

# BiomeFx™

FUNCTIONAL MICROBIOME ANALYSIS

The results from this test kit are for informational purposes only and are not intended to be a substitute for professional medical advice, diagnosis, or treatment. Always seek the advice of your physician or qualified health provider with any questions you may have regarding a medical condition.

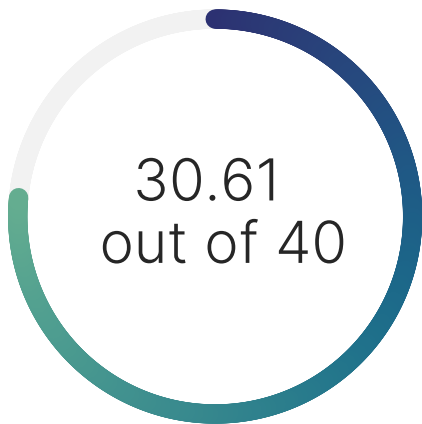
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# Your Report Summary

## Gut Microbiome Index

The Gut Microbiome Index (GMI) is an overall score for gut microbiome health. A score above 30 is considered excellent. Your Gut Microbiome Index: **30.61**



### Alpha Diversity



### Beta Diversity



### Resistome Occurrence Index



### Pathogen Control Index



## Keystone Species out of Range

<i>Akkermansia muciniphila</i>	High
<i>Bifidobacterium longum</i>	Low
<i>Bifidobacterium adolescentis</i>	Low
<i>Faecalibacterium prausnitzii</i>	High
<i>Ruminococcus bromii</i>	Low
<i>Roseburia intestinalis</i>	High
<i>Eubacterium rectale</i>	Low
<i>Limosilactobacillus reuteri</i>	Low
<i>Parabacteroides merdae</i>	High
<i>Parabacteroides goldsteinii</i>	Low
<i>Oxalobacter formigenes</i>	Low
<i>Phocaeicola vulgatus</i>	High
<i>Bifidobacterium pseudocatenulatum</i>	High

## Functions out of Range

Butyrate production	High
Vit B9 Folate	High
Vit B5 Pantothenic acid	High
Polyamine production	High
Vit B2 Riboflavin	High
Vit B1 Thiamin	High
Glutathione production	High
Hydrogen Sulfide (H <sub>2</sub> S) production	High
Histamine production	High
Ammonia production	High
P-Cresol (Phenol)	High

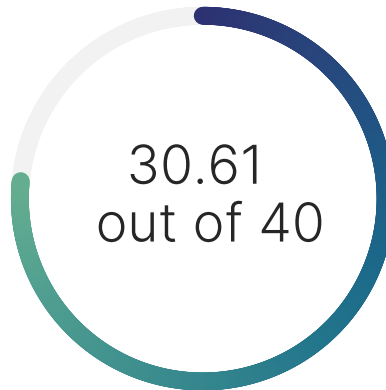
## Dysbiosis Ratios out of Range

No Dysbiosis Ratios out of range

# Your Gut Microbiome Index

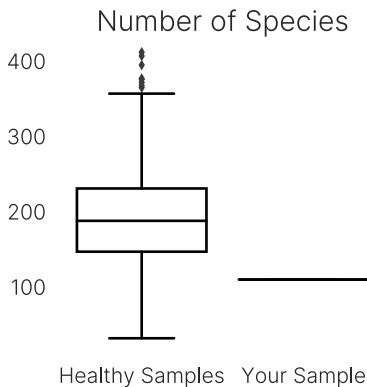
The Gut Microbiome Index (GMI) is an overall score for gut microbiome health. A score above 30 is considered excellent. It is calculated by assessing four key indicators of your gut microbiome's health and comparing them to those of a typical healthy gut microbiome. The four key indicators include Alpha Diversity (species richness), Beta Diversity (composition), Pathogen Occurrence (population of pathogens) and Resistome Occurrence (population of antibiotic resistance genes).

**Your Gut Microbiome Index (out of 40): 30.61**



## Alpha Diversity

Number of species in the gut microbiome: **110**  
 Your Alpha Diversity was found to be: **7.25**



In ecology, Alpha Diversity describes a particular ecosystem by combining information about the number of species observed and their abundance. This marker evaluates your gut microbiome by looking at your own personal species diversity, which can be negatively affected by antibiotics, environmental toxins, stress, diet, or other factors. This can lead to the microbiome being dominated by only a few species. A high Alpha Diversity indicates that the ecosystem has many species and their abundance is balanced, which is typically associated with a healthy microbiome.

The box plot to the left displays the observed species count for the healthy population and your sample. If your sample is within the confines of the box you are within the normal range of the healthy population. The slider below displays the Shannon index which takes into account species abundance and evenness.

**Note.** The Shannon index considers both species abundance and evenness. Consequently, if one or a few species disproportionately dominates the microbiome, the Alpha Diversity score may be low, even if the number of species displayed in the box plot is high.



## Beta Diversity

Your Beta Diversity was found to be: **7.31**

Beta Diversity is the variation of species when comparing the composition of two separate ecosystems. This marker compares the composition of your gut microbiome to healthy populations in order to illustrate notable differences. A higher Beta Diversity is preferred.



## Resistome Occurrence Index

Your Resistome Occurrence Index was found to be: **9.31**

This section explores the presence and abundance of a panel of antibiotic resistance genes in the gut microbiome, and compares that to healthy population. The resistome is the sum of antimicrobial resistance genes in your gut. High number of resistance functions in your gut will make pathogens less likely to be sensitive to antibiotics and may be an indication that virulent strains are flourishing.



