BiomeFx™

FUNCTIONAL MICROBIOME ANALYSIS

SAMPLE REPORT

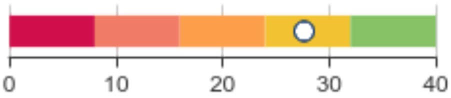
The results from this test kit are for informational purposes only and are not intended to be a substitute for professional medical advice, diagnosis, or treatment. Always seek the advice of your physician or qualified health provider with any questions you may have regarding a medical condition.

Version 2.3

Sample ID: Sample **Date:** 9/9/2020

Report Summary

Gut Microbiome Index

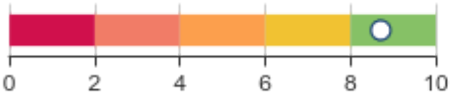


My Gut Microbiome Index:

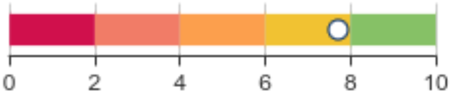
27.65 / **40**

Diversity

Alpha Diversity Index = 8.71

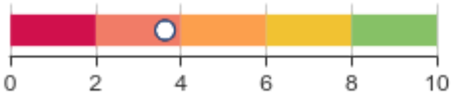


Beta Diversity Index = 7.71



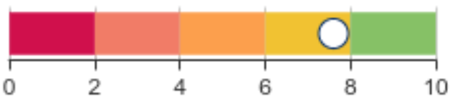
AMR Richness

Resistome Occurrence Index = 3.63



Pathogens

Pathogen Control Index = 7.6



Out of range:

Bilophila wadsworthia	High

Keystone Species

Out of range:

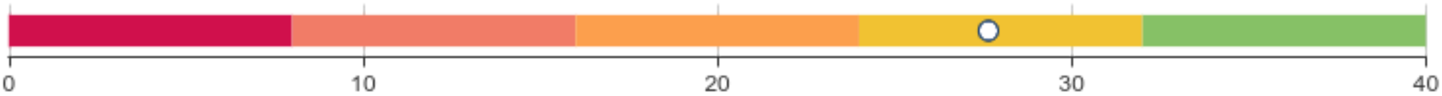
Akkermansia muciniphila	High
Ruminococcus bromii	High
Ruminococcus flavefaciens	Low
Bifidobacterium longum	High
Lactobacillus species	High
Butyricicoccus pullicaecorum	Low

Functions

Out of range:

Butyrate production	Low
Lactate production	High
GABA	Low
Vit B9 - Folate	High
Vit B12 - Cobalamin	High
Proteolytic fermentation	High
Sulfate Reduction	Low

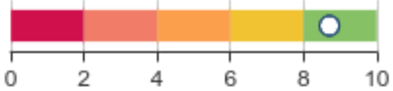
My Gut Microbiome Index (out of 40): 27.65



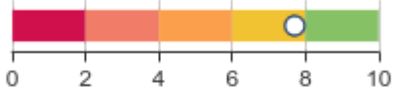
The Gut Microbiome Index (GMI) is an overall score for gut microbiome health. A score above 30 is considered excellent. It is calculated by assessing four key indicators of microbiome health for your gut microbiome and comparing them to the typical healthy gut microbiome. The four key indicators include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

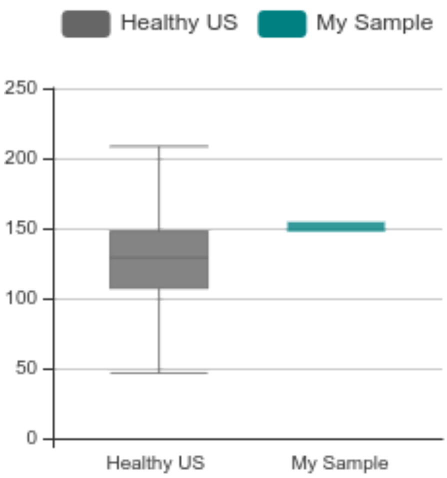
My Gut Microbiome Alpha- and Beta-Diversity

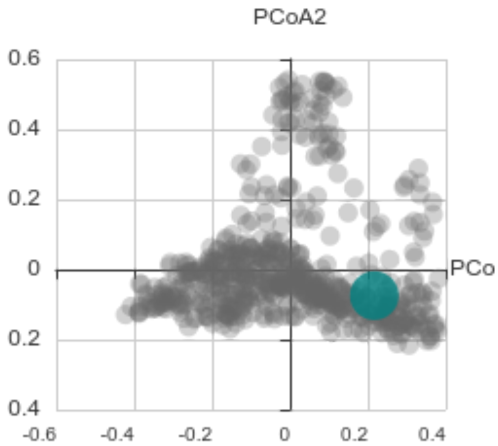
Alpha Diversity Index = 8.71



Beta Diversity Index = 7.71







Number of species in gut microbiome: 151

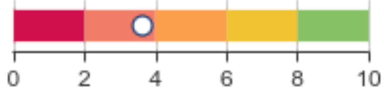
In ecology, Alpha-Diversity refers to the average diversity, or the richness of species, in a particular ecosystem. This marker is looking at your own personal species richness within your gut microbiome.

