



Ben Greenfield

Élie® Test Results

Barcode: 22241080602601

Lab Collection Date:
12.30.2024

Analysis Date:
01.07.2025

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

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***Disclaimer:** This test is not intended to diagnose, treat, or cure any illness or disease. This report should not be used as the sole basis for diagnosis or treatment decisions. It is recommended that individuals review and discuss the results of this report with their licensed healthcare provider before making any decisions or taking any actions based on the information provided.*

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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.

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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.

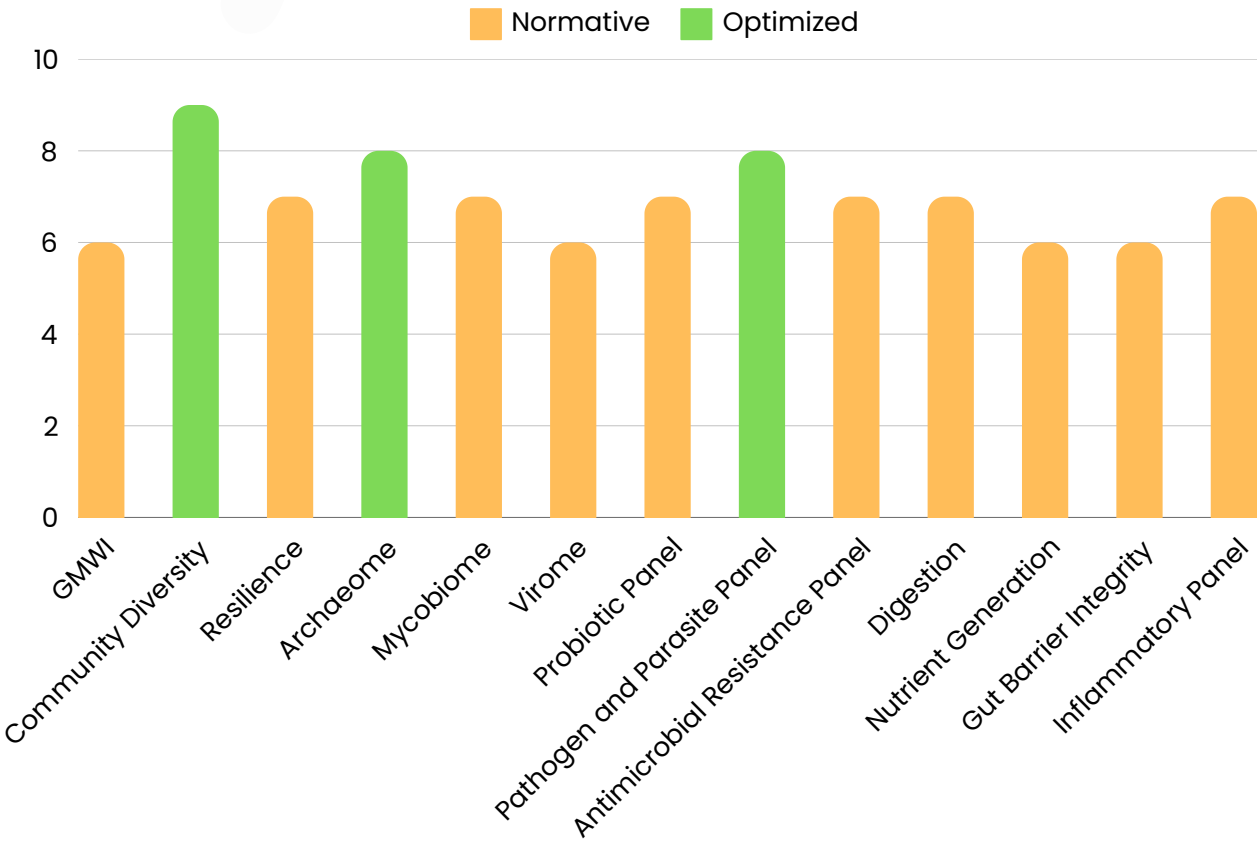
Ben Greenfield



Overall Score:

