Vitract

838 Walker Rd, Dover, Delaware,
19904, United States

For enquiries, email hello@vitract.com

# Gut Microbiome Analysis

Comprehensive Analysis - Deep Shotgun Sequencing

John Doe | VT1-123DC

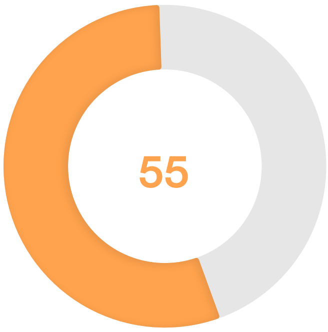
17 Feb 2025

This is your complete gut microbiome analysis containing condition related findings with food and supplements recommendation to optimize your gut health.

## SECTION 1: Summary of your results

0-49 represents Poor • 50-79 represents Needs work • 80-100 represents Satisfactory

Gut Health Score

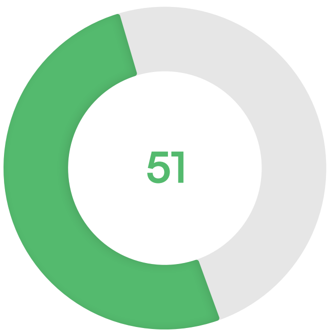



Needs work

### Your Gut Health Score

Your Gut Health Score is the percentage value of all the microbes enlisted in section 2 within the optimal range. Assuming all your scores are within optimal ranges, then your score will be 100. For every taxa that is out of range, your score decreases accordingly.

Diversity Score




Satisfactory

### Your Diversity Score

Your Diversity Score is computed using the Shannon Index. This accounts for the richness and evenness of the species found in your gut. Your score is a percentage value compared to the highest Shannon score of the population who have taken the Vitract Gut Microbiome Test. Note that apart from diet, other factors such as age, geographical location, genetics, sleep patterns, antibiotic use, etc, can affect your diversity score

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## SECTION 2: Microbial life forms

### BACTERIA

**Health-associated bacteria**

Probiotic bacteria
Commensals

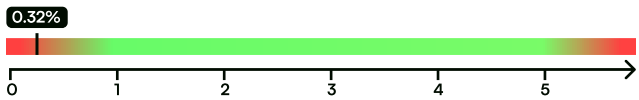
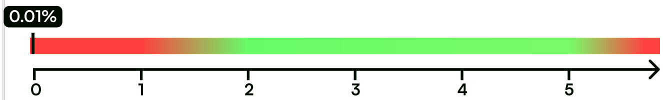
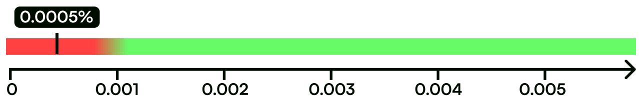
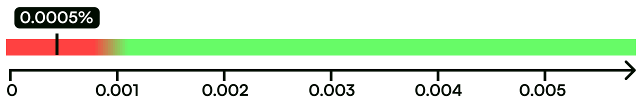
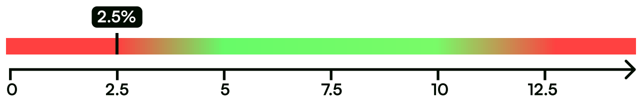
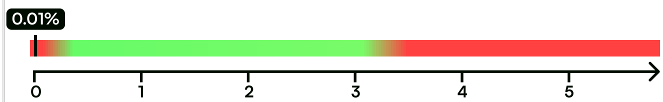
**Disease-associated bacteria**

Pathobiont overgrowth
Pathogens

### Probiotic bacteria - 52

Probiotic bacteria are live microorganisms that, when consumed in sufficient quantities, provide health benefits by promoting a balanced and healthy gut microbiota.

Low Optimal High represents bacteria levels.

| # | Probiotic bacteria | Implication |
|---|---|---|
| 1 | *Akkermansia muciniphila* - 0.32% Low Optimal range (1-5%)<br> | Low<br>Low levels of *A. muciniphila* can lead to impaired gut barrier function, increased inflammation, and metabolic disorders like obesity and insulin resistance. |
| 2 | *Bifidobacterium* - 0.01% Low Optimal range (2-5%)<br> | Low<br>Low amounts of *Bifidobacterium* can lead to dysbiosis, a microbial imbalance associated with various digestive disorders, including IBS, ulcerative colitis and IBD. Additionally, it can weaken the gut's barrier function, making it more susceptible to harmful pathogen invasion. |
| 3 | *Bifidobacterium adolescentis* - 0.005% Low Optimal range (>0.001%)<br> | Low<br>Low levels of *Bifidobacterium adolescentis* are linked to increased gut permeability, obesity and insulin resistance, as well as cognitive decline. |
| 4 | *Bifidobacterium longum* - 0.0005% Low Optimal range (>0.001%)<br> | Low<br>Low levels of *Bifidobacterium longum* can reduce short chain fatty acid production, increase risks of inflammatory bowel diseases, impair digestion of dietary fibers and increase risk of allergies |
| 5 | *Blautia* - 2.5% Low Optimal range (5-10%)<br> | Low<br>Low levels of *Blautia* have been reported in adults and children suffering from type 2 diabetes and Inflammatory bowel disease (IBD), including Crohn's disease (CD) and ulcerative colitis and also liver cirrhosis. |
| 6 | *Blautia obeum* - 0.01% Low Optimal range (0.07-3%)<br> | Low<br>Low levels of *Blautia obeum* may impair fiber fermentation, absorption of nutrients, and butyrate production which can lead to compromised immune function. |