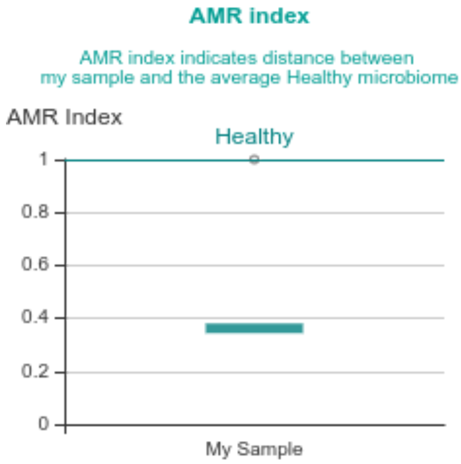
A Low Alpha-Diversity Index suggests that your gut microbiome was recently damaged by antibiotics, environmental toxins, stress, diet, or other factors.

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 = 3.63

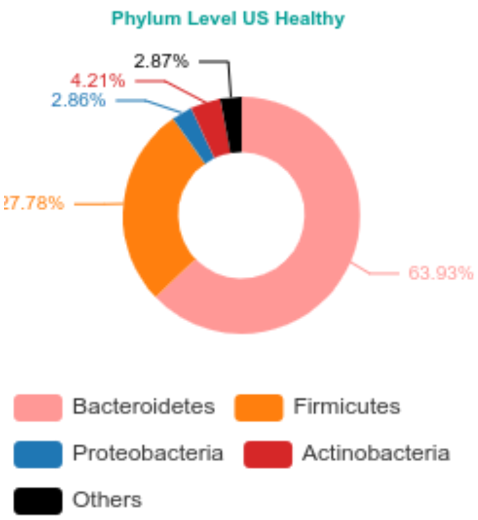


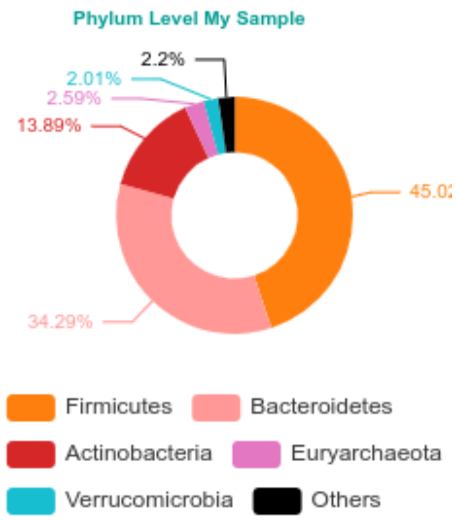


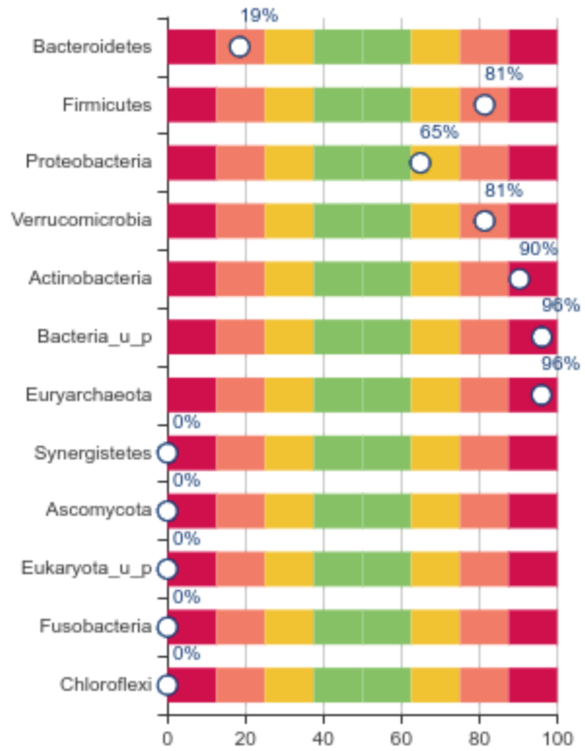
This section explores the richness and stability of your gut microbiome by comparing the resilience of your gut microbiome to Healthy populations. A low index suggests that you have low richness and resilience in your gut.

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.

