Gut Microbiome Report

ANALYSIS

Sequencing type	**16S rRNA, V4 region**
Pipeline	**Consensus**
Generated	**August 27, 2026**

SPECIMEN

Report for	**Member Example**
Collected	**December 13, 2021**

SUMMARY

Your results at a glance

80/100

GUT WELLNESS SCORE

Satisfactory

A single measure combining your diversity, probiotics, commensals and pathobionts.

CORE INDICATORS

Diversity	Probiotics	Commensals	Pathobionts
87%	**81%**	**88%**	**68%**

FUNCTIONAL & METABOLITE HEALTH

SCFAs Needs Improvement	**Neurotransmitters** Satisfactory	**Detoxification** Satisfactory	**Toxins** Needs Improvement
Nutrients Satisfactory	**Permeability** Satisfactory	**Intolerance** Satisfactory	**Longevity** Satisfactory

Where to focus

BACTERIA

- **Methanobacteriaceae** Pathobiont · High
- **Bacteroides** Commensal · High
- **Bifidobacterium** Probiotic · Low
- **Faecalibacterium** Probiotic · Low
- **Lactobacillus** Probiotic · Low
- **Methanobrevibacter** Pathobiont · High
- **Oxalobacter** Commensal · Low
- **Phocaeicola** Commensal · High
- **Roseburia** Probiotic · Low
- **Ruminococcus** Probiotic · High
- **Veillonella** Commensal · Low
- **Desulfobacterota** Pathobiont · High
- **Proteobacteria** Pathobiont · High
- **Bilophila wadsworthia** Pathobiont · High
- **Enterococcus faecalis** Pathobiont · High

FUNCTIONAL & METABOLITE

- **Butyrate** SCFAs · Low
- **Hydrogen Sulfide (H2S)** Toxins · High
- **Methane** Toxins · High

Functional and metabolite ratings are estimated from the bacteria that produce them and are not a direct measure of stool metabolites.

Probiotics

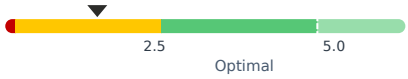
Section score **81** / 100

Optimal · Not optimal · Deficient or overgrown · Beyond optimal — no penalty

Bifidobacterium Low

You 1.46% · Optimal >=2.5–5.0% · 84th percentile · Prevalence 95%

Bifidobacterium is a genus of gram-positive bacteria commonly found in the gastrointestinal tract, playing a crucial role in regulating microbial balance, inhibiting harmful pathogens, modulating immune responses, and enhancing gut health. They may offer various health benefits, such as improving gut barrier function and potentially alleviating symptoms of irritable bowel syndrome, although evidence is not yet conclusive.



Faecalibacterium Low

You 5.90% · Optimal >=10.0–15.0% · 27th percentile · Prevalence 100%

Faecalibacterium, primarily Faecalibacterium prausnitzii, is a key gram-positive bacterium in the human gut microbiota that supports the immune system. Reduced levels are linked to conditions such as Crohn's disease, obesity, asthma, and major depressive disorder, while increased levels are associated with psoriasis.



Lactobacillaceae Optimal

You 0.02% · Optimal 0.01–0.5% · 80th percentile · Prevalence 70%

Lactobacillaceae is a family of lactic acid-producing bacteria in the human gut that supports gut health by inhibiting harmful bacteria and modulating immune responses. They are beneficial for some conditions like IBS, eczema, and allergies, although effects are strain-specific. Their levels can be increased with fermented foods and probiotics but reduced by antibiotics and low-fiber diets.



Lacticaseibacillus (Lactobacillaceae) Optimal

You 0.01% · Optimal 0.001–0.15% · 91th percentile · Prevalence 29%

Lacticaseibacillus is a genus of lactic acid-producing bacteria that reflects recent dietary intake, commonly found in fermented dairy and supplements, rather than establishing a stable gut population. Specific strains like Lcb. rhamnosus GG have been studied for transient gut persistence and effects on acute diarrhoea, though not consistently beneficial; other strains have shown potential positive impacts on metabolic markers, mood, and sleep in small trials.



Lactobacillus (Lactobacillaceae) Low

You 0.00% · Optimal 0.003–0.2% · 77th percentile · Prevalence 34%

Lactobacillus is a genus of beneficial bacteria that plays a key role in human gut health by converting sugars to lactic acid, forming biofilms to persist in challenging environments, and protecting against pathogens. It is a common probiotic in foods like yogurt and can aid in treating conditions such as diarrhea, vaginal infections, and eczema.



Limosilactobacillus (Lactobacillaceae) Optimal

You 0.01% · Optimal 0.003–0.15% · 98th percentile · Prevalence 31%

Limosilactobacillus, including species like L. reuteri and L. fermentum, is a lactic acid-producing bacterium found in the human gut, breast milk, and fermented foods. Some strains have anti-inflammatory and gut barrier-supporting effects, though they are typically low in abundance in the gut. Consuming prebiotic fibers and fermented foods can increase their presence, while reducing simple sugars may help manage overgrowth in cases of dysbiosis. Optimal levels depend on individual microbial balance and health context.



Akkermansia Optimal

You 0.66% · Optimal 0.02–3.0% · 78th percentile · Prevalence 91%

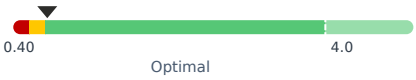
Akkermansia muciniphila, a prominent gut bacterium, plays a key role in maintaining balanced gut flora and is being explored for its potential benefits on metabolism, possibly reducing obesity, type 2 diabetes, and inflammation. However, high levels may be linked to multiple sclerosis and intestinal inflammation. It can degrade mucin, offering competitive inhibition against pathogenic bacteria, and is available as a probiotic supplement.