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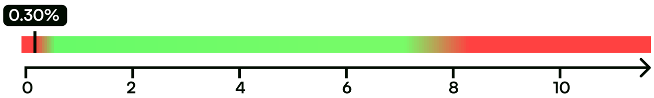
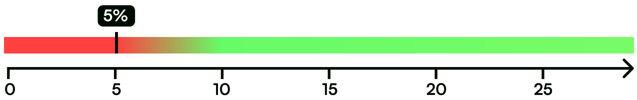
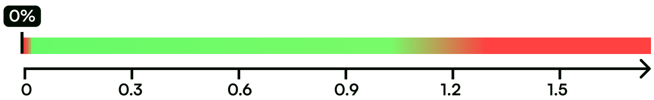
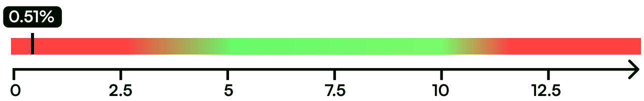
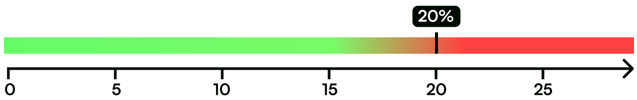
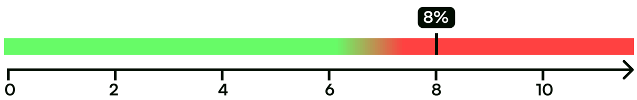
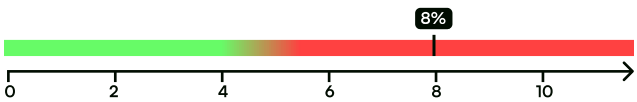
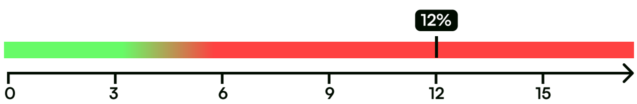
| # | Probiotic bacteria | Implication |
|---|---|---|
| 7 | *Blautia wexlerae* - 0.30% Low Optimal range (0.4-7%)   | Low<br>Low levels of *Blautia wexlerae* may impair fiber digestion, and contribute to digestive issues like constipation and metabolic disorders like type 2 diabetes. |
| 8 | *Faecalibacterium prausnitzii* - 5% Low Optimal range (>=10%)   | Low<br>*F prausnitzii* produces butyrate which serves as an energy source for intestinal cells. Low levels of *F. prausnitzii* can result in reduced nutrient supply to intestinal cells, promote chronic inflammation, and negatively impact gut-brain communication. |
| 9 | *Lactobacillus* - 0% Low Optimal range (0.01-1%)   | Low<br>Low levels of *Lactobacillus* can lead to an imbalance in the gut microbiota, which is associated with various gastrointestinal issues, such as diarrhea, irritable bowel syndrome, and inflammatory bowel diseases. |
| 10 | *Roseburia* - 0.51% Low Optimal range (5-10%)   | Low<br>Low levels of *Roseburia* can lead to an imbalance in the gut microbiota, which is associated with various gastrointestinal disorders, including irritable bowel syndrome (IBS) and inflammatory bowel diseases (IBD). |
| 11 | *Ruminococcus* - 20% High Optimal range (0-15%)   | High<br>An over-abundance of certain strains of *Ruminococcus* has been associated with health conditions, including obesity and metabolic disorders. |
| 12 | *Ruminococcus bromii* - 8% High Optimal range (0-6%)   | High<br>Very high levels of *Ruminococcus bromii* could disrupt gut balance, potentially leading to digestive discomfort like bloating, gas, and poor regulation of butyrate production. |

## Commensals - 84

Gut commensals are microorganisms that coexist with the host in the gastrointestinal tract without causing harm. They contribute to host wellbeing and gut homeostasis.

| # | Commensals | Implication |
|---|---|---|
| 1 | *Agathobacter rectalis (formerly Eubacterium rectale)* - 8% High Optimal range (0-4%)   | High<br>Very high levels of *Agathobacter rectalis* may indicate an imbalance in gut microbiota, leading to intestinal gas production and possibly contributing to mood disorders such as anxiety. |
| 2 | *Alistipes finegoldii* - 12% High Optimal range (0-3%)   | High<br>High levels of *Alistipes finegoldii* are correlated with depression, anxiety and chronic fatigue syndrome. |

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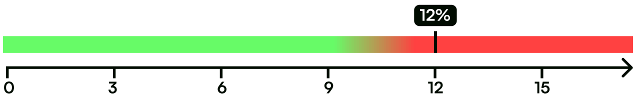
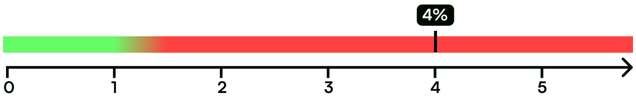
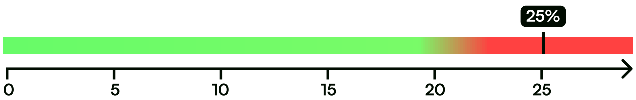
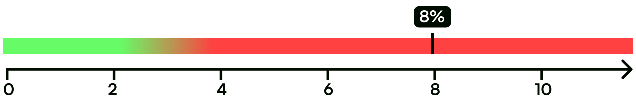
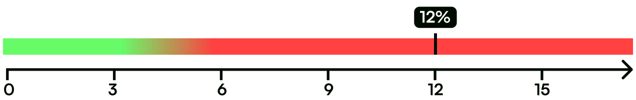
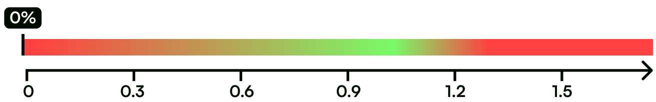
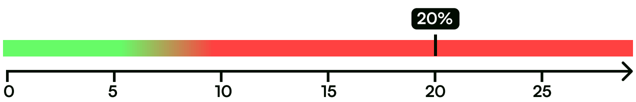
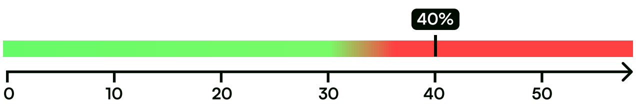
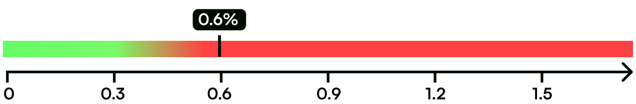
| # | Commensals | Implication |
|---|---|---|
| 3 | *Alistipes putredinis* - 12% High — Optimal range (0-9%)<br> | High<br>High levels of *Alistipes putredinis* are correlated with depression, anxiety and chronic fatigue syndrome. |
| 4 | *Anaerobutyricum hallii (formerly Eubacterium hallii)* - 4% High — Optimal range (0-1%)<br> | High<br>High *Anaerobutyricum hallii* levels could contribute to increased production of hydrogen and methane gases, potentially causing bloating, discomfort, or gas. |
| 5 | *Bacteroides* - 25% High — Optimal range (0-20%)<br> | High<br>Increased levels of certain *Bacteroides spp.* have been associated with increased mucosal inflammation and the development of colorectal and invasive breast cancer. |
| 6 | *Bacteroides fragilis* - 8% High — Optimal range (0-2%)<br> | High<br>Very high levels of *Bacteroides fragilis* has been associated with abscess formation; and an increase in autoimmune conditions like Ulcerative colitis and Crohn's Disease. |
| 7 | *Bacteroides thetaiotaomicron* - 12% High — Optimal range (0-3%)<br> | High<br>Very high levels of *Bacteroides thetaiotaomicron* may lead to overproduction of byproducts from fiber fermentation. |
| 8 | *Oxalobacter formigenes* - 0% Low — Optimal range (0.01-1%)<br> | Low<br>*Oxalobacter formigenes* is crucial for oxalate degradation, and low levels can lead to toxic oxalate buildup, increasing the risk of nephrolithiasis. |
| 9 | *Phocaeicola vulgatus* - 20% High — Optimal range (0-10%)<br> | High<br>Very high levels of *Phocaiecola vulgatus* may interfere with intestinal permeability, increase risk of obesity and insulin resistance, including disrupting normal digestion. |
| 10 | *Prevotella copri (now Segatella copri)* - 40% High — Optimal range (0-20% for non-vegetarians) Optimal range (0-30% for vegetarians)<br> | High<br>Very high levels of *Prevotella copri* may contribute to gut dysbiosis, increased production of proinflammatory markers, and have been associated with arthritis. |
| 11 | *Streptococcus thermophilus* - 0.6% High — Optimal range (0-0.3%)<br> | High<br>Elevated *Streptococcus thermophilus* levels may suggest an overgrowth, possibly influencing fermentation process, leading to an increased production of gas or byproducts that can exacerbate gut irritation. |