## Pathogen Control Index

Your Pathogen Control Index was found to be: **6.75**

Low levels of pathogens can be normal and characteristic of a healthy, diverse gut microbiome. Increased levels of pathogens, however, could indicate that a pathogen is playing a role in symptoms you are experiencing. The Pathogen Control Index compares the relative abundances (RA) of specific pathogens to normal levels present in the healthy gut.

**Note.** BiomeFx is NOT a diagnostic test. If your Pathogen Control Index is low, consult your physician who can make a diagnosis and provide treatment if needed.



## Pathogen Species Found in Your Sample

The table below presents identified pathogen species in your sample. Pathogens that fall outside the IQR reference range are highlighted in bold and marked in red.

Pathogen Species	IQR in Reference (%)	Your Sample Abundance (%)
<i>Bacteroides fragilis</i>	0.0 - 0.065	<b>1.072</b>
<i>Sutterella wadsworthensis</i>	0.0 - 0.331	<b>2.074</b>

## Full List of Pathogen Species Tested

### Bacteria

*Bacteroides fragilis*  
*Bilophila wadsworthia*  
*Campylobacter jejuni*  
*Citrobacter freundii*  
*Clostridioides difficile*  
*Clostridium perfringens*  
*Enterococcus gallinarum*  
*Escherichia coli*  
*Hafnia alvei*  
*Helicobacter pylori*

*Klebsiella pneumoniae*  
*Porphyromonas gingivalis*  
*Proteus mirabilis*  
*Proteus vulgaris*  
*Pseudomonas aeruginosa*  
*Raoultella ornithinolytica*  
*Salmonella enterica*  
*Sutterella wadsworthensis*  
*Vibrio cholerae*  
*Yersinia enterocolitica*

### Protists

*Blastocystis sp subtype 1*  
*Cryptosporidium*

*Entamoeba histolytica*  
*Giardia intestinalis*

### Fungi

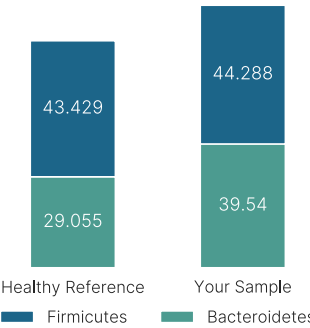
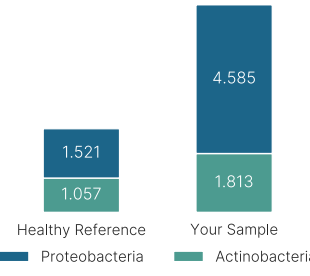
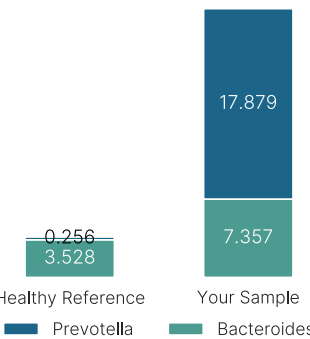
*Candida*  
*Microsporidia*  
*Aspergillus*

*Malassezia*  
*Cryptococcus*

# Your Dysbiosis Ratios

This section compares the abundance of important groups of gut bacteria between your gut and the typical healthy gut microbiome. Elevated dysbiosis ratios for these bacterial phyla or genera point to imbalances in abundance (dysbiosis) which are associated with a range of health conditions.

**Note.** In the table below, **Not Detected** is used when your sample abundance is zero. **Low Concentration (LC)** is used when your sample abundance is above zero but below .001.

	Healthy Ratio IQR	Your Ratio
 <p><b>Firmicutes:Bacteroidetes Ratio</b></p> <p>In adults, Firmicutes and Bacteroidetes are the most abundant bacterial phyla in the gut. The Firmicutes to Bacteroidetes (F/B) abundance ratio was shown to increase from infancy to adulthood and subsequently to decrease again in the elderly. Elevated F/B ratios have been linked to obesity though the evidence is not conclusive.</p>	0.677 - 2.907	1.12
 <p><b>Proteobacteria:Actinobacteria Ratio</b></p> <p>Together these phyla comprise about 10% of total gut microbes. Healthy adults tend to have no more than 4.5% Proteobacteria. Proteobacteria: Actinobacteria (P/A) ratios less than 1.0 are associated with healthy metabolism and cell turnover. Increasing Actinobacteria can be accomplished by consuming plant-derived carbohydrate starch and polysaccharides, such as FOS, GOS, XOS, inulin or arabinoxylan.</p>	0.372 - 7.989	2.528
 <p><b>Prevotella:Bacteroides Ratio</b></p> <p>High Prevotella:Bacteroides ratios are associated with lower BMI and reduced incidence of chronic, inflammatory disease. Low Prevotella:Bacteroides ratios are associated with metabolic imbalances and are positively correlated with high intake of protein and animal fat as typical for a Western diet. Higher abundance of Prevotella is observed in individuals that consume diets rich in carbohydrates and fiber. Bacteroides is increased by sugar and saturated fat intake, while Prevotella generally thrives on fiber rich foods, like fruit, vegetables, beans, and whole grains. Levels of Prevotella tend to decrease with age.</p>	0.0 - 11.298	2.43

## Functional Keystone Species

Keystone species are beneficial bacteria that have a disproportionately large effect on both their habitat and the status of other microbial communities of the gut. Keystone species create an environment that is unfriendly to pathogens yet allows good gut microbes (commensal) to thrive. This section compares relative abundances between your gut and the healthy gut microbiome.

**Note.** In the table below, **Not Detected** is used when your sample abundance is zero. **Low Concentration (LC)** is used when your sample abundance is above zero but below .001.

