

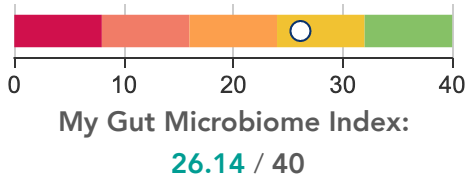
BiomeFx™

FUNCTIONAL MICROBIOME ANALYSIS

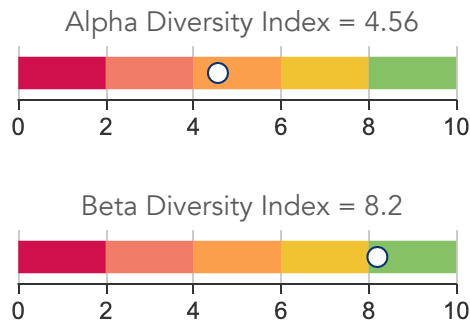
The results from this test kit are for informational purposes only and are not intended to be a substitute for professional medical advice, diagnosis, or treatment. Always seek the advice of your physician or qualified health provider with any questions you may have regarding a medical condition.

Report Summary

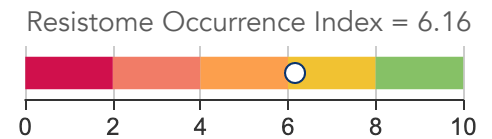
Gut Microbiome Index



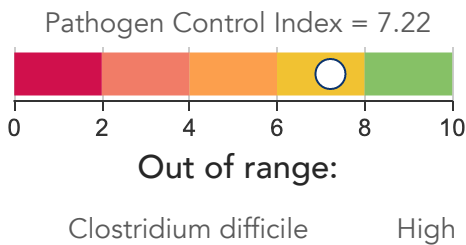
Diversity



AMR Richness



Pathogens



Keystone Species

Out of range:

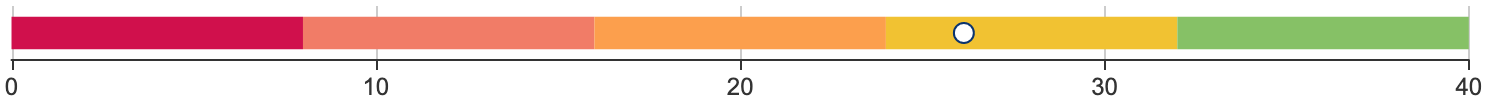
Akkermansia muciniphila	Low
Faecalibacterium prausnitzii	High
Ruminococcus bromii	Low
Ruminococcus flavefaciens	Low
Roseburia intestinalis	Low
Butyricoccus pullicaecorum	Low
Bifidobacterium adolescentis	Low
Lactobacillus rhamnosus	Low
Lactobacillus reuteri	Low
Total Lactobacillus species	Low

Functions

Out of range:

Saccharolytic fermentation	Low
Butyrate production	Low
Propionate production	Low
GABA	Low
Indole production	Low
Vitamin biosynthesis	Low
Methanogens	Low
Sulfate Reduction	High

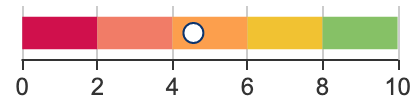
My Gut Microbiome Index (out of 40): **26.14**



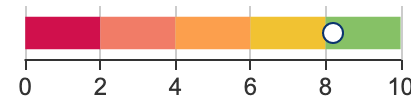
The Gut Microbiome Index (GMI) is an overall score for gut microbiome health. A score above 30 is considered excellent. It is calculated by assessing four key indicators of microbiome health for your gut microbiome and comparing them to the typical healthy gut microbiome. The four key indicators include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

My Gut Microbiome Alpha- and Beta-Diversity

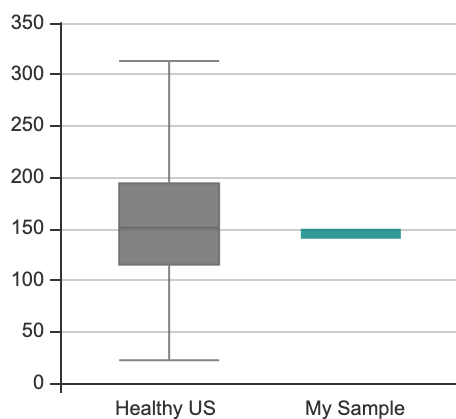
Alpha Diversity Index = 4.56



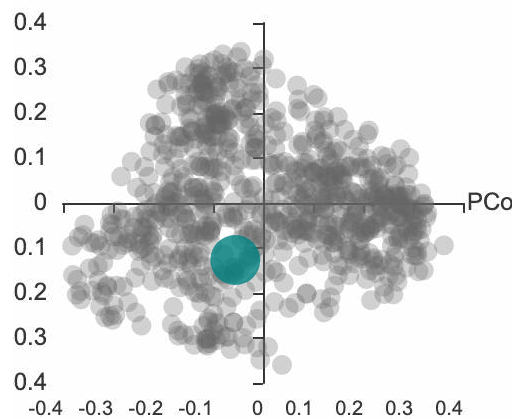
Beta Diversity Index = 8.2



Healthy US My Sample



PCoA2

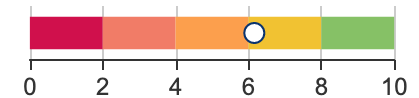


Number of species in gut microbiome: **145**
In ecology, **Alpha-Diversity** refers to the average diversity, or the richness of species, in a particular ecosystem. This marker is looking at your own personal species richness within your gut microbiome. A Low Alpha-Diversity Index suggests that your gut microbiome was recently damaged by antibiotics, environmental toxins, stress, diet, or other factors.

