiota modulation**: Nuts contain fiber, polyphenols, and healthy monounsaturated fatty acids (MUFAs) and act as a prebiotic that may promote a beneficial bacterial population. Adequate nut and seed intake is associated with improved bacterial diversity, reduced inflammation, and increased butyrate production. Almonds specifically have been shown to increase alpha diversity.
Fermented foods	**Gut microbiota modulation:** Consumption of fermented foods may lead to increased microbiome diversity and have a stronger effect than fiber alone. Additionally, adequate intake of fermented foods is associated with increased probiotic abundance, reduced inflammation, and improved microbiota-related immune function. Examples of fermented foods and specific modifications to bacterial composition and gastrointestinal function include: **-Kefir** may increase *Lactobacillus* spp and improve constipation **-Kombucha** may decrease abundance of pathogens such as *E.coli* and *H.pylori* **-Sauerkraut** may improve symptoms in all IBS subtypes **-Kimchi** my increase *Lactobacillus* **-Natto and Miso** may increase *Bifidobacterium* and decrease *Enterobacteriaceae*
Omega 3 and MUFAs	**Gut microbiota modulation:** Omega-3 fatty acids, found in fatty fish and nuts and seeds, may increase the abundance of butyrate-producing bacteria and probiotics such as *Lactobacillus* and *Bifidobacterium* spp. Furthermore, omega-3 may decrease LPS-induced inflammation. MUFAs, found in olive oil, avocado, nuts, and seeds may increase *Bifidobacterium* spp and favour *Bacteroidetes* over *Firmicutes*.
Supplements containing vitamins and minerals	**Gut microbiota modulation:** Effect of different supplement types depends on dosage, length of intervention, combination of nutrients, and genetic and epigenetic factors and may include: **-Vitamin D** may increase diversity, promote *Akkermansia* and *Bifidobacterium* spp, and decrease *Proteobacteria* abundance **-Iron** may increase *Lactobacillus* spp, which are dependent on iron availability. However, as excess iron intake may promote

Foods, nutrients, diets	Main effects
	inflammation, oxidative stress, and increased abundance of pathogenic bacteria, it is recommended to supplement only when a deficiency is identified.
Mediterranean Diet	**Gut microbiota modulation:** The MD is high in fiber, polyphenols, nuts and seeds, omega-3 fatty acids, and MUFAs. The MD may decrease the F/B ratio and abundance of *Proteobacteria* and increase abundance of beneficial bacteria such as probiotics, SCFA-producing bacteria, and mucosa-protective bacteria (as demonstrated in the PREDIMED study).
Ketogenic diet (KD)	**Gut microbiota modulation/ altered microbiota**: Effects of the KD depend on the health status of the host. KD may increase abundance of *Akkermansia* and decrease the F/B ratio. Given the very low intake of carbohydrates and fiber, a KD may also decrease probiotics species, particularly *Bifidobacterium*. KD may increase the abundance of pro-inflammatory *Proteobacteria* like *Bilophila wadsworthia*. While specific beneficial effects of a KD on refractory epilepsy and obesity may be mediated by positive changes in the microbiome composition, regular testing may be necessary to avoid negative intestinal bacterial imbalances.
Vegetarian and vegan diets	**Gut microbiota modulation/ possible alterations in microbiota**: High consumption of plant-based foods and fiber, a characteristic of vegetarian and vegan diets, may increase abundance of SCFA-producing bacteria, improve bacterial diversity, and decrease abundance of potential pathogens. However, sub-optimal intake of essential nutrients such as iron, omega-3, vitamin B12, and protein, associated with unbalanced and strict vegetarian and vegan diets, may negatively affect bacterial distribution and cause an overabundance of some species and should be monitored.
Artificial sweeteners	**Altered microbiota**: In general, artificial sweeteners may affect microbiome diversity. Acesulfame K, saccharine and sucralose consumption has been linked to decreased abundance of *Akkermansia*, though these results are controversial. Because research in this area is still early, it is not yet possible to draw conclusions about individual effects of artificial sweeteners on microbiome composition, which are likely dose-dependent and linked to duration of consumption.
Excess of sugars, saturated fats, salt and ultra-processed foods	**Altered microbiota**: The typical Western Diet (WD) is characterized by high intake of saturated fat, salt, and sugar and inadequate in fiber. The WD can negatively affect microbiome composition and may decrease microbial diversity, increase abundance of *Proteobacteria* and pathogens, and promote LPS biosynthesis. Specifically, excess saturated fat intake may decrease abundance of *F.prausnitzii* and increase abundance of species expressing bile acid hydrolases such as *Clostridium*, *Alistipes*, *Bifidobacterium*, and *Lactobacillus* spp. Furthermore, excessive salt intake may decrease *Lactobacillus* spp.
Alcohol	**Altered microbiota**: Chronic excessive alcohol intake may negatively affect bacterial diversity and distribution, increase abundance of *Proteobacteria*, and promote intestinal inflammation and IBS-related symptoms. However, moderate beer consumption, particularly if unpasteurized, has been demonstrated to exert some prebiotic effects due to polyphenolic compounds and melanoidins, which may increase *Bifidobacterium* spp and *Akkermansia*. Moderate consumption of red wine, which is also rich in polyphenols, may increase microbiota diversity. However, as alcohol has several known detrimental effects, non-alcoholic versions of beer and red wines should be consumed, if consumed at all.