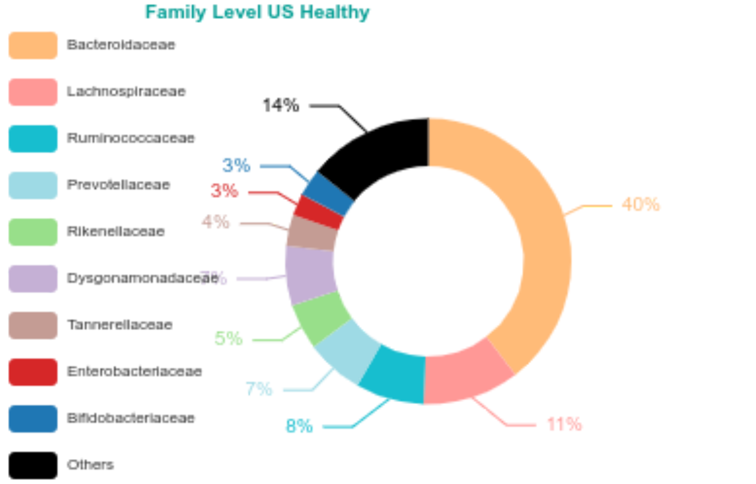
The Percentile Chart to the right compares the relative abundance (RA) for each bacterial phylum between your gut microbiome and the microbiomes typical for healthy populations. Percentile values between around 25% – 75% are typical, low values for a certain phylum suggest that in your case relative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

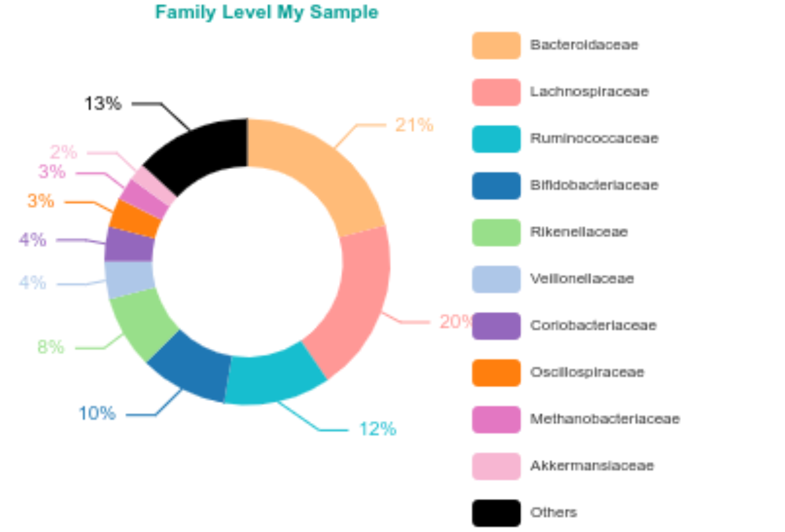
Phylum	Healthy Population Relative Abundance IQR Range [%]	My Sample Relative Abundance[%]	My Sample Percentile
Bacteroidetes	45.38 - 85.04	34.29	18.5
Firmicutes	12.04 - 38.83	45.02	81.34
Proteobacteria	0.41 - 1.74	1.27	64.85
Verrucomicrobia	0.07 - 1.45	2.01	81.34
Actinobacteria	0.07 - 2.33	13.89	90.28
Bacteria_u_p	0.02 - 0.18	0.93	96.04
Euryarchaeota	0.02 - 0.52	2.59	95.93
Synergistetes	0.01 - 0.05	0	0
Ascomycota	0.0 - 0.01	0	0
Eukaryota_u_p	0.0 - 0.02	0	0
Fusobacteria	0.0 - 0.04	0	0
Chloroflexi	0.01 - 0.01	0	0

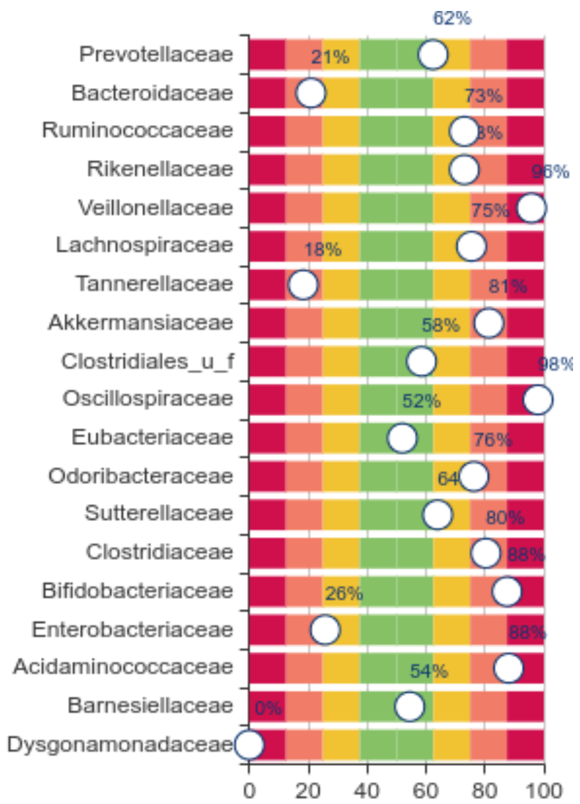
My Gut Microbiome Composition (Family level)

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.