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. The green dot for your sample not falling within the clusters of grey dots (healthy) leads to a low Beta-Diversity Index suggesting that your gut microbiome composition is trending away from a healthy gut to an imbalanced, dysbiotic gut.

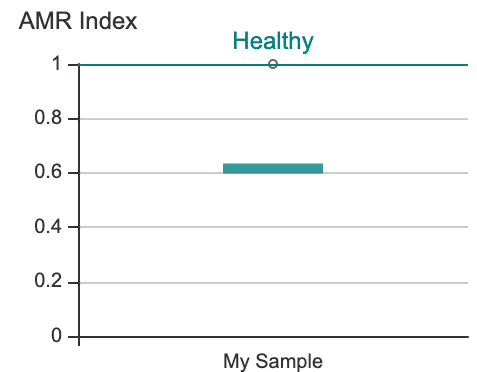
My Gut Stability and Uniformity

Resistome Occurrence Index = 6.16



AMR index

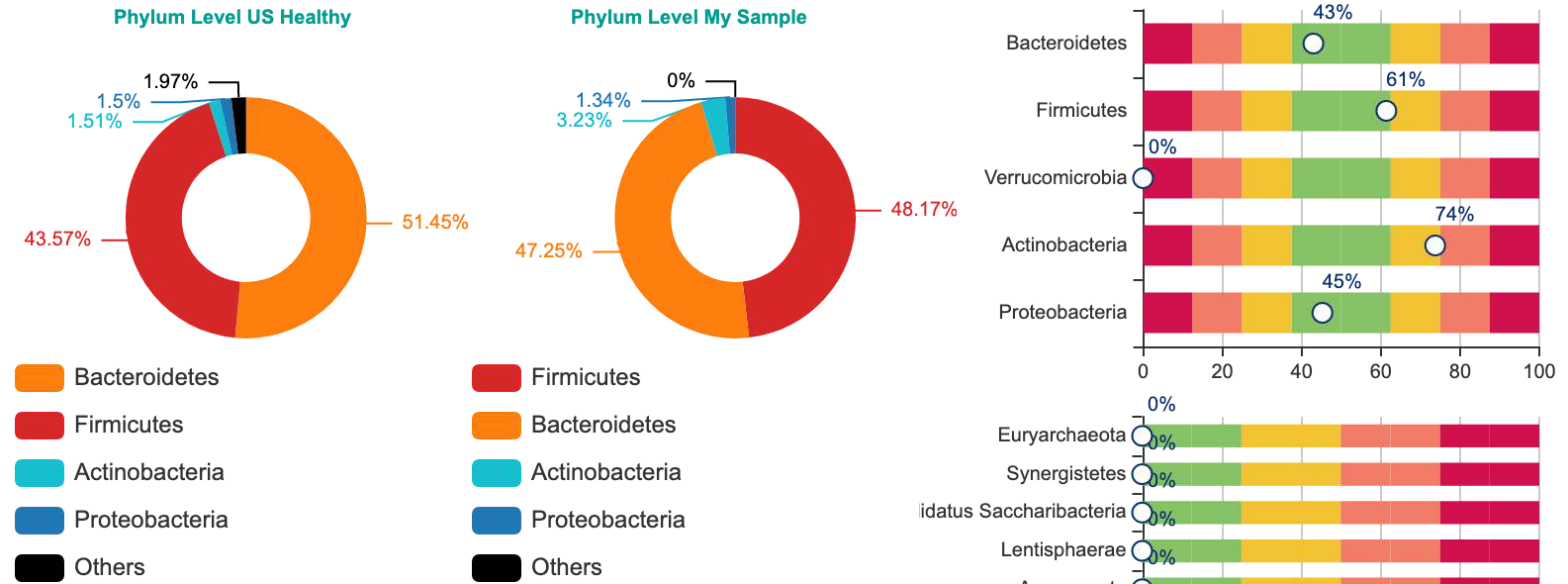
AMR index indicates distance between my sample and the average Healthy microbiome



This section explores the richness and stability of your gut microbiome by comparing the resilience of your gut microbiome to Healthy populations. A low index suggests that you have low richness and resilience in your gut.

My Gut Microbiome Composition (Phylum level)

This section explores the composition of your gut microbiome at phylum level resolution.



The Donut Charts to the left visualizes the most abundant bacterial phyla in your gut.

The Percentile Chart to the right compares the relative abundance (RA) for each bacterial phylum between your gut microbiome and the microbiomes typical for healthy populations. Percentile values between around 25% – 75% are typical, low values for a certain phylum suggest that in your case relative abundances are on the low side, high values suggest that your abundances are on the high side.