Foods High In Specific FODMAPs

Type of FODMAP	Main food sources
Fructose	Monosaccharide found in high quantity in honey, dried fruits (for example raisins, dates, and figs), high fructose corn syrup, mango, watermelon, apple, pear, prunes, grapes, lychee, agave syrup, applesauce, and fruit juices.
Lactose	Disaccharide made of galactose and glucose found in high quantity in animal milk, cream, and some cheeses. Lactose reactions are individual, and some people may not have any problems eating moderate quantities of yogurt. Kefir is naturally very low in lactose. As a result of their processing, some hard cheeses may be better tolerated because their lactose content decreases (i.e. parmesan, gouda, provolone, brie, camembert). Fresh cheeses like ricotta, feta, mascarpone and spreadable cheeses, tend to be high in lactose.
FOS	Fructo-oligosaccharides found in high quantity in artichoke and Jerusalem artichoke, chicory, green bananas, leeks, onion, garlic, shallots, asparagus, yacon.
GOS	Galacto-oligosaccharides found in high quantity in legumes such as beans, lentils, soya and chickpeas, pistachios and cashew. Dairy products may contain some GOS.
Inulin	Mixture of oligo and polysaccharides, similar to FOS but with a longer and more polymerized structure (meaning with cross-links) found in high quantity in Jerusalem artichoke, dandelion, chicory, barley, burdock, stevia, garlic, agave.
Xylitol	Sugar alcohol that is normally used as a sweetener in chewing gum and sugar-free products. It is also naturally occurring in mushrooms, cauliflower, berries, corncob and husk and plant stalks. However, it tends to become problematic when used on its own as a sweetener.
Sorbitol	Sugar alcohol used as a sweetener in sugar-free products. It is naturally occurring in apple, dates, pear, apricots, prunes, raisins, peaches, nectarines, broccoli, fennel, red cabbage and aubergine.
Mannitol	Sugar alcohol used as a sweetener in sugar-free products. It also naturally occurring in mushrooms, pineapple, sweet potatoes, carrot, olives, asparagus, celery, snow peas, butternut squash.
Maltitol	Sugar alcohol used as a sweetener in sugar-free products. It is also naturally occurring in chicory leaves and roasted malt.
Isomalt	Sugar alcohol used as a sweetener derived from sugar beet. It does not naturally occur in foods.

The Microbiome test essential FAQs

What is the Microbiome test essential?