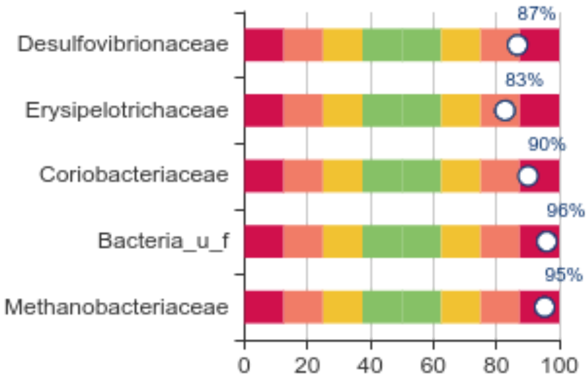




Family	Healthy Population Relative Abundance IQR Range [%]	My Sample Relative Abundance[%]	My Sample Percentile
Prevotellaceae	0.04 - 6.02	1.67	62.42
Bacteroidaceae	25.5 - 67.71	20.88	20.93
Ruminococcaceae	3.64 - 12.61	12.08	73.05
Rikenellaceae	2.8 - 8.58	8.21	73.02
Veillonellaceae	0.02 - 0.8	4.3	95.8
Lachnospiraceae	4.21 - 19.43	19.64	75.44
Tannerellaceae	1.96 - 5.75	1.48	18.3
Akkermansiaceae	0.07 - 1.45	2.01	81.34
Clostridiales_u_f	0.46 - 1.27	0.88	58.49
Oscillospiraceae	0.34 - 1.14	3.3	98.04
Eubacteriaceae	0.27 - 1.15	0.66	51.97
Odoribacteraceae	0.33 - 0.93	0.95	76.24
Sutterellaceae	0.07 - 0.65	0.43	63.96
Clostridiaceae	0.17 - 0.96	1.15	80.35
Bifidobacteriaceae	0.07 - 2.66	9.95	87.55
Enterobacteriaceae	0.05 - 1.0	0.05	25.77
Acidaminococcaceae	0.21 - 1.03	1.87	88.1
Barnesiellaceae	0.32 - 2.01	1.1	54.48
Dysgonamonadaceae	1.93 - 12.33	0	0

My Gut Microbiome Composition (Family level)

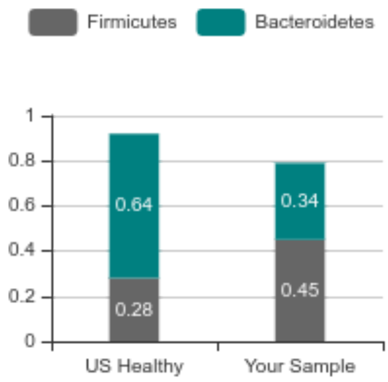
Note: The organisms in the previous page typically occur in the healthy gut at Relative Abundances (RA) of > 0.5%. Organisms from the current page occur more rarely, but have been detected in your gut microbiome.

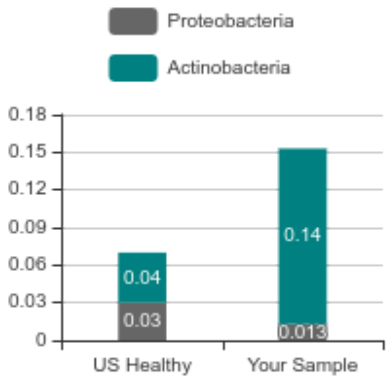


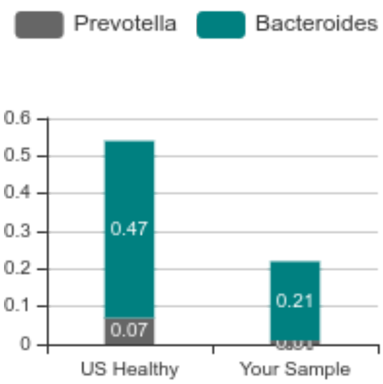
Family	Healthy Population Relative Abundance IQR Range [%]	My Sample Relative Abundance[%]	My Sample Percentile
Desulfovibrionaceae	0.07 - 0.45	0.79	86.75
Erysipelotrichaceae	0.07 - 0.54	0.71	82.78
Coriobacteriaceae	0.05 - 1.16	3.91	90.1
Bacteria_u_f	0.02 - 0.18	0.93	96.04
Methanobacteriaceae	0.01 - 0.54	2.59	95.36

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.



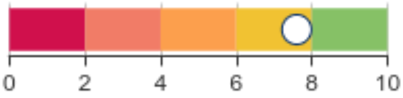




Description	Healthy Ratio IQR	My Ratio
Firmicutes:Bacteroidetes (F/B) Ratio In adults, Firmicutes and Bacteroidetes are the most abundant bacterial phyla in the gut. The Firmicutes to Bacteroidetes (F/B) abundance ratio was shown to increase from infancy to adulthood and subsequently to decrease again 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.	0.14 ~ 0.88	**1.31**
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 arabinoxylan.	0.35 ~ 12.23	**0.09**
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 ~ 0.28	0.03

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.