70 /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 detailed evaluation of your gut microbiome's composition and functionality across 13 key metrics, your overall microbiome health shows a strong foundation with several notable strengths. These include high **Community Diversity**, **Archaeome**, and **Pathogen and Parasite Panel** scores, reflecting robust microbial diversity, functional archaeal contributions, and minimal pathogenic burden. However, there is room for improvement in areas such as **GMWI**, **Virome**, **Nutrient Generation**, and **Gut Barrier Integrity**, which reflect challenges in microbial metabolic efficiency, virome functionality, and gut resilience. These scores, while moderate, indicate opportunities to further enhance gut health and overall functionality. In your Personalized Gut Health Improvement Plan, we outline specific dietary, supplementation, and lifestyle interventions to address these areas and optimize your overall gut ecosystem for better health and resilience.



Overview of Scores

Domain	Score	Score Overview
GMWI	6	Moderate microbiome health profile, supported by positive contributions from SCFA producers and stabilizing host-phage interactions, but hindered by negative associations with <i>Bacteroides</i> species and the <i>Clostridiaceae</i> family.
Community Diversity	9	The sample demonstrates a diverse and balanced microbial ecosystem with high richness, normative Simpson Index, and high Shannon Index.
Resilience	7	The resilience domain demonstrates high microbial diversity and normative interaction networks, but low-normative functional stability and redundancy are offset by high-normative stress response and adaptation.
Archaeome	8	The archaeome demonstrates low-normative methane production, with a diverse composition.
Mycobiome	7	This sample reflects a low-abundance and moderately diverse fungal community, with beneficial genera present in trace amounts and no detection of <i>Candida albicans</i> , which reduces the risk of fungal-related dysbiosis or infection.
Virome	6	This score reflects moderate virome functionality, with high genetic transfer but limited regulatory and stabilizing contributions.
Probiotic Panel	7	While certain strains are strongly represented, the lack of foundational probiotics (e.g., <i>Bifidobacterium</i> and <i>Lactobacillus</i>) may lower the functional resilience of the gut microbiome.
Pathogen and Parasite Panel	8	This panel indicates overall excellent pathogen control with isolated low-level detections. While the presence of ETBF and <i>Salmonella enterica</i> is notable, their levels are low and manageable with targeted strategies.
AMR Panel	7	While the panel shows robust resistance to several important antibiotic classes, there is an absence of resistance genes in some key classes and lack of multidrug efflux genes.
Digestion	7	Normative fiber degradation, protein fermentation, fat metabolism, phytate metabolism, and enzymatic function, but lower gas production and lactose/simple sugar digestion suggest mild inefficiencies in carbohydrate processing.
Nutrient Generation	6	High amino acid synthesis and normative propionate and vitamin K production, but low acetate, lactate, and B-vitamin synthesis, along with low-normative butyrate production.
Gut Barrier Integrity	6	Normative LPS production and tight junction regulation, but low-normative butyrate production, mucus degradation, and gut barrier-related metabolism.
Inflammatory Panel	7	Normative bile acid metabolism, hydrogen sulfide production, cytokine production, and inflammatory-related metabolism, but low tryptophan metabolism.