Agathobacter Optimal

You 0.45% · Optimal >=0.4–4.0% · 26th percentile · Prevalence 100%

Agathobacter is a genus of bacteria in the human gut that produces butyrate, which supports gut health and reduces inflammation. Higher levels are linked to improved cognitive function, reduced neuroinflammation, and better outcomes in Alzheimer's disease and multiple myeloma. Its abundance may also influence lipid metabolism and can be increased through dietary fibers and prebiotics.



Ruminococcus High

You 10.57% · Optimal 0.0–10.0% · 99th percentile · Prevalence 100%

Ruminococcus is a genus of anaerobic, Gram-positive bacteria in the gut, with lower abundances found in individuals with inflammatory bowel disease and Parkinson's disease, indicating a potential link to these conditions.



Roseburia Low

You 0.61% · Optimal 0.75–5.0% · 42th percentile · Prevalence 100%

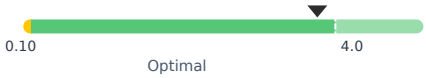
Roseburia are beneficial gut bacteria that produce butyrate, a short-chain fatty acid important for colonic motility, immune system support, and anti-inflammatory effects, with changes in their levels linked to conditions like irritable bowel syndrome, obesity, Type 2 diabetes, neurological disorders, and allergies.



Barnesiella Optimal

You 3.77% · Optimal >=0.1–4.0% · 100th percentile · Prevalence 88%

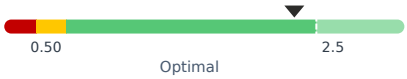
Barnesiella is a genus of beneficial bacteria in the human gut, with Barnesiella intestinihominis supporting gut barrier integrity and possibly reducing inflammation and visceral fat through short-chain fatty acid production. Its abundance can be maintained by diets rich in certain micronutrients and probiotics, but reduced with antibiotics and high-fat diets. High levels might be linked to autoimmunity in mice, though this is not well understood in humans.



Gemmiger Optimal

You 2.33% · Optimal >=0.5–2.5% · 75th percentile · Prevalence 100%

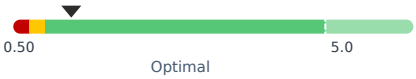
Gemmiger is a genus of gut bacteria that produces butyrate, supporting gut health and having anti-inflammatory benefits. Its presence is linked to improved gut barrier function and reduced liver fat, particularly with a fiber-rich diet, while its reduction is noted in conditions like inflammatory bowel disease and after chemotherapy. Factors like high dietary fiber intake and regular exercise may boost its abundance.



Fusicatenibacter Optimal

You 0.94% · Optimal >=0.5–5.0% · 63th percentile · Prevalence 100%

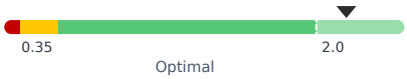
Fusicatenibacter is a genus of gut bacteria known for producing butyrate, a short-chain fatty acid with gut health and anti-inflammatory benefits. Lower levels are linked to mental health issues and certain diseases, while dietary intake of resistant maltodextrin and lion's mane mushroom can increase its abundance, potentially benefiting conditions like psoriasis.



Christensenellaceae Optimal

You 2.89% · Optimal >=0.35–2.0% · 85th percentile · Prevalence 100%

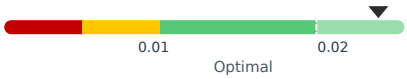
Christensenellaceae is a family of Gram-negative, anaerobic bacteria in the human gut, with the species Christensenella minuta producing beneficial short-chain fatty acids like butyrate. Its presence is associated with a leaner BMI, better metabolic health, reduced inflammation, enhanced gut barrier function, and potential protection against inflammatory bowel diseases, often increased by fiber-rich and prebiotic diets.



Adlercreutzia Optimal

You 0.04% · Optimal >=0.01–0.02% · 94th percentile · Prevalence 61%

Adlercreutzia is a genus of Gram-positive, anaerobic bacteria found in the human gut, with A. equolifaciens known for producing equol, a metabolite with estrogen-like activity. Higher levels of A. equolifaciens are linked to improved lipid metabolism, reduced dyslipidemia risk, lower chances of metabolic liver diseases, and modulation of inflammatory responses. Its abundance may increase with diets rich in soy isoflavones and fermented dairy products.



Blautia Optimal

You 3.41% · Optimal 2.5–10.0% · 59th percentile · Prevalence 100%

Blautia aids in digesting complex carbohydrates and produces anti-inflammatory butyrate, contributing to gut health. Higher levels of Blautia are associated with a healthy gut and are found in lower amounts in individuals with liver disease, colorectal cancer, and diabetes.



Commensals

Section score **88** / 100

Optimal · Not optimal · Deficient or overgrown

Bacteroidota Optimal

You 33.09% · Optimal 0.0–40.0% · 37th percentile · Prevalence 100%

Bacteroidota (Bacteroidetes) is a group of Gram-negative bacteria commonly found in the gut, involved in vital metabolic processes like breaking down proteins and complex sugars, and is established early in life with the help of substances in breast milk. While they can occasionally cause infections, they mostly play a beneficial symbiotic role in the gastrointestinal tract.



Bacteroides (Bacteroidota) High

You 10.47% · Optimal 2.5–10.0% · 53th percentile · Prevalence 100%

Bacteroides are key gut bacteria that assist in breaking down complex molecules into simpler ones, playing a crucial role in digestion. They primarily use complex glycans from the host and plants for energy and can be resistant to many antibiotics, which may lead to overgrowth following frequent antibiotic use. While they contain endotoxin, their pathogenicity is low compared to other gram-negative bacteria.