Phylum	Healthy Population Relative Abundance IQR Range [%]	My Sample Relative Abundance[%]	My Sample Percentile
Bacteroidetes	32.672 - 66.333	47.255	42.986
Firmicutes	27.629 - 57.18	48.169	61.39
Verrucomicrobia	0.22 - 1.794	0	0
Actinobacteria	0.25 - 3.382	3.231	73.726
Proteobacteria	0.731 - 2.739	1.345	45.254
Euryarchaeota	0.055 - 0.602	0	0
Synergistetes	0.022 - 0.277	0	0
Candidatus Saccharibacteria	0.007 - 0.016	0	0
Lentisphaerae	0.049 - 0.414	0	0
Ascomycota	0.001 - 0.002	0	0
Microsporidia	0.002 - 0.016	0	0
Negarnaviricota	0.001 - 0.006	0	0
Tenericutes	0.028 - 0.075	0	0
Spirochaetes	0.079 - 1.299	0	0
Fusobacteria	0.012 - 0.097	0	0

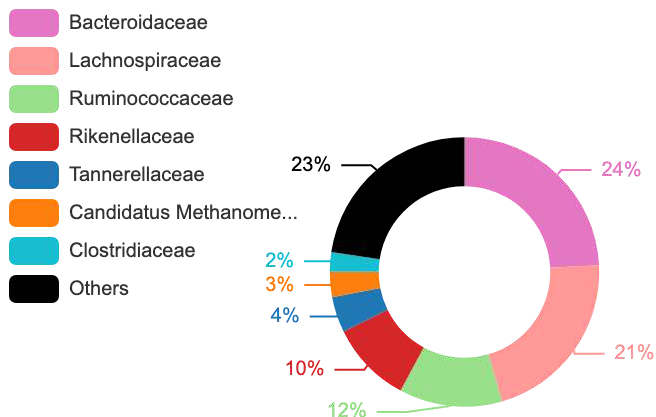
My Gut Microbiome Composition (Family level)

This section explores the composition of your gut microbiome at family level resolution.

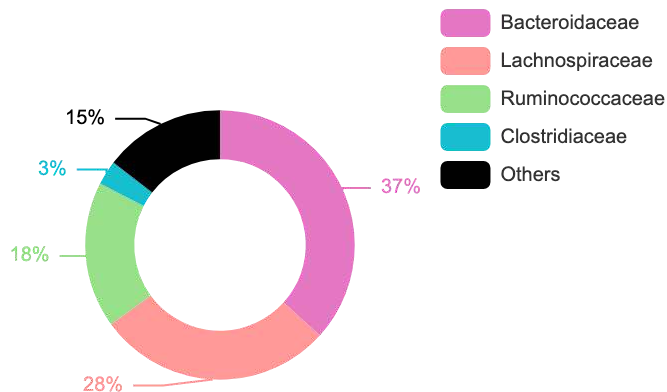
The [Donut Charts](#) visualize the most abundant bacterial genera in your gut.

The [Percentile Chart](#) below compares the relative abundance (RA) for each bacterial genera between your gut microbiome and the microbiomes typical for healthy populations. Percentile values between around 25% – 75% are typical, low values for a certain family suggest that in your case relative abundances are on the low side, high values suggest that your abundances are on the high side.

Family Level US Healthy



Family Level My Sample



Phylum	Family	Healthy Population Relative Abundance IQR Range [%]	My Sample Relative Abundance[%]	My Sample Percentile
Bacteroidetes	Bacteroidaceae	12.62 - 36.79	36.72	75.03
Firmicutes	Lachnospiraceae	11.77 - 30.91	28.28	69.37
Firmicutes	Ruminococcaceae	8.23 - 15.76	17.53	81.6
Firmicutes	Clostridiaceae	1.4 - 3.14	2.94	71.74
Actinobacteria	Bifidobacteriaceae	0.31 - 3.3	1.92	62.46
Bacteroidetes	Rikenellaceae	5.37 - 14.22	1.87	6.7
Firmicutes	Erysipelotrichacea...	0.14 - 1.51	1.26	70.35
Bacteroidetes	Tannerellaceae	2.23 - 6.37	1.1	12.82
Bacteroidetes	Odoribacteraceae	0.49 - 1.66	0.73	36.74
Firmicutes	Eubacteriaceae	0.37 - 1.38	0.68	43.98
Proteobacteria	Sutterellaceae	0.3 - 1.68	0.53	38.11
Firmicutes	Veillonellaceae	0.27 - 2.17	0.31	27.99
Firmicutes	Oscillospiraceae	0.8 - 2.07	0.25	5.4
Bacteroidetes	Porphyromonadaceae	0.09 - 1.28	0.07	22.54
Verrucomicrobia	Akkermansiaceae	0.26 - 2.17	0	0
Bacteroidetes	Barnesiellaceae	0.69 - 2.31	0	0
Firmicutes	Acidaminococcaceae	0.52 - 1.99	0	0
Bacteroidetes	Prevotellaceae	0.06 - 5.91	0	0
Spirochaetes	Brachyspiraceae	0.08 - 1.4	0	0
Euryarchaeota	Candidatus Methano...	3.63 - 3.63	0	0
Phylum unknown	Dysgonomonadaceae	1.15 - 4.8	0	0

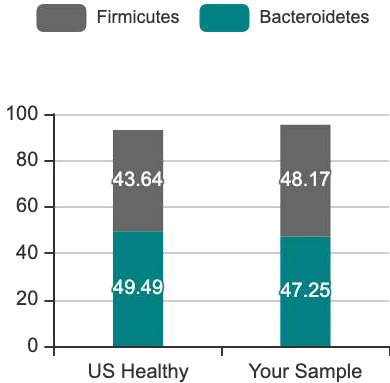
My Gut Microbiome Composition (Family level)

Note: The organisms in the previous page typically occur in the healthy gut at Relative Abundances (RA) of > 0.5%. Organisms from the current page occur more rarely, but have been detected in your gut microbiome.

Phylum	Family	Healthy Population Relative Abundance IQR Range [%]	My Sample Relative Abundance[%]	My Sample Percentile
Firmicutes	Peptostreptococcaceae	0.07 - 0.45	1.03	92.04
Actinobacteria	Eggerthellaceae	0.14 - 0.68	1.91	97.62
Firmicutes	Streptococcaceae	0.04 - 0.37	1.95	96.11

Dysbiosis Ratios

This section compares the abundances 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.



