Personalized Gut Microbiome Report

Theriome

Jane Doe

Élie® Test Results

Barcode: XXXXXXXXXX

Lab Collection Date: 12.12.2024	**Analysis Date:** 12.26.2024	**Sample Collection Method:** Fecal specimen with stabilizing chemistry (22°C to 23°C for 2 Mo.)
Analytical Platform: Illumina NextSeq 500 platform	**Sequencing method:** Shotgun whole genome sequencing Depth: ~10 M. 2x150 bp read pairs	**Report Reviewed By:** Alex Mohr, PhD

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This test provides a comprehensive overview of an individual's gut microbes and can be used to identify potential health issues. The microbiome is now considered a key player in human health (1, 2), and we are passionate about providing you with the most up-to-date, scientifically sound personalized insights on how to optimize and synergize the microorganisms residing in your gastrointestinal tract for better health. To understand this community, we use Whole Genome Sequencing (WGS), a cutting-edge technology that profiles the entire gut microbiome, including all microorganisms, their genomes, associated functions, and actual activity within their surrounding environmental conditions (3). WGS offers superior accuracy and depth compared to other methods like RNA sequencing or culture-based testing, as it captures the complete genetic material of all microbes—bacteria, archaea, fungi, and viruses—present in the gut. This allows us to detect both abundant and low-abundance species and provides a more comprehensive view of the microbial ecosystem, making it the most robust tool for gut microbiome analysis.

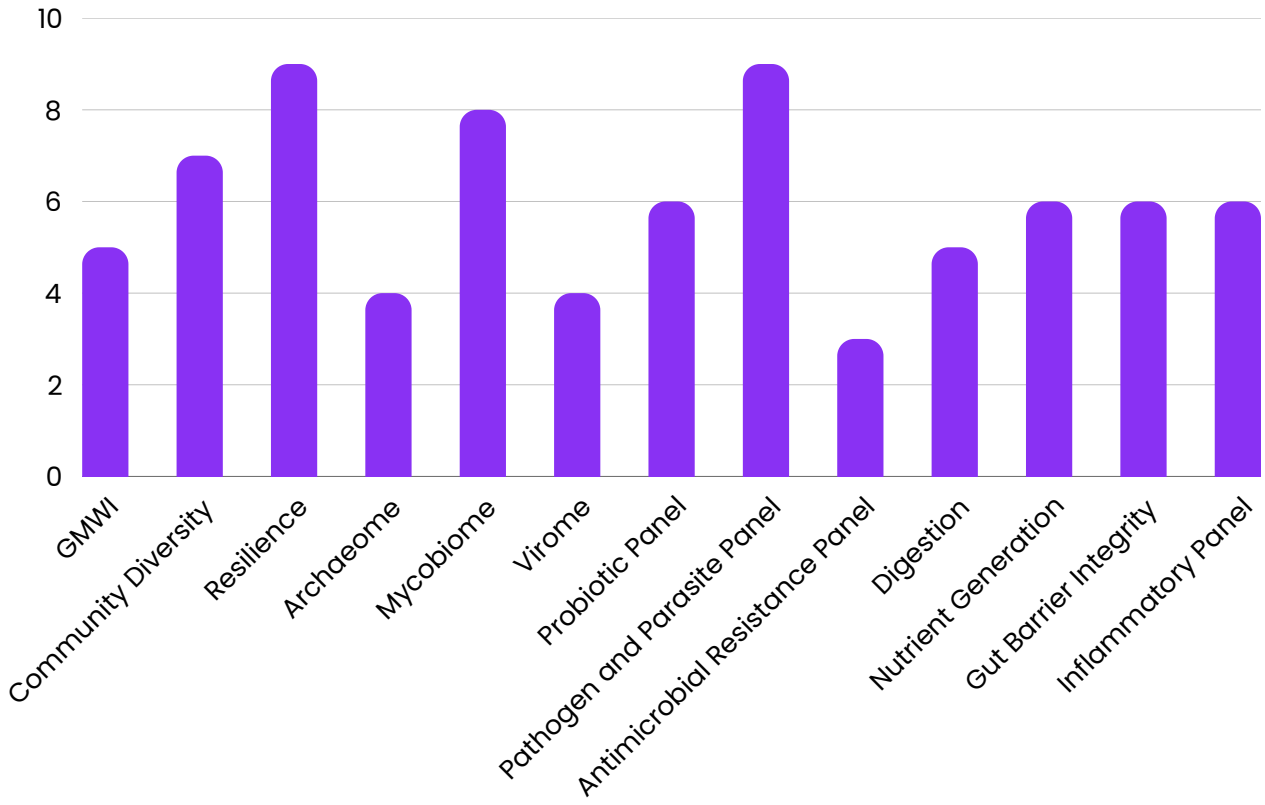
Note: *The report aims to empower individuals with a deep metagenomic understanding of their gut microbiome health, offering actionable insights for lifestyle and dietary adjustments. However, it emphasizes the necessity of consulting with healthcare providers before making significant changes. This document is intended to complement professional medical advice, not replace it, underscoring its role in proactive health management rather than diagnostic purposes.*

Jane Doe

Overall Score:

60/100

Thank you for choosing Theriome's deep microorganism profiling service. Based on your recent gut microbiome panel, we have calculated your health scores across our key analytical domains.



Following our thorough analysis of your gut microbiome's composition and functionality, it's clear that you have room for improvement. Out of the 13 key metrics we evaluated to determine this score, you exhibit excellent **Resilience**, **Mycobiome**, and **Pathogen and Parasite Panel** Scores. While your overall gut microbiome health is commendable, there's room for improvement in certain areas. These include increasing **GMWI**, **Archaeome**, **Virome**, **Antimicrobial Resistance Panel**, and **Digestion** scores. In your Personalized Improvement Plan, we provide a detailed roadmap to help you optimize your overall score and further enhance your gut health.

Overview of Scores

Domain	Score	Score Overview
GMWI	5	Moderate score, indicating room for improvement in overall microbiome balance and resilience against stressors like inflammation and bloating.
Community Diversity	7	Good diversity, indicating a stable microbiome ecosystem, but still opportunities to enhance specific beneficial taxa.
Resilience	9	High resilience suggests a microbiome that can recover well from disturbances.
Archaeome	4	Low archaeal activity, likely contributing to issues such as gas metabolism imbalances and bloating.
Mycobiome	8	A well-balanced fungal community, with potential for optimizing fungal interactions with bacterial populations.
Virome	4	Low viral diversity, limiting beneficial host-phage interactions and the regulation of bacterial populations.
Probiotic Panel	6	Moderate levels of key probiotic species, but some strains like Faecalibacterium prausnitzii are below optimal ranges.
Pathogen and Parasite Panel	9	Minimal detection of pathogens, reflecting a low risk of active infection or dysbiosis-driven pathogen overgrowth.
AMR Panel	3	Burden of AMR genes, including those with high potential for horizontal gene transfer and multi-drug resistance.
Digestion	5	Moderate digestive function, with good fiber degradation but room to improve enzymatic activity and protein fermentation.
Nutrient Generation	6	Moderate SCFA production with potential to improve acetate and butyrate synthesis through dietary and probiotic interventions.
Gut Barrier Integrity	6	Moderate gut barrier integrity with elevated LPS production, indicating potential endotoxemia and inflammatory challenges.
Inflammatory Panel	6	Slightly elevated bile acid metabolism and lower tryptophan metabolism suggest inflammatory pathways that need modulation.

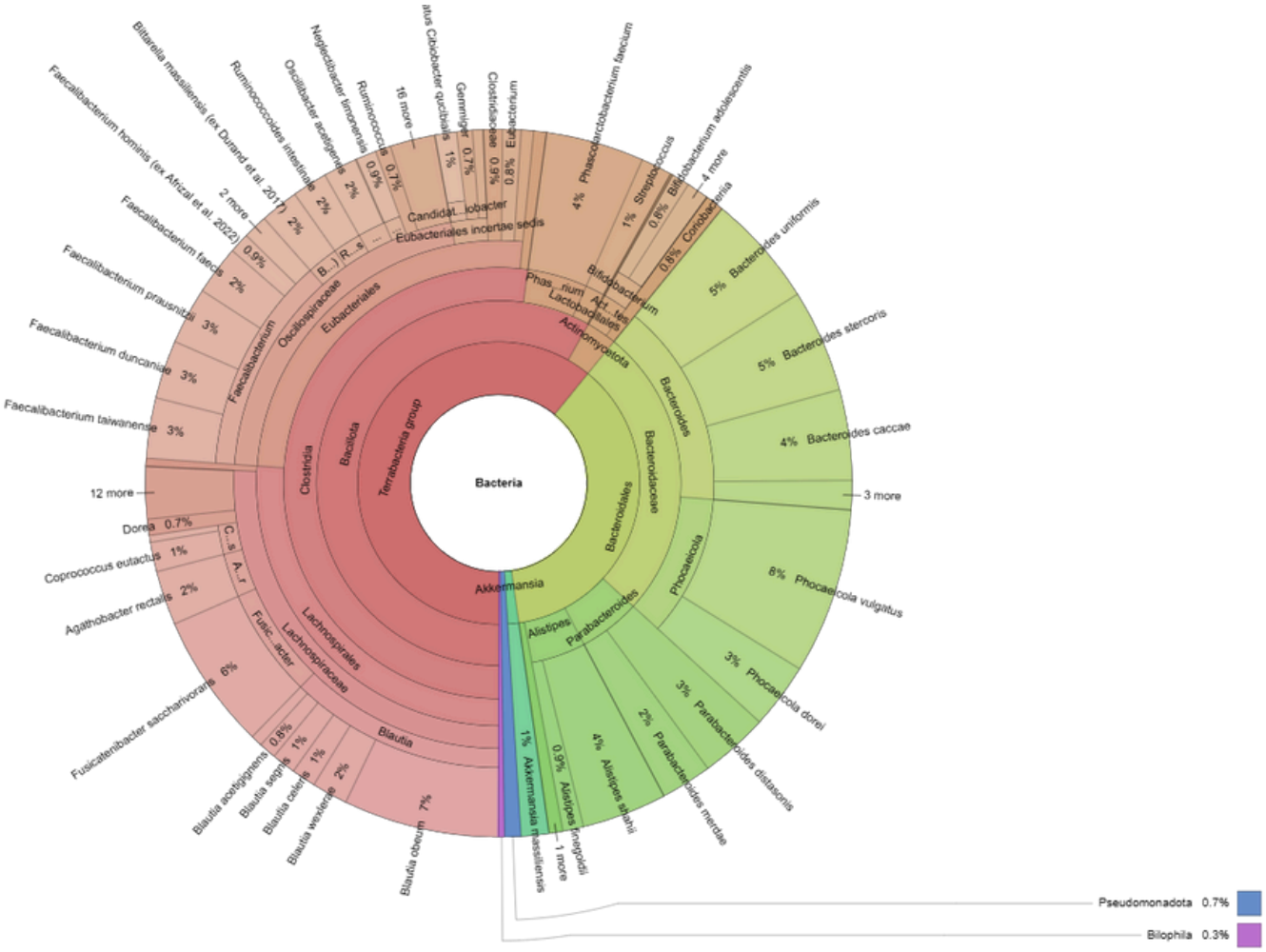
*Find a detailed report of all recommendations see the **Digital Twinning** section of your report.*