The Microbiome test essential is a test that identifies all bacteria present in an individual's microbiome down to the strain level. It is divided into sections that examine how specific bacteria, and their abundance may influence gut symptoms and predisposition to intestinal disorders. To facilitate interpretation and actionability, bacterial abundances are analysed based on well-established indices like diversity and enterotypes, and according to their specific beneficial or detrimental effects. The presence of bacteria that may negatively impact both intestinal and systemic health, such as Fusobacteria and Proteobacteria, is highlighted. Furthermore, a separate section examines the abundance of bacteria involved in certain nutrients metabolism.

Who should use the test?

This test is designed to help users, in collaboration with a healthcare provider, better understand the balance of their gut microbiome and its potential influence on their digestive well-being. It is not a diagnostic tool but rather a way to identify possible bacterial imbalances that may be associated with certain symptoms or an increased risk of chronic intestinal disorders. This information can help guide users and healthcare professionals in adopting personalized strategies to optimize gut health..

How is the microbiome score calculated?

The overall microbiome score is calculated by applying proprietary algorithms that consider both the general features of the microbial population, including bacterial diversity, evenness of distribution, and phyla present in the sample, while also focusing on abundance of potentially pathogenic as well as beneficial bacteria. All measurements in an individual sample are compared to the reference population to generate a quantitative comparison. As a result, scores are designed to indicate where an individual sample differs from the general population, providing guidance for following up with specific actions, rather than providing a diagnosis of disease.

What is the reference population?

The reference population is made up of a significant and expanding number of individuals who have been screened using the test. The reference population includes all samples tested by Intus Biosciences (subcontracting laboratory). The rationale for including all individuals in the reference population, regardless of self-reported health status and symptoms, is to better observe trends associated with health status. Furthermore, as samples are self-collected and health status information is self-reported, inclusion of all data accounts for errors and eliminates scientific assumption bias. As more sample data is compiled, reference population norms will be adjusted to reflect the most updated information, which may result in a slight change to the ranges included in the report. The highest and lowest percentiles are flagged as abnormal values.

What is the meaning of the detrimental, beneficial, and overall species balance?

Specific bacteria likely to be associated with a condition may positively or negatively contribute to it. Therefore, most of the bacteria under specific sections are listed in terms of beneficial, detrimental, and overall species balance. Bacteria that are beneficial may have a positive effect on a given condition if they are present in a balanced abundance and in the correct amount. As a result, we do not want their total to be low. Conversely, other bacteria may negatively affect a disorder or risk of developing it, so we aim to keep them within a normal and not elevated range.

There are, however, some bacterial lists that do not include this distinction. If, for example, certain bacteria are known to be potentially problematic, such as pathogens, or if they can only have a negative impact on a condition, only the detrimental category will be displayed. In contrast, if a group of bacteria is known to generally contribute to the host's health, such as probiotics, only the beneficial category will be displayed.

If a list of bacteria can contribute to both directions, a total of detrimental, beneficial, and their balance is displayed. The sections are flagged in accordance with this balance or the overall abundance of "good" and "bad" species. It is important to note that to facilitate interpretation and actionability of bacterial lists, even when a section has a "green tick" and is considered overall within a normal range, if any species has an abnormal abundance (too low or too high), it will be flagged.

What is more important: The score, or individual sections of the report?

The score provides a general idea of microbiome balance and can be very informative for overall health and well-being. If a specific condition is a concern or as a preventive measure, it may be helpful to pay particular attention to the sections with a flagged indicator.

What does ‘Typical Range’ mean and will the range change?

Typical ranges represent the findings in the majority of the reference population. As the reference population expands, the typical ranges will change to become more refined and precise.

Who provides the test?

The test is provided by AveroDX, using technology under license from Intus Biosciences, LLC. Report content generated by Intus Biosciences, LLC.

What technology generates the results?

The test is powered by the patented, high resolution and high throughput Intus Bio Titan-1™ platform. Titan-1™ uses the latest Next Generation Sequencing (NGS) Technology, with a ‘long’ target sequence of 16S-ITS and partial 23S. Visit intusbio.com for more information.

