



Order: 999999-9999



Client #: 999999

Doctor: Sample Doctor, MD
Doctors Data Inc
123 Main St.
St. Charles, IL 60174 USA

Patient: Sample Patient

Id: 999999

Age: 35 DOB: 01/01/1989

Sex: Female

Sample Collection

Date Collected

Date/Time

08/10/2025

Date Received

08/13/2025

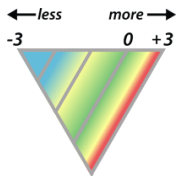
Date Reported

08/16/2025

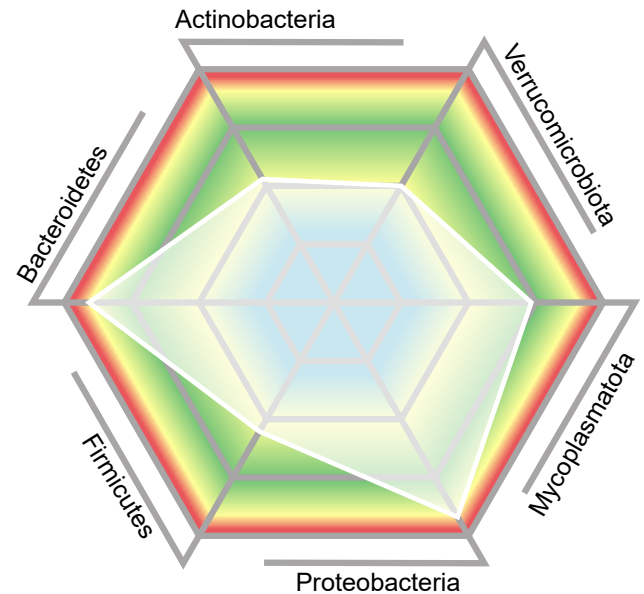
Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.

LEGEND



The web image shows the relative diversity and balance among bacteria belonging to the six primary Phyla. The white shaded area represents the patient's results compared to a normobiotic reference population. The center of the web represents less abundance while the outer edges represent more than normobiotic.

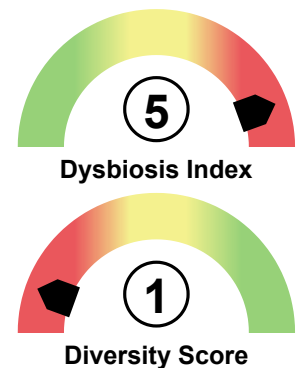


Dysbiosis and Diversity Index

These indexes are calculated from the results of the Microbiome Profile, with scores ranging from 1 to 5, and do not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

The Dysbiosis Index (DI) is calculated strictly from the results of the Microbiome Profile, with scores from 1 to 5. A DI score above 2 indicates dysbiosis; a microbiota profile that differs from the defined normobiotic reference population. The higher the DI above 2, the more the sample deviates from the normobiotic profile. The dysbiosis test and DI does not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

A diversity score of 3 indicates an expected amount of diversity, with 4 & 5 indicating an increased distribution of bacteria based on the number of different species and their abundance in the sample, calculated based on Shannon's diversity index. Scores of 1 or 2 indicate less diversity than the defined normobiotic reference population.