Overall Microbiome

Total number of microbial species detected in your fecal sample **1,110**

In human microbiome fecal samples, several microbial kingdoms are commonly found (4, 5). The relative abundance of these kingdoms can vary depending on factors such as diet, health status, geography, and individual variability (6-9). However, a general overview of the typical kingdoms and their abundance in fecal samples is as follows:

- **Bacteria** dominate the gut microbiome and play essential roles in digestion, nutrient absorption, immune function, and protection against pathogens. Beneficial species help maintain gut balance, while harmful bacteria can lead to infections or gut dysbiosis.
- **Archaea** are involved in methane production in the gut, influencing gas metabolism and overall digestive function.
- **Fungi** are important in maintaining gut balance and contributing to immune regulation. Imbalances in fungal populations can lead to infections or inflammatory responses, especially in immunocompromised individuals.
- **Viruses** help regulate bacterial populations in the gut by infecting and lysing harmful bacteria.
- **Protists** can either play a symbiotic role in the gut or act as pathogens when overgrown.
- **Parasites** can disrupt gut function and cause infections.
- **Yeasts**, such as *Saccharomyces boulardii*, support gut health by preventing harmful bacterial overgrowth, modulating the immune system, and aiding digestion. Imbalances in yeast populations can lead to infections or gut disturbances.



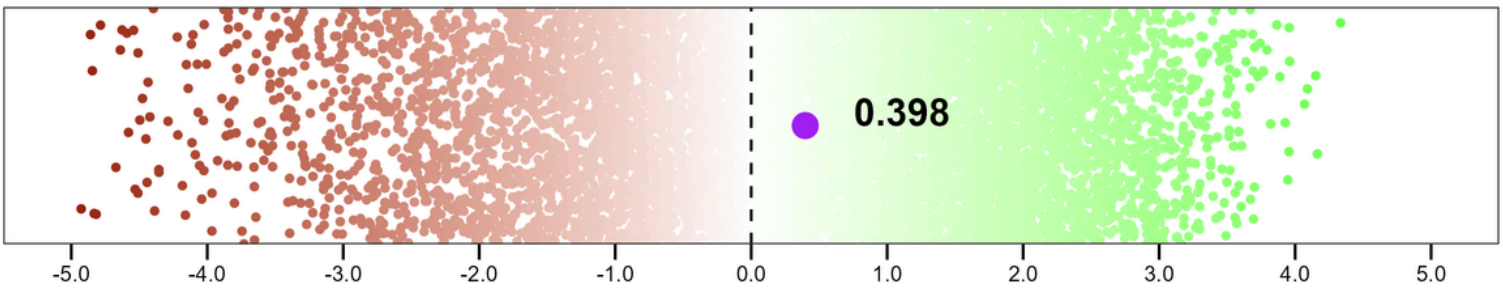
Gut Microbiome Wellness Index

50%

Poor Optimal

The Gut Microbiome Wellness Index 2 (GMWI2) provides a scientifically-validated (10) holistic assessment of gut health by analyzing the composition of your microbiome to estimate your likelihood of having a clinically dysbiotic community. This indicator is disease-agnostic, meaning it assesses general health risk from microbiome composition alone without identifying specific diseases. The GMWI2 was trained on a pooled dataset of 8,069 fecal metagenomic samples from global, cross-study cohorts—5,547 healthy and 2,522 non-healthy individuals—to develop a score that distinguishes healthy from non-healthy microbiome profiles with high accuracy. This health index leverages linear regression modeling to estimate the "log odds" of a sample belonging to a healthy individual, similar to polygenic risk scores. Positive scores indicate a microbiome composition typical of a healthy individual, while negative scores suggest an increased likelihood of disease presence. A score of 0 reflects a neutral state, where health-associated and disease-associated taxa are balanced.

Distribution of Gut Microbiome Wellness Index (GMWI2) Scores Across >8,000 Individuals



Gut Microbiome Wellness Index

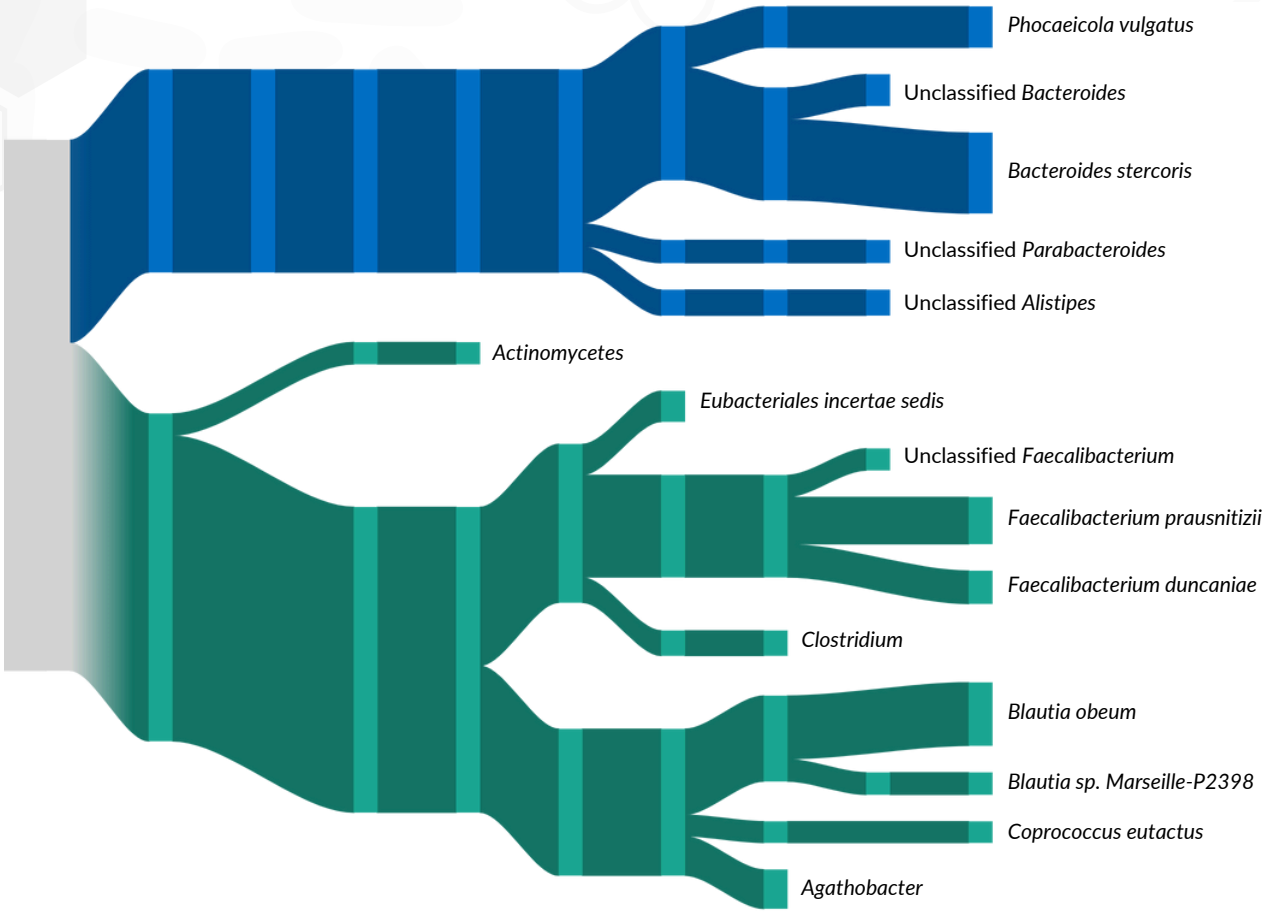
Scientist Notes:

- The Gut Microbiome Wellness Index (GMWI2) score of 0.398 suggests a moderately balanced microbiome with several beneficial contributors, though notable negative taxa may warrant targeted intervention to optimize gut health and resilience.
- Positive Influences: Beneficial taxa such as *Bifidobacterium adolescentis*, *Bifidobacterium animalis*, and *Eubacterium eligens* contribute to SCFA production, promoting gut barrier integrity and anti-inflammatory effects. The presence of *Alistipes shahii* and *Dorea formicigenerans* further supports microbial diversity and resilience.
- Negative Contributors: Elevated levels of *Bacteroides stercoris*, *Bacteroides vulgatus*, and *Clostridium sp. CAG:58* are associated with potential pro-inflammatory activities. Similarly, the presence of *Eisenbergiella* and *Flavonifractor*, which may disrupt microbial harmony, highlights areas for microbial modulation.
- Functional Implications: The positive contribution of SCFA-producing microbes is offset by taxa that may hinder optimal gut health through inflammation and dysbiosis risks. Supporting beneficial populations while addressing potentially harmful ones is recommended to improve the balance.