What makes the test unique?

Side by side analysis of different approaches has demonstrated that the Intus Bio technology is the most effective and accurate method for strain level identification of bacteria - see https://doi.org/10.1099/mgen.0.000794. This is the only test of its type benefiting from the power of the technology.

Are there any drugs, supplements or foods that drastically interfere with the test’s results?

Antibiotics and probiotics can significantly change the microbiota composition, although not necessarily in the long-term. We suggest waiting for a couple of weeks after completing a course of antibiotics before taking this test. If you are interested in monitoring the effects of a probiotic intervention, the test may be performed while on the supplement or after completing treatment. We also recommend that users follow their typical diet in the weeks preceding the test so that the results reflect average and normal food intake (no drastic changes in the diet or new foods should be introduced prior to the test).

How many times should you take this test?

It is strongly recommended to take a test before and after any dietary, medical, or lifestyle interventions. Regular testing can help monitor the development of chronic intestinal diseases and evaluate the effectiveness of treatments over time.

Test Category Definitions

Resilience & Biodiversity

Alpha Diversity

Calculated using the Shannon Index, the alpha diversity score incorporates measures of richness and evenness and is an indicator of microbiome resilience. Resilience can be defined as how resistant the bacterial community is to changes that may push it out of its current state, such as after an infection, course of antibiotics, a long period of ill-health, or another stressor. In general, a healthy and well-balanced gut bacterial community should have many different species that are well-distributed, such that no one species is dominant. Therefore, highest resilience is achieved when richness and evenness are in balance.

Richness

The number of total bacterial species detected in the sample, higher richness values generally are generally associated with a healthier microbiome. In rare cases, however, the presence of several pathogenic species may result in a higher richness score, making it important to evaluate the types and abundance of bacterial species present, including potentially harmful pathogenic species.

Evenness

A measure of how well different bacterial species are distributed throughout the microbiome. Scores closer to 1 indicate a more desirable, even distribution while scores closer to 0 suggest one or more species may be dominant.

Beta diversity
Calculated using the Bray-Curtis dissimilarity, beta diversity compares how similar or different the sample is from the reference population. In general, it is better to have a bacterial composition closer to that of the reference population. A high beta diversity score may be an indicator of an unusual microbial profile, typically dominated by a single species. Although a sample may be different due to a high abundance of beneficial bacteria, gut-related symptoms are frequently associated with higher beta diversity scores.

Firmicutes/Bacteroidetes (F/B) ratio
These two bacterial phyla are the dominant types of bacteria present in the healthy adult human gut. The phyla are usually present at about equal amounts, and together they typically represent more than 90% of the entire bacterial community. The F/B ratio is a well-recognized marker of microbiome health and balance, and an unusual ratio can indicate a predisposition to certain diseases. For example, higher abundance of Firmicutes tends to be associated with obesity, while higher abundance of Bacteroidetes is more common in individuals suffering from Inflammatory Bowel Disease (IBD). However, this result should be considered within the context of overall health rather than used as a primary indicator.

Fusobacteria
Typically absent or in very low abundance in the lower digestive system, Fusobacteria are naturally occurring bacteria that colonize mucosal surfaces, especially in the oral cavity. Fusobacteria are mostly associated with periodontal disease and formation of biofilm. When found in the gut, however, it may indicate that an insufficient immune surveillance and/or low gastric acidity have allowed these bacteria to translocate from the mouth to the intestine, or that disrupted conditions in the gut are allowing Fusobacteria to thrive. High abundance of Fusobacteria in the gut may be an indicator of chronic inflammation and an increased risk of disease and some cancers, such as is the case with Fusobacterium nucleatum.