Phocaeicola (Bacteroidota) High

You 13.26% · Optimal 0.0–11.0% · 59th percentile · Prevalence 100%

Phocaeicola, a common gut bacterium previously classified under Bacteroides, aids in breaking down complex carbohydrates into short-chain fatty acids such as acetate and propionate. These acids are important for supporting gut barrier function, reducing inflammation, and supplying energy to colon cells. Notable species like Phocaeicola vulgatus and Phocaeicola dorei are present early in life and constitute 3–10% of a healthy adult gut microbiome.



Alistipes (Bacteroidota) Optimal

You 2.96% · Optimal 0.0–5.0% · 65th percentile · Prevalence 100%

Alistipes is a genus of Gram-negative, anaerobic bacteria in the human gut involved in metabolic processes, with studies suggesting it may play both protective and harmful roles in health. While it can protect against diseases like liver fibrosis and colitis, it may also be linked to risks such as colorectal cancer and depression. Its abundance is influenced by factors like diet and antibiotics, and deviations could indicate dysbiosis or other health issues.



Parabacteroides (Bacteroidota) Optimal

You 2.12% · Optimal 0.1–5.0% · 67th percentile · Prevalence 100%

Parabacteroides, particularly Parabacteroides distasonis, is a gut bacterium involved in short-chain fatty acid production and bile acid metabolism, promoting gut health and potentially reducing inflammation, improving metabolism, and enhancing immune response. Its role in health and disease is complex, as it may be beneficial in treating metabolic disorders and certain cancers, yet elevated levels are linked to conditions like COVID-19 and colorectal polyps. A diet rich in dietary fibers can increase its abundance.



Prevotella (Bacteroidota) Optimal

You 0.03% · Optimal 0.0–10.0% · 66th percentile · Prevalence 92%

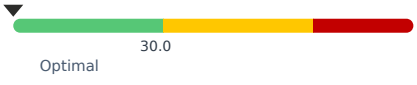
Prevotella is a genus of Gram-negative bacteria found in the oral, vaginal, and gut microbiota, often dominating in individuals consuming high-carbohydrate diets. Prevotella copri feeds on fungal metabolites, suggesting that its overgrowth may indicate a fungal imbalance, particularly in cases not linked to dietary habits.



Segatella (Bacteroidota) Optimal

You 0.01% · Optimal 0.0–30.0% · 6th percentile · Prevalence 100%

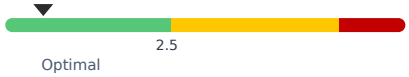
Segatella, including Segatella copri, is a group of anaerobic Gram-negative bacteria that play a key role in the gut by breaking down plant fibers into short-chain fatty acids like propionate and producing sphingolipids, which support gut barrier function, metabolism, and immune signaling. These bacteria are more prevalent in non-Western populations, constituting a significant portion of their gut microbiome.



Streptococcus Optimal

You 0.57% · Optimal 0.0–2.5% · 93th percentile · Prevalence 100%

Streptococcus in the human gut is generally a commensal bacterium, with some species like S. pyogenes and S. pneumoniae being pathogenic by producing toxins that damage cell membranes and can cause immune reactions. Some strains generate beneficial compounds like lactic acid and are found in foods like yogurt. However, Streptococcus is not typically considered a major influencer of the gut microbial ecosystem.



Oxalobacter Low

You 0.00% · Optimal 0.001–0.2% · 29th percentile · Prevalence 43%

Oxalobacter, particularly O. formigenes, is a gut bacteria known for its ability to degrade oxalate, a compound linked to kidney stones. It is under study as a potential therapeutic agent for preventing kidney stones. This bacterium is sensitive to antibiotics, which lowers its prevalence, found in around 39% of samples on our platform. Enhancing other oxalate-degrading bacteria like Bifidobacteria and Lactobacillus may be more sustainable approaches for managing oxalate levels.



Veillonella Low

You 0.00% · Optimal 0.01–1.0% · 39th percentile · Prevalence 80%

Veillonella bacteria in the gut may enhance athletic performance by converting exercise-induced lactate into propionate, which appears to improve endurance. These findings suggest Veillonella's potential as a probiotic to reduce fatigue in athletes.



Eubacterium Optimal

You 0.92% · Optimal 0.0–5.0% · 96th percentile · Prevalence 95%

Eubacterium is a genus of commensal bacteria with both gram-positive and gram-negative species, characterized by a rigid cell wall, and plays a role in maintaining gut health.



Dorea Optimal

You 0.08% · Optimal 0.0–0.6% · 13th percentile · Prevalence 100%

Dorea is a genus of anaerobic bacteria in the Lachnospiraceae family, commonly found in the human gut where it ferments carbohydrates. It is linked to health conditions such as obesity, type 2 diabetes, hypertension, insomnia, and is influenced by diet, pollution exposure, and vitamin D levels. Though its precise role in health is complex, Dorea's normal abundance is usually low in gut microbiome sequencing.



Pathobionts

Section score **68** / 100

Optimal · Not optimal · Deficient or overgrown

Desulfobacterota High

You 0.69% · Optimal 0.0–0.3% · 83th percentile · Prevalence 94%

Desulfobacterota are bacteria in the human gut that reduce sulfate to hydrogen sulfide, which can support gut health at low levels but may cause harm at higher concentrations. An overabundance of these bacteria has been linked to intestinal inflammation and other gut issues, particularly when influenced by dietary sulfate and sulfur. However, their presence alone is not diagnostic of such conditions.