Keystone Species	Function	Healthy Mean	Healthy Relative Abundance IQR (%)	Your Sample Abundance (%)
<b>Phylum: Actinobacteria</b>				
<i>Bifidobacterium longum</i>	GABA Producer	0.584	0.048 - 0.628	<b>0.045</b>
<i>Bifidobacterium adolescentis</i>	Acetate Producer	1.291	0.085 - 1.397	<b>Not Detected</b>
<i>Bifidobacterium pseudocatenulatum</i>	Acetate Producer	0.608	0.023 - 0.382	<b>0.481</b>
<b>Phylum: Bacteroidetes</b>				
<i>Parabacteroides merdae</i>	Bile Acids Metabolism	0.782	0.131 - 0.841	<b>2.116</b>
<i>Parabacteroides goldsteinii</i>	Bile Acids Metabolism	0.126	0.011 - 0.092	<b>Not Detected</b>
<i>Phocaeicola vulgatus</i>	Propionate Producer	4.455	0.244 - 5.262	<b>5.619</b>
<b>Phylum: Firmicutes</b>				
<i>Faecalibacterium prausnitzii</i>	Butyrate Producer	3.06	1.086 - 3.962	<b>4.569</b>
<i>Ruminococcus bromii</i>	Cellulose Degradar	1.453	0.139 - 2.122	<b>Not Detected</b>
<i>Roseburia intestinalis</i>	Butyrate Producer	0.38	0.031 - 0.422	<b>0.937</b>
<i>Eubacterium rectale</i>	Butyrate Producer	2.398	0.393 - 3.438	<b>Not Detected</b>
<i>Limosilactobacillus reuteri</i>	Lactate Producer	0.193	0.003 - 0.14	<b>Not Detected</b>
<i>Clostridium scindens</i>	Bile Acids Metabolism	0.046	0.003 - 0.039	0.026
<b>Phylum: Proteobacteria</b>				
<i>Oxalobacter formigenes</i>	Oxalate Degradation	0.044	0.011 - 0.06	<b>0.001</b>
<b>Phylum: Verrucomicrobia</b>				
<i>Akkermansia muciniphila</i>	Acetate Producer	1.217	0.071 - 1.275	<b>5.58</b>



## Functional Analysis of your Gut Microbiome

The Functional Analysis explores your gut microbiome for genes known to contribute metabolically important functions. A higher value means that more microbial genes contributing to a function have been identified. A low value in your gut (or the typical healthy gut) microbiome does not mean that your metabolite levels are low. It only reflects the extent to which your gut microbiome can contribute to your levels.

**Note.** In the next section of the report, **density plots** are used. The shaded bell curve shows the distribution of the healthy population for that specific pathway. The dotted line represents your sample percentile, meaning where on the distribution you reside. If the dotted line is within the shaded bell curve, then you are within the range of the healthy population. The x-axis shows the abundance of the pathway.

**Note.** Below, **Not Detected** is used when your sample abundance is zero. **Low Concentration (LC)** is used when your sample abundance is above zero but below .001.

### Saccharolytic vs. Proteolytic Pathway

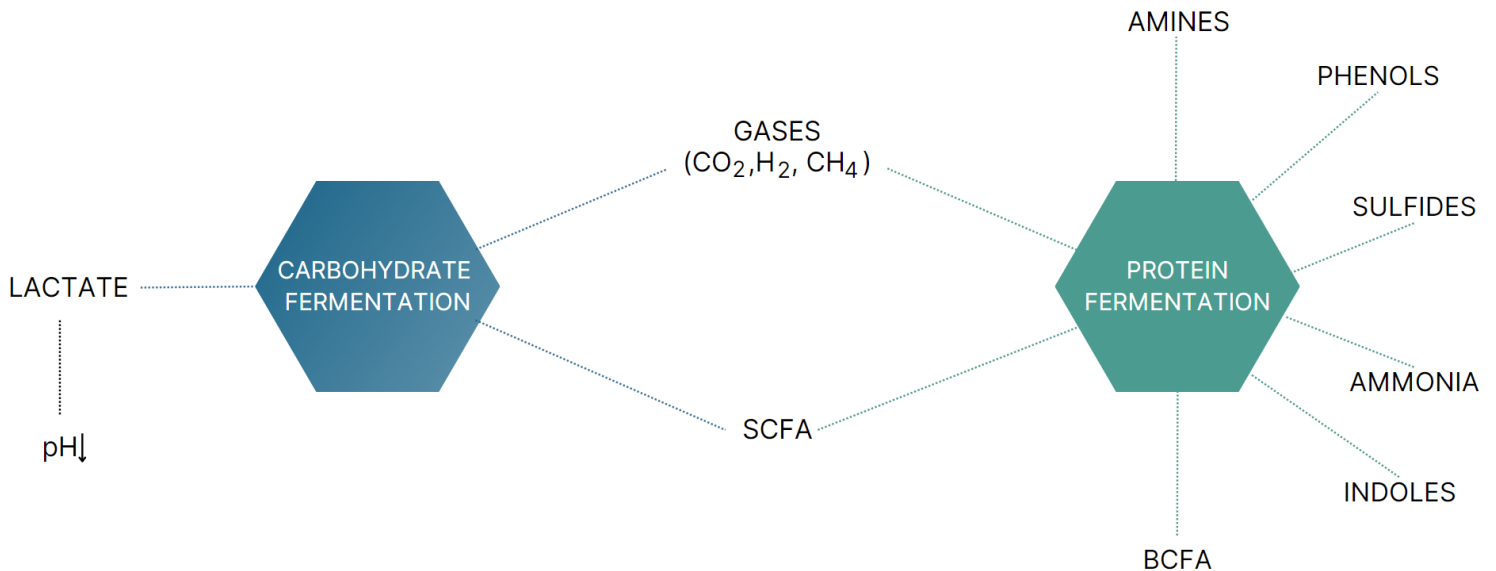


Figure 1. This image shows a comparison of the byproducts that result from carbohydrate and protein fermentation in the gut microbiome. In the image, SCFA is used to abbreviate Short-Chain Fatty Acids while BCFA is used to abbreviate Branched-Chain Fatty Acids.