Resistome
The concept of resistome has been introduced quite recently and refers to the presence of antibiotic resistant genes (ARGs) in bacteria present in a specific environment that play a significant role in the spread of antibiotic resistance, a significant threat to health. Antibiotic resistance reduces the effectiveness of antibiotics, and as bacteria develop resistance to multiple antibiotics, it limits the available treatment options, making infections more severe, prolonged, and difficult to treat and may lead to complications, morbidity and mortality, as well as an increased burden on healthcare systems. Antibiotic resistant bacteria can be transferred between individuals, and antibiotic resistant genes can be transferred between bacteria, even across different species. This horizontal gene transfer allows the rapid spread of resistance within bacterial populations. This means that resistance can emerge in one location and quickly become a global problem. The "Resistome Score" measures the number and types of bacteria likely to harbor ARGs in this gut microbiome sample as compared to the samples in the reference database. Problematic species are common in the genera *Escherichia*, *Klebsiella*, and *Enterococcus*. These species have been found to harbor a large number of ARGs. Additionally, species belonging to the genera *Bacteroides*, *Prevotella*, and *Streptococcus* also contribute to the gut microbiome resistome.

Enterotype
The identification of intestinal enterotypes that may reflect an individual's typical diet was first proposed by Arumugam et al. in 2011. Even though this concept has evolved, many still recognize and stratify the human microbiome based on enterotypes, most notably *Bacteroides* and *Prevotella*. The Intus Bio research team has also identified a fourth possible enterotype dominated by Bifidobacterium spp. We are continuously gathering data to determine whether this enterotype is linked to a specific diet, medication and supplement use or predisposition to a particular condition.

Proteobacteria
Proteobacteria are gram-negative bacteria characterized by the presence of lipopolysaccharide (LPS) on the outer membrane, that may activate the immune system response and cause systemic inflammation. Common examples of Proteobacteria include *Shigella*, *E. coli*, *Salmonella*, *Enterobacter*, and *Klebsiella*. As emerging research suggests that not all Proteobacteria negatively affect health, this score takes into consideration both the overall abundance of Proteobacteria as well as the presence of highly-pathogenic species.

Pathogens
Although many common human pathogenic bacteria belong to the Proteobacteria phylum, there are species belonging to other phyla, such as *Streptococcus*, *Staphylococcus* and *Clostridium* from the Firmicutes phylum. While Firmicutes do not have LPS, they are often associated with GI and systemic conditions. It is important to note that a microbiome test is not intended to diagnose a bacterial infection. While detection of small amounts of pathogenic bacteria in the absence of symptoms may not be a cause for concern, chronic presence of a high pathogen abundance may indicate that the microbiome is providing a favorable environment for pathogens to thrive. Abundance of pathogenic bacteria may increase after a course of antibiotics, surgery, serious illness, and/or elevated stress levels. Additionally, unhealthy dietary patterns, such as diets high in saturated fats and sugars, may favor increased levels of pathogenic bacteria in the gut. The term pathobionts is sometimes used instead of pathogens. Pathogens are bacteria known to cause infections while pathobionts are bacteria that are potentially pathogenic under specific circumstances such as during immune system dysfunction.

Top 10 Species
No scientific study has demonstrated the utility of indicating the top 10 most abundant species within an individual microbiome. From a clinical standpoint, however, knowing the species that are more abundant and often over dominant may offer an effective starting point when deciding whether or not to intervene. Overabundant bacteria, regardless of whether they are commensal or probiotics, should prompt further investigation into how diet, pharmaceuticals, and/or supplements may be altering microbial balance. Furthermore, tracking the changes in the top 10 species over time may help determine the effectiveness of interventions.

Beneficial Bacteria
Several intestinal bacterial species and strains confer protection and health benefits to the host by supporting gut mucosa permeability and barrier function, producing anti-microbial molecules such as bacteriocins, regulating GI motility, optimizing metabolic health, metabolizing xenobiotics, and modulating the local and systemic immune system. Contrary to common perception, probiotic bacteria are not the only beneficial gut micro-organisms, as other common commensal bacteria can protect the host from opportunistic pathogens and sustain overall health. However, all bacteria, even those deemed as beneficial, may become pathobionts by negatively affecting diversity if present in excessive abundance. This report analyses the presence and abundance of three distinct categories of beneficial bacteria: probiotics, mucosa protective bacteria, and short chain fatty acid (SCFA) producing bacteria.