*Find a detailed health protocol for your **Gut Microbiome Wellness Index** in the digital twinning section of your report.*

Core Microbiome

The core gut microbiome of an individual comprises a consistent group of microorganisms inhabiting the gastrointestinal tract that dominant functional capacity (11-13). This microbiome remains relatively stable over time and plays a pivotal role in numerous aspects of health and digestive function. To provide a visual overview of your core microbiome, which includes the most prevalent microbes detected in your microbiome sample, we've created a graphical representation. In this taxonomic chart of classified reads, the horizontal bars represents your overall core microbiome, with each node denoting different microbial taxa. The width of each section corresponds to the relative abundance of a particular microbial taxon.



Scientist Notes:

- The core microbiome demonstrates a well-balanced composition with a strong representation of SCFA producers and fiber-degrading species. Key beneficial taxa such as *Faecalibacterium prausnitzii* and *Phocaeicola vulgatus* highlight the potential for anti-inflammatory effects, while a diverse array of *Bacteroides* species supports robust polysaccharide metabolism.
    - High relative abundances of *Bacteroides uniformis*, *Bacteroides stercoris*, and *Blautia obeum* suggest a fiber-degrading profile, but an overrepresentation of these taxa can sometimes correlate with pro-inflammatory tendencies if unbalanced with other anti-inflammatory species.
    - Lower Representation of *Faecalibacterium* and *Oscillibacter*: These taxa play key roles in gut barrier maintenance and mucosal integrity. Their moderate presence may limit optimal gut resilience.

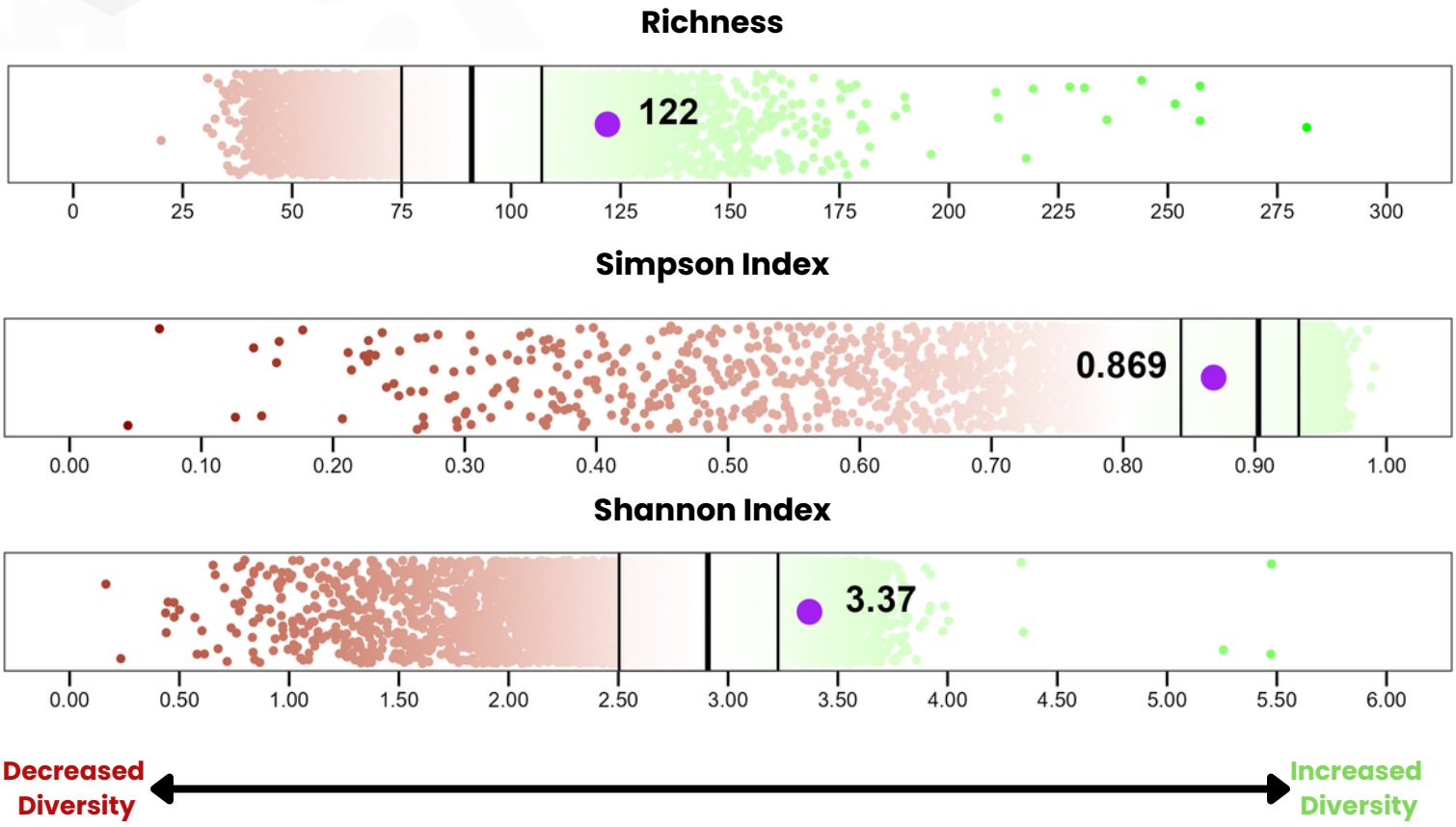
*Find a detailed description of the top microbes normally detected in samples, see the **Appendix of Keystone Taxa** of your report.*

Community Diversity

70%

Poor — Optimal

Diversity in the gut microbiome is defined as the number and abundance of distinct types of microorganisms present (14). An unhealthy state is characterized by an ecosystem often characterized by low microbial diversity, with a depletion of health-associated microbes and expansion of pathogens; a state associated with disease; often called 'dysbiosis' (15). We want to promote a health-associated state for the gut microbiota, characterized by a high microbial diversity, which favors functional diversity and microbe–microbe and host–microbe interactions. Also referred as equilibrium state, balanced state or homeostatic state (13, 16).



Scientist Notes:

- The high taxonomic richness indicates a wide variety of microbial species, enhancing the microbiome's adaptability to environmental and dietary changes while promoting resilience against disturbances like pathogen colonization.
- The Simpson index, within the normal range, suggests a fairly even distribution of microbial species without excessive dominance by any single taxon. This indicates a healthy microbial balance.
- The slightly elevated Shannon index highlights both richness and evenness, suggesting a proportional abundance of diverse taxa. This supports robust functional diversity and a lower risk of dysbiosis.

*Find a detailed health protocol for your **Community Diversity** in the digital twinning section of your report.*

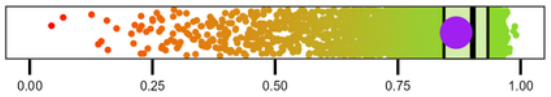
Resilience Score

90%

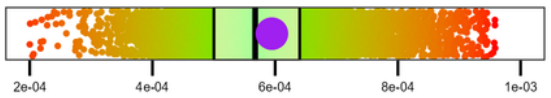
Poor **Optimal**

The gut microbiome Resilience Score measures the ability of your microbiome to recover and maintain balance after disruptions such as illness, antibiotic use, or dietary changes (17, 18). A resilient microbiome consists of diverse, stable microbial populations that can quickly restore equilibrium following stressors. Higher resilience is associated with better overall gut health, reduced inflammation, and a lower likelihood of infections or dysbiosis. This score is derived from key indicators such as microbial diversity, stability, and functional redundancy, offering insights into how well your microbiome can adapt and protect your health over time.

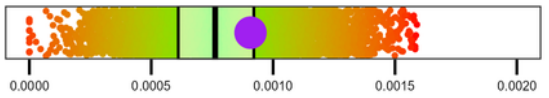
Microbial Diversity
Higher species richness is associated with greater resilience because a more diverse ecosystem is better equipped to recover from disturbances.



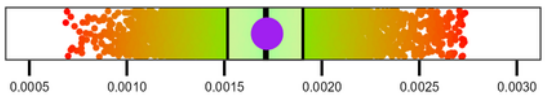
Functional Stability
Pathways are essential for maintaining diverse and stable microbial populations by ensuring proper protein synthesis and regulation.



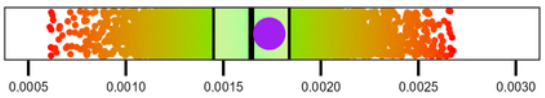
Functional Redundancy
High redundancy allows the microbiome to maintain key activities like fermentation or SCFA production even if specific species are lost or reduced.



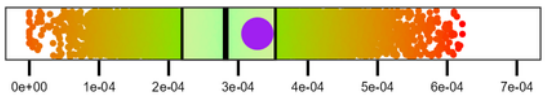
Stress Response and Adaptation
Pathways involved in stress response, adaptation to environmental changes, and utilization of various energy sources, contributing to microbiome resilience.



Microbial Interaction Networks
The complexity of interactions between different microbial species, which can be measured using network analysis. More interconnected and robust networks tend to support a resilient microbial community.



Microbe-Host Interaction
These pathways are involved in the production of metabolites that can influence host-microbe interactions and contribute to overall gut health.



*Find a detailed health protocol for your **Resilience Score** in the digital twinning section of your report.*

Archaeome

40%

Poor **Optimal**

The Archaeome refers to the community of archaea present within the gut microbiome. Although less abundant than bacteria, archaea play essential roles in maintaining microbial balance, particularly in methane production and gas metabolism (19). Key species such as *Methanobrevibacter smithii* and *Methanosphaera stadtmanae* contribute to the breakdown of complex carbohydrates and fermentation processes, producing gases like methane that can affect digestion (20). Understanding the composition and activity of the Archaeome provides insights into how these microorganisms influence gut health and metabolic processes.

Composition

Methane Production

Scientist Notes:

- Dominance of *Candidatus Methanomassiliicoccus intestinalis*: A methanogenic archaeon crucial for hydrogen turnover and methane production. Notably, this species also metabolizes methylamines, such as trimethylamine, which are linked to cardiovascular health markers like TMAO. Research has linked *Candidatus Methanomassiliicoccus intestinalis* with inflammatory bowel disease (IBD).
- Elevated methane production is likely driven by active methanogenic pathways, converting substrates like hydrogen and methyl compounds into methane. This process plays a key role in microbial fermentation and maintaining redox balance in the gut.
- Increased methane production has been associated with slowed intestinal transit, which may contribute to bloating or constipation in sensitive individuals. However, methane also stabilizes the gut environment and may support microbial fermentation efficiency.

