GutID

Clinicians' Guide

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Clinicians' Guide

GutID microbiome tests have been created with clinicians in mind, to assist you in understanding the complex microbiome results of your patients.

GutID has been designed to target specific areas of concern so that you do not have to worry about determining the kind of impact an imbalanced abundance of specific bacteria is having on your patients' symptoms, or will have in the future.

Key Characteristics

✓ **MICROBIOME SCORE**

An overall microbiome score to check if your patient's profile is typical

✓ **SUMMARY**

A quick overview of the microbiome's health, including indications of areas to review, enterotype and resistome

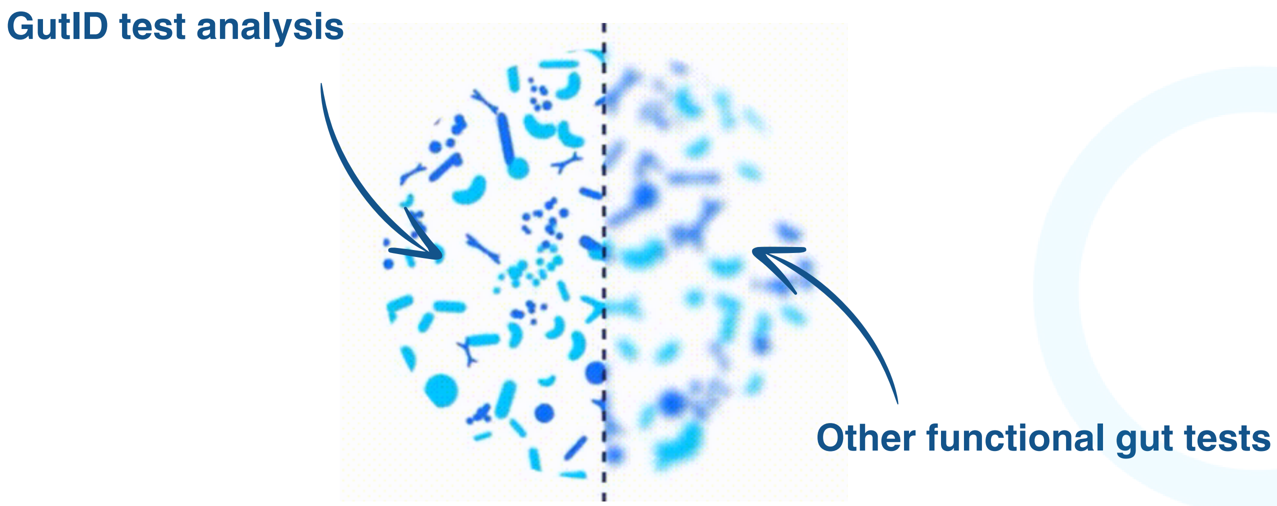
✓ **TARGET PLOT**

Colourful graph that illustrates all bacteria detected in the stool, up to the strain level

✓ **AREAS OF CLINICAL INTEREST**

Clinically relevant sections which indicate which function and type of bacteria need to be addressed

How does our tech compare?



GutID tests identify and analyze ALL bacteria present in a sample and interpret the main indicators of microbiome health and balance, such as diversity, resistome, etc.

The **GutID CGI** test, focuses primarily on gut health and the bacterial causes of intestinal symptoms. The **GutID CMA**, on the other hand, interprets any bacterial imbalance in terms of its potential impact on any body system from a **“gut axis”** point of view.

Although the two tests interpret the microbiome composition from slightly different perspectives, the analysis of the bacteria present in the stool sample is complete and unbiased. Similar tests are available on the market, but they are not comprehensive analyses of the entire microbiome, but rather provide a snapshot of a few bacteria considered to have clinical significance.