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



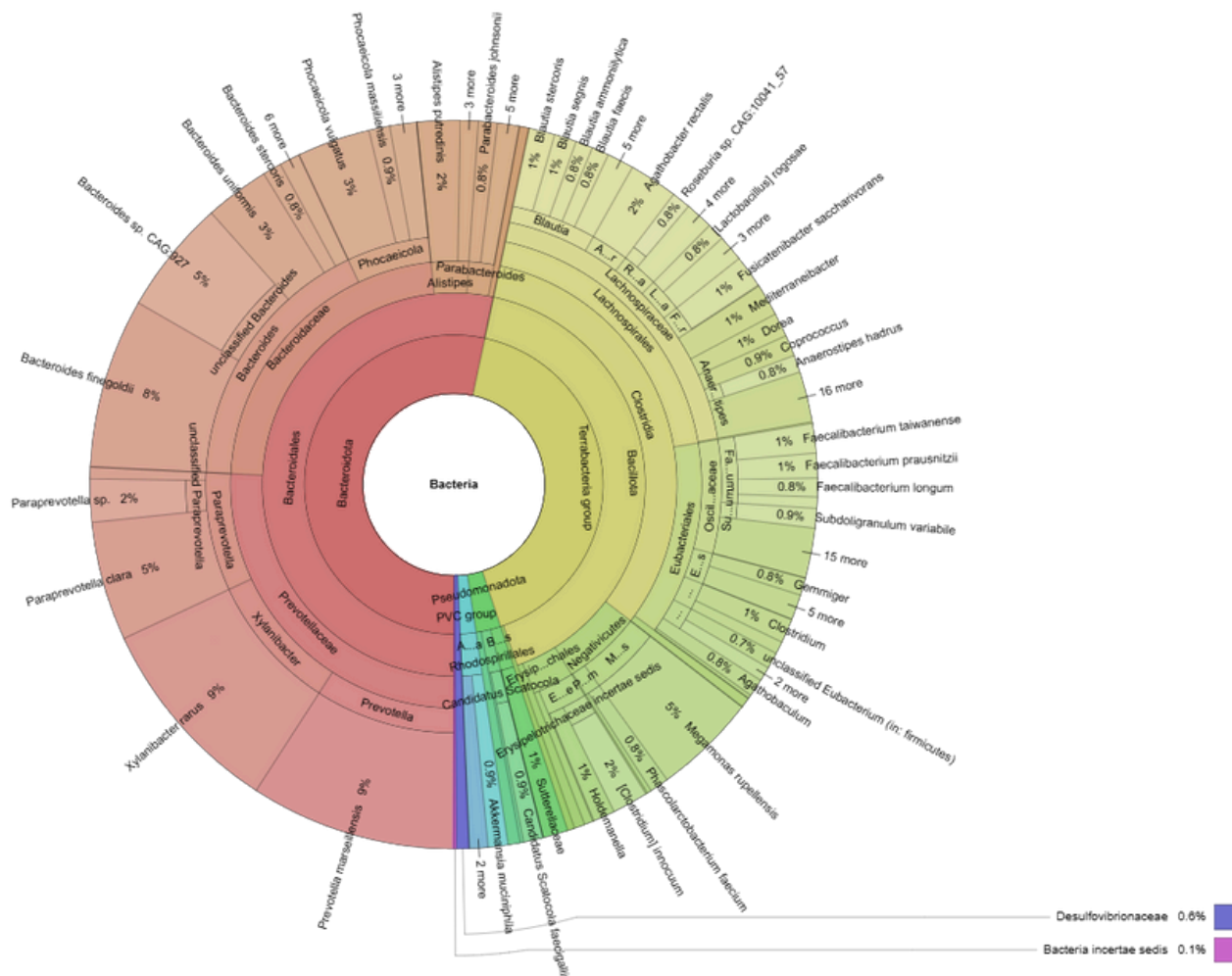
Overall Microbiome

Total number of microbial species
detected in your fecal sample

1,711

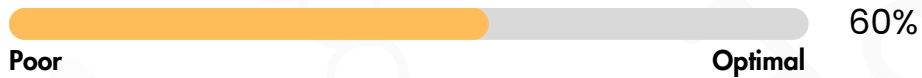
In human microbiome fecal samples, several microbial kingdoms are commonly found (4, 5). The relative abundance of these kingdoms can vary depending on factors such as diet, health status, geography, and individual variability (6-9). However, a general overview of the typical kingdoms and their abundance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