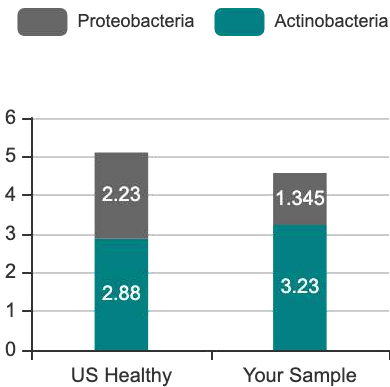
Description	Healthy Ratio IQR	My Ratio
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Firmicutes:Bacteroidetes (F/B) Ratio

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. Healthy F/B ratios differ significantly between studies and can exceed 0.25 (shown here), in some studies even 1.

0.42 ~ 1.73

1.02

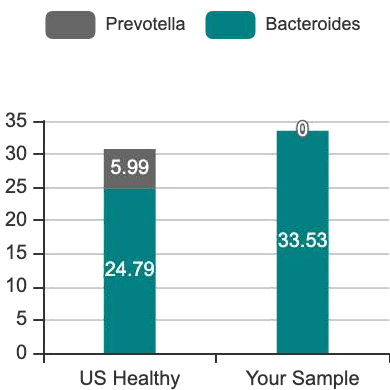


Proteobacteria:Actinobacteria (P/A) Ratio

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 arabinosylin.

0.28 ~ 5.64

0.42



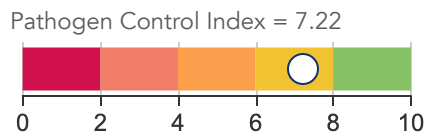
Prevotella:Bacteroides (P/B) Ratio

High Prevotella:Bacteroides ratios are associated with lower BMI and reduced incidence of chronic, inflammatory disease. Low Prevotella:Bacteroides ratios (smaller numbers) 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, particularly among centenarian populations.

0.0 ~ 0.52

0

Pathobiome 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. This section compares the relative abundances (RA) of specific pathogens to normal levels present in the healthy gut.



BiomeFX is NOT a diagnostic test. If your Pathogen levels are abnormally high consult your physician who can make a diagnosis and provide treatment if needed.

Pathogen Species	Healthy RA IQR %	My Sample RA %
Clostridium difficile	0.02 - 0.17	0.6326
Escherichia coli	0.04 - 0.47	0.0752
Bacteroides fragilis	0.07 - 0.79	0.5249

Virulence Factors Tested in Your Sample

Virulence factors are genes that when transcribed enable a microorganism to establish itself on or within a host and enhance its potential to cause disease (they help bacteria invade the host, cause disease, and evade host defenses), and include bacterial toxins, cell surface proteins that mediate bacterial attachment, cell surface carbohydrates and proteins that protect a bacterium, and hydrolytic enzymes that may contribute to the pathogenicity of the bacterium.

Virulence Factors	My Sample
Clostridiodes difficile cdtA	Not Detected
Clostridiodes difficile cdtB	Not Detected
Clostridiodes difficile tcdA	Not Detected
Clostridiodes difficile tcdB	Not Detected
Bacteroides fragilis BFT	Not Detected

Pathobiome 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. This section compares the relative abundances (RA) of specific pathogens to normal levels present in the healthy gut.

BiomeFX is NOT a diagnostic test. If your Pathogen levels are abnormally high consult your physician who can make a diagnosis and provide treatment if needed.

Full List of Pathogen Species Tested

Bacteria

Bacteroides fragilis	Bilophila wadsworthia
Campylobacter	Campylobacter jejuni
Citrobacter freundii	Clostridiodes difficile
Clostridiodes perfringens	Enterococcus gallinarum
Escherichia coli	Hafnia alvei
Helicobacter pylori	Klebsiella pneumoniae
Porphyromonas gingivalis	Proteus mirabilis
Proteus vulgaris	Pseudomonas aeruginosa
Raoultella ornithinolytica	Salmonella enterica
Sutterella stercoricanis	Sutterella wadsworthensis
Vibrio cholerae	Yersinia enterocolitica

Protists

Blastocystis hominis	Cryptosporidium
Cyclospora cayetanensis	Entamoeba histolytica
Giardia lamblia	

Fungi

Candida	Geotrichum spp
Microsporidia spp	Rhodotorula spp

Viruses

Adenovirus	Cytomegalovirus
Epstein Barr Virus	

Functional Keystone Species in My Gut

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.

Keystone Species	Function	Healthy Relative Abundance IQR Range[%]	My Sample Relative Abundance
Phylum: Verrucomicrobia			
Akkermansia muciniphila	Acetate Producer	0.15 - 2.295	Not Detected
Phylum: Actinobacteria			
Bifidobacterium longum	Acetate Producer	0.127 - 1.268	0.837
Bifidobacterium adolescentis	GABA Producer	0.077 - 1.536	0.016
Phylum: Firmicutes			
Faecalibacterium prausnitzii	Butyrate Producer	0.675 - 2.032	3.393
Ruminococcus bromii	Cellulose Degradar	0.155 - 1.391	Not Detected
Ruminococcus flavefaciens	Cellulose Degradar	0.007 - 0.014	Not Detected
Roseburia intestinalis	Butyrate Producer	0.062 - 1.116	0.061
Eubacterium rectale	Butyrate Producer	0.665 - 2.238	1.278
Butyricoccus pullicaecorum	Butyrate Producer	0.011 - 0.04	Not Detected
Lactobacillus rhamnosus	Lactate Producer	0.016 - 0.051	Not Detected
Lactobacillus reuteri	Lactate Producer	0.011 - 0.016	Not Detected
Total Lactobacillus species	Lactate Producer	0.032 - 0.196	Not Detected

Short Chain Fatty Acid (SCFA) Producers

In the functional analysis section we measure the genes and pathways identified for SCFA production.