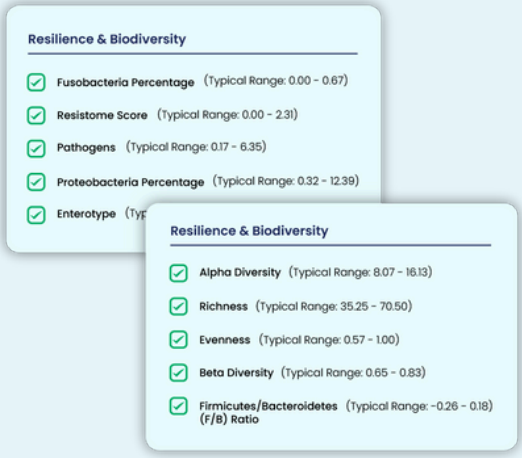
The tests may contain additional markers, such as calprotectin or **Short Chain Fatty Acids (SCFAs)**, but they cannot be considered microbiome tests in the traditional sense.

GutID Technology Vs Others

	CGI	CMA	Other Tests
ID of ALL bacteria in sample	🟢	🟢	🔴
Strain Level ID	🟢	🟢	🔴
Resistome Score	🟢	🟢	🔴
FODMAP Sensitivity Score	🟢	🟢	🔴
Association with major chronic intestinal disorders	🟢	🟢	🔴
Association with major systemic chronic diseases	🔴	🟢	🔴
Additional Fungi,Parasites & Viruses	🔴	🔴	🟢

State-of-the-art

microbiome testing for the identification of bacterial causes of intestinal issues and general health improvement.



Resilience & Biodiversity

☑ **Fusobacteria Percentage** (Typical Range: 0.00 - 0.67)
☑ **Resistome Score** (Typical Range: 0.00 - 2.31)
☑ **Pathogens** (Typical Range: 0.17 - 6.35)
☑ **Proteobacteria Percentage** (Typical Range: 0.32 - 12.39)
☑ **Enterotype** (Typ

Resilience & Biodiversity

☑ **Alpha Diversity** (Typical Range: 8.07 - 16.13)
☑ **Richness** (Typical Range: 35.25 - 70.50)
☑ **Evenness** (Typical Range: 0.57 - 1.00)
☑ **Beta Diversity** (Typical Range: 0.65 - 0.83)
☑ **Firmicutes/Bacteroidetes (F/B) Ratio** (Typical Range: -0.26 - 0.18)