Pathogen Control Index = 7.6



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 %
Escherichia coli	0.05 - 0.86	0.05
Bilophila wadsworthia	0.05 - 0.27	**0.62**

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.

Full List of Pathogen Species Tested

Helicobacter pylori	Clostridium difficile
Escherichia coli	Campylobacter
Salmonella enterica	Vibrio cholerae
Yersinia enterocolitica	Klebsiella pneumoniae
Citrobacter freundii	Hafnia alvei
Raoultella ornithinolytica	Candida
Blastocystis hominis	Giardia lamblia
Cryptosporidium	Entamoeba histolytica
Adenovirus	Cytomegalovirus
Epstein Barr Virus	Geotrichum spp
Microsporidia spp	Rhodotorula spp
Cyclospora cayetanensis	Bilophila wadsworthia

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.

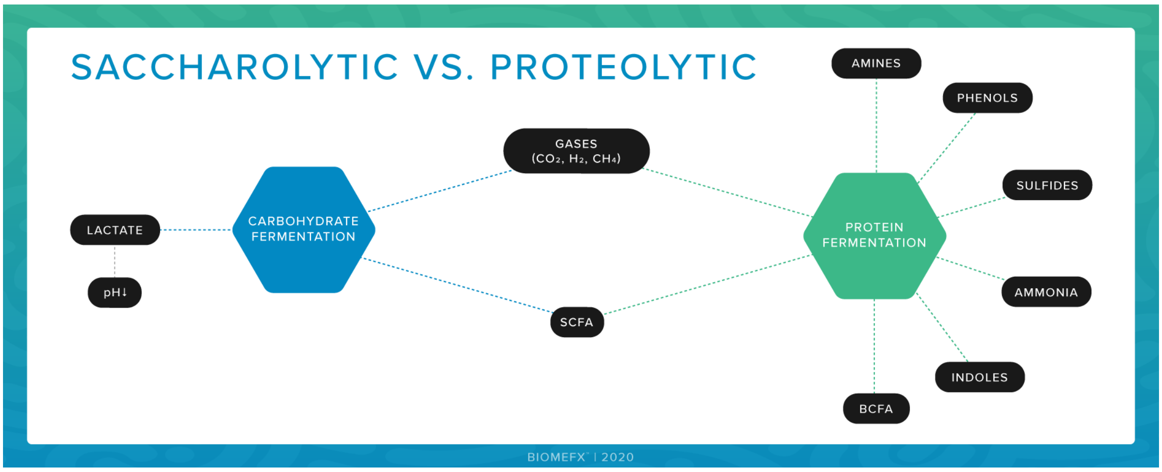
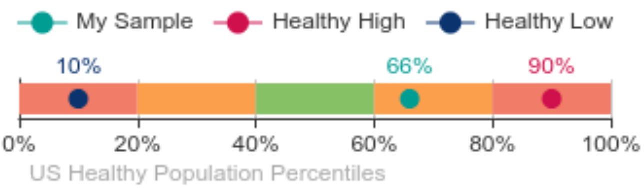


Figure 1. This image shows a comparison of the byproducts that result from carbohydrate and protein fermentation in the gut microbiome.

Saccharolytic fermentation

Summary:



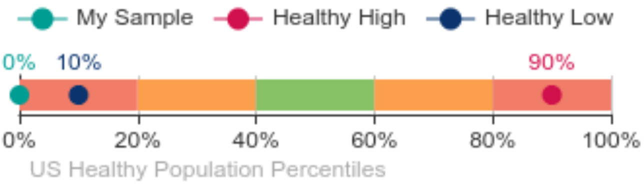
My Gut	US Healthy Range
438	117 to 809

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

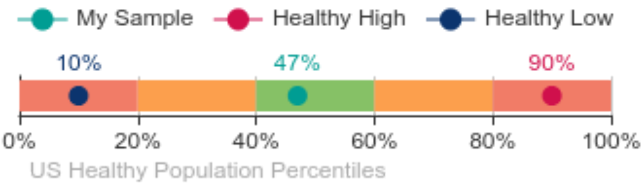


My Gut	US Healthy Range
Not Detected in my sample	36 to 302

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

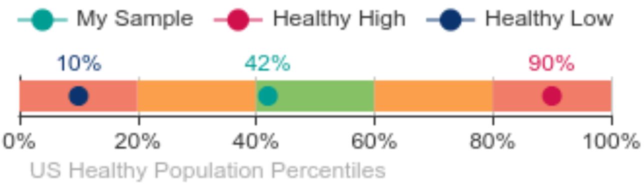


My Gut	US Healthy Range
518	132 to 1523

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

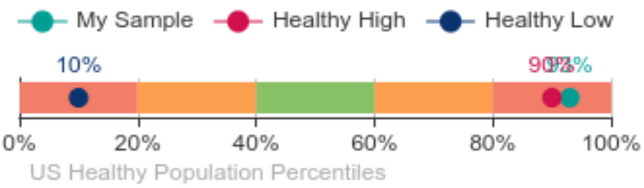


My Gut	US Healthy Range
719	428 to 1234

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



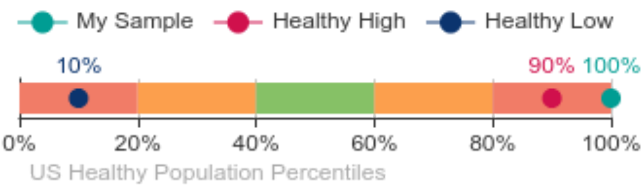
My Gut	US Healthy Range
4146	1546 to 3791