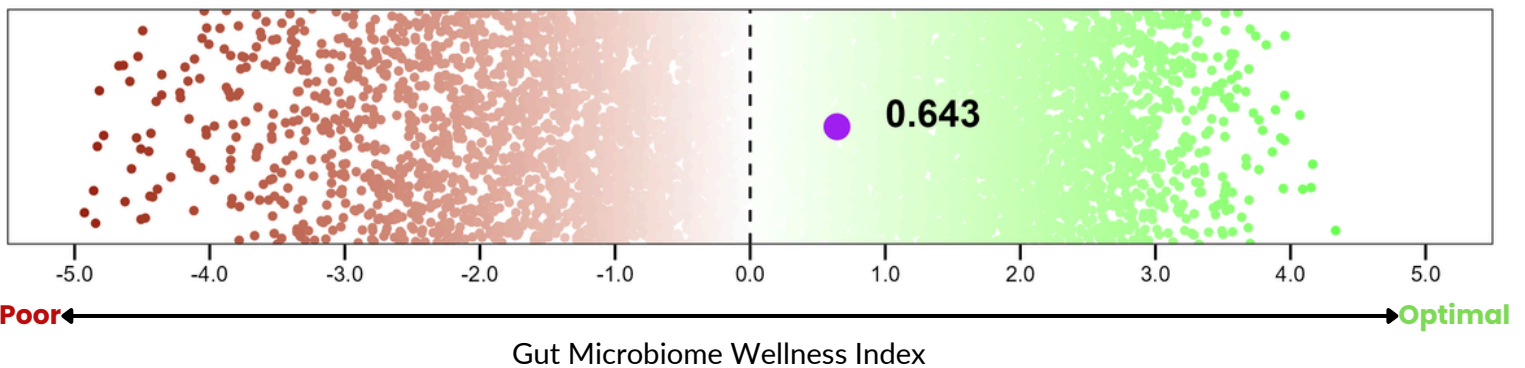


Gut Microbiome Wellness Index



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



Scientist Notes:

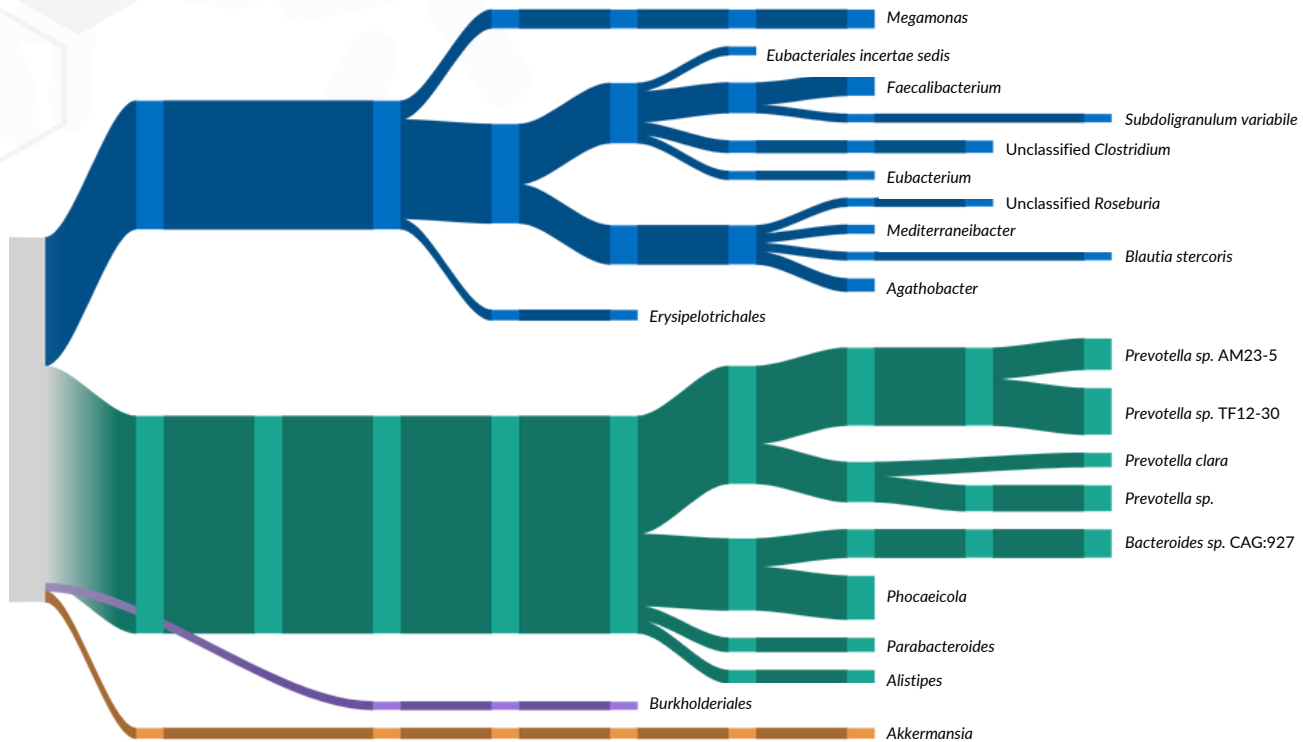
- Score: 0.643, indicating a moderate microbiome health profile with room for improvement in balance and functional resilience.
- Positive Contributors:
 - *Gemmiger formicilis*: Strongest positive association, known for its SCFA production, supporting gut barrier integrity and anti-inflammatory pathways.
 - *Dorea formicigenerans* and *Dorea longicatena*: Associated with carbohydrate metabolism and metabolic stability.
 - *Eubacterium eligens* and *Roseburia hominis*: SCFA producers contributing to anti-inflammatory properties.
 - Viruses: Moderate positive correlation, likely indicative of host-phage interactions stabilizing bacterial populations.
- Negative Contributors:
 - *Bacteroides* species (e.g., *B. stercoris* and *B. plebeius*): Notable negative associations, linked to dysbiosis and potential inflammatory pathways.
 - *Clostridiaceae* family: Weak negative influence, possibly indicative of opportunistic or pathogenic behavior.