Overview of the Report Key Sections

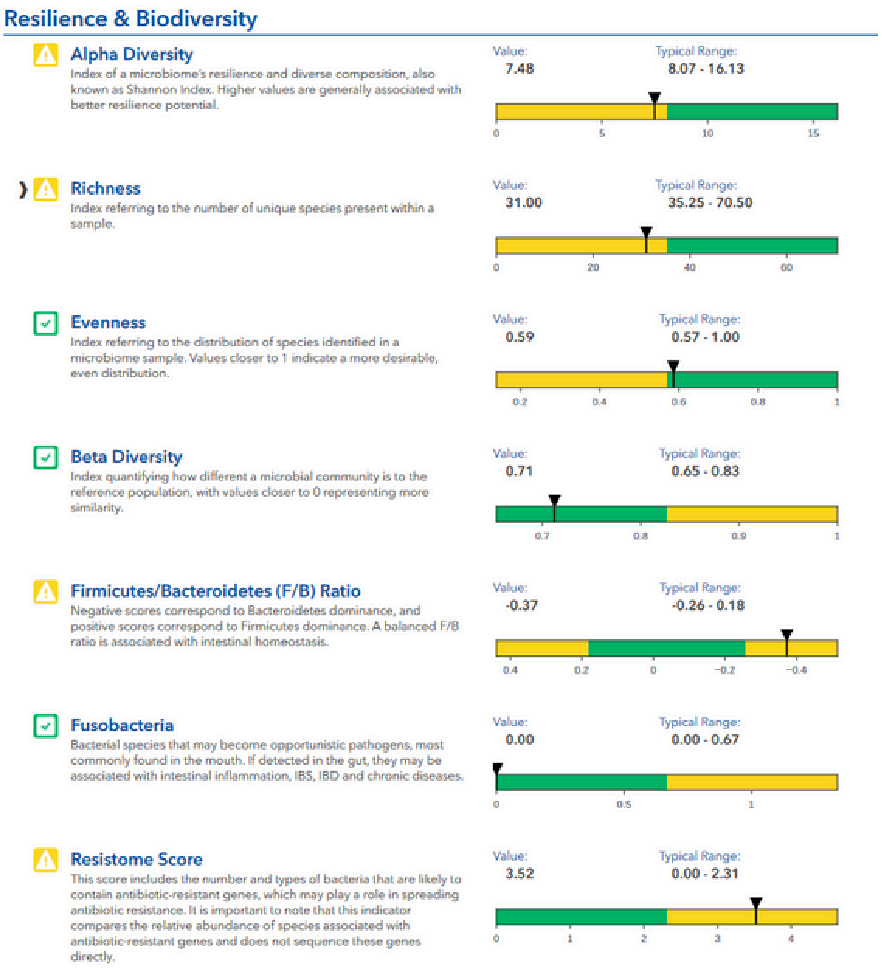
Resilience and Biodiversity

The purpose of this section is to describe the most well-known markers of microbiome health and balance, including **alpha** and **beta diversity**, the **Firmicutes/Bacteroidetes** ratio, and the relative abundance of potentially pathogenic bacteria such as ***Proteobacteria*** and ***Fusobacteria***.

Moreover, it provides a new indicator of microbiome health, the resistome, which measures the abundance of bacteria likely to carry **antibiotic-resistance genes**. Finally, the top ten species reveal a snapshot of the individual's microbiota at a glance.

Clinical Utility

Quick overview of patient microbiome composition and balance. Practical recommendations are also provided to improve these indicators.



Resilience & Biodiversity

⚠ **Alpha Diversity**
Index of a microbiome's resilience and diverse composition, also known as Shannon Index. Higher values are generally associated with better resilience potential.
Value: 7.48
Typical Range: 8.07 - 16.13

⚠ **Richness**
Index referring to the number of unique species present within a sample.
Value: 31.00
Typical Range: 35.25 - 70.50

✓ **Evenness**
Index referring to the distribution of species identified in a microbiome sample. Values closer to 1 indicate a more desirable, even distribution.
Value: 0.59
Typical Range: 0.57 - 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: 0.71
Typical Range: 0.65 - 0.83

⚠ **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: -0.37
Typical Range: -0.26 - 0.18

✓ **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: 0.00
Typical Range: 0.00 - 0.67

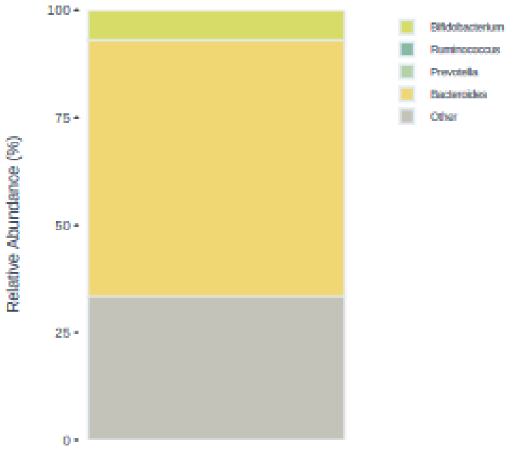
⚠ **Resistome Score**
This score includes the number and types of bacteria that are likely to contain antibiotic-resistant genes, which may play a role in spreading antibiotic resistance. It is important to note that this indicator compares the relative abundance of species associated with antibiotic-resistant genes and does not sequence these genes directly.
Value: 3.52
Typical Range: 0.00 - 2.31

Enterotype

In microbiome research, enterotypes serve as a classification method for identifying particular clusters of microbial species that tend to be more prevalent: Bacteroides (Type 1) is most likely to be observed in individuals consuming a diet high in protein and animal fat, Prevotella (Type 2) is usually associated with a plant based diet rich in carbohydrates and simple sugars, whereas Ruminococcus (Type 3) is found in individuals consuming a diet rich in complex carbohydrates, fruits, and vegetables. Bifidobacterium-dominant enterotypes (Type 4) have also been observed, though their significance is unclear.