*Find a detailed health protocol for your **Archaeome** in the digital twinning section of your report.*

Mycobiome

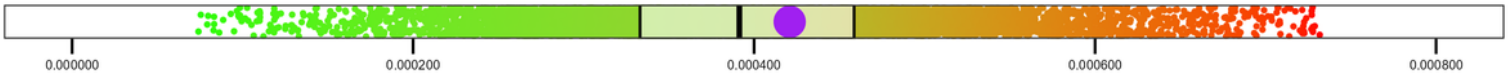
80%

Poor **Optimal**

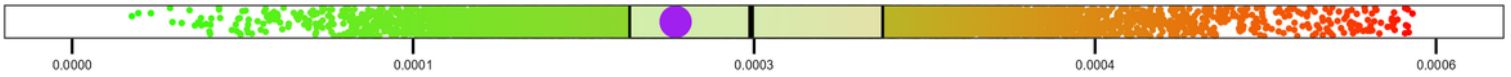
The Mycobiome represents the community of fungi within the gut microbiome. Although present in much lower abundance compared to bacteria, fungi play a significant role in health, maintaining microbial balance, supporting digestion, and regulating immune responses (21, 22). Common fungal species such as *Candida albicans* and *Saccharomyces* are critical for gut health, with *Saccharomyces* acting as a beneficial probiotic (23) and *Candida* becoming pathogenic if overgrown (24). The balance of the mycobiome is crucial, as disruptions can contribute to conditions such as inflammatory bowel disease (IBD) and other gastrointestinal disorders. Studying the mycobiome provides insights into its influence on gut health and disease prevention.

Composition

Yeast Carbohydrate Metabolism



Fungal Virulence



Scientist Notes:

- The mycobiome is primarily composed of *Saccharomyces*, *Magnaporthiopsis*, and *Trichosporon*, with additional low-abundance taxa contributing minimally to overall diversity.
- Both yeast carbohydrate metabolism and fungal virulence are within normative ranges, indicating balanced fungal activity without excessive fermentation or pathogenic potential.

Mycobiome

Mycotoxin Bioremediation Capacity

Mycotoxins are toxic secondary metabolites produced by fungi, such as Fusarium, Penicillium, Aspergillus, and Alternaria, that frequently contaminate food and feed, impacting 60–80% of global agricultural commodities (25). These toxins pose significant health risks, including immune suppression, endocrine disruption, and gastrointestinal inflammation.

Bioremediation, the use of microorganisms to detoxify mycotoxins, is a promising alternative due to its low cost, wide applicability, and minimal nutrient disruption (26). Certain gut microorganisms possess enzymatic and adsorption capabilities that neutralize mycotoxins (27), reducing their bioavailability and systemic effects. Key enzymes, classified by Enzyme Commission (EC) numbers, drive these detoxification processes. These include oxidoreductases, hydrolases, and methyltransferases, which break down mycotoxins like aflatoxins, ochratoxins, zearalenone, fumonisins, and deoxynivalenol. The table below summarizes key enzymes and associated microorganisms involved in mycotoxin bioremediation.

Mycotoxin	EC number	Description	Result*	Reference
Aflatoxins	1.11.1.7: Peroxidase	Catalyzes the degradation of toxic compounds, including aflatoxins, by oxidative cleavage.	Absent	10 to 100 CPM
	3.1.1.2: Arylesterase	Hydrolyzes ester bonds in aflatoxins to reduce toxicity.	**3.61 CPM**	3 to 50 CPM
	1.6.3.1: NAD(P)H oxidase	Works in tandem with other oxidative enzymes to detoxify aflatoxins.	Absent	10 to 80 CPM
Ochratoxins	3.4.17.1: Carboxypeptidase A	Cleaves peptide bonds in ochratoxins, reducing their toxic impact.	**9.77 CPM**	3 to 20 CPM
	4.2.1.1: Carbonic anhydrase	Participates in detoxification processes through hydration reactions.	**22.13 CPM**	10 to 40 CPM
Zearalenone	3.2.1.75: glucan endo-1,6-beta-glucosidase	Facilitates the hydrolysis of glycosidic bonds in zearalenone, making it less bioavailable.	Absent	5 to 50 CPM
	1.1.1.209: Hydroxysteroid dehydrogenase	Converts zearalenone into non-toxic metabolites through hydroxylation.	Absent	3 to 30 CPM
Deoxynivalenol	1.3.1.122: Trichothecene 3-ketoreductase	Converts deoxynivalenol to de-epoxidated forms that are less toxic.	**0.67 CPM**	5 to 50 CPM
	4.1.1: Decarboxylase	Facilitates the removal of carboxyl groups in mycotoxins, neutralizing their effects.	Absent	10 to 100 CPM

Mycobiome

Mycotoxin	EC number	Description	Result*	Reference
General Mycotoxin Detoxification	3.5.1.4: Amidase	Acts on amide bonds in various mycotoxins, breaking them down into non-toxic metabolites.	**19.41 CPM**	5 to 50 CPM
	2.1.1.45: Methyltransferase	Adds methyl groups to alter toxic functional groups in mycotoxins, reducing their activity.	**73.80 CPM**	20 to 150 CPM
	1.14.14.1: Monooxygenase	A broad enzyme family that oxidizes various toxins, including fungal metabolites.	Absent	10 to 80 CPM
Fumonisins	3.1.4.3: Phospholipase C	Involved in breaking down sphingolipid analogs produced by fumonisins, mitigating their effects.	**2.47 CPM**	10 to 60 CPM
	4.1.2.27: Sphinganine-1-phosphate lyase	Metabolizes fumonisins by breaking down sphinganine intermediates.	Absent	5 to 50 CPM
Patulin	1.10.3.2: Laccase	Known to degrade patulin and other fungal toxins through oxidative polymerization.	Absent	5 to 40 CPM
	1.1.1.21: Aldose reductase	Reduces patulin by converting it into less toxic compounds.	**8.13 CPM**	0 to 50 CPM

Scientist Notes:

- Aflatoxins: Limited detoxification with low arylesterase (3.61 CPM) and absence of key oxidative enzymes.
- Ochratoxins: Moderate detoxification supported by carboxypeptidase A (9.77 CPM) and carbonic anhydrase (22.13 CPM).
- Zearalenone & DON: Minimal capacity due to absence or suboptimal activity of key enzymes.
- General Detoxification: Strong potential with elevated methyltransferase (73.80 CPM) and amidase (19.41 CPM).
- Fumonisins & Patulin: Limited detoxification capacity due to low or absent enzyme activity.

**Note:* This panel uses shotgun metagenomic sequencing to analyze the complete DNA content of fecal samples, focusing on enzymes and pathways involved in mycotoxin detoxification. The panel reports the estimated enzyme copy number in copies per million (CPM), providing a measure of detoxification potential relative to the total microbial content. Detection limits ensure even low-abundance enzymes are identified with high accuracy. Results are compared to reference ranges from healthy microbiomes to evaluate the microbiome's capacity to neutralize harmful mycotoxins, offering valuable insights into gut health and resilience against toxin exposure.*

*Find a detailed health protocol for your **Mycobiome** in the digital twinning section of your report.*

Virome

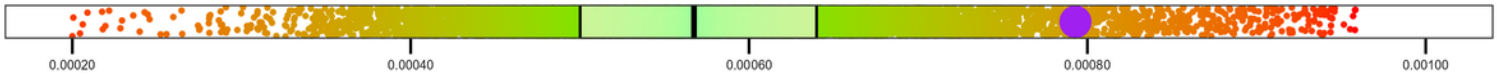
40%

Poor **Optimal**

The Virome refers to the collection of viruses within the gut microbiome, including bacteriophages (viruses that infect bacteria) and eukaryotic viruses that interact with human cells (28). Bacteriophages play a crucial role in regulating bacterial populations, shaping microbial diversity, and maintaining a balanced gut ecosystem (29). They help control harmful bacterial overgrowth, contributing to gut stability and resilience (30). The presence of specific enteric viruses can influence gut health and immune function, with some associated with infections or inflammatory conditions (31). Understanding the functionality of the virome is essential for assessing how these viral populations impact overall gut health and microbial dynamics.

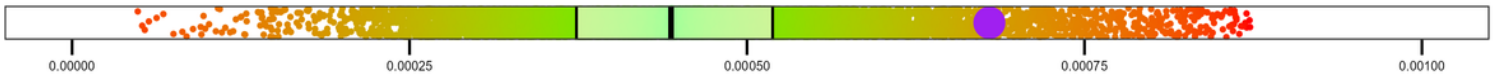
Composition

Viral Replication and Life Cycle



Host-Phage Interactions

Phage-Mediated Horizontal Gene Transfer



Scientist Notes:

- This sample shows a virome dominated by *Brigitvirus*, with trace levels of *Carjivirus* and *Culoivirus*, and a few low-abundant genera like *Slopekvirus*. Notably, *Brigitvirus* is recognized for its role in the bacteriophage-host ecosystem, potentially impacting microbial dynamics.
- The high activity in viral replication and phage-mediated gene transfer suggests an active and potentially adaptive virome. While this could support bacterial diversity, it may also influence the spread of antimicrobial resistance or virulence genes.

*Find a detailed health protocol for your **Virome** in the digital twinning section of your report.*

Probiotic Panel

60%

Poor Optimal

This panel identifies and quantifies beneficial microbial strains within your gut microbiome that are known for their health-promoting properties. Probiotics, defined as live microorganisms that confer a health benefit to the host when administered in adequate amounts, play a crucial role in maintaining gut health, supporting digestion, and enhancing immune function.