## Saccharolytic Fermentation

Gut bacteria prefer to ferment carbohydrates rather than protein. Saccharolytic fermentation produces Short-Chain Fatty Acids (SCFAs), like butyrate, acetate, and propionate, as by-products. These SCFAs are the preferred energy source of intestinal cells and, as a result, can support healthy gut barrier function. Higher levels of saccharolytic fermentation are associated with healthy metabolism and reduced intestinal pH, which supports a healthy gut environment. Saccharolytic fermentation levels may be low as a result of a high-protein diet, low-fiber diet, or insufficient keystone species.

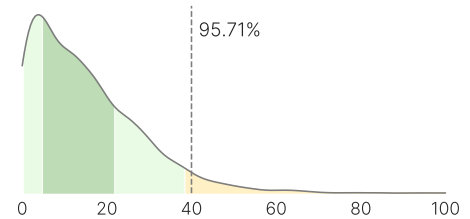
### Butyrate production

Butyrate is arguably the most important SCFA, yet it comprises only 15-20% of total SCFA production. Butyrate enhances intestinal barrier function, acts as a fuel source for enterocytes, scavenges ammonia, regulates the immune system, reduces oxidative stress, and much more. Butyrate production is mostly associated with microbial fermentation of fibers such as bran, oligosaccharides, arabinoxylan, resistant starches, and others. Furthermore, butyrate production requires an acidic environment in the gut.

**Healthy Relative Abundance IQR:** 4.843 - 21.875

**Your Sample Abundance:** 39.995

**Your Sample Percentile:** 95.71



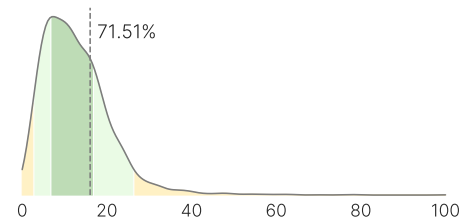
### Propionate production

Propionate is a SCFA that can be produced by gut bacteria through the fermentation of key fibers or the metabolism of lactate. Propionate supports a healthy immune system by encouraging regulatory T cell differentiation in gut associated lymphoid tissues (GALT), and it also promotes gluconeogenesis in the liver, supports insulin sensitivity, and improves gut hormone production. Propionate and butyrate both work together to support healthy inflammatory responses by inhibiting histone deacetylases (HDACs) in macrophages and dendritic cells.

**Healthy Relative Abundance IQR:** 6.863 - 16.909

**Your Sample Abundance:** 16.053

**Your Sample Percentile:** 71.51



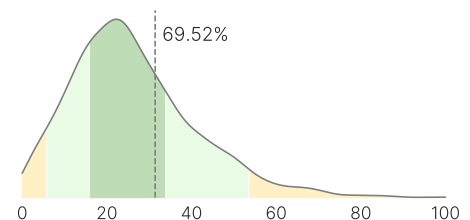
### Acetate production

Acetate is another SCFA produced by gut bacteria through the fermentation of prebiotic fibers like inulin and GOS or unabsorbed peptides and fats. Gut-derived acetate production is tightly regulated within the microbiome and determined by the presence of prebiotic fiber and the balance between saccharolytic and proteolytic fermentation. Acetate is used for cholesterol synthesis and lipogenesis but can also be utilized by muscle tissue. Additionally, some gut bacteria like *Roseburia spp* and *Faecalibacterium prausnitzii* can convert acetate into butyrate. Excessive acetate production combined with insufficient butyrate production can lead to fat gain, particularly around the liver.

**Healthy Relative Abundance IQR:** 15.848 - 34.164

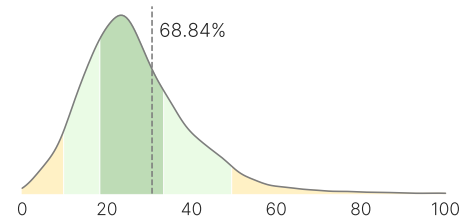
**Your Sample Abundance:** 31.408

**Your Sample Percentile:** 69.52



### Lactate production

Lactate is an intermediate of carbohydrate metabolism, produced from pyruvate during lactic acid fermentation. Lactate also plays important roles in immunomodulation and inflammation modulation. These species use lactate as a substrate for SCFA production. However, if there is an overabundance of lactate producers paired with low abundance of lactate utilizers (SCFA producers) this will cause a surge of lactate in the gut which can be toxic and harmful to host tissues.



**Healthy Relative Abundance IQR:** 18.163 - 33.445

**Your Sample Abundance:** 30.674

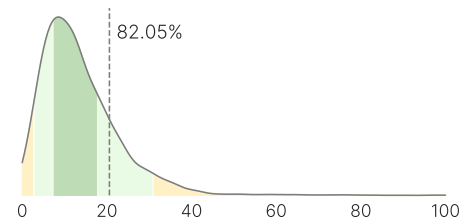
**Your Sample Percentile:** 68.84

### Proteolytic Fermentation

While both saccharolytic and proteolytic fermentation can yield beneficial SCFAs, studies show that protein fermentation also produces unfavorable metabolites like p-cresol, phenol, ammonia, and H<sub>2</sub>S that can increase inflammation in the body. Protein-degrading microbes generally only ferment protein after all dietary carbohydrates have been utilized. Higher levels of proteolytic fermentation are associated with gut dysbiosis and inflammation. Proteolytic fermentation levels may be low when the gut microbiome is more diverse and utilizing more saccharolytic fermentation.