Value:

Bacteroides



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		0.27	0.17 - 6.35	
	Escherichia coli	0.22	0.04 - 5.33	
	Bilophila wadsworthia	0.06	0.1 - 1.24	

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		7.27	0.32 - 12.39	
	Parasutterella excrementihominis	7.03	0.07 - 10.25	
	Escherichia coli	0.22	0.04 - 5.33	
	Turicimonas muris	0.02	0.02 - 4.18	

Top 10 Species

An indication of the overall composition of a 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.

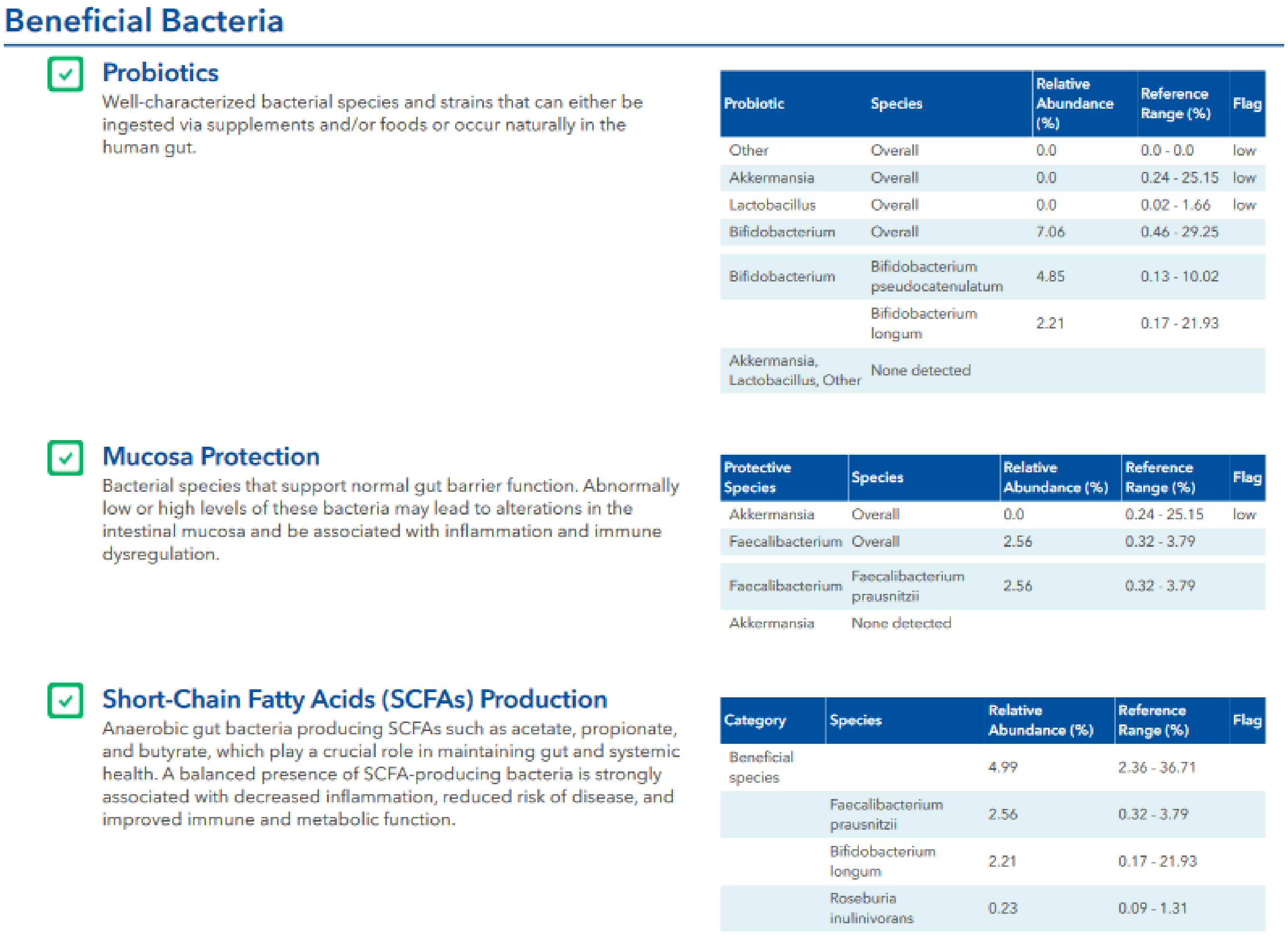
Species	Relative Abundance (%)	Reference Range (%)	Flag
Phocaeicola vulgatus	42.90	3.75 - 51.08	
Phocaeicola dorei	16.65	0.12 - 37.69	
Parasutterella excrementihominis	7.03	0.07 - 10.25	
Megasphaera massiliensis	6.28	0.84 - 9.22	
Faecalibacillus intestinalis	5.53	0.08 - 5.14	high
Faecalibacterium sp. I4-3-84	5.04	0.1 - 3.99	high
Bifidobacterium pseudocatenulatum	4.85	0.13 - 10.02	
Faecalibacterium prausnitzii	2.56	0.32 - 3.79	
Bifidobacterium longum	2.21	0.17 - 21.93	
Phascolarctobacterium faecium	1.88	0.43 - 11.78	