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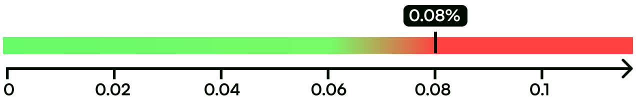
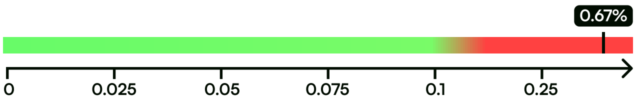
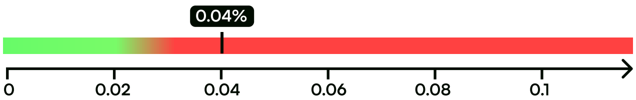
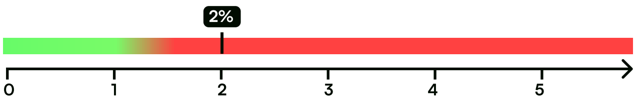
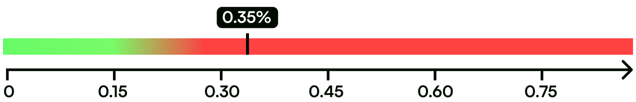
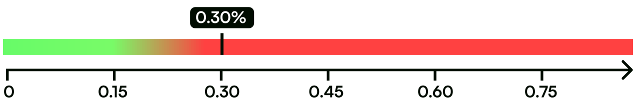
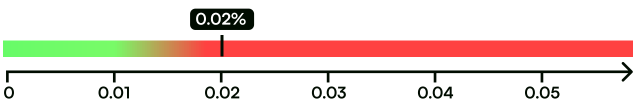
## Pathobionts - 64

Pathobionts are microorganisms that typically reside harmlessly in the gut but have the potential to cause disease under certain conditions or when the host's immune system is compromised. Pathobionts in this test are shown in 4 sub-categories:

| # | Enterotoxic & Inflammatory Pathobionts | Implication |
|---|---|---|
| 1 | *Enterococcus faecalis* - 0.08% High — Optimal range (0-0.06%)<br><br> | High<br>High levels produce hemolysin that lyses the host cell and may drive the endocarditis infections, biofilm production protects the bacteria from immune responses and antibiotics. |
| 2 | *Escherichia coli* - 0.67% High — Optimal range (0-0.1%)<br><br> | High<br>When present in high levels, pathogenic *Escherichia coli* strains may produce heat liable and heat stable toxins that cause diarrhea and host cell death, leading to conditions such as hemolytic uremic syndrome. |
| 3 | *Klebsiella pneumoniae* - 0.04% High — Optimal range (0-0.02%)<br><br> | High<br>Synthesizes polysaccharides that protect against immune responses and siderophores that sequester iron from the host leaving the host vulnerable to other bacteria infections in an iron limited environment. |
| 4 | *Ruminococcus gnavus (now Mediterraneibacter gnavus)* - 2% High — Optimal range (0-1%)<br><br> | High<br>*Ruminococcus gnavus* has been found to produce an inflammatory polysaccharide that induces inflammation in the gut, as a result contributing to inflammatory bowel diseases. |

| # | Hydrogen Sulfide Producers | Implication |
|---|---|---|
| 1 | *Bilophila wadsworthia* - 0.35% High — Optimal range (0-0.15%)<br><br> | High<br>*Bilophila wadsworthia* is a hydrogen sulfide-producing bacterium enriched by a high-fat diet, with high levels linked to inflammation, bile acid dysmetabolism, and intestinal barrier dysfunction. |
| 2 | *Desulfovibrio* - 0.30% High — Optimal range (0-0.15%)<br><br> | High<br>An increased abundance of *Desulfovibrio* (DSV) can result in the overproduction of hydrogen sulfide, increasing the risk of gastrointestinal problems and inflammatory bowel diseases (IBD). In ulcerative colitis conditions, DSV has been associated with ulcerative colitis in individuals with anxiety and depression comorbidities. |
| 3 | *Fusobacterium nucleatum* - 0.02% High — Optimal range (0-0.01%)<br><br> | High<br>*Fusobacterium nucleatum* can invade the intestinal epithelium, with high levels triggering systemic inflammation and promoting colorectal cancer formation. |

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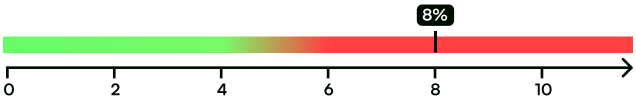
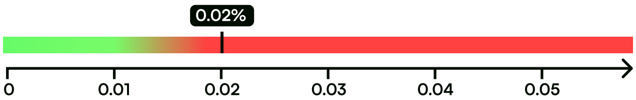
| # | Inflammatory Lipopolysaccharide Producer | Implication |
|---|---|---|
| 1 | *Proteobacteria* - 8% High — Optimal range (0-4%)   | High<br>High levels of *Proteobacteria* can trigger systemic inflammation as a result of lipopolysaccharide production, increasing the risk of metabolic disorders such as insulin resistance and cardiovascular diseases. |

| # | Methane Producing Archaea | Implication |
|---|---|---|
| 1 | *Methanobrevibacter smithii* - 0.02% High — Optimal range (0-0.01%)   | High<br>*Methanobrevibacter smithii* produces high levels of methane and may lead to methane-associated constipation by slowing transit time. |

## Pathogens

Pathogens in the gut can cause disease or infection when they colonize the gastrointestinal tract.

Detected Not detected

| # | Pathogens | Implication |
|---|---|---|
| 1 | *Campylobacter jejuni* - 1.2% Detected | *Campylobacter jejuni* can penetrate the gut surface and produce enterotoxins that disrupt the host functions, triggering inflammation and cell death. |
| 2 | *Clostridiodes difficile* - 1.3% Detected | *C. difficile* produces toxin A and B that disrupts epithelial cell cytoskeletons leading to cell death and loss of gut barrier integrity and triggering inflammatory responses. |
| 3 | *Helicobacter pylori* - 1.2% Detected | *H. pylori* neutralizes gastric acids by producing ammonia in the stomach, creating an environment suitable for opportunistic pathogens to colonize the stomach. *H. pylori* also promotes inflammation and cell death, leading to formation of stomach ulcers. |
| 4 | *Salmonella enterica* - 1.2% Detected | *Salmonella enterica* at high levels can cause diarrhea and gastrointestinal issues. |
| 5 | *Salmonella typhi* - 1.2% Detected | *Salmonella typhi* can hijack immune cells in the body to spread systemically to sites such as the liver and spleen to cause infections such as typhoid fever. |
| 6 | *Shigella dysenteriae* - 1.3% Detected | *Shigella dysenteriae* produces shiga toxin that disrupts the host metabolic functions and contributes to cell death and eventually systemic complications such as hemolytic uremic syndrome. |
| 7 | *Staphylococcus aureus* - 1.3% Detected | *S. aureus* produces a toxin (Panton-Valentine leukocidin) that forms pores in host cells causing cell lysis and may cause extensive tissue damage. |
| 8 | *Vibrio cholerae* - 1.2% Detected | Cholera toxins increase intestinal permeability to water, leaving the intestine vulnerable to water loss and watery diarrhea. |
| 9 | *Yersinia enterolytica* - 1.2% Detected | Inject molecules called yop effectors that disrupts cellular process, inhibit uptake by immune cells and suppress host response and can cause yersiniosis. |
| 10 | *Yersinia pestis* - 1.2% Detected | *Y pestis* produce proteins called Yop effectors inhibit immune cell uptake and activation and may cause plague. *Y. pestis* multiplies primarily in the blood, leading to tissue necrosis and shock. |
| 11 | *Yersinia pseudotuberculosis* - 1.2% Detected | *Y. pseudotuberculosis* uses yop proteins to evade the immune system causing mesenteric lymphadenitis by targeting the Peyer's patches in the gut. |