GI Health Markers

Butyrate producing bacteria



Gut barrier protective bacteria



Gut intestinal health marker



Pro-inflammatory bacteria



Gut barrier protective bacteria vs. opportunistic bacteria



= Expected

= Imbalanced

Key Findings



Microbiome Bacterial Abundance; Multiplex PCR



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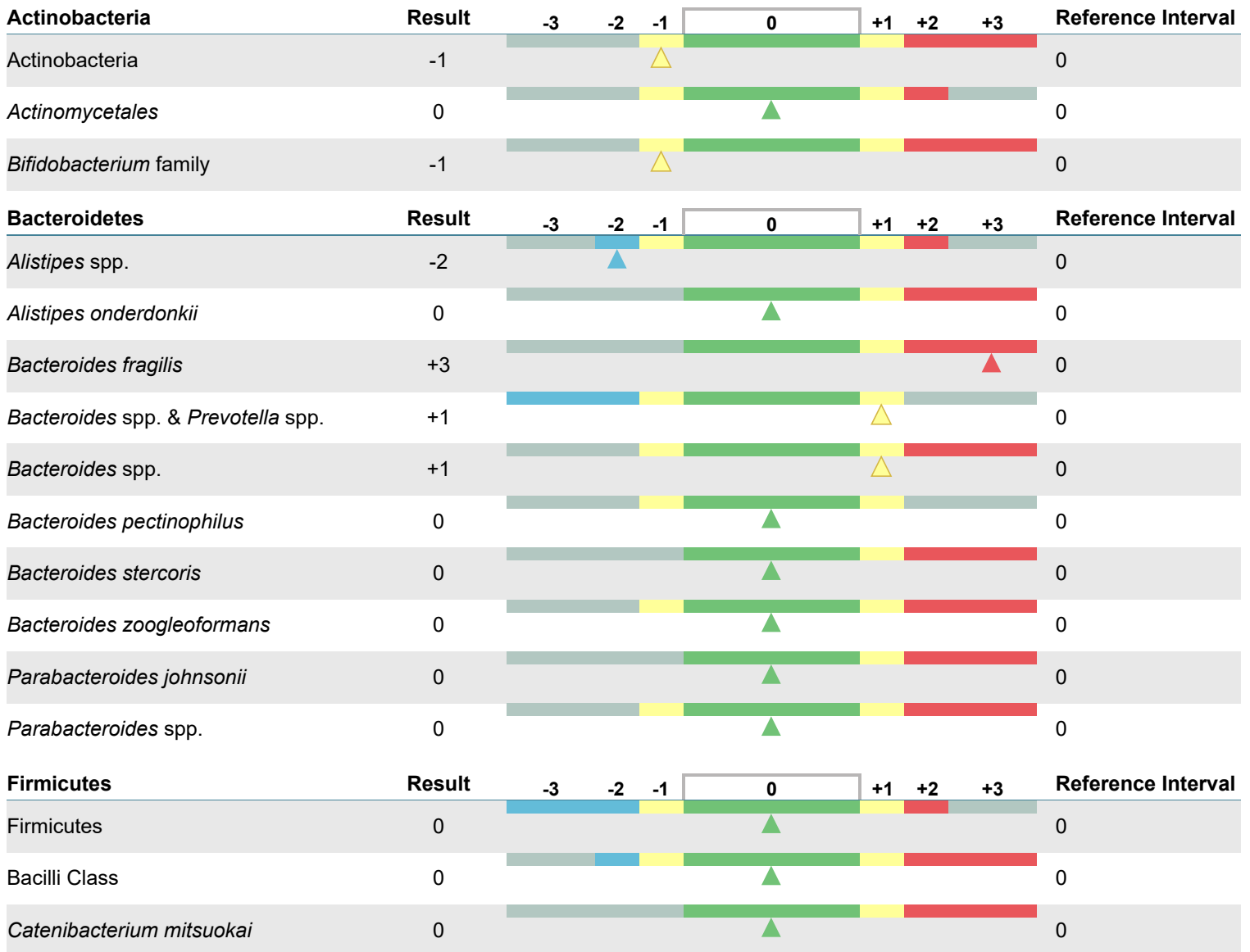
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Results are graphed as deviations from a normobiotic population. Normobiosis or a normobiotic state characterizes a composition of the microbiota profile in which microorganisms with potential health benefits predominate in abundance and diversity over potentially harmful ones.



Notes:

The gray-shaded area of the bar graph represents reference values outside the reporting limits for this test.

*This test was developed and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements. The U. S. Food and Drug Administration (FDA) has not approved or cleared this test; however, FDA clearance is not currently required for clinical use. The results are not intended to be used as a sole means for clinical diagnosis or patient management decisions.