Beneficial Bacteria

Listed under this section are tables that show the relative abundance of bacteria most commonly associated with a positive effect on the host, such as probiotics, **Short Chain Fatty Acids (SCFAs)** producers, and mucosa protective bacteria.

Clinical Utility

The tables can be used to detect the absence of beneficial bacteria as well as to monitor the effectiveness of supplements and treatments



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	0.0 - 0.0	low
Akkermansia	Overall	0.0	0.24 - 25.15	low
Lactobacillus	Overall	0.0	0.02 - 1.66	low
Bifidobacterium	Overall	7.06	0.46 - 29.25	
Bifidobacterium	Bifidobacterium pseudocatenulatum	4.85	0.13 - 10.02	
	Bifidobacterium longum	2.21	0.17 - 21.93	
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.

Protective Species	Species	Relative Abundance (%)	Reference Range (%)	Flag
Akkermansia	Overall	0.0	0.24 - 25.15	low
Faecalibacterium	Overall	2.56	0.32 - 3.79	
Faecalibacterium	Faecalibacterium prausnitzii	2.56	0.32 - 3.79	
Akkermansia	None detected			

☑ **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.

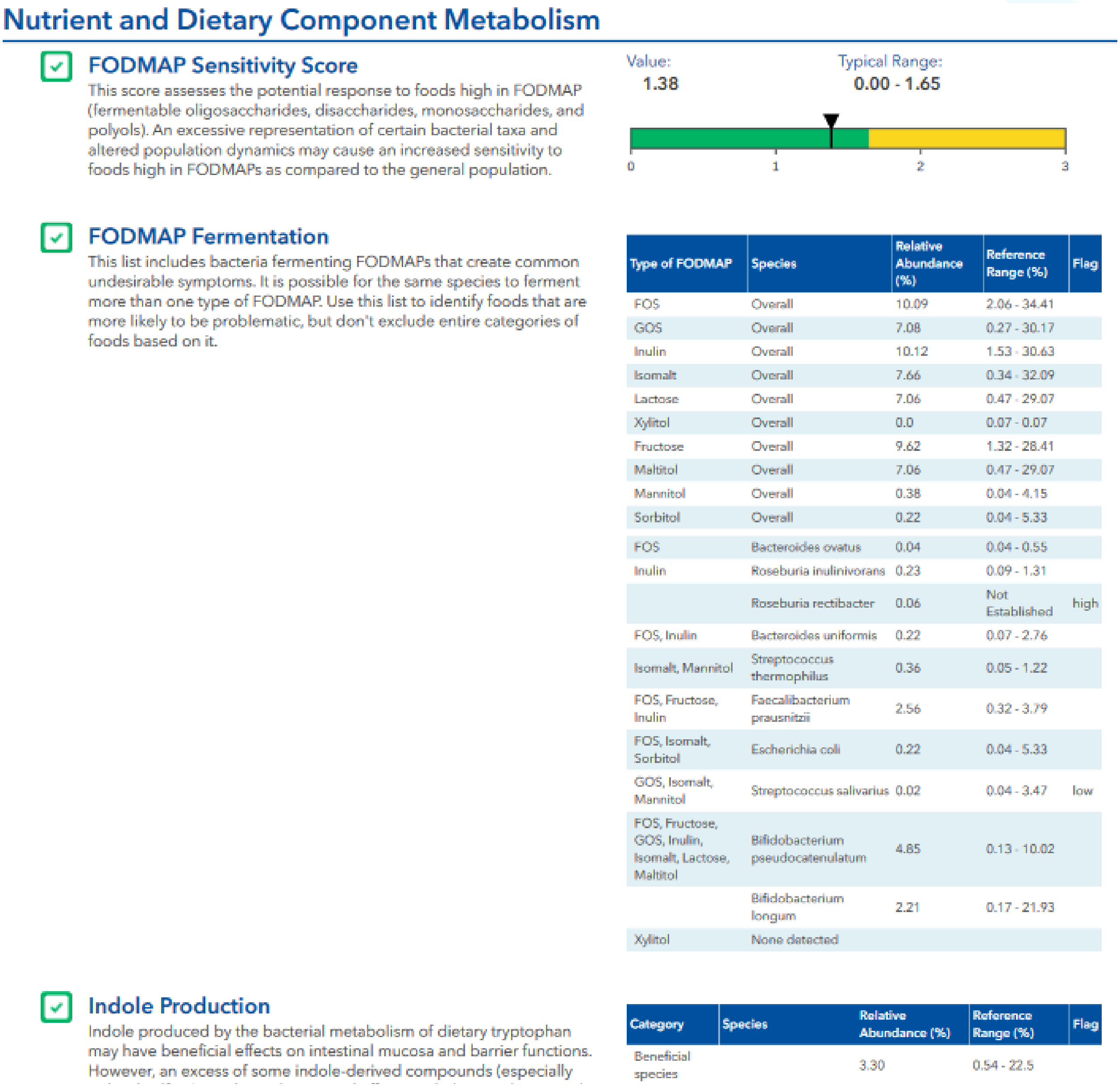
Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		4.99	2.36 - 36.71	
	Faecalibacterium prausnitzii	2.56	0.32 - 3.79	
	Bifidobacterium longum	2.21	0.17 - 21.93	
	Roseburia inulinivorans	0.23	0.09 - 1.31	

Nutrients and Dietary Components Metabolism