Probiotics
According to the definition provided by the International Scientific Association for Probiotics and Prebiotics (ISAPP), the term probiotic should be applied only to “live microorganisms that, when administered in adequate amounts, confer a health benefit on the host”. Although certain gut commensals can be considered probiotic strains, these must be well-characterized and clearly demonstrated to be beneficial. If well-recognized probiotic species such as Lactobacillus and Bifidobacterium are detected in the sample, relative abundance is reported in the probiotic table. *Akkermansia muciniphila* is a newly recognized probiotic that may confer metabolic health benefits and be imbalanced in individuals with type 2 diabetes, obesity and/or metabolic syndrome. However, as abnormally high levels of *Akkermansia muciniphilia* have been observed in those with autoimmune and neurodegenerative disorders, careful evaluation of probiotic abundance is important.

Probiotic Supplementation
Supplements containing specific strains of probiotics are increasingly being used inclinical practices. As probiotic strain(s), dose, and duration are individualized, supplementation should be overseen by a trained practitioner. If abnormally high levels of *Lactobacilli*, *Bifidobacterium*, and/or *Akkermansia* are detected, current pre- and probiotic supplements may need to be reevaluated. Probiotic abundance may also be affected by pharmaceutical drugs, as is seen with metformin, which may promote intestinal barrier function and the production of beneficial short chain fatty acid (SCFA) producing bacteria.

Mucosa Protective Bacteria

Mucosa protective bacteria, including *Akkermansia muciniphila* and *Faecalibacterium prausnitzii*, have been demonstrated to support a normal intestinal barrier function, regulate mucosal inflammation and act as “sentinels of the gut”. While several chronic diseases may be associated with a low abundance of these species, abnormally high levels may also be harmful. High abundance of *Akkermansia muciniphila*, for example, has been observed in some neurodegenerative and autoimmune disorders. It is possible that inflammatory conditions may increase mucosal protective bacteria abundance as a defensive response.

Short chain Fatty Acid (SCFA) Producing Bacteria

Dietary fibre is metabolized by SCFA-producing bacteria to generate acetate, propionate, and butyrate, which play an important role in metabolic health and regulation of the immune system. For example butyrate is the main energy supply for colonocytes and has been extensively studied for its antiproliferative effects due to epigenetic regulation via histone deacetylase activity. Moreover, SCFAs can influence bacterial gene expression and reduce virulence of intestinal pathogens. A very high level of a single species, although not necessarily cause for concern, should be evaluated as dietary patterns, pharmaceuticals and supplements may cause alterations in bacterial distribution.

Gut Systems Bacterial Groups

This section is intended to assist in identifying potential areas of concern more quickly. There are three major intestinal disorders included in this section: IBS, IBD, and SIBO, as well as the production of two crucial bacterial metabolites: TMA and LPS. There may be a need to rebalance the abundance and distribution of the species related to each disorder or molecule to prevent the worsening of symptoms or triggering potential pathogenic responses.

Irritable Bowel Syndrome (IBS)

IBS is a chronic bowel disorder of a functional nature. Thus, despite the constant presence of bothersome and relapsing symptoms such as constipation, diarrhoea, bloating, and abdominal pain, no "real" organic causes have been identified. IBS patients suffer from ongoing symptoms that have a significant impact on their daily lives. While doctors assure patients that this condition does not pose a risk for cancer or IBD (Inflammatory Bowel Disease), many still suffer "in silence" due to a lack of understanding and appreciation of their distress.

IBS is known to be exacerbated by disturbances in the gut microbiome. Although it can’t be directly linked to any one bug, certain bacterial species and/or their associations aggravate symptoms and cause flare-ups. The Microbiome essential test identifies bacteria strongly linked to IBS or other functional intestinal disorders based on scientific research. Functional intestinal disorders like IBS are chronic conditions that may come and go but knowing whether your intestinal bacteria are contributing to your symptoms maximizes your chances of controlling them.