In this section we are measuring the abundance of certain bacteria that are known to produce SCFAs. Frequently, the keystone species known to produce these SCFAs are found at low abundance in the microbiome. This means that the entire genome may not be available, including the genes and pathways for SCFA production. This table provides the aggregated relative abundance of the SCFA producing bacteria.

SCFA Name	Healthy IQR	My Sample	My Sample Percentile [%]
Acetate Producers	5.23 - 13.99	12.53	69
Butyrate Producers	2.67 - 5.72	7.14	86
D-Lactate Producers	3.30 - 8.79	24.07	99
L-Lactate Producers	1.10 - 6.46	10.47	89
Propionate Producers	6.68 - 15.16	10.53	49

Functional Analysis of Your Gut Microbiome

This section 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. The report shows absolute values and your functional gut microbiome composition as a percentile relative to the typical healthy microbiome.

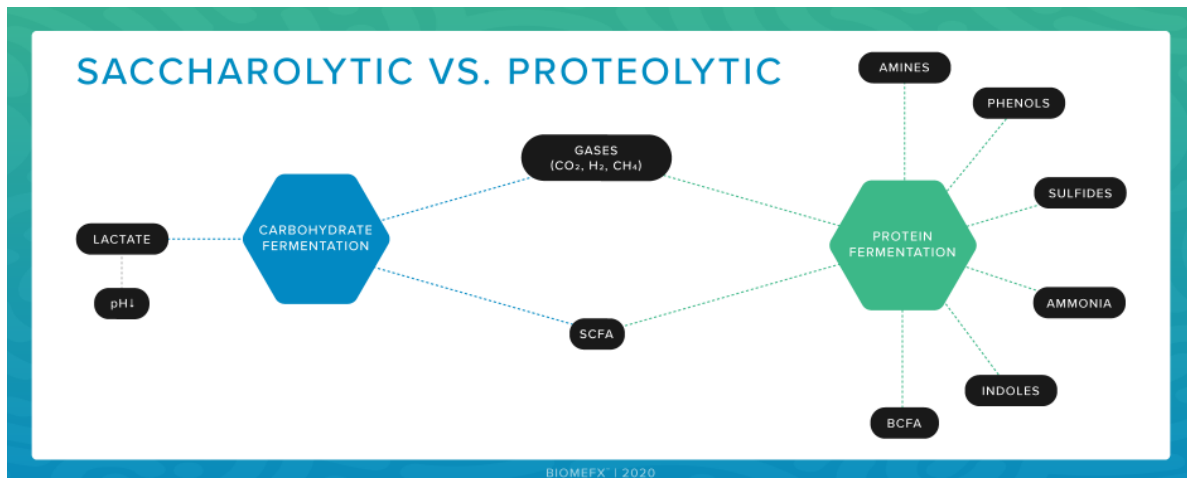
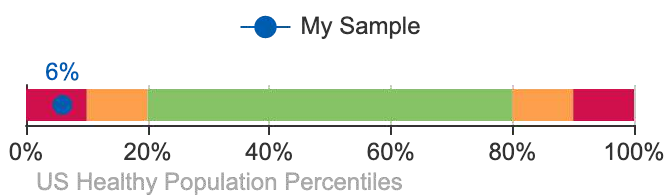


Figure 1. This image shows a comparison of the byproducts that result from carbohydrate and protein fermentation in the gut microbiome.

Saccharolytic fermentation

Summary:



My Gut	US Healthy Range
432	535 to 1573

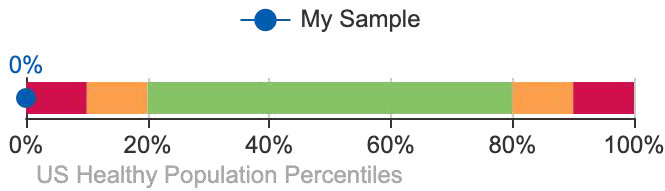
Report Descriptions

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.

 Functional Analysis of Your Gut Microbiome

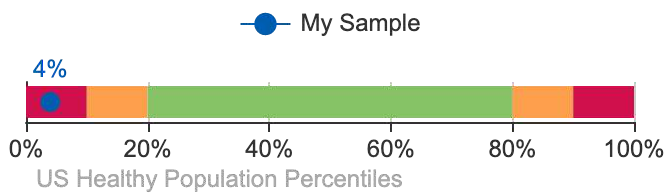
Butyrate production



Report Descriptions

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.

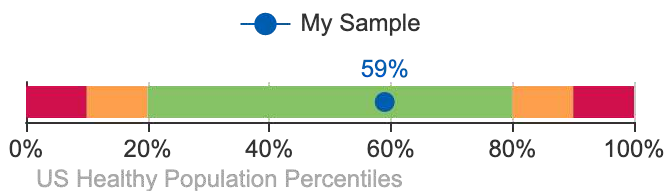
Propionate production



Report Descriptions

Propionate is a short-chain fatty acid 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 inulin 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.