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



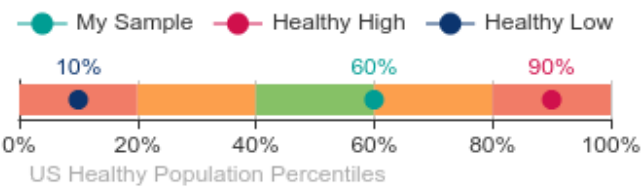
My Gut	US Healthy Range
1320	30 to 197

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



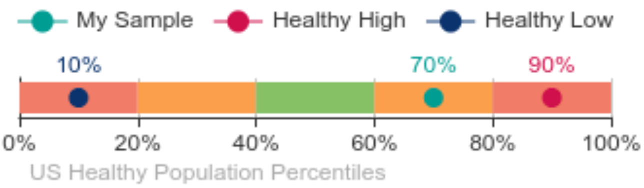
My Gut	US Healthy Range
1320	695 to 1740

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

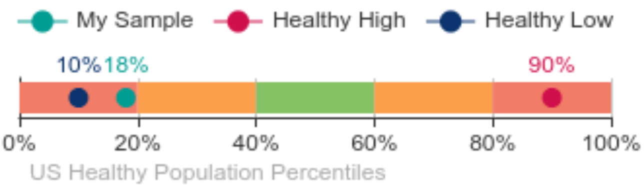


My Gut	US Healthy Range
22	2 to 56

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

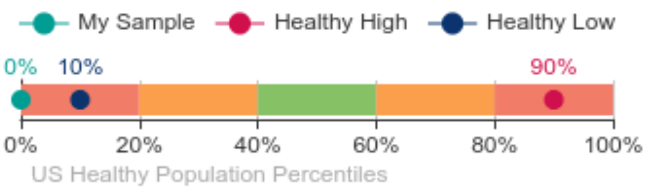


My Gut	US Healthy Range
0.01	0 to 0.39

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

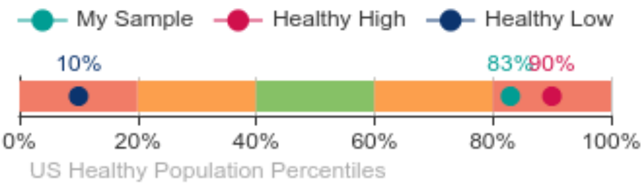


My Gut	US Healthy Range
Not Detected in my sample	0.01 to 8.83

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.

Methane production



My Gut	US Healthy Range
0.9	0 to 1.65

Report Descriptions

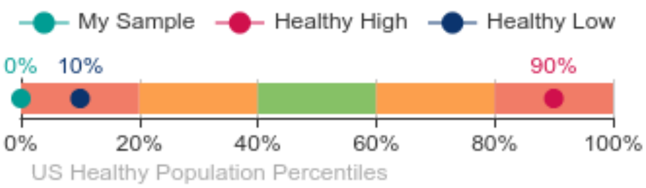
Methanogens convert acetate, ammonia, hydrogen gas, and trimethylamines (TMA) to methane gas. Methane gas also slows the intestinal transit and affects gut motility, which may also allow increased time for nutrient absorption. Furthermore, methane producers compete with acetate producers for substrate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

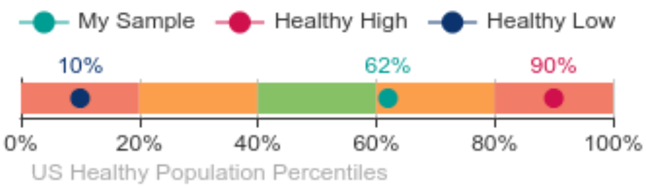


My Gut	US Healthy Range
Not Detected in my sample	87 to 767

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	US Healthy Range
144	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 detoxifaction 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 through out the body. Recent evidence suggests that the gut microbiome determines levels of glutathione throughout the body.