Bilophila wadsworthia (Desulfobacterota) High

You 0.60% · Optimal 0.0–0.25% · 89th percentile · Prevalence 90%

Bilophila wadsworthia is a gram-negative bacterium that produces hydrogen sulfide, contributing to, and possibly exacerbating, conditions like irritable bowel disease and colorectal cancer by damaging the gut's mucus layer. It can also inhibit mitochondrial function and promote antibiotic resistance by aiding the growth of opportunistic bacteria during antibiotic treatments.



Desulfovibrio (Desulfobacterota) Optimal

You 0.00% · Optimal 0.0–0.15% · 24th percentile · Prevalence 52%

Desulfovibrio is a genus of Gram-negative bacteria found in the gut that produces hydrogen sulfide, which can inhibit mitochondrial function. While this hydrogen sulfide has some health benefits, it is also associated with the progression of irritable bowel disease and colorectal cancer, and can promote antibiotic resistance by supporting opportunistic bacteria growth during antibiotic treatment.



Proteobacteria High

You 4.48% · Optimal 0.0–4.0% · 78th percentile · Prevalence 100%

Proteobacteria is a major phylum of Gram-negative bacteria that includes both pathogenic genera and nonparasitic types responsible for processes like nitrogen fixation. An increased abundance of these bacteria has been linked to inflammatory bowel diseases, including Crohn's disease.



Klebsiella (Proteobacteria) Optimal

You 0.00% · Optimal 0.0–0.01% · 51th percentile · Prevalence 60%

Klebsiella is a genus of bacteria that is part of the normal intestinal flora in humans, with K. oxytoca found in 8-10% of healthy adults. However, Klebsiella pneumoniae is commonly isolated in patients with gastrointestinal conditions and contributes to small intestinal bacterial overgrowth (SIBO). It produces hydrogen sulfide and may require dietary adjustments such as reducing starch and lactose intake, though these should not be long-term. Testing focused on pathogens and antibacterial susceptibility might be necessary depending on symptoms and overgrowth extent.



Parasutterella (Proteobacteria) Optimal

You 2.49% · Optimal 0.0–2.5% · 96th percentile · Prevalence 93%

Parasutterella is a genus of bacteria in the human gut linked to obesity, type 2 diabetes, and depression, with its levels influenced by diet, hormones, and dietary interventions.



Sutterella (Proteobacteria) Optimal

You 0.01% · Optimal 0.0–2.5% · 34th percentile · Prevalence 91%

Sutterella is a common gut bacterium with a mild pro-inflammatory effect, linked to digestive issues such as irritable bowel disease and Crohn's disease, as well as neurological conditions like autism spectrum disorder, although the exact causal mechanisms remain under investigation.



Citrobacter freundii (Proteobacteria) Optimal

You 0.00% · Optimal 0.0–0.01% · 50th percentile · Prevalence 0%

Citrobacter freundii, present in diverse environments and human intestines, can form biofilms and is linked to opportunistic infections due to its toxin production, while also showing potential in cancer treatment.



Escherichia (Proteobacteria) Optimal

You 0.02% · Optimal 0.0–0.3% · 45th percentile · Prevalence 91%

Escherichia, primarily represented by E. coli, are aerobic commensal bacteria in the human gut capable of surviving anaerobically, synthesizing vitamin K, and producing toxins like endotoxins and shiga toxins, which can be pathogenic.



Escherichia coli (Escherichia) Optimal

You 0.00% · Optimal 0.0–0.1% · 47th percentile · Prevalence 6%

Escherichia coli is commonly found in the intestines of healthy individuals and animals, where most strains are harmless and contribute positively by producing vitamin K2 and inhibiting pathogenic bacteria. However, certain strains can cause severe gastrointestinal symptoms when contracted from contaminated food or water.



Fusobacteriota Optimal

You 0.00% · Optimal 0.0–0.03% · 28th percentile · Prevalence 44%

Fusobacteriota, particularly Fusobacterium nucleatum, are gram-negative, anaerobic bacteria present in the human gut and mouth, linked to various diseases including periodontal disease, abscesses, sepsis, colorectal cancer, and inflammatory bowel disease. While generally considered harmful, there is limited research on their role in healthy individuals.



Enterococcus faecalis High

You 0.03% · Optimal 0.0–0.01% · 96th percentile · Prevalence 45%

Enterococcus faecalis is a gut bacterium that functions as both a commensal and pathobiont, offering strain-dependent health benefits like oxalate degradation and antioxidant support when used as a probiotic. However, it can also produce toxins that cause gastrointestinal issues and displays high antibiotic resistance.



Clostridium perfringens Optimal

You 0.00% · Optimal 0.0–0.01% · 43th percentile · Prevalence 14%

Clostridium perfringens is a common cause of food poisoning, particularly from type A strains that produce an enterotoxin leading to diarrhea and abdominal pain, though it can sometimes be ingested without causing harm.



Methanobacteriaceae High

You 0.21% · Optimal 0.0–0.02% · 99th percentile · Prevalence 27%

Methanobacteriaceae are methane-producing archaea (not bacteria, despite the name) and make up almost all of the gut's methanogens, mainly *Methanobrevibacter* and *Methanosphaera*. They consume hydrogen from fermentation to produce methane. Higher levels, and the methane they generate, are associated with slower gut transit and constipation, particularly in constipation-predominant IBS. Note that standard 16S sequencing can under-detect archaea, so low readings should be interpreted with caution.



Methanobrevibacter (Methanobacteriaceae) High

You 0.21% · Optimal 0.0–0.01% · 99th percentile · Prevalence 26%

Methanobrevibacter is a genus of methane-producing archaea in the human intestine, mainly by reducing carbon dioxide with hydrogen. It is associated with gastrointestinal disorders such as chronic constipation and constipation-predominant irritable bowel syndrome, and may also play a role in metabolic diseases like obesity.