Bacterial Probiotics	Result*	Reference*
Akkermansia muciniphila	< detection limit	10 to 5,000 CPM
Bacillus cereus	< detection limit	<1 to 10 CPM
Bacillus clausii	< detection limit	<10 to 100 CPM
Bacillus coagulans	< detection limit	<10 to 50 CPM
Bacillus licheniformis	< detection limit	<10 to 50 CPM
Bacillus megaterium	< detection limit	<10 to 50 CPM
Bacillus pumilus	< detection limit	<1 to 10 CPM
Bacillus subtilis	< detection limit	<10 to 100 CPM
Bifidobacterium animalis (subsp. animalis)	< detection limit	10 to 500 CPM
Bifidobacterium animalis (subsp. lactis)	**518.02 CPM**	50 to 1,000 CPM
Bifidobacterium bifidum	**16.64 CPM**	20 to 1,000 CPM
Bifidobacterium breve	**60.45 CPM**	50 to 1,000 CPM
Bifidobacterium longum (subsp. infantis)	**53.15 CPM**	50 to 1,500 CPM
Bifidobacterium longum (subsp. longum)	**150.30 CPM**	100 to 5,000 CPM

Probiotic Panel

Bacterial Probiotics	Result*	Reference*
Faecalibacterium prausnitzii	**22,409.88 CPM**	1,000 to 5,000 CPM
Lactobacillus acidophilus	**9.92 CPM**	10 to 1,000 CPM
Levilactobacillus brevis	< detection limit	10 to 500 CPM
Lactobacillus casei	< detection limit	50 to 1,000 CPM
Lactobacillus delbrueckii (subsp. bulgaricus)	< detection limit	<10 to 50 CPM
Lactobacillus delbrueckii (subsp. delbrueckii)	< detection limit	<10 to 50 CPM
Limosilactobacillus fermentum	< detection limit	10 to 500 CPM
Lactobacillus gasseri	< detection limit	10 to 200 CPM
Lactobacillus helveticus	< detection limit	10 to 500 CPM
Lacticaseibacillus paracasei	< detection limit	50 to 1,000 CPM
Lactiplantibacillus plantarum	**20.44 CPM**	50 to 1,000 CPM
Limosilactobacillus reuteri	< detection limit	10 to 500 CPM
Lacticaseibacillus rhamnosus	< detection limit	10 to 1,000 CPM
Lactobacillus salivarius	< detection limit	10 to 500 CPM
Lactococcus lactis	< detection limit	10 to 1,000 CPM
Propionibacterium freudenreichii	< detection limit	10 to 500 CPM
Streptococcus salivarius	**123.23 CPM**	50 to 1,500 CPM

Probiotic Panel

Bacterial Probiotics	Result*	Reference*
Streptococcus thermophilus	**74.74 CPM**	100 to 1,000 CPM
Veillonella atypica	< detection limit	10 to 500 CPM

Fungal Probiotics	Result*	Reference*
Saccharomyces boulardii	< detection limit	10 to 1,000 CPM
Saccharomyces cerevisiae	< detection limit	10 to 500 CPM

Scientist Notes:

- This patient's probiotic profile reveals modest colonization potential for several beneficial bacterial strains, but notable deficiencies in key genera that could support gastrointestinal health. The patient's reported supplement regimen (PB8) provides several strains found in the panel, yet levels of some species are below detection limits, suggesting potential issues with colonization or efficacy.
- Strengths:
  - *Bifidobacterium animalis* (subsp. lactis) and *Bifidobacterium longum (subsp. longum)* are within the reference range, suggesting some degree of colonization by these critical SCFA-producing probiotics.
  - *Lactobacillus acidophilus* and *Lactiplantibacillus plantarum*, both included in the PB8 supplement, were detectable at low levels, indicating some activity but with room for improvement.
  - *Streptococcus thermophilus* and *Streptococcus salivarius* are in the normal range, which may support lactic acid production and oral health.
- Weaknesses:
  - Most *Lactobacillus* species (e.g., *L. rhamnosus*, *L. casei*, *and L. reuteri*) and all *Bacillus* species were below detection limits, despite their presence in the supplement. This suggests poor colonization or a need for dosage adjustment.
  - Key anti-inflammatory species such as *Faecalibacterium prausnitzii* were elevated, exceeding the reference range, which could indicate compensatory activity in response to inflammation.
  - Fungal probiotics (*Saccharomyces boulardii* and *Saccharomyces cerevisiae*) were below detection limits, which may reduce gut resilience.

**Note:* *This panel uses shotgun metagenomic sequencing to analyze the complete DNA content of fecal samples, identifying and quantifying beneficial microorganisms, including probiotic bacteria and yeasts. The panel reports the estimated copy number of each species, providing a direct measure of microbial load per gram of feces. Detection limits ensure even low-abundance species can be identified with high accuracy. Results are compared to reference ranges from healthy microbiomes to assess the balance of beneficial microbes and provide valuable insights into gut health.*

Pathogen and Parasite Panel

90%

Poor — Optimal

This section identifies and measures pathogens and parasites that are known to influence gut health. It's important to note that while these organisms may be present in the gut, not all individuals with positive findings will experience gastrointestinal symptoms. Some pathogens can exist in a subclinical state, or their presence may be transient without leading to poor health status. The results of this panel should be interpreted in the context of other clinical information and individual health status.

Bacterial Pathogens	Result*	Reference*
Camphylobacter spp.	< detection limit	<10 CPM
Clostridioides difficile (formerly *Clostridium difficile*)	**8.47 CPM**	10 to 1,000 CPM
Enterotoxigenic Bacteroides fragilis (ETBF)	< detection limit	10 to 1,000 CPM
Escherichia coli O157	**2.92 CPM**	10 to 1,000 CPM
Helicobater pylori	< detection limit	<10 CPM
Mycobacterium avium subsp. paratuberculosis (MAP)	< detection limit	<10 CPM
Salmonella enterica	< detection limit	<10 CPM
Shigella spp.	< detection limit	<10 CPM
Vibrio chloerae	< detection limit	Typically undetected
Yasinia enterocolitica	< detection limit	<10 CPM

Fungal Pathogens	Result*	Reference*
Aspergillus spp.	< detection limit	10 to 1,000 CPM
Candida albicans	< detection limit	<10 to 500 CPM

Pathogen and Parasite Panel

Viral Pathogens	Result*	Reference*
Astrovirus	< detection limit	Typically undetectable
Enteric adenoviruses	< detection limit	Typically undetectable
Norovirus	< detection limit	Typically undetectable
Rotavirus	< detection limit	Typically undetectable
Sapovirus	< detection limit	Typically undetectable

Protists Pathogens	Result*	Reference*
Balantidium coli	< detection limit	Typically undetectable
Blastocystis hominis	< detection limit	<10 to 1,000 CPM
Cryptosporidium spp.	< detection limit	Typically undetectable
Cyclospora cayetanensis	< detection limit	Typically undetectable
Entamoeba histolytica	< detection limit	Typically undetectable
Giardia lamblia (also known as *Giardia intestinalis*)	< detection limit	Typically undetectable
Isospora belli (Cystoisospora)	< detection limit	Typically undetectable

Pathogen and Parasite Panel

Parasites	Result*	Reference*
Ascaris lumbricoides (Roundworm)	< detection limit	Typically undetectable
Enterobius vermicularis (Pinworm)	< detection limit	Typically undetectable
Strongyloides stercoralis	< detection limit	Typically undetectable
Schistosoma mansoni	< detection limit	Typically undetectable
Taenia spp. (Tapeworms)	< detection limit	Typically undetectable
Toxocara spp.	< detection limit	Typically undetectable
Trichuris trichiura (Whipworm)	< detection limit	Typically undetectable

Scientist Notes:

- The presence of low levels of *C. difficile* and *E. coli O157* is unlikely to contribute to significant gastrointestinal symptoms in isolation, particularly without additional clinical signs of infection. These findings may reflect transient exposure or colonization, not active disease. However, they underscore the importance of gut microbial resilience and barrier integrity to mitigate potential risks from opportunistic or toxin-producing pathogens.

**__Note:__ Note: This panel uses shotgun metagenomic sequencing to accurately identify and quantify pathogenic microorganisms and parasites in fecal samples. The results provide an estimated copy number, representing the number of pathogen or parasite genome copies per gram of stool. If a pathogenic species is present in significant amounts, it may indicate potential infection or dysbiosis. Each result is compared to a Reference Range, which reflects the typical copy number ranges found in healthy individuals. For most pathogens, this range is extremely low or undetectable in healthy microbiomes. Detection of pathogens with higher copy numbers suggests active infection or colonization.*

Key Considerations:

- *Infection Threshold: Elevated copy numbers above reference ranges suggest a higher risk of infection or disease.*
- *Clinical Relevance: The copy number provides a clearer picture of the pathogen load, which can be used to monitor the severity of the infection or the effectiveness of treatment.*

*Find a detailed health protocol for your **Pathogen and Parasite Panel** in the digital twinning section of your report.*

Antimicrobial Resistance Panel

30%

Poor Optimal

This section summarizes the results of the Ion AmpliSeq™ Antimicrobial Resistance (AMR) Research Panel. This panel is comprised of a total of 814 amplicons to assess the presence of 478 antimicrobial resistance genes across 25 antibiotic classes (32, 33). AMR occurs when bacteria and fungi develop the ability to defeat drugs that are designed to kill them. This can make resistant infections difficult to treat. Some causes of AMR include: Natural processes, the use of antibiotics, poor hygiene, and travel. A status of “present” is predictive of resistance, while a “probable” status may confer resistance. The results of this panel should be interpreted in the context of other clinical information and individual health status.