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## FUNGI

| # | Fungi | Implication |
|---|---|---|
| 1 | *Candida albicans* - 0.5% Detected | *Candida albicans* is a fungus that overgrows during dysbiosis, leading to fungal infections and gut inflammation by disrupting epithelial integrity. |
| 2 | *Candida spp.* - 0.5% Not detected | Not detected |
| 3 | *Geotrichum spp.* - 2.5% Not detected | Not detected |
| 4 | *Microsporidium spp.* - 0.5% Not detected | Not detected |
| 5 | *Rhodotorula spp.* - 1.2% Not detected | Not detected |

## VIRUSES

| # | Viruses | Implication |
|---|---|---|
| 1 | Adenovirus F40/41 Detected | Adenovirus F40/41 is a leading cause of viral gastroenteritis, particularly in children. Overabundance triggers diarrhea and inflammation by infecting intestinal epithelial cells and disrupting barrier integrity. |
| 2 | Astrovirus Not detected | Not detected |
| 3 | Cytomegalovirus (CMV) Not detected | Not detected |
| 4 | Epstein-Barr virus (EBV) Not detected | Not detected |
| 5 | Norovirus GI Detected | Norovirus GI is highly infectious and the leading cause of acute gastroenteritis. It disrupts epithelial tight junctions and induces cytokine storms, leading to diarrhea and inflammation. NoV infections are linked to post-infectious irritable bowel syndrome (IBS) and possibly inflammatory bowel disease (IBD). |
| 6 | Norovirus GII Not detected | Not detected |
| 7 | Rotavirus A Not detected | Not detected |
| 8 | Sapovirus Not detected | Not detected |

## PROTOZOA

| # | Protozoa | Implication |
|---|---|---|
| 1 | *Balantidium coli* Not detected | Not detected |
| 2 | *Blastocystis spp.* Not detected | Not detected |
| 3 | *Chilomastix mesnili* Not detected | Not detected |
| 4 | *Cryptosporidium* Not detected | Not detected |
| 5 | *Cyclospora spp.* Not detected | Not detected |
| 6 | *Dientamoeba fragilis* Not detected | Not detected |
| 7 | *Entamoeba coli* Not detected | Not detected |
| 8 | *Entamoeba hartmanni* Detected | *Entamoeba hartmanni* is a non-pathogenic amoeba commonly found in the human gastrointestinal tract. Currently, there is limited evidence to suggest that an overabundance of *E. hartmanni* adversely affects gut health or contributes to diseases. However, high levels of *E. hartmanni* may indicate poor sanitary conditions or exposure to contaminated food or water sources, raising concerns about potential exposure to other pathogens. |
| 9 | *Entamoeba histolytica* Not detected | Not detected |
| 10 | *Giardia* Detected | *Giardia* is a flagellated protozoan causing giardiasis. Overgrowth disrupts nutrient absorption by damaging villi, leading to malabsorption, diarrhea, and chronic gut inflammation. |
| 11 | *Pentatrichomonas hominis* Not detected | Not detected |

## PARASITIC HELMINTHS (WORMS)

| # | Parasitic Helminths (Worms) | Implication |
|---|---|---|
| 1 | *Ancylostoma duodenale*<br>Not detected | Not detected |
| 2 | *Ascaris lumbricoides*<br>Not detected | Not detected |
| 3 | *Diphyllobothrium latum*<br>Not detected | Not detected |
| 4 | *Dipylidium caninum*<br>Not detected | Not detected |
| 5 | *Enterobius vermicularis*<br>Not detected | Not detected |
| 6 | *Fasciola spp.*<br>Not detected | Not detected |
| 7 | *Hymenolepis*<br>Not detected | Not detected |
| 8 | *Mansonella spp.*<br>Detected | *Mansonella species* are filarial nematodes. Human mansonellosis is caused by three filarial species: *Mansonella perstans, M. ozzardi*, and *M. streptocerca*. They induce immune activation, which can impair gut function indirectly. |
| 9 | *Necator americanus*<br>Not detected | Not detected |
| 10 | *Schistosoma*<br>Detected | *Schistosoma species* are trematodes causing schistosomiasis. The adult parasite can evade the immune system for years and induce granulomatous inflammation, leading to fibrosis and portal hypertension, disrupting gut and liver function. |
| 11 | *Strongyloides stercoralis*<br>Not detected | Not detected |
| 12 | *Taenia solium*<br>Not detected | Not detected |
| 13 | *Taenia spp*<br>Not detected | Not detected |
| 14 | *Trichuris trichiura*<br>Not detected | Not detected |

## SECTION 3: Antimicrobial resistance genes

| Universal Antimicrobial resistance | Result |
|---|---|
| b-lactams | Positive |
| Aminoglycosides | Positive |
| Fluoroquinolones | Negative |
| Macrolides_lincosamines_streptogramin B | Positive |
| Polymixin_colistin | Negative |
| Sulfonamides_Trimethoprim | Negative |
| Vancomycin | Positive |