Methanosphaera (Methanobacteriaceae) Optimal

You 0.00% · Optimal 0.0–0.01% · 48th percentile · Prevalence 4%

Methanosphaera is the gut's second methanogen, represented almost entirely by *Methanosphaera stadtmanae*. Unlike other methanogens, it makes methane only by reducing methanol with hydrogen, and its methanol supply comes largely from dietary pectin. It's usually uncommon and low in abundance. When elevated alongside *Methanobrevibacter*, it supports a picture of a methanogen-rich gut rather than being a concern on its own.



Mediterraneibacter gnavus Optimal

You 0.07% · Optimal 0.0–0.5% · 69th percentile · Prevalence 87%

Mediterraneibacter gnavus is a gut bacterium normally found in healthy microbiota but is often overrepresented in diseases such as long COVID, obesity, Type 2 diabetes, Crohn’s disease, IBD, and ulcerative colitis, with diet influencing its prevalence, particularly pro-inflammatory diets.



Helicobacter Optimal

You 0.00% · Optimal 0.0–1e-05% · 50th percentile · Prevalence 1%

Helicobacter is a genus of bacteria known for H. pylori, which infects half the global population and is a leading cause of gastritis, peptic ulcers, and gastric cancer. It colonizes the stomach lining by neutralizing acid. Non-pylori Helicobacters are rare in stool, as they primarily inhabit the stomach. Accurate detection of H. pylori in suspected cases requires specific testing, as general 16S tests may lack sufficient sensitivity.



Clostridioides difficile Optimal

You 0.00% · Optimal 0.0–1e-05% · 49th percentile · Prevalence 1%

Clostridioides difficile, commonly known as C. diff, is a bacterium that can cause inflammation of the colon and symptoms like diarrhea, particularly following antibiotic use which disrupts the normal gut microbiome. While C. diff may be detected in healthy individuals, it becomes concerning if symptoms such as persistent diarrhea, abdominal pain, or fever appear post-antibiotics. Diagnosis typically involves specific stool tests for toxins or toxin genes rather than relying on microbiome sequencing, which is less conclusive.



Short Chain Fatty Acids

Section rating **Needs Improvement**

SCFAs (Short Chain Fatty Acids) are beneficial anti-inflammatory end or intermediate metabolites produced by gut bacteria.

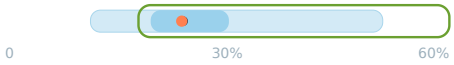
Not a direct measure of stool metabolites.

Optimal range · Distribution · Typical range · Median · Your sample

Acetate

Satisfactory

You 23.84% · Aim ≥ 18% · 49th percentile



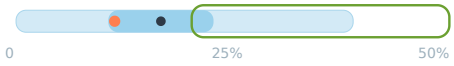
Weight Management

In general, acetate may modulate body weight control through different mechanisms that can affect central appetite regulation, gut-satiety hormones, and improvements in lipid metabolism and energy expenditure.

Butyrate

Low

You 12.32% · Aim ≥ 21% · 28th percentile



Gut Barrier Integrity · Immune System Support · Protection against colorectal cancer

Butyrate is an essential short chain fatty acid, produced by colonic bacteria. The cells of the gut lining feed on butyrate and this makes butyrate essential for gut barrier maintenance. A shortage of butyrate has been implicated in diseases involving colonic inflammation such as ulcerative collitis. Due to the importance of butyrate as an inflammatory regulator and immune system contributor, butyrate depletions could be a key factor influencing the pathogenesis of many vasculitic conditions.

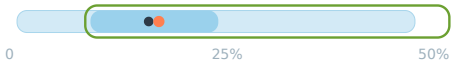
The anti-inflammatory capacity of butyrate has been extensively analyzed and supported by many studies. It has been found that microorganism-produced butyrate expedites the production of regulatory T cells. An increase in regulatory T cell numbers was observed upon a butyrate provision. More recently, it has been shown that butyrate plays an essential and direct role in modulating gene expression of cytotoxic T-cells. Although specific mechanism by which butyrate aids in the differentiation of T-cells is unclear, it has been determined that butyrate promotes the generation of regulatory T cells. This makes butyrate producing bacteria key for supporting the immune system.

Butyrate producers in the optimal range is likely to have a systemic anti-inflammatory effect.

Propionate

Satisfactory

You 17.30% · Aim ≥ 9% · 54th percentile



Blood Pressure Control · Weight Management · Lowers Cholesterol

Propionate is observed to be among the most common short-chain fatty acids produced by human gut microbiota in response to indigestible carbohydrates (fiber) in the diet. Another study found that fatty acid propionate can calm the immune cells that drive up blood pressure, thereby protecting the body from damaging effects of high blood pressure.

Detoxification

Section rating **Satisfactory**

Gut bacteria affect the body's detoxification pathways through the production of enzymes causing toxins bound in the liver to be freed up and reabsorbed in the colon.

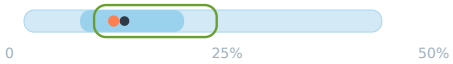
Not a direct measure of stool metabolites.

Optimal range · Distribution · Typical range · Median · Your sample

Beta-glucuronidase (B-GUS) Satisfactory

You 12.21% · Aim 10% to 23.8% · 44th percentile

Estrogen Dominance | Fatigue | Inflammation



The liver excretes toxins by attaching them to glucuronic acid and sending this complex into the small intestine to eventually be excreted from the body. Beta-glucuronidase is an enzyme produced by intestinal bacteria that can break the bond between toxins and glucuronic acid. This enzyme needs to be present just the right amount - not too little and not too much. When beta-glucuronidase is in excess, the bonds between toxins and glucuronic acid are broken, and toxins and hormones that were meant to be excreted are then reabsorbed into the body.