### Polyamine production

Polyamines like putrescine, spermidine, and cadaverine are metabolites of arginine and tyrosine that have many important roles in the gut like stabilizing RNA and DNA structures, supporting protein synthesis, and scavenging free radicals. However, high amounts of polyamines can be toxic to the gut microbiome. Gut bacteria primarily synthesize amines from amino acids. Generally speaking, Gram-positive bacteria tend to reduce the concentration of amines, while Gram-negative species produce amines and increase their concentration.



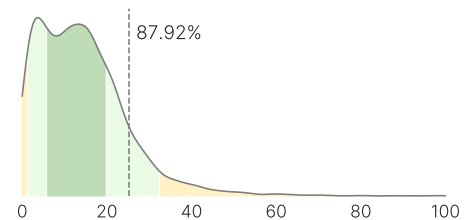
**Healthy Relative Abundance IQR:** 7.078 - 17.934

**Your Sample Abundance:** 20.606

**Your Sample Percentile:** 82.05

### P-Cresol (Phenol)

P-cresol is a byproduct of tyrosine metabolism by gut bacteria that can be toxic to intestinal cells and impair intestinal barrier function. P-cresol is also toxic to a wide range of gut microbiota, particularly Gram-negative species.



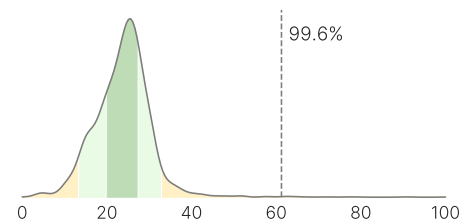
**Healthy Relative Abundance IQR:** 5.845 - 19.715

**Your Sample Abundance:** 25.233

**Your Sample Percentile:** 87.92

### Ammonia production

Ammonia is a normal byproduct of amino acid fermentation by gut microbes. Ammonia is also produced in the small intestine through the bacterial degradation of glutamine. Healthy liver and kidneys can filter and excrete ammonia through the urine.



**Healthy Relative Abundance IQR:** 19.852 - 27.41

**Your Sample Abundance:** 61.25

**Your Sample Percentile:** 99.6

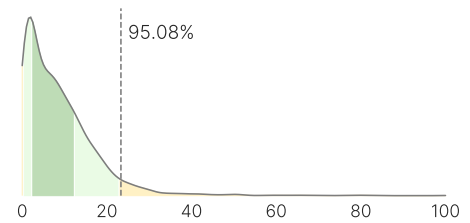
## Hydrogen Sulfide (H<sub>2</sub>S) production

Sulfate-reducing bacteria convert dietary sulfur and taurine to H<sub>2</sub>S, a toxic compound that impairs intestinal detoxification pathways and can cause gas that smells like rotten eggs. H<sub>2</sub>S production is associated with high-protein, low-fiber diets. Sulfate-reducing bacteria compete with methane-producers and acetate-producers for the same H<sub>2</sub> substrate; and as a result, it is important to maintain a delicate balance among all three.

**Healthy Relative Abundance IQR:** 2.227 - 12.414

**Your Sample Abundance:** **23.326**

**Your Sample Percentile:** 95.08



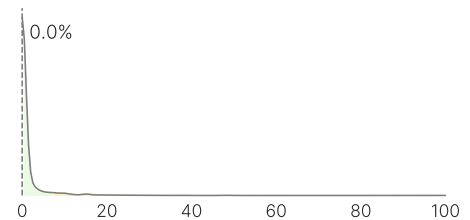
## Methane Production

Methanogens convert acetate, ammonia, hydrogen gas, and trimethylamines (TMA) to methane gas. Methane gas also slows the intestinal transit and affects gut motility, which may also allow increased time for nutrient absorption. Furthermore, methane producers compete with acetate producers for substrate utilization, which may explain why methanogens are indirectly associated with digestive issues. Methanogens convert acetate, ammonia, hydrogen gas, and TMA to methane gas. Methane gas also slows the intestinal transit and affects gut motility, which may also allow increased time for nutrient absorption. Furthermore, methane producers compete with acetate producers for substrate utilization, which may explain why methanogens are indirectly associated with digestive issues.

**Healthy Relative Abundance IQR:** 0.0 - 0.044

**Your Sample Abundance:** Not Detected

**Your Sample Percentile:** 0.0



## Hormones and Neurotransmitters

Hormones are produced in endocrine glands and are transmitted through the blood stream. Neurotransmitters are released by presynaptic nerve terminal into the synapse and transmitted across the synaptic cleft.

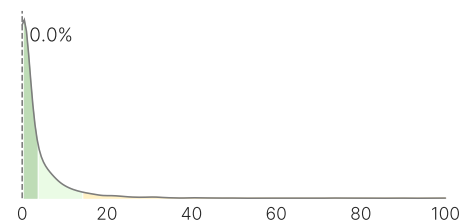
### GABA production

Gamma-aminobutyric acid (GABA) is a neurotransmitter, or chemical messenger, in the brain that blocks specific signals in the central nervous system in order to slow down the brain. This provides a protective and calming effect on the brain and body. High fat diets are shown to reduce GABA levels in the prefrontal cortex by 40% which can result in various mood imbalances and difficulty sleeping.