The last section focuses on bacteria that are involved in the metabolism of some nutrients of interest. The **FODMAP sensitivity** score as well as the abundance of major bacteria fermenting them are provided to help you optimize the symptoms of your patients. In addition, bacteria involved in indole production and vitamin B metabolism and biosynthesis are present.

Clinical Utility

The tables can be used to detect the absence of beneficial bacteria as well as to monitor the effectiveness of supplements and treatments.



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). 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:
1.38

Typical Range:
0.00 - 1.65

☑ 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	10.09	2.06 - 34.41	
GOS	Overall	7.08	0.27 - 30.17	
Inulin	Overall	10.12	1.53 - 30.63	
Isomalt	Overall	7.66	0.34 - 32.09	
Lactose	Overall	7.06	0.47 - 29.07	
Xylitol	Overall	0.0	0.07 - 0.07	
Fructose	Overall	9.62	1.32 - 28.41	
Maltitol	Overall	7.06	0.47 - 29.07	
Mannitol	Overall	0.38	0.04 - 4.15	
Sorbitol	Overall	0.22	0.04 - 5.33	
FOS	Bacteroides ovatus	0.04	0.04 - 0.55	
Inulin	Roseburia inulinivorans	0.23	0.09 - 1.31	
	Roseburia rectibacter	0.06	Not Established	high
FOS, Inulin	Bacteroides uniformis	0.22	0.07 - 2.76	
Isomalt, Mannitol	Streptococcus thermophilus	0.36	0.05 - 1.22	
FOS, Fructose, Inulin	Faecalibacterium prausnitzii	2.56	0.32 - 3.79	
FOS, Isomalt, Sorbitol	Escherichia coli	0.22	0.04 - 5.33	
GOS, Isomalt, Mannitol	Streptococcus salivarius	0.02	0.04 - 3.47	low
FOS, Fructose, GOS, Inulin, Isomalt, Lactose, Maltitol	Bifidobacterium pseudocatenulatum	4.85	0.13 - 10.02	
	Bifidobacterium longum	2.21	0.17 - 21.93	
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