Toxins

Section rating **Needs Improvement**

Pathogenic gut bacteria produce small amounts of end or intermediate substances with various degrees of toxicity to humans.

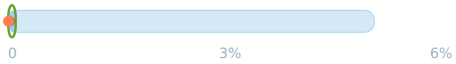
Not a direct measure of stool metabolites.

Optimal range | Distribution | Typical range | Median | Your sample

Colibactin Satisfactory

You 0.01% · Aim ≤ 0.1% · 23th percentile

Ageing

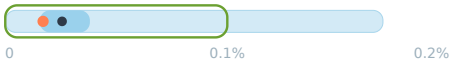


Colibactin is a toxin produced by gut bacteria that induce chromosomal instability and DNA damage, which leads to senescence of epithelial cells and apoptosis of immune cells.

D-Lactate Satisfactory

You 0.02% · Aim ≤ 0.1% · 28th percentile

Fatigue | Brain Fog



D-lactate is produced by bacteria residing in the colon when carbohydrates are not completely absorbed in the small intestine. When not metabolized and transformed into other substrates, it will be eliminated from the body through renal excretion.

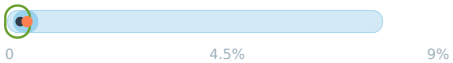
The D-Lactate percentage we display here represents an approximation of the amount of D-lactate producing bacterial species that you have in your colon. Even if we calculate that you have a high level of D-lactate producing bacteria, that does not mean you produce elevated D-lactate, unless you have undigested carbohydrates reaching your colon.

Elevated D-lactate levels in the blood are highly unusual. D-lactic acidosis is typically only observed in patients with a malabsorptive disorder, such as short-bowel syndrome.

Ethanol Satisfactory

You 0.44% · Aim ≤ 0.5% · 63th percentile

Fatigue

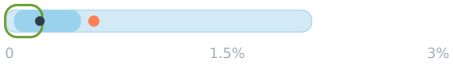


Ethanol is the form of alcohol contained in beverages including beer, wine, and liquor.

Hydrogen Sulfide (H2S) High

You 0.60% · Aim ≤ 0.25% · 80th percentile

Fatigue | Inflammation | Bloat



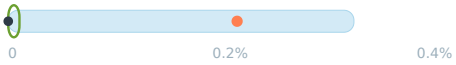
Sulfate-reducing bacteria are the main producers of hydrogen sulfide in the gut. High concentrations of hydrogen sulfide are involved in gut inflammation. Lactic acid bacteria can be sensitive to hydrogen sulfide. Although there are some benefits to hydrogen sulfide production in the gut like cardioprotection, hydrogen sulfide production also contributes to disease pathology. Production of hydrogen sulfide has been linked to irritable bowel disease (IBD) by damaging the gut epithelium's mucus layer and to colorectal cancer. In addition, during treatments with antibiotics, hydrogen sulfide can aide opportunistic bacteria growth leading to antibiotic resistance.

Hydrogen sulfide can inhibit mitochondrial function directly. Mitochondria are the energy powerhouses of cells and runs a range of biological processes.

Methane High

You 0.21% · Aim ≤ 0.01% · 99th percentile

Constipation | Obesity



Methane gas is produced by intestinal methanogens that metabolize hydrogen gas, a product itself of bacterial fermentation of sugar substrates. Currently the main producers are thought to be single celled organisms belonging to the Kingdom Archaea including Methanobrevibacter smithii and Methanospaera stadmagnae and to a lesser extent some of the bacteria species of the clostridium and bacteroides type.

Methane has been associated with gastrointestinal disorders, mainly chronic constipation and constipation predominant irritable bowel syndrome as well as metabolic diseases like obesity.

Neurotransmitters

Section rating **Satisfactory**

*Please note: The section does **not** reflect the neurotransmitters in your brain. Optimal ranges are provided for guidance only and are still under review.*

The gut microbiota communicate with the brain through several different mechanisms. This includes production of neurotransmitters or modulation of host neurotransmitter catabolism, innervation via the vagus nerve, or activation of the HPA axis. These microbial molecules do not act directly on the brain, which is isolated and protected by a membrane called the blood-brain barrier. It appears that neurotransmitters produced by gut bacteria act on the cells lining the gastrointestinal wall in order to have them transmit their message to the central nervous system through the neurons of the gastrointestinal tract that are connected to the brain.

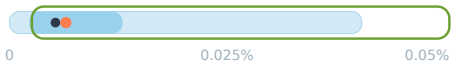
Not a direct measure of stool metabolites.

Optimal range | Distribution | Typical range | Median | Your sample

Dopamine Satisfactory

You 0.01% · Aim ≥ 0.003% · 56th percentile

Motivation | Motor function

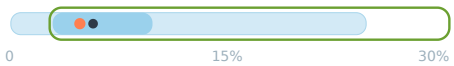


Dopamine is one of the major neurotransmitters in reward-motivated behavior - it is well-known for its role in movement, motivation, and addiction. Dopamine is a precursor for other catecholamines, like norepinephrine and epinephrine. Dopamine is involved in many brain functions.