**Healthy Relative Abundance IQR:** 0.0 - 3.576

**Your Sample Abundance:** Not Detected

**Your Sample Percentile:** 0.0



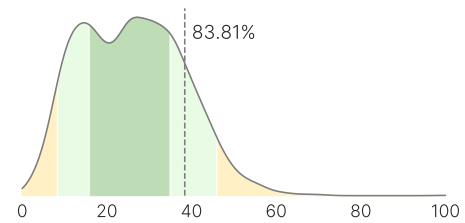
### Glutathione production

Glutathione is the most powerful antioxidant in the human body. It is found in nearly every cell in the body and is the primary agent of detoxification in the liver. Glutathione can also act as a hormone, regulating the release of GABA and dopamine. Glutathione is produced from three amino acids glutamate, cysteine, and glycine which are obtained from food or supplementation. Deficiency in glutathione may lead to production of free radicals and oxidative damage throughout the body. Recent evidence suggests that the gut microbiome determines levels of glutathione throughout the body.

**Healthy Relative Abundance IQR:** 15.809 - 34.812

**Your Sample Abundance:** **38.405**

**Your Sample Percentile:** 83.81



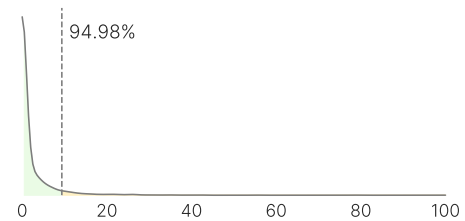
### Histamine production

Histamine can be produced in the gut and travel to distant areas of the body, where it may induce unfavorable symptoms. Patients with an overabundance of histamine-producing bacteria should focus on strengthening intestinal barrier function, as a leaky gut can allow gut derived histamines to enter circulation and promote dietary intolerances or disruption in healthy allergic responses. High levels of gut derived histamine are associated with high abundance of Proteobacteria, Roseburia, Morganii morganii, and Klebsiella pneumoniae and decreased abundance of Bifidobacterium.

**Healthy Relative Abundance IQR:** 0.0 - 0.0

**Your Sample Abundance:** **9.366**

**Your Sample Percentile:** 94.98



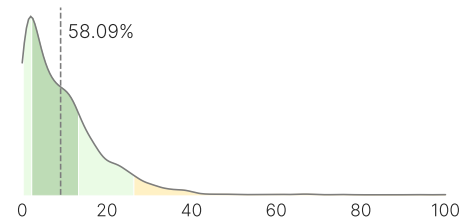
### Indole production

Indole is a byproduct of the microbial degradation of tryptophan that can be utilized in a variety of ways in the gut microbiome. Indole can bind to serotonin receptors in order to regulate behavior, gut motility, and food intake, and it can support immune and intestinal health by interacting with gut microbes, scavenging free radicals, and increasing the expression of xenobiotic-metabolizing enzymes like cytochrome P450. Indole also functions as a signaling molecule that may be increased during latent infections. Indole production must be balanced, as too much indole may produce unwanted changes in mood or cognition, yet insufficient indole production may damage the gut barrier.

**Healthy Relative Abundance IQR:** 2.452 - 13.432

**Your Sample Abundance:** 9.079

**Your Sample Percentile:** 58.09



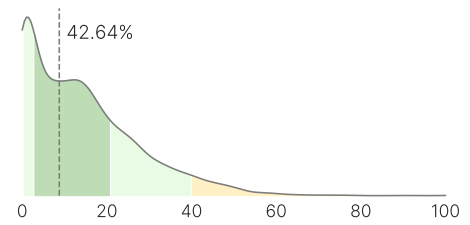
## Estrogen recycling (Estrobolome)

The estrobolome is a network of over 60 genera of bacteria that can recycle or deconjugate inactivated estrogens for reabsorption into circulation by producing very powerful enzymes. This recycling process is handled by gut bacteria with beta-glucuronidase and beta-glucosidase activity. When the estrobolome is too abundant, the body is unable to efficiently eliminate estrogen, causing estrogens to build up and ultimately leading to estrogen dominance. On the other hand, if estrogen recycling (estrobolome) is too low, then this may lead to insufficient levels of estrogen in circulation.

**Healthy Relative Abundance IQR:** 2.595 - 21.054

**Your Sample Abundance:** 8.761

**Your Sample Percentile:** 42.64



## Vitamin Biosynthesis

Gut bacteria synthesize vitamin K2 and many of the B vitamins including biotin (B7), cobalamin (B12), folates (B8), nicotinic acid (B3), pantothenic acid (B5), pyridoxine (B6), riboflavin (B2), and thiamine (B1). Vitamin production levels may be low as a result of low Alpha Diversity the gut.

**Note.** In this section, the **percentile charts** to the right compare the relative abundance for each vitamin between your gut microbiome and the microbiomes typical for healthy populations.

**Note.** Below, **Not Detected** is used when your sample abundance is zero. **Low Concentration (LC)** is used when your sample abundance is above zero but below .001.

### Vit B2 Riboflavin

Vitamin B2 (riboflavin) is a cofactor needed for energy production and fat metabolism that also plays an important role in immune cell function.

**Healthy Relative Abundance IQR:** 36.18 - 52.516

**Your Sample Abundance:** 54.486



### Vit B5 Pantothenic acid

Vitamin B5 (pantothenic acid) is essential for energy production and fat metabolism. *Bacteroides fragilis*, *Prevotella copri*, *Ruminococcus spp*, *Salmonella enterica*, and *Helicobacter pylori* can all produce vitamin B5 in the gut. However, there are many species that rely on vitamin B5 for growth but cannot synthesize it, like most *Fusobacterium*, *Bifidobacterium spp*, *Faecalibacterium spp*, *Lactobacillus spp*, and some strains of *Clostridium difficile*, suggesting that these bacteria may compete with the host for vitamin B5.