Drug Class	Gene	Accession	Status*	Coverage | Depth | ID
Aminoglycosides	aadS	M72415	Present	100.00% / 1.95x / 99.26%
	aph2prime-Ib	AF337947	Present	87.83% / 1.44x / 99.26%
Bacitracin			Absent	-
Beta-lactams	cfxA	U75371	Present	100.00% / 65.79x / 99.80%
Bleomycin	-	-	Absent	-
Chloramphenicol	cat.C.coli	M35190	Present	100.00% / 4.59x / 98.95%
Fosfomycin	-	-	Absent	-
Fusaric acid	-	-	Absent	-
Fusidic acid	-	-	Absent	-
Integrase	-	-	Absent	-
Lincosamides	-	-	Absent	-
Mls (macrolides, lincosamides, streptogramins)	-	-	Absent	-
Macrolides	ermF	M14730	Present	100.00% / 4.01x / 98.96%
	ermG	M15332	Present	100.00% / 28.29x / 98.59%

Antimicrobial Resistance Panel

Drug Class	Gene	Accession	Status*	Coverage | Depth | ID
	mefA	AF227520	Present	98.58% / 23.99x / 99.15%
	msrD_or_mel	AF227521	Present	100.00% / 31.89x / 97.36%
Multidrug efflux	-	-	Absent	-
Mupirocin	-	-	Absent	-
Nitroimidazole	-	-	Absent	-
Platensimycin	-	-	Absent	-
Polymyxin	-	-	Absent	-
Quarternary ammonium compounds	-	-	Absent	-
Quinolones	-	-	Absent	-
Streptogramins	-	-	Absent	-
Streptothricins	-	-	Absent	-
Sulfonamides	-	-	Absent	-
Tetracyclines	tet32	AJ295238	Present	100.00% / 13.37x / 99.51%
	tet40	AJ295238	Present	100.00% / 3.32x / 97.77%
	tetO	M18896	Present	100.00% / 13.40x / 99.51%
	tetQ	X58717	Present	100.00% / 38.09x / 96.52%
	tetW	AJ222769	Present	100.00% / 16.41x / 96.86%

Antimicrobial Resistance Panel

Drug Class	Gene	Accession	Status*	Coverage | Depth | ID
	tetX-1	AJ311171	**Present**	**100.00% / 2.14x / 99.77%**
Trimethoprim	-	-	Absent	-
Vancomycin	-	-	Absent	-

Scientist Notes:

The sample reflects a significant burden of AMR genes, including those with high potential for horizontal gene transfer and multi-drug resistance. While this does not necessarily indicate active resistance in pathogenic bacteria, the findings suggest heightened risks that warrant proactive gut health and antibiotic stewardship strategies.

- Key Resistance Genes and Mechanisms:
  - Aminoglycosides: Genes such as aadS and aph2'-Ib encode enzymes that modify and inactivate aminoglycosides.
  - Beta-lactams: The presence of cfxA highlights resistance to this critical antibiotic class, likely through enzymatic degradation.
  - Macrolides: Genes such as ermF, ermG, mefA, and msrD confer resistance through mechanisms like ribosomal methylation and efflux pumps.
  - Tetracyclines: A high number of tetracycline-resistance genes (tet32, tet40, tetO, tetQ, tetW, and tetX-1) suggest robust resistance via target protection and degradation.
  - Chloramphenicol: The cat.C.coli gene encodes an enzyme that inactivates chloramphenicol through acetylation.
- Functional Implications:
  - The diversity and redundancy of AMR genes enhance the microbiome's capacity to resist multiple antibiotic classes simultaneously.
  - Resistance encoded by genes within mobile genetic elements (tetX, ermF, ermG) increases the potential for horizontal gene transfer, which may disseminate resistance to other commensal or pathogenic bacteria.
- Clinical Considerations:
  - Resistance to beta-lactams, macrolides, and tetracyclines could pose treatment challenges for common bacterial infections if pathogenic bacteria acquire these genes.
  - The sample's AMR profile highlights the need for careful antibiotic stewardship and monitoring of clinical symptoms, particularly in case of gastrointestinal disturbances or infections.

**Note:* *For each gene, the status is called as 'Present' if coverage is >=85% and identity is >=95%, and 'Probable' if coverage is >80% and identity is >90%. The coverage, depth, and identity statistics for each resistance gene are calculated as a weighted average of the corresponding markers with the highest detection status. These statistics are calculated from a sequence alignment to a curated reference database.*

*Find a detailed health protocol for your **Antimicrobial Resistance Panel** in the digital twinning section of your report.*

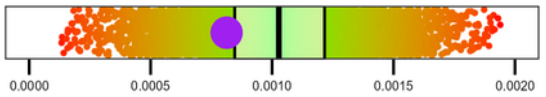
Digestion

50%

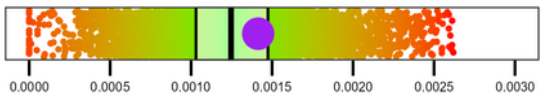
Poor **Optimal**

The Digestion section examines the microbiome's role in breaking down food and absorbing nutrients. Microorganisms in the gut, particularly bacteria, play a crucial role in digesting complex carbohydrates, fibers, and proteins that the human body cannot fully break down on its own. Key metabolic byproducts, such as short-chain fatty acids (SCFAs), are produced during this process, supporting gut health, immune function, and energy production (34, 35). Imbalances in the digestive microbiome can lead to issues such as bloating, malabsorption, or discomfort (36). This section evaluates microbial functions that influence digestion efficiency and identifies potential areas for improvement to optimize gut health.

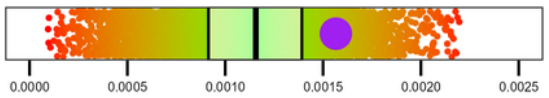
Fiber Degradation Capacity
The ability of the microbiome to break down complex carbohydrates (fibers) is a key indicator of digestive efficiency. This involves the presence of microbes that produce enzymes like cellulase and hemicellulase to degrade fibers.



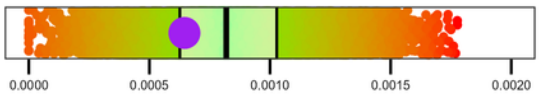
Protein Fermentation
Protein fermentation by gut bacteria can produce beneficial or harmful byproducts (e.g., amino acids vs. ammonia or hydrogen sulfide). Efficient protein digestion supports gut and overall health, while excessive harmful byproducts can indicate dysbiosis.



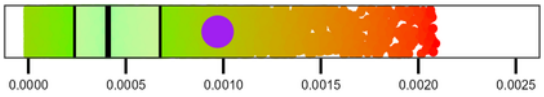
Gas Production
Fermentation by gut bacteria produces gases such as methane, hydrogen, and carbon dioxide. Excessive gas production can indicate an imbalance in microbial fermentation processes, leading to bloating or discomfort.



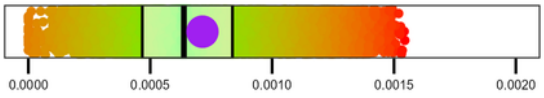
Lactose and Simple Sugar Digestion
The ability of the microbiome to digest simple sugars and lactose efficiently without causing intolerance symptoms like bloating or diarrhea.



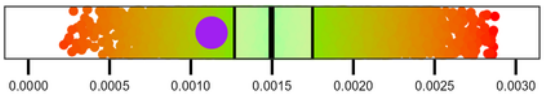
Fat Metabolism
Certain gut microbes contribute to the digestion and metabolism of fats. Their presence can affect lipid metabolism and energy extraction from fats.



Phytate Metabolism
This subdomain evaluates the microbiome's capacity to degrade phytates, anti-nutrients commonly found in plant-based foods that can reduce mineral absorption.



Enzymatic Function
Microbial production of digestive enzymes, such as amylase, protease, and lipase, is key to efficient digestion. A well-functioning microbiome supports the production of these enzymes.



*Find a detailed health protocol for your **Digestion** in the digital twinning section of your report.*

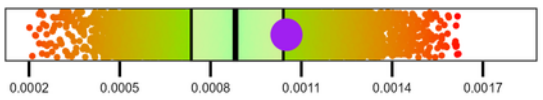
Nutrient Generation

60%

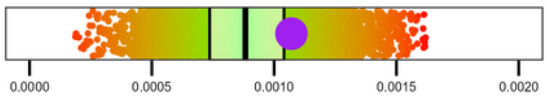
Poor — Optimal

The Nutrient Generation section evaluates the ability of your gut microbiome to produce essential nutrients that support overall health. Certain gut bacteria synthesize vitamins, short-chain fatty acids (SCFAs), and other metabolites crucial for maintaining a healthy gut lining, regulating immune function, and supplying energy (37). A well-functioning microbiome contributes significantly to nutrient availability, aiding in the production of compounds like vitamin K, B vitamins, and SCFAs. This section highlights the microbial functions and pathways that generate these critical nutrients, helping assess how effectively your microbiome contributes to your overall nutritional status.

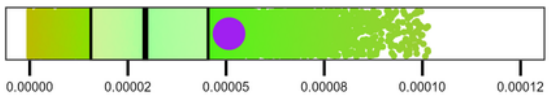
Butyrate Production
Butyrate is a key SCFA that provides energy to colon cells, reduces inflammation, and supports gut barrier integrity. Higher butyrate levels are linked to better gut health.



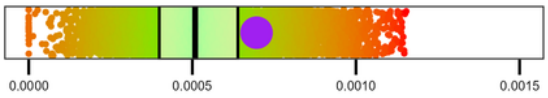
Acetate Production
Acetate is the most abundant SCFA in the gut and serves as a precursor for the synthesis of other SCFAs like butyrate. It supports energy production, helps maintain gut pH, and has systemic effects on cholesterol regulation and appetite control.



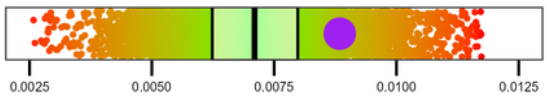
Propionate Production
Propionate is a SCFA that plays a role in regulating lipid metabolism, reducing cholesterol levels, and serving as an energy source for the liver. It also influences glucose metabolism and has anti-inflammatory properties in the gut.



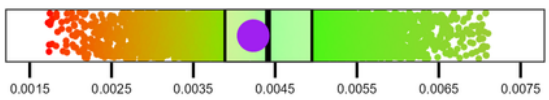
Lactate Production
Lactate is a key intermediate metabolite produced by certain gut bacteria during the fermentation of carbohydrates. While it can be further metabolized into other beneficial SCFAs like butyrate or propionate, an overaccumulation of lactate can lead to issues like acidosis. Lactate plays an important role in energy metabolism, gut pH regulation, and serves as a precursor for cross-feeding between bacterial species that further break it down into SCFAs.



Amino Acid Synthesis
Some gut bacteria contribute to the synthesis of amino acids, which are essential for protein production, tissue repair, and various metabolic functions.



B-Vitamin Synthesis Capacity
Certain gut bacteria are capable of synthesizing essential B-vitamins, including B12 (cobalamin), B6 (pyridoxine), B7 (biotin), and folate (B9). These vitamins play vital roles in energy metabolism, red blood cell formation, neurological function, and DNA synthesis. A healthy microbiome can significantly contribute to the body's supply of B-vitamins, especially in individuals with diets low in these nutrients.