GABA Satisfactory

You 5.04% · Aim ≥ 3% · 42th percentile

Calmness | Improved Sleep

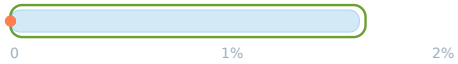


Gamma-aminobutyric acid (GABA) is the major inhibitory neurotransmitter of the central nervous system, and it and its receptors are widely distributed throughout the mammalian host. Substantial literature supports the link between altered GABAergic neurotransmission and numerous CNS disorders, including behavioral disorders, pain, and sleep, as well in the disruption of important functions of the ENS, such as intestinal motility and gastric emptying.

Histamine Satisfactory

You 0.00% · Aim 0% to 1.6% · 32th percentile

Neuromodulation | Wakefulness



Histamine is an biogenic amine that is endogenously produced by mast cells and basophils as part of inflammatory immune responses. Recent evidence also suggests that certain gut bacteria can convert histidine in food to histamine via histamine decarboxylase (HDC) enzyme production. It also performs several important functions in the bowel and acts as a neurotransmitter or chemical messenger that carries signals from one nerve to another.

Nutrients

Section rating **Satisfactory**

Our gut bacteria produces many nutrients, many of which are plentiful in our diets. This section focuses on nutrients that are beneficial (or even essential), but are uniquely produced by our gut bacteria. These nutrients are not present in foods (unless fermented or added) and cannot be synthesized by the human body itself.

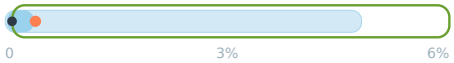
Not a direct measure of stool metabolites.

Optimal range | Distribution | Typical range | Median | Your sample

Equol Satisfactory

You 0.41% · Aim ≥ 0.1% · 76th percentile

Reduce skin ageing | Anti-oxidant | Reduce menopause symptoms



Equol is an isoflavonoid estrogen (phytoestrogen) metabolized from daidzein, a type of isoflavone found in soybeans and other plant sources, by bacterial flora in the intestines. Equol is a nonsteroidal estrogen. Not all humans can produce (S)-equol after soy consumption. The ability to do so depends on having certain strains of bacteria living within the intestine. Note that equol will only be produced if soy products are consumed.

Lipopolysaccharides (LPS)

Section rating **Satisfactory**

Gut microbiome tests like ours cannot measure the degree of intestinal permeability. Instead, this section contains markers of bacterial byproducts that influence the extent to which you would be impacted by a compromised barrier, if it is compromised.

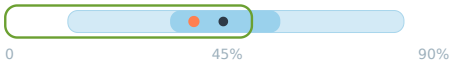
Not a direct measure of stool metabolites.

Optimal range | Distribution | Typical range | Median | Your sample

Gram Negative Satisfactory

You 38.24% · Aim ≤ 50% · 36th percentile

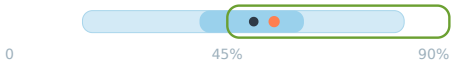
Fatigue | Inflammation | Obesity | Metabolic disorders



The cell membranes of Gram-negative bacteria contain LPS and is therefore of concern to those with higher levels of intestinal pereability. Note that while all Gram-negative bacteria contain LPS in their cell walls, the potency of the LPS differs between organisms. Proteobacteria that's found under the Pathobionts section contain more harmful LPS than those from Bacteroidetes (Commensals) and other bacteria.

Gram Positive Satisfactory

You 54.47% · Aim ≥ 45% · 60th percentile



The cell membranes of Gram-positive bacteria do not contain LPS and is therefore not of concern in relation to LPS.

Food Intolerances

Section rating **Satisfactory**

While many intolerances are predetermined genetically (e.g. through lack of enzyme production), some are also impacted by our gut microbiota. Many gut bacteria produce enzymes relevant to degrading substrates ingested both through diet as well as those produced as byproducts of metabolizing other substrates. Intolerance should not be confused with allergies. Intolerances are milder reactions based on lack of enzymes and not an immune reaction. For both lactose & oxalate degraders, close to or higher than the median is desired.

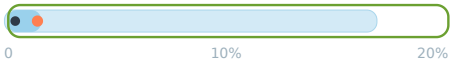
Not a direct measure of stool metabolites.

Optimal range | Distribution | Typical range | Median | Your sample

Lactose Satisfactory

You 1.50% · Aim ≥ 0.18% · 73th percentile

Bloat Diarrhoea

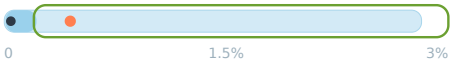


Lactose digestion is determined by the ability to produce the lactase enzyme. While all human babies produce lactase, many adults produce very little. Lactose intolerance (via endogenous lactase enzyme production) can be determined through a genetic test. A further factor influencing lactose intolerance is the presence/absence of lactose degrading bacteria in the small intestine and to a lesser degree in the colon.

Oxalates Satisfactory

You 0.45% · Aim ≥ 0.2% · 86th percentile

Kidney Stones Reduced mineral absorpion Inflammation Autoimmunity



Leafy greens and other popular plant foods contain an antinutrient called oxalate. Gut bacteria contribute to oxalate metabolism through the production of enzymes that degrade oxalate. Oxalates are not just ingested through the dietary intake but are also synthesized by the body. Most oxalates are produced by the body through the breakdown of Dehydroascorbic acid (DHA), an oxidized form of ascorbic acid (vitamin C). One of the main health concerns around oxalates is that it can bind to minerals in the gut and prevent the body from absorbing them. It also increases the risk of developing kidney stones as it is excreted through urine and stool.

Longevity

Section rating **Satisfactory**

Our gut microbiota are capable of producing enzymes implicated in longevity which we cannot produce ourselves. These enzymes are responsible for processing substrates from food into beneficial metabolites. They increase longevity by decreasing the slow damage associated with aging via their antioxidative properties. Additionally, these metabolites have been found to combat the three leading causes of death in both the USA and UK: cancer, heart disease, and neurological diseases such as dementia and Alzheimer's disease. Myrosinase producers close to or higher than the median is desired.