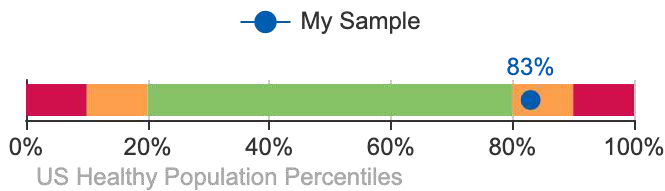
Acetate production



Report Descriptions

Acetate is another short-chain fatty acid 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.

Lactate production



My Gut

3592

US Healthy Range

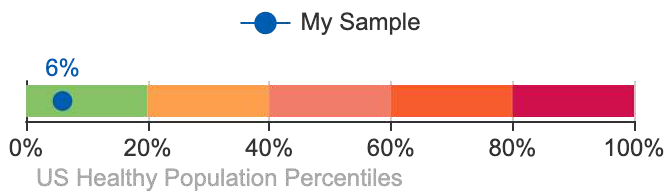
1641 to 3913

Report Descriptions

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 short-chain fatty acid 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.

Proteolytic fermentation

Summary



My Gut

1199

US Healthy Range

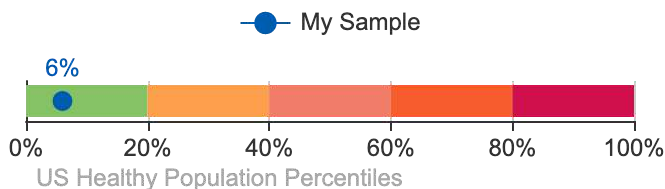
1358 to 3464

Report Descriptions

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 H₂S 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.

Amines

Polyamine production



My Gut

1199

US Healthy Range

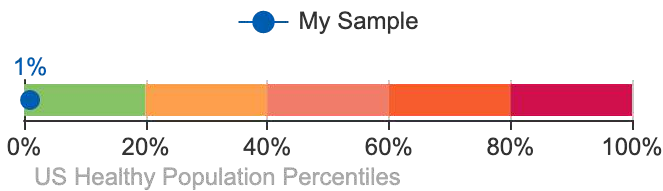
1368 to 3480

Report Descriptions

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.

 Functional Analysis of Your Gut Microbiome

Phenols

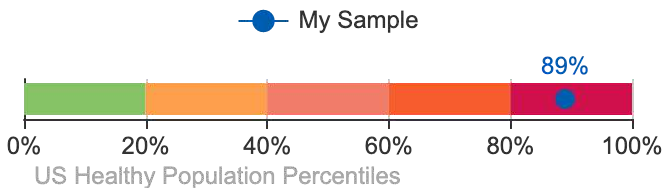


My Gut	US Healthy Range
3	8 to 121

Report Descriptions

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.

Ammonia production

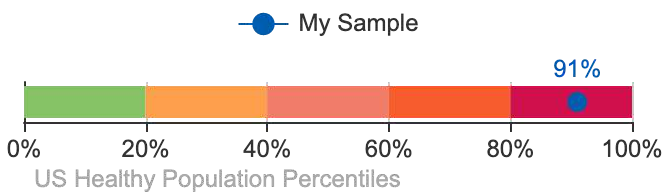


My Gut	US Healthy Range
0.2481	0.01 to 0.26

Report Descriptions

Ammonia is a normal by-product 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.

Hydrogen Sulfide (H2S) production



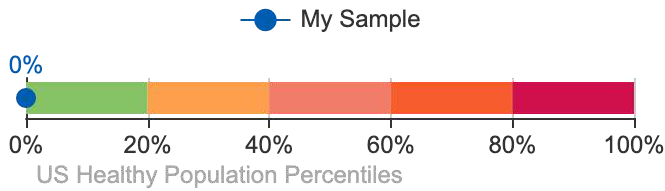
My Gut	US Healthy Range
0.4015	0.02 to 0.38

Report Descriptions

Sulfate-reducing bacteria (SRB) convert dietary sulfur and taurine to H₂S, or hydrogen sulfide, a toxic compound that impairs intestinal detoxification pathways and can cause gas that smells like rotten eggs. H₂S production is associated with high-protein, low-fiber diets. Sulfate-reducing bacteria compete with methane-producers and acetate-producers for the same H₂ substrate; and as a result, it is important to maintain a delicate balance among all 3.

 Functional Analysis of Your Gut Microbiome

Methane production



My Gut

Not Detected in my sample

US Healthy Range

0.01 to 0.91

Report Descriptions

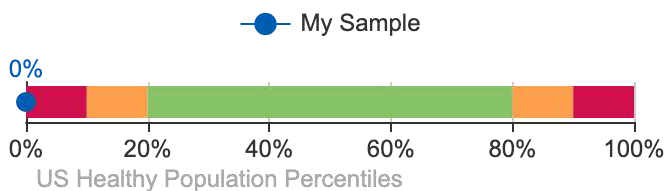
Methanogens convert acetate, ammonia, hydrogen gas, and trimethylamines (TMA) to methane gas. Methane gas also slows the intestinal transit and affects gut motility, which may also allow increased time for nutrient absorption. Furthermore, methane producers compete with acetate producers for substrate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

Hormones & 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.

Psychobiome

GABA production



My Gut

Not Detected in my sample

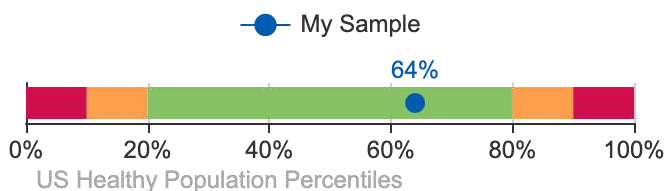
US Healthy Range

87 to 767

Report Descriptions

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.