*Reference bacteria can be found on supplementary pages.*

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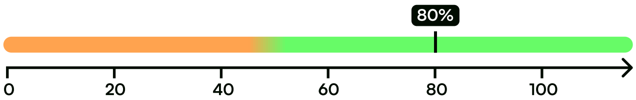
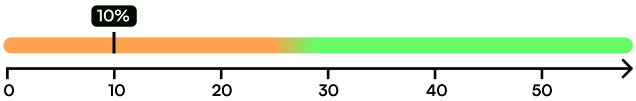
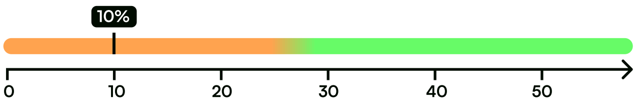
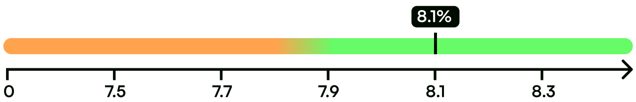
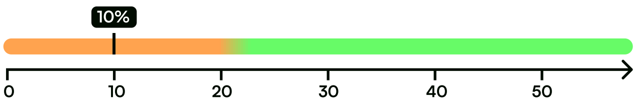
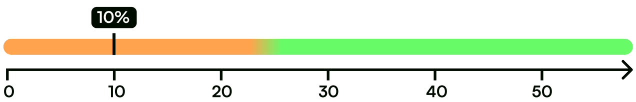
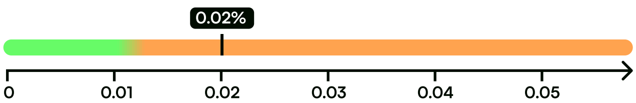
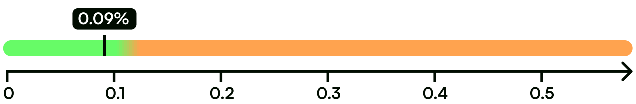
## SECTION 4: Insights into metabolites, inflammatory and digestive markers

**Please note that the metabolites are computed based on the microbial gene content and metabolic pathways related to metabolite production. This is not a direct measurement of the metabolite or enzyme.**

Satisfactory Needs work High represents rating.

| # | Short Chain Fatty Acids Producers | Impact |
|---|---|---|
| 1 | Acetate - 80% Satisfactory Optimal range (>= 46%)<br> | Metabolic regulation<br>Anti-inflammatory effects<br>Neuroprotection and cognitive function |
| 2 | Butyrate - 10% Needs work Optimal range (>= 28%)<br> | Energy source for colonocytes<br>Anti-inflammatory effects<br>Maintenance of gut barrier function |
| 3 | Propionate - 10% Needs work Optimal range (>= 28%)<br> | Colonic pH regulation<br>Appetite regulation<br>Anti-inflammatory effects by promoting immune regulatory responses |

| # | Neurotransmitter Producers | Impact |
|---|---|---|
| 1 | Acetylcholine - 8.1% Satisfactory Optimal range (>= 7.9%)<br> | Key mediator of peristalsis<br>Stimulates the release of digestive enzymes from glands in the digestive system |
| 2 | Dopamine - 10% Needs work Optimal range (>= 21%)<br> | Cognitive function<br>Regulates mood and sleep |
| 3 | GABA - 10% Needs work Optimal range (>= 24%)<br> | Influences smooth muscle contraction and relaxation<br>Contributes to mood regulation and relaxation |
| 4 | Histamine - 0.02% Needs work Optimal range (0-0.01%)<br> | Contributes to the body's defense mechanisms against pathogens<br>Involved in the regulation of wakefulness, arousal, and cognitive functions |
| 5 | Norepinephrine - 0.09% Satisfactory Optimal range (0-0.1%)<br> | Increases alertness<br>Involved in cognitive functions such as attention, learning, and memory |

*Reference bacteria can be found on supplementary pages.*

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| # | Neurotransmitter Producers | Impact |
|---|---|---|
| 6 | Serotonin - 1.4% Satisfactory; Optimal range (>= 1.3%) | Mood regulation; Gastrointestinal motility; Involved in the regulation of appetite and satiety |

| # | Vitamins Producers | Impact |
|---|---|---|
| 1 | Vitamin B1 (Thiamin) - 0.8% Satisfactory; Optimal range (>= 0.7%) | Serves as a coenzyme in carbohydrate metabolism; Cellular growth and repair; Essential for the proper functioning of the enteric nervous system |
| 2 | Vitamin B2 (Riboflavin) - 20% Needs work; Optimal range (>= 48%) | Aids in the breakdown of carbohydrates, proteins, and fats for energy; Antioxidant defense; Supports the growth and maintenance of gut epithelial cells |
| 3 | Vitamin B3 (Niacin) - 0.4% Satisfactory; Optimal range (>= 0.3%) | Aids metabolism of fats, carbohydrates and proteins; Aids in neurotransmitter synthesis; Essential for maintaining skin health |
| 4 | Vitamin B5 (Pantothenic Acid) - 1.0% Satisfactory; Optimal range (>= 0.8%) | Energy production through metabolism of carbohydrates, proteins, and fats; Contributes to the synthesis of acetylcholine; Fatty acid and hormone synthesis |
| 5 | Vitamin B6 (Pyridoxine) - 1.0% Satisfactory; Optimal range (>= 0.4%) | Essential for the synthesis of neurotransmitters like serotonin, dopamine, and GABA; Supports the immune system |
| 6 | Vitamin B7 (Biotin) - 0.4% Satisfactory; Optimal range (>= 0.3%) | Fatty acid synthesis; Carbohydrate metabolism; Cell growth and maintenance of gene expression |
| 7 | Vitamin B9 (Folate) - 1.0% Satisfactory; Optimal range (>= 0.6%) | DNA synthesis and repair; Metabolism of amino acids; Involved in the synthesis of serotonin, dopamine, and norepinephrine |

*Reference bacteria can be found on supplementary pages.*

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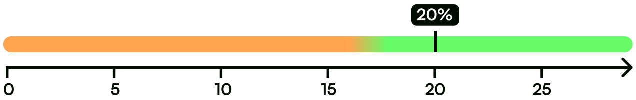
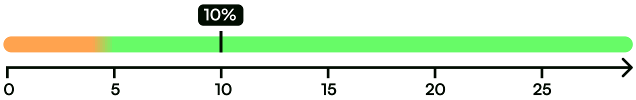
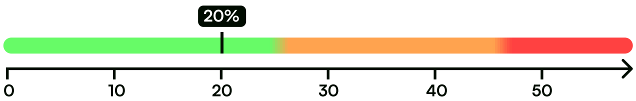
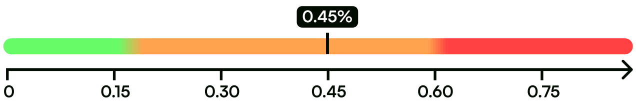
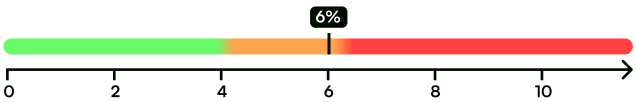
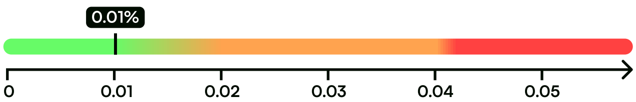
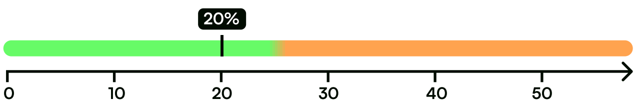
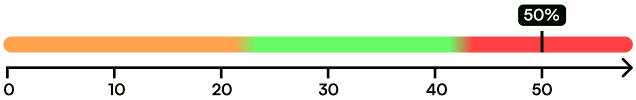
John Doe | VT1-123DC