Methodology: Multiplex PCR



Microbiome Bacterial Abundance; Multiplex PCR



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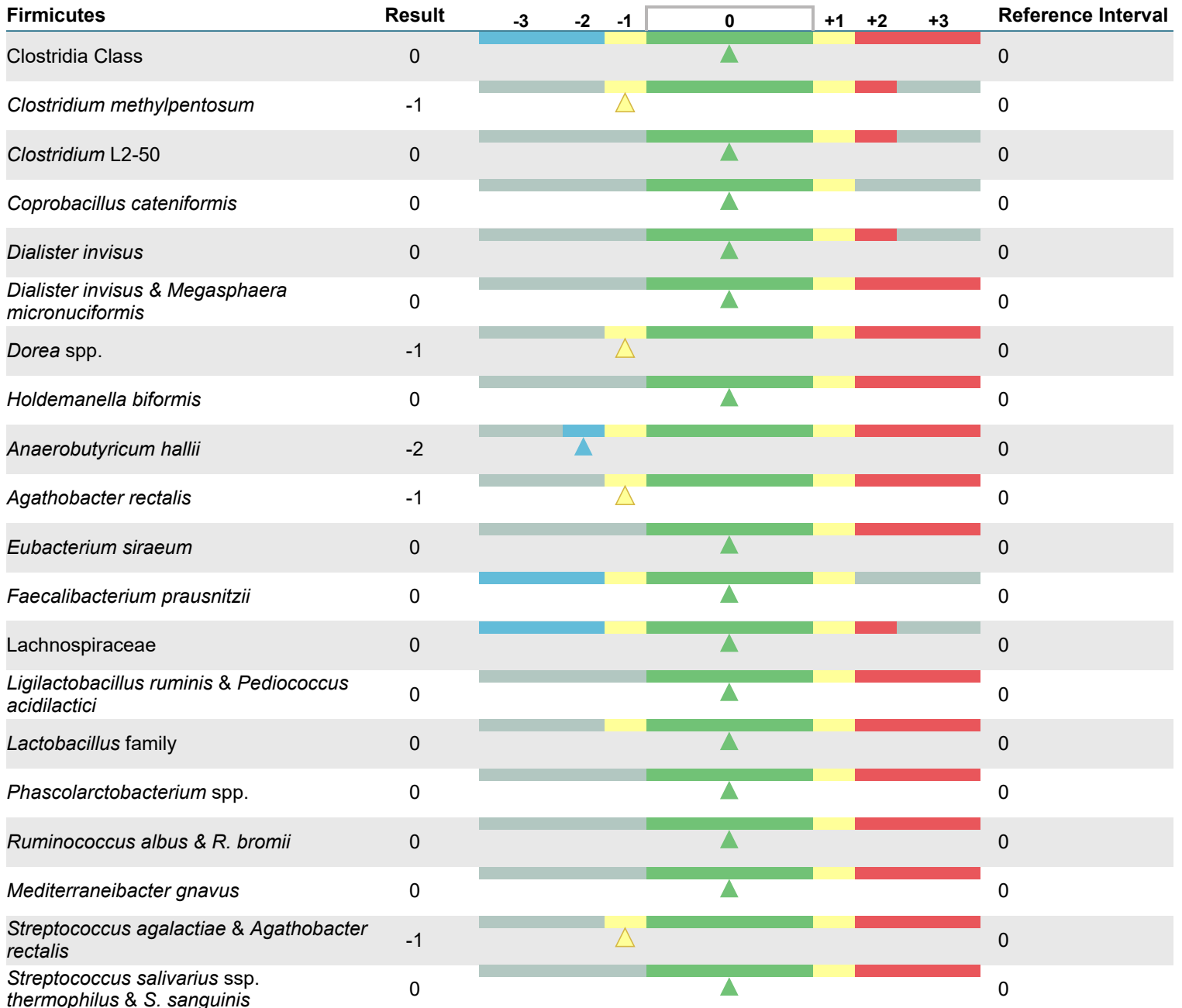
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Firmicutes	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i>	-1			▲					0
<i>Streptococcus</i> spp.	+1					▲			0
<i>Veillonella</i> spp.	0				▲				0
Proteobacteria	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
Proteobacteria	+2						▲		0
<i>Enterobacteriaceae</i>	0				▲				0
<i>Escherichia</i> spp.	+2						▲		0
<i>Acinetobacter junii</i>	0				▲				0
Mycoplasmata	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Metamycoplasma hominis</i>	0				▲				0
Verrucomicrobiota	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Akkermansia muciniphila</i>	-1			▲					0



Microbiome Abundance Information:

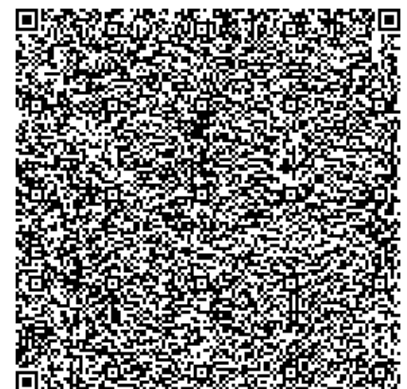
- The GI360™ Microbiome Profile is a focused gut microbiota DNA analysis tool that identifies more than 45 targeted analytes across six phyla using a CE-marked multiplex PCR system. Patient results are compared to a highly defined normobiotic reference population (n > 1,100). The white shadowed web plot within the hexagonal diagram illustrates the degree to which an individual's microbiome profile deviates from normobiosis. The center of the diagram represents less bacterial abundance while the outer edges represent greater than normobiosis. Deviation from a hexagon-shaped plot indicates variant diversity of the microbial community. Key findings for patient's microbiome profile are summarized in the table below the diagram, and detailed results for all of the analytes are presented on the next 3 pages of the report. Detailed results for the specific bacteria are reported as -3 to +3 standard deviations, as compared to the normobiotic reference population.

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Introduction

This analysis of the stool specimen provides fundamental information about the overall gastrointestinal health of the patient. When abnormal microflora or significant aberrations in intestinal health markers are detected, specific commentaries are presented. If no significant abnormalities are found, commentaries are not presented.

The majority of reference intervals are established from adult populations. Results may differ in pediatric populations and care should be taken when interpreting these values.

Microbiome Abundance Information

Actinobacteria (phylum)

Actinobacteria is one of the largest bacterial phyla, comprised of Gram-positive bacteria. This phylum includes a wide range of species, with different morphological and physiological characteristics. Significant groups in the human colon include Actinomycetales and Bifidobacteriales. Actinomycetales were inversely associated with clinically significant depression in IBS patients, suggesting these bacteria may be depleted in depressed IBS patients. A strict vegetarian diet may increase the total count of *Actinomyces* spp. compared to following a Western diet.

↓ Bifidobacterium (genus)

Considered amongst the most beneficial commensal bacteria in the human gut, *Bifidobacterium* spp. are able to degrade monosaccharides, galacto-, manno-, and fructo-oligosaccharides, as well as some complex carbohydrates. Many of the non-digestible oligosaccharides, found as natural components in mother's milk, select for colonization of these species which dominate the infant gut shortly after birth. Bifidobacteria may provide health benefits directly through interactions with the host, and indirectly through interactions with other microorganisms. *Bifidobacterium* spp. take part in production and adsorption of vitamins, such as vitamins K and B12, biotin, folate, thiamine, riboflavin, and pyridoxine. They are also involved in lipid absorption and metabolism, glucose and energy homeostasis, and regulating intestinal barrier function. Although *Bifidobacterium* produce acetate over butyrate, healthy levels of *Bifidobacterium* spp. facilitate colonization of *Faecalibacterium. prausnitzii*. Polyphenols derived from chocolate, green tea, blackcurrant, red wine and grape seed extracts have been shown to increase *Bifidobacterium* species. The increased abundance of *Bifidobacterium* species has been associated with amelioration of inflammation. Multiple published studies have suggested that there is an association between obesity and a lower abundance of bifidobacteria. They may also be less abundant in elderly populations, patients with rheumatoid arthritis, and in individuals diagnosed with Alzheimer's disease. Patients with active inflammatory bowel disease (IBD) have a lower abundance of *Bifidobacterium* spp. than patients whose IBD is in remission. Taking a probiotic containing bifidobacteria, lactobacilli, and streptococci might help in controlling ulcerative colitis symptoms and preventing their recurrence. Some *Bifidobacterium* strains have been shown to have beneficial effects in irritable bowel syndrome (IBS). *Bifidobacterium* spp. abundance has been shown to be diminished with IBD and with long term use of macrolide antibiotics. Luminal bifidobacteria is reduced with restriction of fermentable carbohydrates, i.e. a low FODMAP diet. High fat dietary feeding is also associated with reduced abundance of bifidobacteria. Consumption of maize and barley-based whole grain products and red berries, which are comprised of anthocyanins, are known to increase levels of bifidobacteria.