**Healthy Relative Abundance IQR:** 31.762 - 42.418

**Your Sample Abundance:** 46.668



### Vit B6 Pyridoxine

Vitamin B6 (pyridoxine) is an incredibly versatile nutrient that supports immunity, brain function, and protein metabolism.

**Healthy Relative Abundance IQR:** 7.897 - 25.467

**Your Sample Abundance:** 24.941



### Vit K2 Menaquinone

Vitamin K2 is a fat-soluble vitamin necessary for calcium metabolism and critical for the health of teeth, bones, nerves, and the cardiovascular system. Most K2 comes from dietary sources, however, gut bacteria including *Escherichia coli*, *Bacteroides vulgatus*, *Bacillus subtilis* and *Bacteroides fragilis* can also produce K2 endogenously. However, microbially derived K2 has protective role against oxidative tissue damage in the gut.

**Healthy Relative Abundance IQR:** 0.0 - 6.347

**Your Sample Abundance:** Not Detected



### Vit B1 Thiamin

Thiamin is a vitamin that plays a critical role in energy metabolism, especially in the brain and nervous system. Thiamin also plays an important role in muscle contraction and nerve conduction.

*Faecalibacterium spp* utilize thiamine but do not produce it, indicating that there is a competition for vitamins within the gut microbiome.

**Healthy Relative Abundance IQR:** 37.323 - 50.4

**Your Sample Abundance:** 64.547

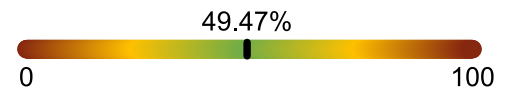


### Vit B7 Biotin

Biotin (also known as Vitamin H, Vitamin B7, or Vitamin B8) is a water soluble vitamin necessary for growth, development, and cellular energy production that can support healthy hair, skin, and nails and support healthy immune responses. Biotin is synthesized from tryptophan by intestinal bacteria like *Bacteroides fragilis*, *Prevotella copri*, *Ruminococcus lactaris*, *Clostridium difficile*, *Bifidobacterium infantis*, *Helicobacter pylori*, and *Fusobacterium varium*. In contrast, some species of *Prevotella*, *Bifidobacterium*, *Clostridium*, *Ruminococcus*, *Faecalibacterium*, and *Lactobacillus* may steal biotin from the host as they need it for survival.

**Healthy Relative Abundance IQR:** 10.514 - 29.686

**Your Sample Abundance:** 18.797



### Vit B9 Folate

Vitamin B9 (folate or tetrahydrofolate), is essential for healthy blood cells. Gut-derived folate is directly absorbed into the colon, contributing up to 37% of the daily recommended intake. If vitamin B9 producers are low, there could be low levels of this nutrient available to the body.

**Healthy Relative Abundance IQR:** 0.0 - 10.795

**Your Sample Abundance:** 11.784



### Vit B12 Cobalamin

Vitamin B12 (cobalamin) is crucial for healthy red blood cells, brain and nervous system function, DNA regulation, and metabolism. Production of B12 by gut bacteria contribute up to 31% of the daily recommended intake for this nutrient.

**Healthy Relative Abundance IQR:** 16.185 - 38.666

**Your Sample Abundance:** 36.864





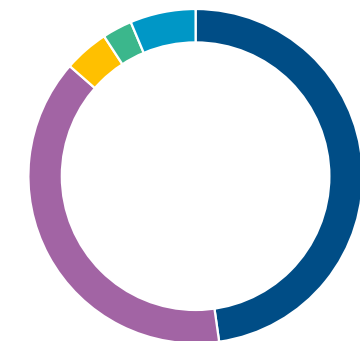
# Your Gut Microbiome Composition

## Phylum level

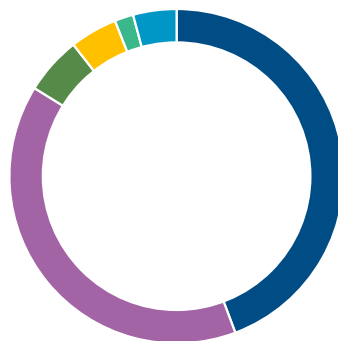
This section explores the composition of your gut microbiome at phylum level resolution. The **donut charts** visualize the most abundant bacterial phyla in both the healthy population and your gut. The **percentile charts** to the right compare the relative abundance for each bacterial phylum between your gut microbiome and the microbiomes typical for healthy populations. The table below provides a detailed overview of the phyla data.

Phylum Level Healthy

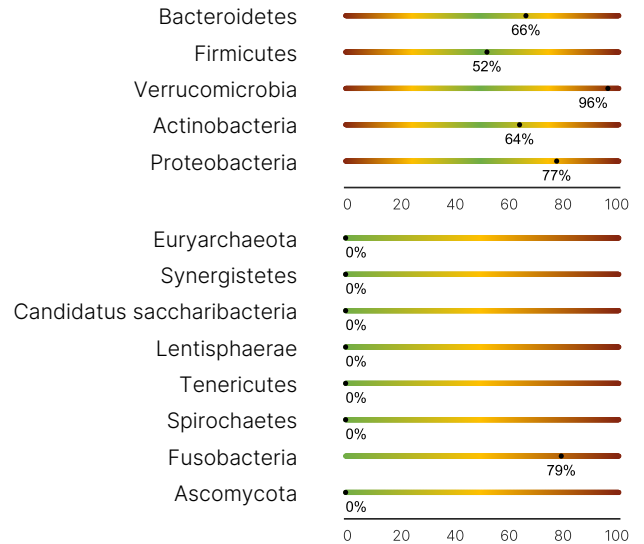
Phylum Level Your Sample



- Firmicutes 47.75%
- Bacteroidetes 38.69%
- Proteobacteria 4.34%
- Actinobacteria 2.88%
- Others 6.34%