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		3.30	0.54 - 22.5	

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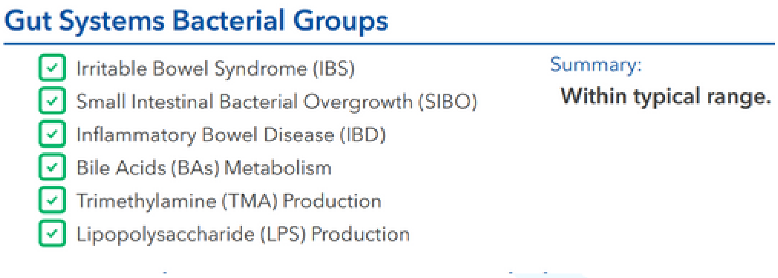
Gut System Bacterial Group

Among the bacteria listed in this section are those which the scientific literature strongly associates with chronic intestinal disorders such as **IBS**, **IBD**, and **SIBO**. Additionally, we present the relative abundance of bacteria that produce key metabolites and molecules that affect the health of the host, including **LPS**, **indoles**, and **TMA**.

Clinical Utility

Quick identification of bacteria or metabolites out of balance that may affect the most common intestinal disorders or symptoms in order to provide targeted treatment.



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

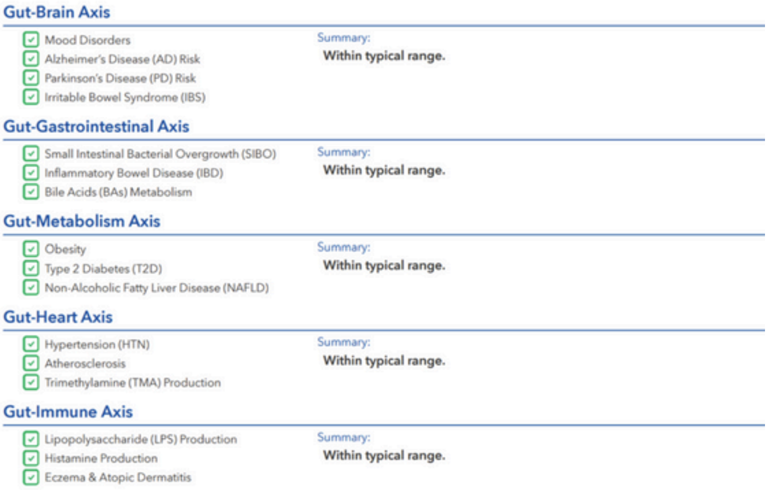
Summary:
Within typical range.

Gut Body System-Axis

In this section, the most well-studied gut axes systems are analyzed to provide the clinician with an indication of any imbalances in bacteria that may increase the risk of chronic diseases.

Clinical Utility

This section is especially helpful for clinicians working in the areas of prevention, longevity, and personalized medicine and nutrition, in order to incorporate the risk of chronic disorders caused by gut bacteria into their holistic approach and comprehensive treatment plans.



Gut-Brain Axis

☑ Mood Disorders
☑ Alzheimer’s Disease (AD) Risk
☑ Parkinson’s Disease (PD) Risk
☑ Irritable Bowel Syndrome (IBS)

Summary:
Within typical range.

Gut-Gastrointestinal Axis

☑ Small Intestinal Bacterial Overgrowth (SIBO)
☑ Inflammatory Bowel Disease (IBD)
☑ Bile Acids (BAs) Metabolism

Summary:
Within typical range.

Gut-Metabolism Axis

☑ Obesity
☑ Type 2 Diabetes (T2D)
☑ Non-Alcoholic Fatty Liver Disease (NAFLD)

Summary:
Within typical range.

Gut-Heart Axis

☑ Hypertension (HTN)
☑ Atherosclerosis
☑ Trimethylamine (TMA) Production

Summary:
Within typical range.

Gut-Immune Axis

☑ Lipopolysaccharide (LPS) Production
☑ Histamine Production
☑ Eczema & Atopic Dermatitis

Summary:
Within typical range.