Vitamin K Production
Gut bacteria, especially from the Bacteroides and Eubacterium genera, produce vitamin K, which is critical for blood clotting and bone health.

*Find a detailed health protocol for your **Nutrient Generation** in the digital twinning section of your report.*

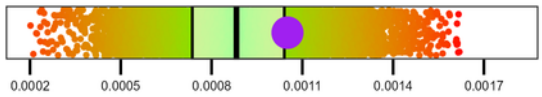
Gut Barrier Integrity

60%

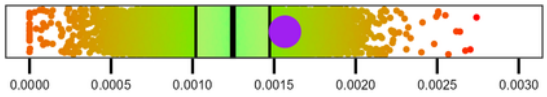
Poor **Optimal**

The Gut Barrier Integrity section assesses the health and functionality of the intestinal barrier, which plays a critical role in protecting the body from harmful pathogens, toxins, and undigested food particles. A well-functioning gut barrier ensures that nutrients are absorbed efficiently while preventing the entry of harmful substances. Key microbes, such as *Akkermansia muciniphila* and butyrate-producing bacteria, contribute to maintaining the mucus layer and strengthening the gut lining (38, 39). Compromised gut barrier integrity, also known as "leaky gut," can lead to increased inflammation, immune system activation, and various health issues (40). This section evaluates the microbial and metabolic factors that support or compromise the gut barrier's function.

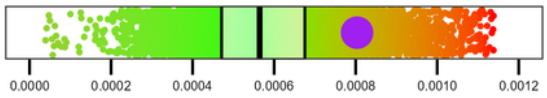
Butyrate Production
Butyrate is a short-chain fatty acid (SCFA) produced by gut bacteria that strengthens the gut barrier by nourishing colonocytes (gut lining cells) and reducing inflammation. It helps maintain tight junctions between cells, preventing "leaky gut."



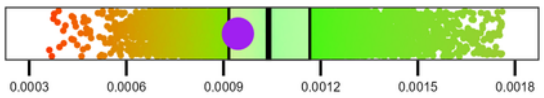
Mucus Degradation
Some bacteria degrade the mucus layer in the intestines, affecting nutrient absorption and gut barrier integrity. Balanced mucus degradation supports both digestion and gut health.



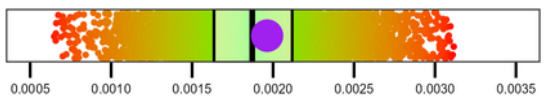
LPS-Production (Endotoxemia Risk)
Lipopolysaccharides (LPS) are inflammatory molecules produced by certain Gram-negative bacteria. High levels of LPS in the bloodstream can weaken the gut barrier and lead to systemic inflammation.



Tight Junction Regulation
Tight junction proteins between epithelial cells help maintain the integrity of the gut lining. Disruption in these proteins can lead to "leaky gut." This can be influenced by certain microbes and their metabolites.



Gut Barrier-Related Metabolism
This subdomain evaluates microbial metabolic pathways that influence gut barrier integrity by producing key metabolites such as indole derivatives (which regulate gut permeability), polyamines like spermidine (which support epithelial cell function and repair), and secondary bile acids (which enhance mucus layer integrity and modulate inflammation).



*Find a detailed health protocol for your **Gut Barrier Integrity** in the digital twinning section of your report.*

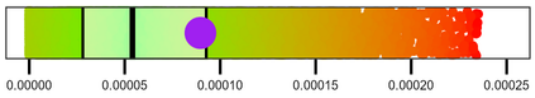
Inflammatory Panel

60%

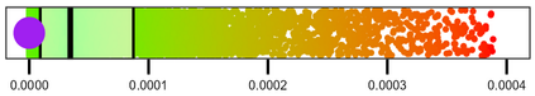
Poor **Optimal**

The Inflammatory Panel evaluates the balance of pro-inflammatory and anti-inflammatory microorganisms in the gut microbiome, which plays a crucial role in regulating systemic inflammation. Chronic low-grade inflammation, often driven by an imbalanced microbiome, can contribute to various health issues such as autoimmune disorders, metabolic syndrome, and gut-related diseases like inflammatory bowel disease (41). This panel assesses the presence and activity of key bacterial species and metabolites associated with inflammation, highlighting potential imbalances that could be driving or mitigating inflammatory responses. Understanding these dynamics helps guide personalized strategies for reducing inflammation and supporting overall immune health.

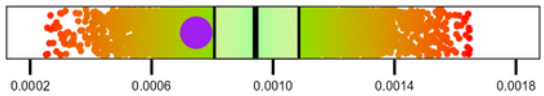
Bile Acid Metabolism
Secondary bile acids produced by gut microbiota can modulate inflammation and affect gut barrier function. Alterations in bile acid composition have been associated with inflammatory conditions.



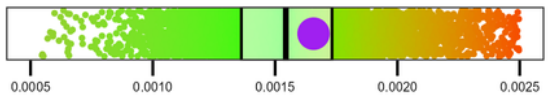
Hydrogen Sulfide (H2S) Production
The microbiome's capacity to produce hydrogen sulfide, a microbial metabolite that, at balanced levels, supports gut health but, in excess, can contribute to inflammation and gut barrier dysfunction.



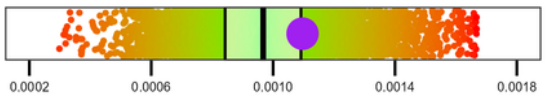
Tryptophan Metabolism
Tryptophan metabolites, such as indole derivatives, play a role in maintaining intestinal homeostasis and have anti-inflammatory effects. Levels of tryptophan-metabolizing bacteria and associated metabolites (e.g., indole, kynurenine pathways).



Cytokine Production
Certain microbes influence the production of pro-inflammatory cytokines like TNF-alpha and IL-6 or anti-inflammatory cytokines like IL-10, affecting the body's inflammatory response. Microbial activity linked to cytokine production and balance, measured indirectly by the presence of species that stimulate or suppress cytokine responses.



Inflammatory-Related Metabolism
Assesses microbial contributions to inflammation by analyzing the production of pro-inflammatory and anti-inflammatory metabolites.



*Find a detailed health protocol for your **Inflammatory Panel** in the digital twinning section of your report.*

Digital Twinning Personal Protocol

Next Steps Re-test in: 3 Months

The insights below are derived from our cutting-edge "Digital Twinning" *in silico* experimental platform, where a digital counterpart of your biological self is created to simulate various health scenarios. To ensure the highest accuracy and relevance to your individual needs, each recommendation undergoes 1,000 iterations, incorporating elements of randomness at every stage. This process is akin to testing out 1,000 slightly different versions of an intervention in a virtual setting to find the optimal health strategies. Considering the overall health state of your gut microbiome, we recommend retesting in 3 months.

Recommendation	Domain(s)	Score*
Avoid high-protein meals (e.g., >30g protein per serving) to limit ammonia production and hydrogen availability for methane producers.	Archaeome, Core Microbiome	5
May continue with PB8. but incorporate phage-based supplements (e.g., Bacillus coagulans GBI-30, 6086, 5 billion CFUs daily) to improve microbial balance, reduce abdominal pain and bloating, and improve protein absorption and utilization. In addition, supplement with Saccharomyces boulardii (5 billion CFUs daily) to mitigate potential PPI-induced dysbiosis and reduce pathogenic overgrowth risk.	AMR Panel, Probiotic Panel, Core Microbiome, Inflammatory Panel	5
Guaifenesin can increase mucus flow, which could theoretically interact with gut mucosal health. Supplement with Akkermansia muciniphila (1 billion CFUs, pasteurized) to improve mucin degradation, strengthen the gut barrier, and reduce LPS production.	Gut Barrier Integrity, Inflammatory Panel	5
Limit choline-rich foods (e.g., eggs, liver, red meat) to reduce trimethylamine (TMA) precursors for Candidatus Methanomassiliicoccus intestinalis.	Archaeome, Digestion	5
Add betaine HCl with meals (starting at 250-500 mg) to support digestion and prevent undigested carbohydrates from fueling gas-producing bacteria.	Digestion, Nutrient Generation	5
Rotate low-FODMAP fibers to improve SCFA production and limit the fermentation of gas-producing species.	Core Microbiome, Nutrient Generation	5
Incorporate arabinogalactan-rich fibers to selectively feed beneficial bacteria and crowd out AMR-associated species like Flavonifractor.	AMR Panel, Nutrient Generation, Core Microbiome	5
Consider replacing fiber gummies with partially hydrolyzed guar gum (5 g daily) to selectively promote beneficial bacteria and reduce hydrogen production.	Core Microbiome, Archaeome	5

Digital Twinning Personal Protocol

Next Steps Re-test in: 3 Months

Recommendation	Domain	Score*
Reduce raw cruciferous vegetables (e.g., broccoli, cauliflower) and switch to lightly steamed options to minimize sulfur-driven fermentation and gas production.	Digestion, Inflammatory Panel	5
Supplement with butyrate (300 mg twice daily) to improve gut lining repair, enhance SCFA production, and reduce inflammation.	Gut Barrier Integrity, Inflammatory Panel	4
Slowly incorporate resistant starch (green bananas, cooled potatoes) 2-3 times weekly to increase acetate and butyrate production while reducing Bacteroides vulgatus activity. Assess tolerance.	Nutrient Generation, Core Microbiome	4
Avoid processed plant-based snacks and opt for whole, minimally processed foods to reduce starch degradation pathways driving gas production.	Core Microbiome, Digestion	4
Limit high-fat meals to <4 oz per serving and replace with lean options (e.g., poultry, fish) to balance bile acid metabolism and reduce gas.	Digestion, Inflammatory Panel	4
Add anti-inflammatory polyphenols (e.g., pomegranate, green tea) to reduce cytokine production and support microbial balance.	Inflammatory Panel, Core Microbiome	3
Avoid environmental toxins and pollutants (e.g., pesticides) by consuming organic produce to limit gut microbiome disruptions that favor AMR gene persistence.	AMR Panel, Inflammatory Panel	3
In addition to fiber gummies already consuming, include pectin-rich fruits (apples, citrus, 1 serving daily) to target inflammatory species like Eisenbergiella and promote acetate and butyrate production.	Core Microbiome, Inflammatory Panel"	3
Avoid unnecessary antibiotic use and antimicrobial products (e.g., triclosan-containing soaps) to limit selective pressures that promote the spread of resistance genes.	AMR Panel, Core Microbiome	3
Avoid overuse of dietary supplements with antimicrobial properties (e.g., oregano oil) that could disrupt the microbiome and promote AMR species.	AMR Panel, Probiotic Panel	2
Use curcumin (500 mg daily) to modulate cytokine production and inflammation associated with methane metabolism.	Inflammatory Panel, Core Microbiome	2