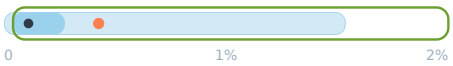
Not a direct measure of stool metabolites.

Optimal range Distribution Typical range Median Your sample

Myrosinase Satisfactory

You 0.43% · Aim ≥ 0.04% · 85th percentile

Anti-carcinogenic Anti-ageing



Inherently, humans cannot produce the enzyme myrosinase so instead, we rely on our gut microbiota to produce it. This enzyme is responsible for processing glucosinolate compounds into their isothiocyanate products. These glucosinolate compounds are typically found in vegetables from the Brassicaceae family, which includes cruciferous vegetables such as broccoli, Brussels sprouts, cabbage, and capers. The primary focus of research on these compounds is the glucosinolate **glucoraphanin**, and its isothiocyanate product **sulforaphane**. These glucosinolates cannot be fully metabolised by the vegetable's own myrosinase after being cooked, since the heat partially inactivates or denatures the myrosinase enzymes. Despite this, the leftover glucosinolates are still metabolised to isothiocyanates in humans. This is explained by the gut microflora because within the gut of humans are myrosinase-producing bacteria. Sulforaphane is a powerful organic sulfur-containing phytochemical that has been found to be associated with a wide range of health benefits, such as: protecting against cancer by inducing the detoxification and excretion of carcinogens, protecting against otherwise lethal pathogens such as SARS-CoV-2, and reducing blood sugar levels associated with type 2 diabetes.
Naturally, these antioxidative properties also extend to the reduction of other age-associated oxidative stress processes such as neurodegeneration, skin damage caused by UV radiation, build-up of plaque in the arteries, and increased blood pressure.

OVERALL RECOMMENDATIONS

Your personalised plan

Built from your completed health profile and your microbiome sample from 13 Dec 2021.

TO ADD	TO REDUCE	BIGGEST IMPACT
71 items	**13** items	**cranberries** · 6 bacteria

Before you start. These suggestions feed or crowd out specific bacteria — they don't imply personal tolerance. Introduce new items gradually, one at a time and starting with a low dose.

Foods

32 to add · 1 to reduce

The number on each card shows how many beneficial bacteria this food is expected to improve.

- 6 cranberries
- 6 strawberries
- 6 zhenjiang aromatic vinegar
- 5 chickpeas
- 5 lentils
- 5 green tea
- 5 matcha
- 5 pomegranate
- 4 beans
- 4 beetroot
- 4 fennel
- 4 lettuce
- 4 raddichio
- 3 broccoli
- 3 pistachios
- 3 cinnamon
- 3 cloves
- 2 cottonseed flour
- 2 soy flour
- 2 chamomile
- 2 vanilla
- 1 oyster mushrooms
- 1 red yeast rice
- 1 mushrooms
- 1 multi-fiber bread
- 1 black pepper
- 1 cayenne pepper
- 1 ginger
- 1 oregano
- 1 rosemary
- 1 turmeric
- 1 holy basil

To reduce

The number shows how many bacteria this food is expected to worsen. Don't cut these completely — just dial back.

- 1 rosemary extract

Prebiotics & ingredients

24 to add · 9 to reduce

The number on each card shows how many beneficial bacteria this item is expected to improve.

- 5 lactulose
- 4 Galactooligosaccharides
- 3 Yeast beta-glucan
- 3 resveratrol
- 3 calanus oil
- 3 Omega-3
- 2 acacia fiber
- 2 Arabinogalactan
- 2 raffinose
- 2 stachyose
- 2 xylooligosaccharides
- 2 turmeric
- 2 garlic
- 2 nicotinamide mononucleotide
- 2 quercetin
- 2 ShenLing BaiZhu San
- 1 Canna edulis RS3
- 1 beta-glucan
- 1 konjac glucomannan
- 1 cinnamon
- 1 ginger
- 1 oregano ▲
- 1 codonopsis
- 1 berberine ▲

▲ Use with caution and for a limited time only — these can decrease your probiotic and commensal bacteria. Please consult your practitioner.

To reduce

The number shows how many bacteria this item is expected to worsen.

- 2 resistant starch
- 2 taurine
- 1 milk oligosaccharides
- 1 pea fiber
- 1 gum arabic
- 1 Partially Hydrolyzed Guar Gum
- 1 psyllium
- 1 cellulose
- 1 licorice

Probiotics

8 to add

The number on each card shows how many beneficial bacteria this item is expected to improve.

- 3 Lactobacillus rhamnosus HN001
- 3 Bifidobacterium longum BB536
- 2 Bacillus coagulans
- 2 Lactobacillus rhamnosus GG
- 1 Bifidobacterium longum
- 1 Lactobacillus acidophilus
- 1 Lactobacillus plantarum
- 1 Lactobacillus casei

Lifestyle

7 to add · 3 to reduce

The number on each card shows how many microbiome markers this change is expected to improve.

- 4 High fiber foods
- 4 Exercise
- 1 Plant based diet
- 1 eat the rainbow
- 1 seasonal foods
- 1 Avoid snacking
- 1 spend time in nature

To reduce

The number shows how many microbiome markers this habit is expected to worsen.

- 6 Reduce animal products and fat
- 2 Reduce milk fats
- 1 Reduce sulfur additives

Numbers show how many of your flagged bacteria (or microbiome markers) each item is expected to affect. Recommendations do not imply tolerance for any particular item; introduce changes gently and consult your practitioner before starting supplements.