Small Intestinal Bacterial Overgrowth (SIBO)

SIBO is a specific form of dysbiosis caused by high levels of specific bacteria in the small intestine. A variety of symptoms have been attributed to SIBO which may depend on the specific bacteria involved and may include excessive bloating, diarrhoea, macronutrient malabsorption, and less commonly, constipation. Bacteria categories associated with SIBO include Proteobacteria, hydrogen-producing bacteria, and hydrogen-sulfide producing bacteria. Proteobacteria and hydrogen-producing bacteria may cause or exacerbate diarrhoea in both IBS and SIBO, while hydrogen sulfide-producing bacteria may be associated with constipation and/or diarrhoea, foul smelling stools, excessive gas and bloating, and may negatively affect gut barrier function and inflammation. This test measures the abundance of species that are commonly present in duodenal and/or jejunal aspirates of patients with SIBO (as demonstrated by the REIMAGINE study, 2019) and indicates if relative abundance of these species is higher than in the reference population. This test does not diagnose SIBO and detection of SIBO-associated bacteria may need to be followed-up with additional diagnostic testing, based on the clinical presentation.

Inflammatory Bowel Disease (IBD)

The pathogenesis of IBD is largely unknown, but it appears to be related to immune activation, environmental factors, genetics, and the microbiome composition. Studies suggest that a dysbiotic state may precede or accompany the onset of the disease and determine the severity of flare-ups. Consequently, any imbalance in the abundance of potentially pathogenic species should be monitored and controlled. To maximize the chances of a full recovery and increase the time in between flare-ups, a balanced presence of protective species, most notably probiotics and mucosa-protecting species, should be ensured. The abundance of SCFAs and BAs producing bacteria should also be monitored in order to regulate mucosal immunity and facilitate epithelial repair mechanisms.

Bile Acid (BA) Metabolizing Bacteria

BAs are synthesized from cholesterol in the liver and enter the intestine as conjugated BAs where they are converted into secondary BAs by intestinal bacteria. Several types of bacteria express BA-metabolizing enzymes, including *Clostridium*, *Bacteroides* and *Listeria* species as well as some *Lactobacilli* and *Bifidobacterium*. Secondary BAs affect enterochromaffin cells (EC) and levels of 5-hydroxytryptamine (5-HT, serotonin) causing increased visceral sensitivity and intestinal motility. Upregulation of intestinal serotonin availability leads to increased bowel peristalsis and may cause diarrhea in individuals predisposed to IBS-D. Moreover, *Clostridium* species can promote a higher liver biosynthesis of BAs and increase their secretion. There is evidence that almost 70% of patients with IBS-D have high fecal BAs or some form of BA malabsorption. The association between certain bacterial species metabolizing BAs and IBS symptoms is stronger for the diarrhea subtype, with increased BA production and secretion and corresponding increased intestinal serotonin. However, a decreased abundance or impaired distribution of BA metabolizing bacteria may cause constipation. Detection of an abnormal abundance in the main bacteria involved in BA metabolism may help personalize treatment by addressing underling dysbiosis and evaluate other factors affecting BA production and absorption. Secondary BAs may be associated with neurodegenerative disorders, metabolic disturbances, and colorectal cancer. It is therefore essential to monitor any abnormal abundance of BA-metabolizing bacteria.

Trimethylamine (TMA) Production

Intestinal bacteria can produce TMA by metabolizing its precursors, such as choline and L-carnitine. After TMA is taken up by the liver, it is oxidized by flavin monooxygenases (FMOs). TMAO concentrations in the blood have been linked directly and indirectly to cardiovascular diseases (CVDs) and atherosclerosis. Therefore, regulating and controlling species that produce TMA may reduce circulating TMAO and moderate the risk associated with it. TMAO levels may be decreased by fibres (in particular resistant starch), fermented foods, and *Lactobacillus rhamnosus* GG.