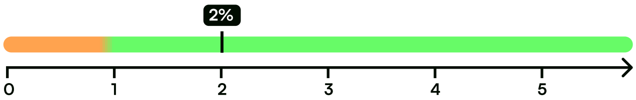
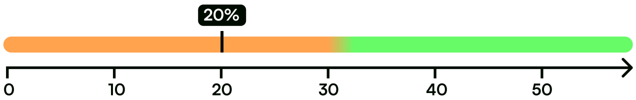
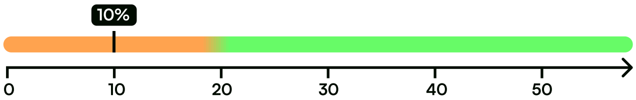
17 Feb 2025

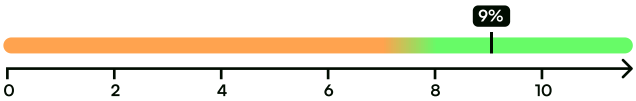
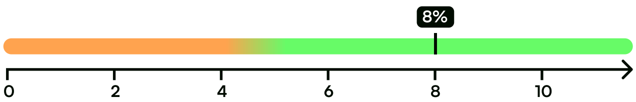
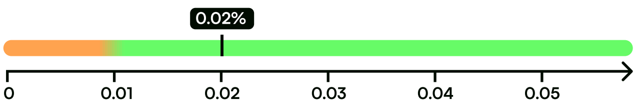
| # | Vitamins Producers | Impact |
|---|---|---|
| 8 | Vitamin B12 (Cobalamine) - 20% Satisfactory Optimal range (>= 17%)<br> | Supports neurological function<br>Red blood cell formation<br>Energy production |
| 9 | Vitamin K2 - 10% Satisfactory Optimal range (>= 5%)<br> | Essential for proper blood clotting and coagulation<br>Improves bone health<br>Prevents arterial calcification and reduces the risk of atherosclerosis |

| # | Inflammatory Markers and Toxin Producers | Impact |
|---|---|---|
| 1 | Ammonia - 20% Satisfactory Optimal range (0-24%)<br> | Disruptions in the intestinal barrier function<br>Inflammation and abdominal pain<br>Neurotoxic effect<br>Gut microbiota disruption |
| 2 | Hydrogen sulfide - 0.45% Needs work Optimal range (0-0.15%)<br> | Increased risk of colorectal cancer<br>Impaired mucin production<br>Bloating and abdominal pain<br>Malodorous breath |
| 3 | Lipopolysaccharides (LPS) - 6% Needs work Optimal range (0-4%)<br> | Increased inflammation<br>Metabolic dysfunction and insulin resistance<br>Neurological effect<br>Increased contribution to chronic diseases |
| 4 | Methane - 0.01% Satisfactory Optimal range (0-0.01%)<br> | Abdominal distension or bloating<br>Constipation, cramping and flatulence<br>Increased methane breath |
| 5 | Trimethylamine (TMA) - 20% Satisfactory Optimal range (0-24%)<br> | Increased cardiovascular health risk<br>Cognitive function and neurological disorders<br>Inflammation and lipid accumulation in the blood vessels |

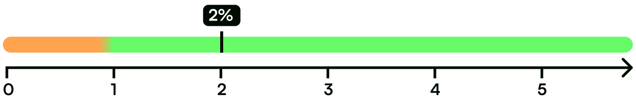
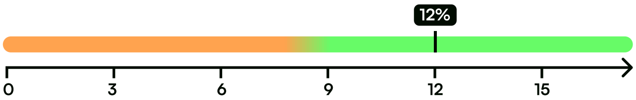
*Reference bacteria can be found on supplementary pages.*

| # | Detoxification Biomarkers and Women's Health | Impact |
|---|---|---|
| 1 | Beta glucoronidase - 50% High — Optimal range (22 - 41%)   | Deconjugation of bile acids; Influence the pharmacokinetics of drugs; Regulation of physiological estrogen metabolism |

| # | Longevity | Impact |
|---|---|---|
| 1 | Indoles and Phenols - 2% Satisfactory — Optimal range (>= 1%)   | Indole is a precursor for neurotransmitter synthesis; Indoles regulates mood and sleep-wake cycles; Phenol reduces oxidative stress and inflammation |
| 2 | Myrosinase - 20% Needs work — Optimal range (>= 31%)   | Anti-cancer potential; Antioxidant and anti-inflammatory properties; Detoxification of harmful substances |
| 3 | Urolithin - 10% Needs work — Optimal range (>= 20%)   | Antioxidant activity; Mitochondrial health; Muscle health and exercise performance; Cellular senescence regulation |

| # | Digestive Markers | Impact |
|---|---|---|
| 1 | Carbohydrate metabolizers - 9% Satisfactory — Optimal range (>= 8%)   | Promote SCFA production; Enhance energy extraction; Improve glucose regulation |
| 2 | Fat metabolizers - 8% Satisfactory — Optimal range (>= 5%)   | Regulation of enrgy balance; Bile acid modification |
| 3 | Lactose degraders - 0.02% Satisfactory — Optimal range (>= 0.01%)   | Digestive efficiency and nutrient absorption; Immune system modulation |

*Reference bacteria can be found on supplementary pages.*

| # | Digestive Markers | Impact |
| --- | --- | --- |
| 4 | Oxalate degraders - 2% Satisfactory Optimal range (>=1%)   | Prevention of kidney stone formation; Maintain gut microbial balance |
| 5 | Protein metabolizers - 12% Satisfactory Optimal range (>= 9 %)   | Nitrogen utilization and recycling; Muscle protein synthesis |

## SECTION 5: Food and supplement recommendation

### Bacteria out of range

*Akkermansia* Low , *Bifidobacterium* Low , *Bilophila* High *Blautia* Low *Clostridium* High *Coprococcus* Optimal *Escherichia coli* High