Bacteroidetes (phylum)

Bacteroidetes make up approximately 28% of the gut microbiota in healthy human adults. They are early colonizers of the infant gut and are amongst the most stable, at a species and strain level, in the host. A low preponderance of Bacteroidetes in relation to Firmicutes has been associated with obesity, though this can increase with weight loss and restricted calorie intake.

↓ Alistipes (genus)

Alistipes does not contribute significantly to short chain fatty acid production. A diet rich in animal protein and fat increases the abundance of *Alistipes*. High abundance of *Alistipes* was identified as a possible predictor of successful weight loss. Increased abundance of *Alistipes* has been correlated with a greater frequency of pain in pediatric irritable bowel syndrome patients. In contrast, *Alistipes onderdonkii* was shown to be decreased in patients diagnosed with ulcerative colitis. Lower abundance of the *Alistipes* genus has been observed in patients with psoriatic arthritis and pediatric Crohn's disease. *Alistipes* may positively correlate with depression.

↑ Prevotella (genus)

Prevotella-rich dysbiosis has been associated with insulin-resistance, obesity and hypertension. *Prevotella* have been shown to be significantly decreased in Crohn's disease and Parkinson's disease. High levels of fiber and carbohydrates from fruits and vegetables in a Mediterranean diet have been shown to increase the relative abundance of *Prevotella*.



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Microbiome Abundance Information continued...

↑ *Bacteroides* (species)

Species in the genus *Bacteroides* carry out broad metabolic functions, including degradation of complex plant polysaccharides, proteolytic activities, de-conjugation of bile acids, mucosal barrier integrity, short chain fatty acid production, fatty acid storage and glucose metabolism. *Bacteroides* spp. are maintained at a higher abundance in breastfed individuals into adulthood. *Bacteroides fragilis* plays an important role in the prevention of intestinal inflammation. An energy-restricted diet has been shown to increase *B. fragilis* in overweight adolescents. An increase in *B. stercoris* has been associated with higher risk of colon cancer. Decreased levels of *Bacteroides* spp. have been reported in association with multiple sclerosis, rheumatoid arthritis and Parkinson's disease.

Firmicutes (phylum)

The phylum Firmicutes constitutes the most diverse and abundant group of gastrointestinal microbiota which are grouped into four classes, Bacilli, Clostridia, Erysipelotrichia, and Negativicutes. They constitute about 39% of gut bacteria in healthy adults, but may increase to as high as 80% in an imbalanced microbial community.

↓ *Clostridium methylpentosum* (species)

Appropriate digestion and metabolism of complex dietary carbohydrates from plants drives healthy diversity in the gut microbiota. *Clostridium methylpentosum* ferments the naturally occurring sugar L-rhamnose that is released by microbial breakdown of plant-derived pectin. Rhamnose is fermented to propionate and acetate which are short chain fatty acids that have pivotal regulatory roles in the maintenance of mucosal barrier integrity, gut microbiota balance, post-prandial appetite suppression and normoglycemia. Lower levels of *C. methylpentosum* were reported for children with autism and pervasive developmental disorder compared to neurotypicals controls. Consumption of probiotic yogurt LKM512 containing *Bifidobacterium animalis* (subspecies lactis LKM512) increased the levels of *C. methylpentosum*.

↓ *Dorea* (genus)

Dorea is a genus within the *Lachnospiraceae* family that is in the Firmicutes phylum. *Dorea* species are known to produce hydrogen and carbon dioxide as end-products of glucose fermentation and may be associated with bloating. Decreased levels of *Dorea* spp. were observed in patients with Parkinson's disease. Recent studies have identified increased levels of *Dorea* spp. in patients diagnosed with IBS, nonalcoholic fatty liver disease and non-alcoholic steatohepatitis, multiple sclerosis and colorectal cancer.

↓ *Anaerobutyricum hallii* (species)

Anaerobutyricum hallii and *Agathobacter rectalis* (*Eubacterium rectale*) are both part of the *Lachnospiraceae* family that is in the Firmicutes family. *A. hallii* and *A. rectalis* produce butyrate that is a key regulator of mucosal barrier integrity and function. Decreased levels of *Anaerobutyricum*/*Agathobacter* spp have been associated with very high protein diets. *Anaerobutyricum hallii* is capable of metabolizing glucose products with antimicrobial properties.