Lipopolysaccharide (LPS) Production

The presence of elevated LPS has been associated with inflammatory and immune responses in several body systems. As a result, they have been implicated in the pathogenesis of several diseases, ranging from neuroinflammatory/neurodegenerative diseases such as Alzheimer's and Parkinson's disease to autoimmune disorders. In all situations, it is recommended to keep the abundance of LPS-containing bacteria under control, particularly if inflammatory conditions (including those affecting the gut) are already present.

Nutrient and Dietary Component Metabolism.

This section is intended to assist in determining the abundance of bacteria involved in production and/or metabolism of nutrients and dietary components, including FODMAPs, vitamins B, and indoles.

FODMAP Sensitivity Score and Fermenting bacteria.

FODMAPs are short-chain carbohydrates that are poorly absorbed in the small intestine and fermented in the colon by bacteria. Overabundance of FODMAP-fermenting bacteria may cause GI symptoms such as gas, bloating, abdominal pain, diarrhoea and/or constipation. IBS and/or SIBO sufferers may be particularly sensitive to FODMAP-containing foods. Being aware of a potential FODMAP sensitivity can assist in personalizing a low-FODMAP diet trial. However, as a low-FODMAP diet is highly restrictive, it should only be followed for a short period of time and overseen by a knowledgeable practitioner who can determine specific intolerances and liberalize the diet as much as tolerated.

As the sensitivity score assesses the potential negative response to food high in FODMAP, the table describing species that ferment some specific FODMAP may assist the clinician in making the most appropriate dietary recommendations. However, since some species ferment more than one type of FODMAP, it is not recommended to implement a diet solely based on the abundance of the species, but rather to rebalance their distribution and evenness.

Indole production.

There is considerable evidence that tryptophan-derived microbial indoles play a crucial role in regulating intestinal mucosal integrity and health, as they modulate inflammatory and immunological responses. A positive effect of Indoles is their ability to increase the abundance of beneficial strains while at the same time reducing the abundance of pathogens, thereby regulating their virulence factors and gene expression. Nevertheless, it is important to ensure that the abundance of Indole-producing bacteria is not excessive to avoid the development of potential side effects, particularly at the renal and neurological levels.

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Disclaimers

This test is not intended to diagnose, treat, or cure any medical condition. It is provided for informational purposes only, and the results should be interpreted with care. No medical treatment, supplement, or significant lifestyle change should be initiated, modified, or discontinued without first consulting a qualified healthcare professional (such as a physician, nutritionist, or dietitian).

This report is not a substitute for a culture-based test or PCR test used for diagnosing gastrointestinal infections, nor is it a replacement for specialized clinical assessments such as the SIBO test. It presents bacteria identified through sequencing and expressed in terms of relative abundance, whether they are potentially pathogenic, commensal, or beneficial.

The analysis focuses solely on bacterial species associated with functional gastrointestinal disorders, as supported by the scientific literature. The species included in this report are selected based on the most robust evidence currently available. However, the field of gut microbiome research is rapidly evolving and is still considered emerging from a medical standpoint. Interpretations should therefore be contextualized within the latest scientific knowledge and do not replace clinical judgment. A normal test result does not rule out the presence of symptoms, and conversely, symptoms may occur even when bacterial composition appears normal. The effects of dysbiosis can vary from person to person.

The gut microbiome is highly dynamic and influenced by multiple factors—including diet, medications, and supplements—any of which can alter test results. It is recommended to repeat this test before and after any major intervention. Neither the test provider nor its affiliates can be held responsible for decisions made based on these results.

The testing methodology, scoring criteria, and selection of bacterial species are subject to updates in line with emerging scientific evidence. By using this test, the individual consents to the anonymized collection and use of their data for research and development purposes. The provider guarantees that these data will not be used for commercial purposes or shared with third parties without explicit consent. The user acknowledges the limitations of this test and releases the provider from any liability related to the interpretation, use, or storage of their data.