- Firmicutes 44.29%
- Bacteroidetes 39.54%
- Verrucomicrobia 5.58%
- Proteobacteria 4.58%
- Actinobacteria 1.81%
- Others 4.19%

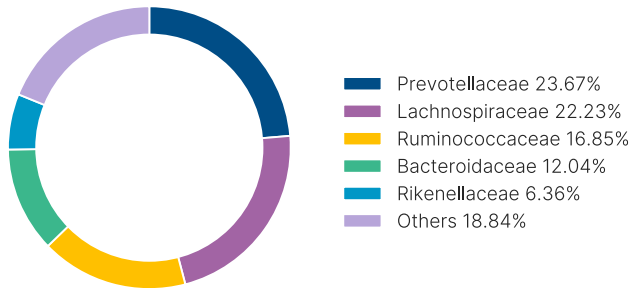


Phylum	Healthy Relative Abundance IQR (%)	Your Sample Relative Abundance (%)	Your Sample Percentile
Firmicutes	28.832 - 54.715	44.288	51.727
Bacteroidetes	18.481 - 47.19	39.54	65.994
Proteobacteria	0.689 - 4.022	4.585	77.244
Actinobacteria	0.351 - 2.756	1.813	63.662
Spirochaetes	0.267 - 1.775	0.0	0.0
Verrucomicrobia	0.071 - 1.224	5.58	95.997
Euryarchaeota	0.035 - 0.766	0.0	0.0
Tenericutes	0.016 - 0.45	0.0	0.0
Lentisphaerae	0.023 - 0.296	0.0	0.0
Synergistetes	0.004 - 0.035	0.0	0.0
Fusobacteria	0.003 - 0.106	0.137	78.93
Candidatus saccharibacteria	0.002 - 0.009	0.0	0.0
Ascomycota	0.002 - 0.009	0.0	0.0

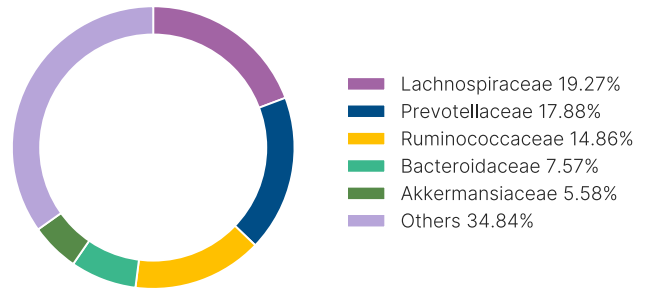
## Family level

This section explores the composition of your gut microbiome at family level resolution. The **donut charts** to the left visualize the most abundant bacterial genera in both the healthy population and your gut. The table below provides a detailed overview of the family data.

### Family Level Healthy



### Family Level Your Sample



Phylum	Family	Healthy Relative Abundance IQR (%)	Your Sample Relative Abundance (%)	Your Sample Percentile
Firmicutes	Lachnospiraceae	7.761 - 20.713	19.273	70.229
Firmicutes	Ruminococcaceae	5.527 - 16.279	14.862	68.424
Bacteroidetes	Prevotellaceae	0.507 - 29.47	17.879	64.558
Bacteroidetes	Bacteroidaceae	1.442 - 10.406	7.569	66.937
Bacteroidetes	Rikenellaceae	1.108 - 5.811	4.713	67.145
Firmicutes	Clostridiaceae	0.76 - 2.715	4.725	92.399
Firmicutes	Veillonellaceae	0.131 - 1.745	0.0	0.0
Bacteroidetes	Tannerellaceae	0.224 - 1.456	3.157	91.14
Actinobacteria	Bifidobacteriaceae	0.127 - 2.109	0.527	47.338
Spirochaetes	Brachyspiraceae	0.148 - 1.026	0.0	0.0
Firmicutes	Acidaminococcaceae	0.179 - 1.054	1.089	76.344
Proteobacteria	Sutterellaceae	0.19 - 0.808	2.074	95.525
Firmicutes	Erysipelotrichaceae	0.172 - 0.765	0.237	32.884
Verrucomicrobia	Akkermansiaceae	0.075 - 1.288	5.58	95.622
Firmicutes	Oscillospiraceae	0.16 - 0.768	0.744	73.843
Bacteroidetes	Barnesiellaceae	0.108 - 0.871	0.0	0.0
Bacteroidetes	Odoribacteraceae	0.097 - 0.547	0.0	0.0
Firmicutes	Eubacteriaceae	0.115 - 0.627	0.0	0.0
Bacteroidetes	Dysgonomonadaceae	0.015 - 0.022	0.0	0.0
Bacteroidetes	Porphyromonadaceae	0.003 - 0.022	0.0	0.0

## Additional Observed Families in your Microbiome

The organisms in the previous page typically occur in the healthy gut at Relative Abundances of above 0.5%. Organisms from the table below occur more rarely, but have been detected in your gut microbiome.

Phylum	Family	Healthy Relative Abundance IQR (%)	Your Sample Relative Abundance (%)	Your Sample Percentile
Actinobacteria	Eggerthellaceae	0.03 - 0.261	0.649	93.71
Proteobacteria	Desulfovibrionaceae	0.047 - 0.232	0.56	95.812