Functional Analysis of Your Gut Microbiome

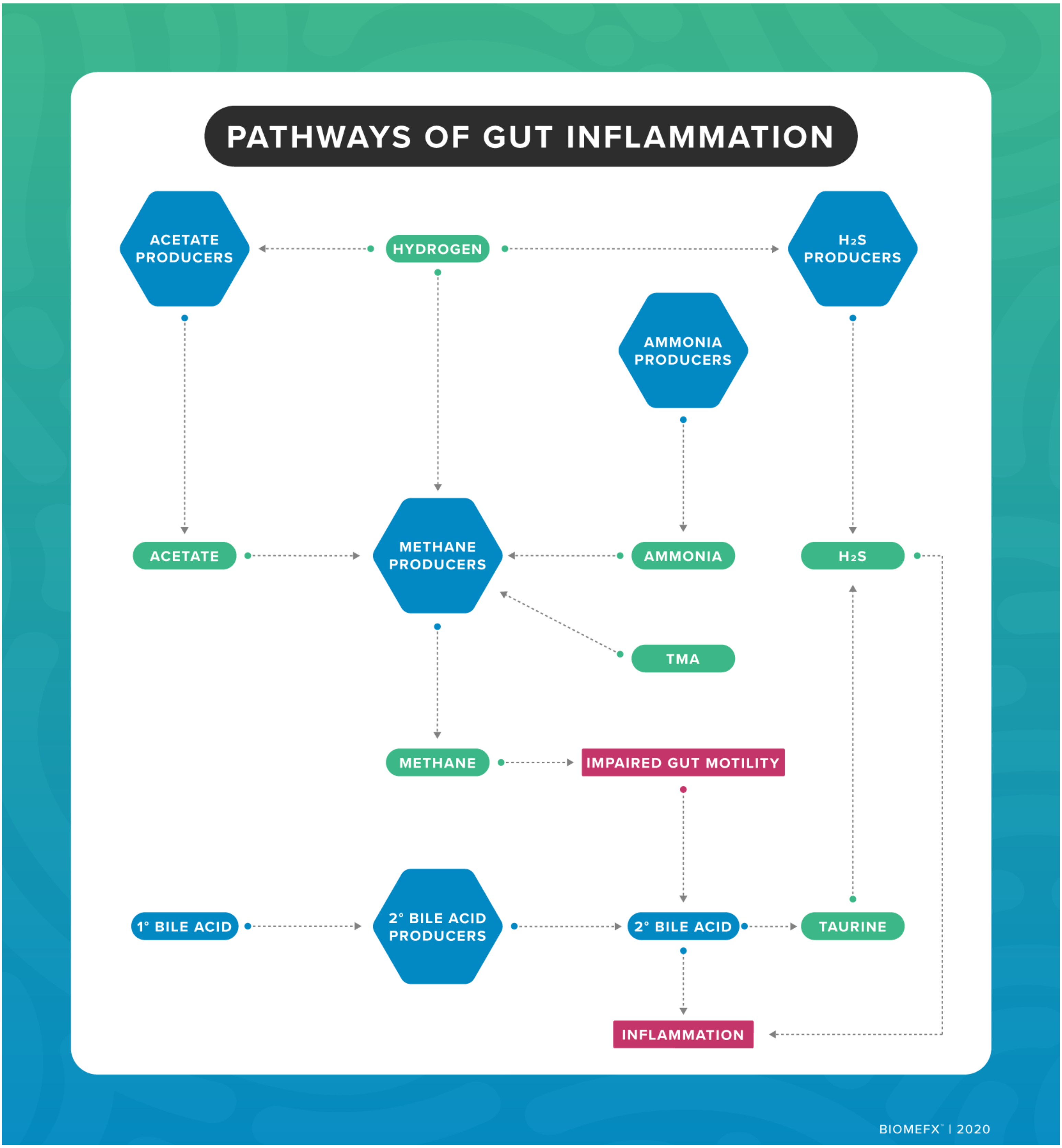
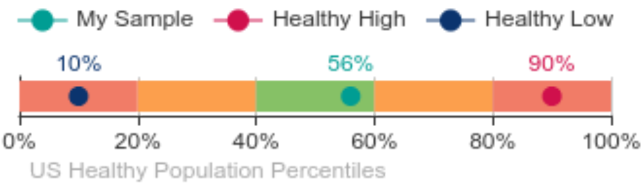


Figure 2. This image depicts some of the cross-feeding relationships in the gut microbiome that can lead to intestinal inflammation.

Functional Analysis of Your Gut Microbiome

Indole production



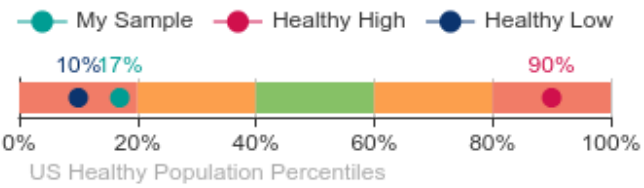
My Gut	US Healthy Range
87	13 to 286

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)