| Modifier | Bacteria shifted | Scientific evidence |
|---|---|---|
| **FOOD**<br>**To include:** extra virgin olive oil[1], sea weed[2], chaga (mushroom)[3], Pulses[5], Konjaku flour[7], white button mushrooms[8], rye[9], buckwheat[10], Pistachio[11], grapes [12], Garlic[13], pomegranate[15], high amylose cornstarch[16] , broccoli[17], almonds/ almond skins[19], green tea[20], potatoes[22], gallic acid(food additive)[23], basil[24], pomegranate blossom tea[25], walnuts[28], Okra[29], rhubarb[30], mulberry fruit polysaccharide[31], Kiwifruit[33]<br>**To avoid:** oats, pork[4], red wine polyphenols[14], wheat[18], lemon[27], glucose (sugar)[34] | Increase *Akkermansia*[1,3,4]<br>Increase *Bifidobacterium*[5,7,8]<br>Reduce *Bilophila*[9,10,11,12,13]<br>Increase *Blautia*[2,15,16,17]<br>Reduce *Clostridium*[19,20,21]<br>Reduce *Coprococcus*[22]<br>Reduce *Escherichia coli*[23,24,25,26]<br>Reduce *Proteobacteria*[3,28,29,30,31]<br>Increase *Roseburia*[32,15,33]<br>Reduces *Akkermansia*[4]<br>Increase *Bilophila*[14]<br>Reduces *Blautia*[18]<br>Increase *Escherichia coli*[27]<br>Reduces *Roseburia*[34] | 1. Fish Oil, but Not Olive Oil, Ameliorates Depressive-Like Behavi...<br>2. Ascophyllum nodosum polysaccharide regulates gut microbio...<br>3. Methanol extract of Inonotus obliquus improves type 2 diabe...<br>4. Concentrated Raw Fibers Enhance the Fiber-Degrading Capa...<br>5. In vitro fermentation of lupin seeds (Lupinus albus) and broa...<br>6. Dietary supplementation with olive oil co-products rich in...<br>7. Amelioration of gut dysbiosis and gastrointestinal motility by ...<br>8. Effect of Agaricus bisporus Polysaccharides on Human Gut...<br>9. The effects of fermented rye products on gut microbiota and...<br>10. Tartary Buckwheat (Fagopyrum tataricum) Ameliorates Lipid...<br>11. Pistachio Consumption Alleviates Inflammation and Improves..<br>12. Table grape consumption reduces adiposity and markers of ...<br>13. Black garlic melanoidins prevent obesity, reduce serum LPS...<br>14. Resveratrol modulates the gut microbiota of cholestasis in...<br>15. Effects of Pomegranate Peel Polyphenols Combined with Inu...<br>***full references for recommendations can be found on supplementarypages*** |
| **PROBIOTICS**<br>**To include:** Lactobacillus Johnsonii[1], Bifidobacterium longum[2], Bifidobacterium adolescentis[3], Bifidobacterium bifidum[5], Lactobacillus plantarum[6], Lactobacillus rhamnosus[8], Lactobacillus fermentum[10], Lactobacillus caseishirota[11], Saccharomyces boulardii[14], Lactobacillus rhamnosus gg[17], Bacillus amyloliquefaciens[19]<br>**To avoid:** Koji aspergillus oryzae[4], Pediococcus pentosaceus[9], bacillus subtilis,Lactobacillus acidophilus[12], Bifidobacterium breve[15], Bacillus subtilis[18], Lactobacillus paracasei[21], LentiLactobacillus buchneri[23] | Increase *Akkermansia*[1,2]<br>Increase *Bifidobacterium*[3]<br>Reduce *Bilophila*[5,6]<br>Increase *Blautia*[7,8]<br>Reduce *Clostridium*[10,11]<br>Reduce *Coprococcus*[14]<br>Reduce *Escherichia coli*[16,17]<br>Reduce *Proteobacteria*[19]<br>Increase *Roseburia*[22]<br>Reduces *Bifidobacterium*[4]<br>Reduces *Blautia*[9]<br>Increase *Clostridium*[12]<br>Increase *Coprococcus*[15]<br>Increase *Escherichia coli*[18]<br>Increase *Proteobacteria*[21]<br>Reduces *Roseburia*[23] | 1. Probiotic Lactobacilli Administration Induces Changes in the F...<br>2. Bifidobacterium longum subsp. longum BL21 ameliorates alc...<br>3. Mouse intestinal microbiome modulation by oral administrat...<br>4. Administration of Aspergillus oryzae suppresses DSS-induced...<br>5. Bifidobacterium bifidum TMC3115 ameliorates milk protein a...<br>6. Effects of microencapsulated Lactobacillus plantarum LIP-1 on...<br>7. Exopolysaccharides from Lactobacillus plantarum YW11 impr ...<br>8. Effect of Lactobacillus rhamnosus HN001 and Bifidobacterium..<br>9. Protective effect of Pediococcus pentosaceus Li05 on diarrh...<br>10. The Impact in Intestines and Microbiota in BALB/c Mice Thr...<br>11. Intestinal Microbiota Profiles of Healthy Pre-School and Sch..<br>12. Gaseous CO2 signal initiates growth of butyric-acid-produci ...<br>13. Lactobacillus plantarum-Derived Extracellular Vesicles Modul...<br>14. Saccharomyces cerevisiae boulardii CNCM I-1079 suppleme...<br>15. Evaluation of the therapeutic effect and dose-effect of Bifido...<br>***full references for recommendations can be found on supplementarypages*** |

*Scientific evidences for recommendations can be found on the reference pages.*

## SECTION 5: Food and supplement recommendation

### Bacteria out of range

*Akkermansia* Low , *Bifidobacterium* Low , *Bilophila* High *Blautia* Low *Clostridium* High *Coprococcus* Optimal *Escherichia coli* High

| Modifier | Bacteria shifted | Scientific evidence |
|---|---|---|
| **SUPPLEMENTS**<br>**To include:** Rutin[1], quercetin[5], bentonite[7], Curcumin[9], whey protein supplement[10], Glucomannan[12], Baicalin[14] | Increase *Akkermansia*[1]<br>Reduce *Bilophila*[5]<br>Increase *Blautia*[7]<br>Reduce *Clostridium*[9]<br>Reduce *Coprococcus*[10]<br>Reduce *Escherichia coli*[12]<br>Reduce *Proteobacteria*[14] | 1. Rutin alleviates colon lesions and regulates gut microbiota in d...<br>2.Increasing breast milk betaine modulates Akkermansia abund...<br>3.Structural Insights into Amelioration Effects of Quercetin and I...<br>4. Shen-Ling-Bai-Zhu-San (SL) and SL Derived-Polysaccha...<br>5.A combination of quercetin and resveratrol reduces obesity in...<br>6. Propionate-Producing Consortium Restores Antibiotic-Induc...<br>7. Microbiome Remodeling via the Montmorillonite Adsorption...<br>8. Glucosamine Ameliorates Symptoms of High-Fat Diet-Fed Mic...<br>9. Prebiotic Potential and Chemical Composition of Seven Culi...<br>10. Effect of a Co-Feed Liquid Whey-Integrated Diet on Crossbr...<br>11. Taxifolin increased semen quality of Duroc boars by improving..<br>12. Antibacterial activity of konjac glucomannan/chitosan blend ...<br>13. Preparation of selenium/zinc-enriched probiotics and their ef..<br>14. Protective effect of baicalin on the regulation of Treg/Th17...<br>15. Helicobacter pylori eradication with bismuth quadruple thera...<br>***full references for recommendations can be found on supplementarypages*** |
| **To avoid:** betaine[2], Shen Ling Bai Zhu San[4], propionate[6] , Glucosamine[8], Taxifolin[11], selenium[13], Bismuth Salts[15], cannabinoids[16] | Reduces *Akkermansia*[2]<br>Reduces *Bifidobacterium*[4]<br>Increase *Bilophila*[6]<br>Reduces *Blautia*[8]<br>Increase *Coprococcus*[11]<br>Increase *Escherichia coli*[13]<br>Increase *Proteobacteria*[15]<br>Reduces *Roseburia*[16] | |
| **PREBIOTICS**<br>**To include:** chitooligosaccharides[1], arabinogalactan[2], inulin[4], lactulose[5], gum arabic[7], galacto-oligosaccharides[8], fructo-oligosaccharides[9], mastic gum[10] | Increase *Akkermansia*[1]<br>Increase *Bifidobacterium*[2]<br>Reduce *Bilophila*[4,5]<br>Reduce *Clostridium*[7,8]<br>Reduce *Escherichia coli*[9,10] | 1. Pretreatment with chitosan oligosaccharides attenuate experi...<br>2. Relative abundance of the Prevotella genus within the human...<br>3. Characterization of fecal fat composition and gut derived fec...<br>4. Prebiotic inulin-type fructans induce specific changes in the h...<br>5. Effect of lactulose intervention on gut microbiota and short ch...<br>6. Diets high in resistant starch and arabinoxylan modulate diges...<br>7. Pharmacological benefits of Acacia against metabolic disease ...<br>8. Prebiotic effect of an infant formula supplemented with galac..<br>9. Dietary cellulose, fructooligosaccharides, and pectin modify...<br>10. Spices as Sustainable Food Preservatives: A Comprehensive...<br>11. In vitro fermentation of raffinose by the human gut bacteria<br>12. Chitooligosaccahrides: Digestion characterization and effect ...<br>13. Effect of Prebiotic on Microbiota, Intestinal Permeability, and ...<br>***full references for recommendations can be found on supplementarypages*** |
| **To avoid:** raffinose(sugar beet)[11], oligofructose-enriched inulin[13] | Increase *Escherichia coli*[11]<br>Reduces *Roseburia*[13] | |