Glutathione production



My Gut

150

US Healthy Range

42 to 232

Report Descriptions

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.

PATHWAYS OF GUT INFLAMMATION

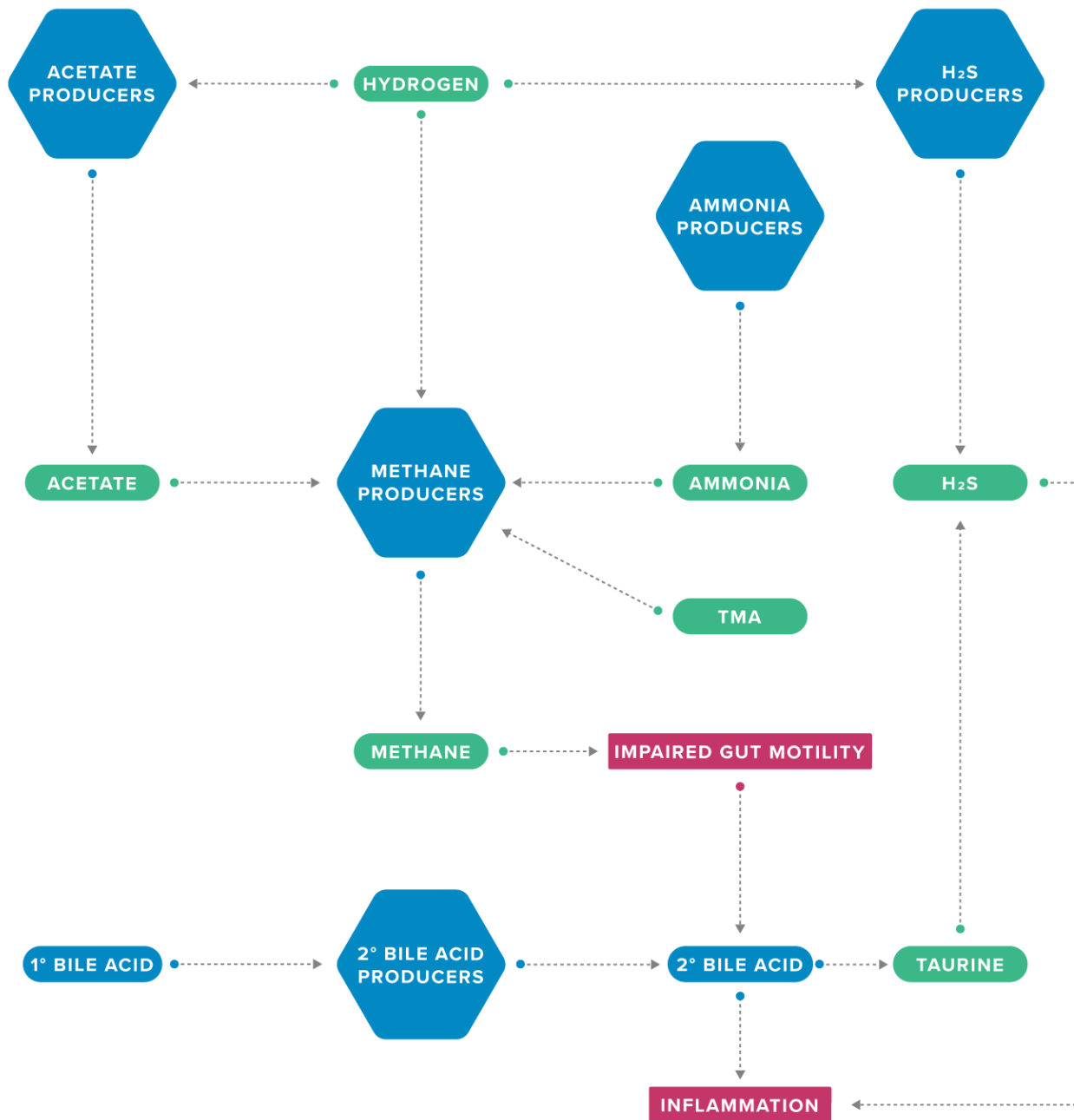
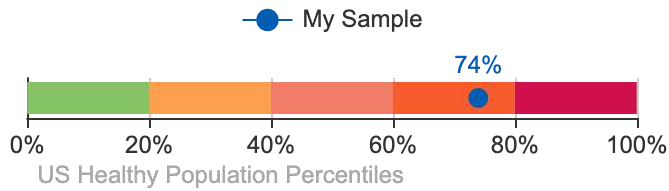


Figure 2. This image depicts some of the cross-feeding relationships in the gut microbiome that can lead to intestinal inflammation.

 Functional Analysis of Your Gut Microbiome

Histamine production

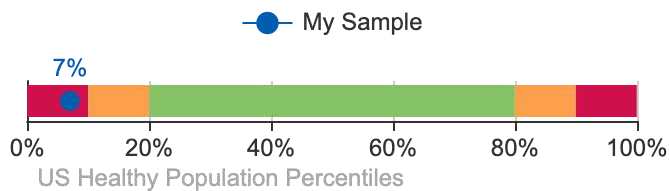


My Gut	US Healthy Range
0.1232	0 to 0.32

Report Descriptions

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

Indole production



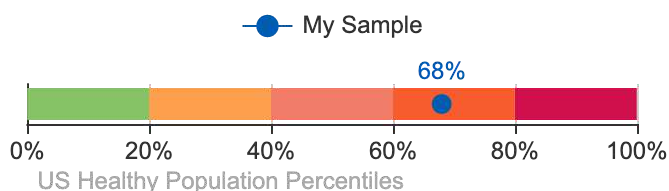
My Gut	US Healthy Range
10	13 to 286

Report Descriptions

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.