Digital Twinning Personal Protocol

Next Steps Re-test in: **3** **Months**

Recommendation	Domain	Score*
Increase light aerobic activity (e.g., walking 20-30 minutes, 4-5 times weekly) to improve motility and microbial diversity.	Resilience, Digestion	2
Hydrate evenly over the day, adding electrolytes if necessary, to support motility and reduce hard stools	Digestion, Gut Barrier Integrity	2
Continue IB Guard and FD Guard as needed but monitor symptom relief. Add ginger tea or peppermint tea (1-2 cups daily) for natural motility enhancement.	Digestion, Inflammatory Panel	4
Store grains and nuts properly to avoid environmental mycotoxin exposure, which could exacerbate gut inflammation.	Mycotoxin Bioremediation, Inflammatory Panel	2
Use zinc carnosine (30 mg daily) to strengthen tight junctions, improve gut barrier integrity, and reduce LPS translocation.	Gut Barrier Integrity, Inflammatory Panel	2

**Note:* The importance Score ranges from 1-5, with 5 indicating the highest impact and 1 the lowest. These scores are informed by our study database and tailored to your unique microbiome profile. Recommendations with a score of 3 and below are more optional but are still advised for maximal benefit to your health and gut balance.*

Keystone Microbes

Microbe	Description	Result*	Reference*
Akkermansia muciniphila	Degrades mucin and supports gut barrier integrity and metabolic health (42-44).	< 0.01%	0.5-3%
Alistipes putredinis	Ferments amino acids and is involved in immune regulation and inflammation (45).	< 0.01%	1-3%
Bacteroides fragilis	Breaks down complex carbohydrates and aids in immune regulation (46).	0.23%	5-10%
Bacteroides ovatus	Aids in digestion of plant-derived polysaccharides, essential for fiber breakdown (47).	< 0.01%	2-6%
Bacteroides vulgatus	Breaks down polysaccharides and plays a role in immune modulation (48, 49).	< 0.01%	3-7%
Bifidobacterium bifidum	Digests human milk oligosaccharides and supporting gut health (50).	< 0.01%	0.5-3%
Bifidobacterium breve	Plays a role in digesting dietary fiber and producing vitamins (51).	< 0.01%	0.5-4%
Bifidobacterium longum	Supports digestion and immune function, commonly found in infants and adults (52).	0.36%	1-5%
Blautia obeum	Produces SCFAs, helps maintain gut pH and suppress pathogens (53).	7.13%	1-4%
Clostridium leptum	Helps in the fermentation of dietary fiber, producing short-chain fatty acids (54).	< 0.01%	3-6%
Coprococcus comes	Produces short-chain fatty acids, playing a role in maintaining gut homeostasis (55).	0.31%	2-5%
Desulfovibrio piger	Produces hydrogen sulfide and is involved in sulfate reduction in the gut (56).	< 0.01%	0.1-1%
Enterococcus faecalis	Common, but can become pathogenic if overgrown, linked to dysbiosis (57).	< 0.01%	0-1%
Escherichia coli	Common gut resident, but pathogenic strains like O157 can cause disease (58).	< 0.01%	0-1%
Eubacterium rectale	Butyrate producer important for maintaining gut barrier and reducing inflammation (59).	< 0.01%	3-7%
Faecalibacterium prausnitzii	Major producer of butyrate, a SCFA with anti-inflammatory properties (60).	2.60%	3-7%

Keystone Microbes

Microbe	Description	Result*	Reference*
Fusobacterium nucleatum	Linked to inflammation and gut disease; naturally present in low levels (61).	< 0.01%	0-0.5%
Lactobacillus acidophilus	Common probiotic that supports lactose digestion and gut health (62).	< 0.01%	0.1-5%
Lactiplantibacillus plantarum	Produces lactic acid, supports gut barrier function and has probiotic effects (63).	0.01%	0.1-5%
Lacticaseibacillus rhamnosus	Probiotic species known for supporting gut health and immune modulation (64).	< 0.01%	0.1-3%
Lactococcus lactis	Ferments lactose, often found in fermented dairy, supports gut health (65).	< 0.01%	0.1-2%
Methanobrevibacter smithii	Archaea that produces methane and aids in reducing intestinal hydrogen levels (66).	< 0.01%	0.1-2%
Parabacteroides distasonis	Role in bile acid metabolism and breaking down complex carbohydrates (67).	3.13%	1-3%
Peptostreptococcus anaerobius	Involved in the fermentation of proteins and can become pathogenic in dysbiosis (68, 69).	< 0.01%	0-1%
Prevotella copri	Associated with high-fiber diets and involved in carbohydrate fermentation (70).	< 0.01%	2-6%
Roseburia inulinivorans	Ferments dietary fibers to produce butyrate, supporting gut health (71).	< 0.01%	2-7%
Ruminococcus bromii	Specializes in breaking down resistant starches, aiding digestion and fermentation (72).	0.17%	1-5%
Ruminococcus gnavus	Ferments sugars and contributes to inflammation in some cases of dysbiosis (73).	< 0.01%	0.1-4%
Streptococcus thermophilus	Ferments lactose, commonly found in dairy products, supports digestion (74).	0.08%	0.1-2%
Veillonella parvula	Lactate fermenter that plays a role in anaerobic digestion in the gut (75).	< 0.01%	0.5-2%

**Note:* *This panel reports the relative abundance of each species, providing insight into their proportional presence within the microbial community. Detection limits ensure even low-abundance species are identified with high accuracy. Results are compared to reference ranges from healthy microbiomes, allowing for the assessment of microbial balance and valuable insights into overall gut health.*

Methodology

1. **Fecal Sample Collection and Preservation:** Your fecal sample was collected using the OMNIgene·GUT® collection device (DNA Genotek), which stabilizes microbial DNA at room temperature for up to 60 days, ensuring minimal degradation and preserving the microbial community composition during transport and storage (76). Your sample was then stored at -80°C upon receipt until processing.
2. **DNA Extraction Optimization and Automation:** DNA extraction is a critical step in microbiome analysis, as it is often the primary source of bias. We developed a robust, fully automated process for DNA extraction that ensures consistent and reproducible results. Given the diversity of microbial cell types in stool, we carefully optimized our lysis protocol to balance between:
    - Effective Lysis: Achieving thorough lysis of difficult-to-lyse organisms such as Gram-positive bacteria while preventing DNA degradation.
    - Avoiding Over-Aggressive Lysis: Protecting high molecular weight DNA from shearing, which can occur with overly aggressive mechanical or chemical lysis.
    - Inhibitor Removal: Stool contains enzymatic inhibitors (e.g., bile salts, polysaccharides) that can interfere with downstream reactions. Our protocol includes inhibitor removal steps to ensure high-quality, inhibitor-free genomic DNA, capturing the true microbial diversity.
    - The extracted DNA was then evaluated for quality and quantity using a Qubit Fluorometer (Thermo Fisher Scientific) and an Agilent TapeStation, ensuring sufficient yield and integrity for sequencing.
3. **Library Preparation:** After DNA extraction and QC, genomic DNA was prepared for sequencing. The library preparation process can introduce bias, particularly related to GC content, which can affect the representation of certain organisms. To mitigate this:
    - We selected a library preparation method optimized for minimal GC bias, ensuring even representation of diverse microbial species.
    - Unique Dual Indexed (UDI) adapters were used to prevent index hopping and misassignment of reads to incorrect samples. This step ensures the integrity and accuracy of sample identification throughout the sequencing process.
    - Libraries were prepared using the Illumina Nextera DNA Flex Library Preparation Kit, followed by amplification and purification.
4. **Sequencing Platform and Parameters:** Shotgun metagenomic sequencing was performed on the Illumina NextSeq 500 platform. Paired-end sequencing was conducted with 2 × 150 bp read pairs, generating high-resolution data for comprehensive microbial profiling. Each sample was sequenced to a depth of approximately 10 million reads, allowing for high sensitivity in detecting rare microbial species while providing sufficient coverage to quantify community diversity and abundance.
5. **Data Upload and Analysis:** Sequencing data was automatically uploaded to our platform for analysis. In partnership with our sequencing center, we utilize a highly sensitive and rapid k-mer classification algorithm to map sequencing reads back to its database, which includes more than 115,000 whole microbial reference genomes. The raw classification data underwent rigorous post-processing steps to eliminate false positives caused by potential contaminants or sequencing artifacts. This statistical filtering ensures high-confidence microbial identification and quantification. This analysis provides a detailed, accurate picture of the microbial composition, giving insight into the diversity and function of the gut microbiome.
6. **Post-Sequencing Quality Control**: Post-sequencing quality control was performed using FastQC (v0.11.9) to assess read quality, GC content, and adapter contamination. Low-quality reads and adapters were trimmed using Trimmomatic (v0.39), ensuring that only high-quality reads were used for analysis. Sequencing depth and coverage were evaluated to confirm that each sample met the minimum required read depth for comprehensive analysis.
7. **Data Analysis:** Taxonomic profiling was conducted using a k-mer-based classification algorithm, which maps reads to microbial reference genomes for highly accurate identification and quantification. Functional profiling was performed using HUMAnN2 (v2.8) to map reads to known metabolic pathways, enabling the exploration of microbial functional potential. Diversity metrics, including alpha and beta diversity, were calculated to assess community richness and composition. Statistical analysis and visualization were performed using Python with libraries such as Pandas, SciPy, Seaborn, and Matplotlib. These tools were used to identify patterns and associations between microbial composition, functional pathways, and health-related outcomes, providing comprehensive insights into the microbiome's influence on health.

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