↓ *Agathobacter rectalis* (*Eubacterium rectale*)

Agathobacter rectalis (*Eubacterium rectale*) is part of the *Lachnospiraceae* family and produce butyrate. *Agathobacter rectalis* was found to be in lower abundance in patients with type 2 diabetes, colorectal cancer, and chronic idiopathic diarrhea. There is a negative correlation between *Agathobacter rectalis* and the symptomology of irritable bowel syndrome (IBS). Decreased levels of *Anaerobutyricum*/*Agathobacter* spp. have been associated with very high protein diets.

↓ *Streptococcus* (genus)

Higher abundance of *S. salivarius* and *S. thermophilus* (Firmicutes phylum) have been associated with a moderate to severe disease course in newly diagnosed ulcerative colitis (UC) patients. These findings are in accordance with a study that showed that UC patients have significantly increased *Streptococcus* spp. and depletion of *Bifidobacterium* spp. Higher levels of *Streptococcus* spp. were also observed in patients with colorectal cancer compared to healthy controls. Administration of *S. salivarius* together with *Bifidobacterium bifidum* was shown to reduce the incidence of acute diarrhea and rotavirus shedding in infants. *S. salivarius* and *S. thermophilus* are also widely used in dairy products like yogurt and cheese.



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Microbiome Abundance Information continued...

Proteobacteria (phylum)

Proteobacteria include a wide variety of pathogens, including species within the *Escherichia*, *Shigella*, *Salmonella*, *Vibrio*, and *Helicobacter* genera. The phylum includes a number of species that are permanent residents of the microbiota and capable of inducing nonspecific inflammation and diarrhea when their presence is increased. Proteobacteria make up approximately 2% of the gut microbiota in healthy adults.

↑ Proteobacteria

A high-fat diet is positively associated with an abundance of Proteobacteria. Slightly increased abundance of Proteobacteria may be associated with low-grade inflammation. Proteobacteria are increased in inflammatory bowel disease and irritable bowel syndrome. Higher abundance of Proteobacteria has been associated with a moderate to severe disease course in newly discovered ulcerative colitis patients. They are associated with diarrhea in IBS.

↑ Escherichia (genus)

Clinically, *Escherichia* has been reported to contribute to irritable bowel syndrome. *Escherichia* spp. are commonly recovered from inflamed tissues of both Crohn's disease and ulcerative colitis patients. Untreated inflammatory bowel disease patients were shown to have higher abundance of *Escherichia* and lower abundance of *Faecalibacterium prausnitzii*. Increased levels of *Escherichia* were observed in colorectal cancer patients. Patients diagnosed with nonalcoholic steatohepatitis have higher abundance of *Escherichia*. Consumption of a Western diet is positively associated with *Escherichia* levels. Increased levels of *E. coli* were observed in people on a gluten-free diet. A non-pathogenic strain of *Escherichia*, *Escherichia nissle*, is a widely used probiotic for treating gut related diseases such as chronic constipation.

Mycoplasmata (Tenericutes) (phylum)

Mycoplasmata are cell wall-less bacteria that do not synthesize precursors of peptidoglycan. Mycoplasmatota consist of four main clades designated as the *Acholeplasma*, *Spiroplasma*, *Pneumoniae* and *Hominis* clusters. Mycoplasmatotas are typically parasites or commensals of eukaryotic hosts.

Verrucomicrobiota (Verrucomicrobia) (phylum)

Verrucomicrobiota is a less common phylum in the human microbiota, but one with increasing recognition with regards to health. Verrucomicrobiota includes *Akkermansia muciniphila*. The obligate anaerobe *A. muciniphila* constitutes 3-5% of total bacteria in a healthy microbiome, and has a protective or anti-inflammatory role in the intestinal mucosa.

↓ Akkermansia muciniphila (genus)

Higher abundance of *Akkermansia muciniphila* has been associated with a milder disease course in newly discovered ulcerative colitis patients. Archaea and *Akkermansia* were significantly more prevalent after weight reduction. A Low FODMAP diet has been shown to decrease the abundance of *A. muciniphila* leading to recommendations against long-term use of such a diet. *A. muciniphila* is a mucolytic specialist that has potent anti-inflammatory effects in part associated with a specific surface coat protein (Amuc- 1100).