Sex Hormones

Estrogen recycling (Estrobolome)



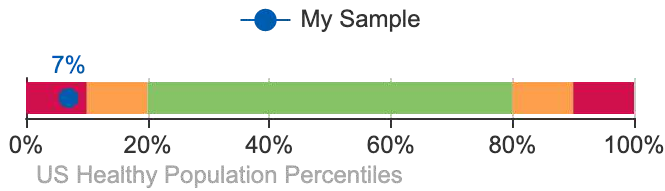
My Gut	US Healthy Range
0.1301	0.06 to 0.24

Report Descriptions

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 β -glucuronidase and β -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.

Vitamin Biosynthesis



My Gut

769

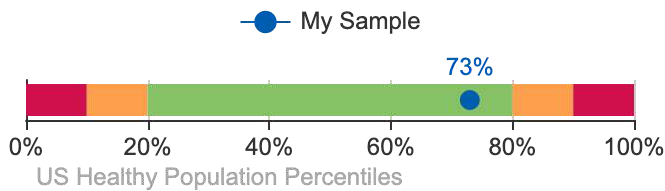
US Healthy Range

876 to 3843

Report Descriptions

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- and beta-diversity in the gut.

Vit B1 Thiamin



My Gut

4304

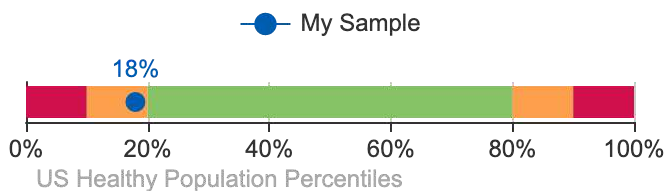
US Healthy Range

2000 to 5183

Report Descriptions

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.

Vit B2 Riboflavin



My Gut

2479

US Healthy Range

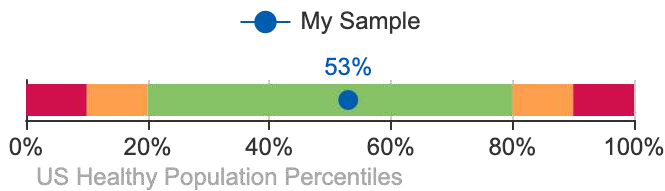
2048 to 5504

Report Descriptions

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

 Functional Analysis of Your Gut Microbiome

Vit B5 - Pantothenic acid



My Gut

10703

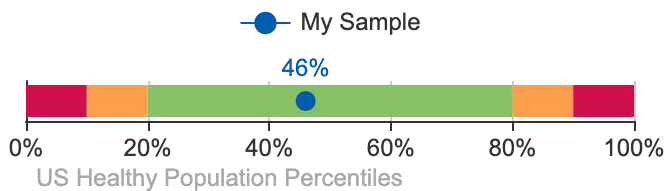
US Healthy Range

7372 to 13593

Report Descriptions

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.

Vit B6 - Pyridoxine



My Gut

3798

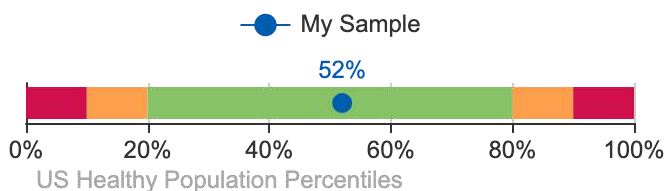
US Healthy Range

1051 to 8271

Report Descriptions

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

Vit B7 - Biotin



My Gut

628

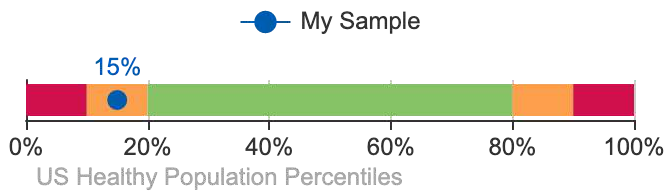
US Healthy Range

291 to 1574

Report Descriptions

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.

Vit B9 - Folate



My Gut

2719

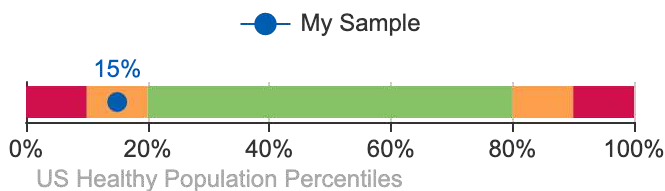
US Healthy Range

2499 to 5903

Report Descriptions

Vitamin B9 (folate/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.

Vit B12 - Cobalamin



My Gut

2719

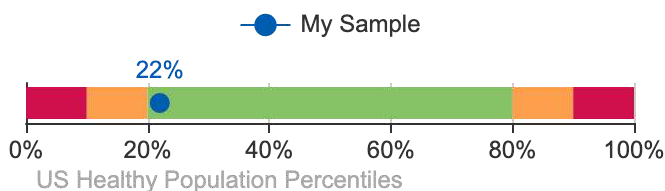
US Healthy Range

2499 to 5903

Report Descriptions

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.

Vit K2 - Menaquinone



My Gut

523

US Healthy Range

361 to 1511

Report Descriptions

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.