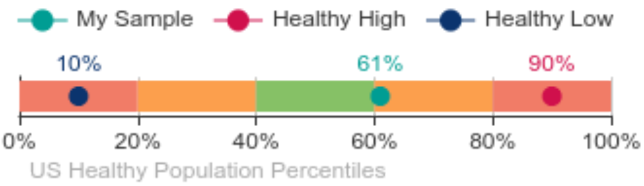
My Gut	US Healthy Range
0.02	0 to 0.31

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

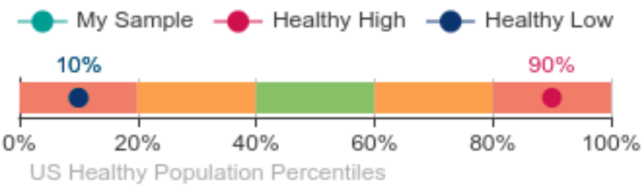


My Gut	US Healthy Range
897	343 to 1764

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

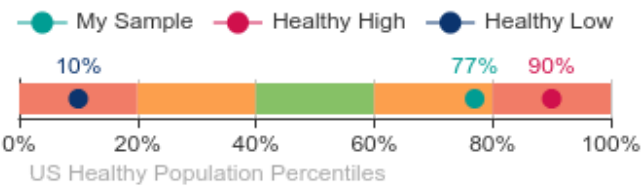


My Gut	US Healthy Range
1654	1671 to 4489

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



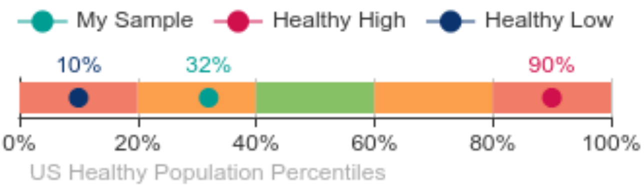
My Gut	US Healthy Range
3824	1357 to 4564

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

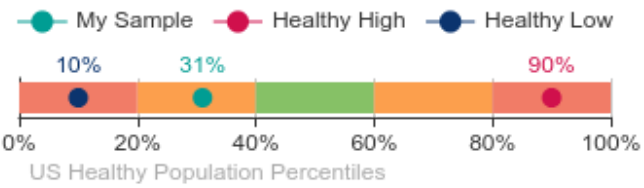


My Gut	US Healthy Range
9415	7372 to 13593

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

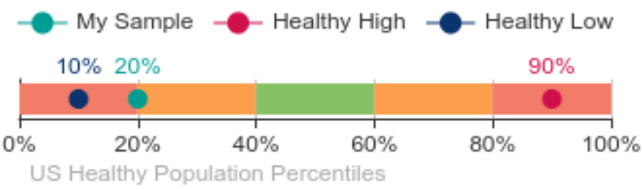


My Gut	US Healthy Range
2535	911 to 8154

Report Descriptions

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

Vit B7 - Biotin

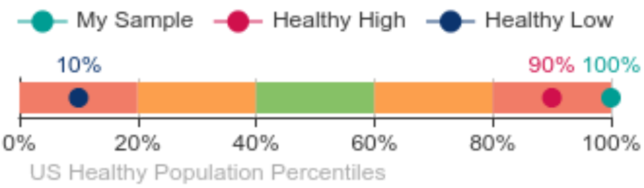


My Gut	US Healthy Range
251	173 to 1288

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

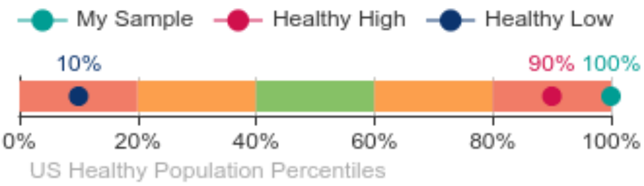


My Gut	US Healthy Range
3354	481 to 1978

Report Descriptions

Vitamin B9 (folate/tetrahydrafolate), 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

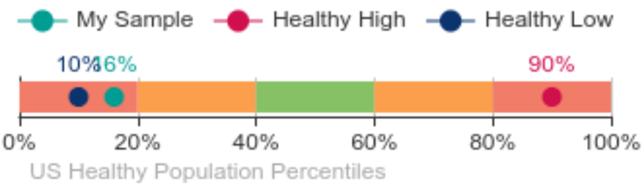


My Gut	US Healthy Range
3354	481 to 1978

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	US Healthy Range
428	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 dervied K2 has protective role against oxidative tissue damage in the gut.

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
Akkermansia muciniphila	metabolism and SCFA	0.07 - 1.45	**2.01**
Faecalibacterium prausnitzii	intestinal health and SCFA	1.14 - 4.83	1.84
Ruminococcus bromii	cellulose degrader	0.13 - 1.64	**2.63**
Ruminococcus flavefaciens	cellulose degrader	0.0 - 0.01	**Not Detected**
Roseburia intestinalis	beta-mannan degrader, butyrate producer	0.15 - 1.18	0.24
Eubacterium rectale	butyrate producer	0.61 - 3.46	2.09
Bifidobacterium longum	acetate producer	0.04 - 1.01	**1.45**
Lactobacillus species	lactate producer	0.02 - 0.27	**2.49**
Butyricicoccus pullicaecorum	butyrate producer	0.02 - 0.06	**Not Detected**