*Scientific evidences for recommendations can be found on the reference pages.*

Vitract

838 Walker Rd, Dover, Delaware,
19904, United States

For enquiries, email hello@vitract.com

# Gut Microbiome Analysis

Comprehensive Analysis - Deep Shotgun Sequencing

John Doe | VT1-123DC

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## SECTION 5: Food and supplement recommendation

### Bacteria out of range

*Akkermansia* Low , *Bifidobacterium* Low , *Bilophila* High *Blautia* Low *Clostridium* High *Coprococcus* Optimal *Escherichia coli* High

| Modifier | Bacteria shifted | Scientific evidence |
|---|---|---|
| **LIFESTYLE CHANGES**<br>**To include:** mediterranean diet[2], nuts[3], Fiber[6], Exercise[9] | Increase *Bifidobacterium*[2]<br>Reduce *Bilophila*[3]<br>Reduce *Clostridium*[6]<br>Reduce *Proteobacteria*[9] | 1. Fucoidan Improves D-Galactose-Induced Cognitive Dysfunct...<br>2.The gut microbial community in metabolic syndrome patients...<br>3. Pistachio Consumption Alleviates Inflammation and Improves...<br>4. Interactions between Diet, Bile Acid Metabolism, Gut Microbi...<br>5. Smoking cessation alters intestinal microbiota: insights from...<br>6. [Clinical benefits after soluble dietary fiber supplementation...<br>7. Gut Microbiome Composition in Non-human Primates...<br>8. Effects of the dietary protein level on the microbial compositio...<br>9. Effect of an 8-week Exercise Training on Gut Microbiota in...<br>10. Metagenomic analyses of alcohol induced pathogenic alte...<br>11. Nuts and their Effect on Gut Microbiota, Gut Function and..<br>12. Gut microbiome and metabolome in a non-human primate ...<br>***full references for recommendations can be found on supplementarypages*** |
| **To avoid:** high-saturated fat diet[1], smoking[5], low protein diet[8], alcoholic beverages[10] | Reduces *Akkermansia*[1]<br>Reduces *Blautia*[5]<br>Increase *Coprococcus*[8]<br>Increase *Proteobacteria*[10] | |

*Scientific evidences for recommendations can be found on the reference pages.*

## **SUPPLEMENTARY TABLE 1:** References for dietary recommendations.

### Food references

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10. Tartary Buckwheat (Fagopyrum tataricum) Ameliorates Lipid Metabolism Disorders and Gut Microbiota Dysbiosis in High-Fat Diet-Fed Mice.

11. Pistachio Consumption Alleviates Inflammation and Improves Gut Microbiota Composition in Mice Fed a High-Fat Diet.

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21. Effect of garlic powder on the growth of commensal bacteria from the gastrointestinal tract.

22. Potato resistant starch inhibits diet-induced obesity by modifying the composition of intestinal microbiota and their metabolites in obese mice.

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25. Antimicrobial activities of widely consumed herbal teas, alone or in combination with antibiotics: an in vitro study.

26. Tartary buckwheat protein prevented dyslipidemia in high-fat diet-fed mice associated with gut microbiota changes.

27. Ascorbic acid-dependent gene expression in Streptococcus pneumoniae and the activator function of the transcriptional regulator UlaR2.

28. Effects of Walnut and Pumpkin on Selective Neurophenotypes of Autism Spectrum Disorders: A Case Study.

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30. What we already know about rhubarb: a comprehensive review.

31. Mulberry leaves ameliorate obesity through enhancing brown adipose tissue activity and modulating gut microbiota.

32. Effects of Konjaku Flour on the Gut Microbiota of Obese Patients.

33. Butyrogenic, bifidogenic and slight anti-inflammatory effects of a green kiwifruit powder (Kiwi FFG®) in a human gastrointestinal model simulating mild constipation.

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## SUPPLEMENTARY TABLE 1: References for dietary recommendations.

### Probiotics references

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11. Intestinal Microbiota Profiles of Healthy Pre-School and School-Age Children and Effects of Probiotic Supplementation.

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13. Lactobacillus plantarum-Derived Extracellular Vesicles Modulate Macrophage Polarization and Gut Homeostasis for Alleviating Ulcerative Colitis.

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22. A metagenomic study of the preventive effect of Lactobacillus rhamnosus GG on intestinal polyp formation in Apc(Min/+) mice.

23. Exopolysaccharides from Lactobacillus buchneri TCP016 Attenuate LPS- and d-GalN-Induced Liver Injury by Modulating the Gut Microbiota.

### Supplements references

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4. Shen-Ling-Bai-Zhu-San (SL) and SL Derived-Polysaccharide (PL) Ameliorate the Severity of Diarrhea-Induced by High Lactose via Modification of Colonic Fermentation.

5. A combination of quercetin and resveratrol reduces obesity in high-fat diet-fed rats by modulation of gut microbiota.

6. Propionate-Producing Consortium Restores Antibiotic-Induced Dysbiosis in a Dynamic in vitro Model of the Human Intestinal Microbial Ecosystem.

7. Microbiome Remodeling via the Montmorillonite Adsorption-Excretion Axis Prevents Obesity-related Metabolic Disorders.

8. Glucosamine Ameliorates Symptoms of High-Fat Diet-Fed Mice by Reversing Imbalanced Gut Microbiota.

9. Prebiotic Potential and Chemical Composition of Seven Culinary Spice Extracts.

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## SUPPLEMENTARY TABLE 1: References for dietary recommendations.


### Prebiotics references

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### Lifestyle changes references

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12. Gut microbiome and metabolome in a non-human primate model of chronic excessive alcohol drinking.


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