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:

- **Key Taxa and Roles:** Includes *Faecalibacterium*, *Subdoligranulum variabile*, *Akkermansia*, and *Prevotella* species, contributing to SCFA production, gut barrier integrity, and carbohydrate metabolism.
- **Functional Highlights:** SCFA producers like *Roseburia* and *Mediterraneibacter* support anti-inflammatory pathways, while *Bacteroides* and *Parabacteroides* modulate bile acid metabolism.
- **Virome and AMR:** Host-phage interactions enhance microbial diversity; AMR genes in taxa like *Blautia stercoris* highlight the need for cautious antibiotic use.
- **Clinical Implications:** Dysbiosis-linked taxa (e.g., *Erysipelotrichales*) may indicate metabolic imbalance; fiber-rich diets support beneficial microbial activity.

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

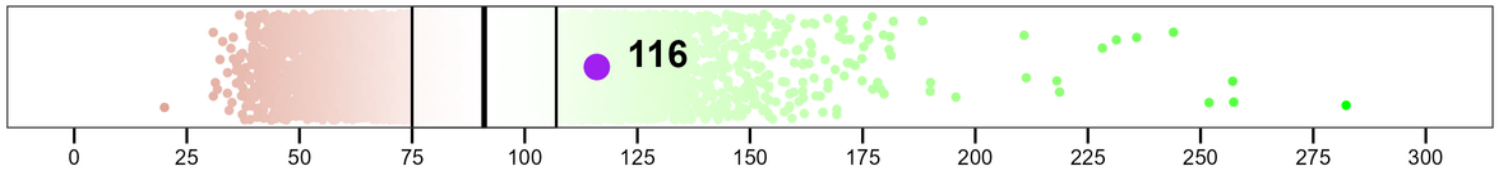


Community Diversity

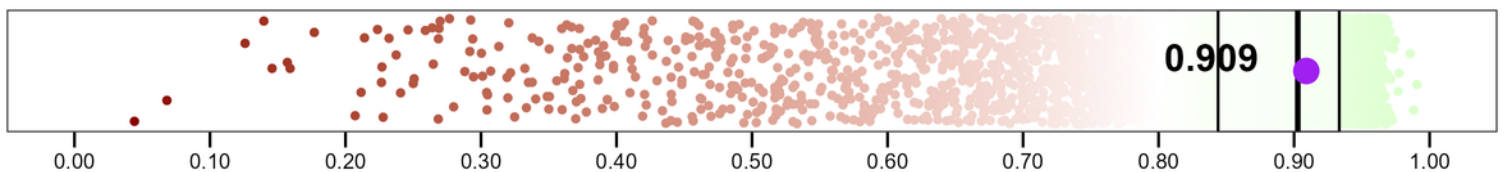


Diversity in the gut microbiome is defined as the number and abundance of distinct types of microorganisms present (14). An unhealthy state is characterized by an ecosystem often characterized by low microbial diversity, with a depletion of health-associated microbes and expansion of pathogens; a state 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).

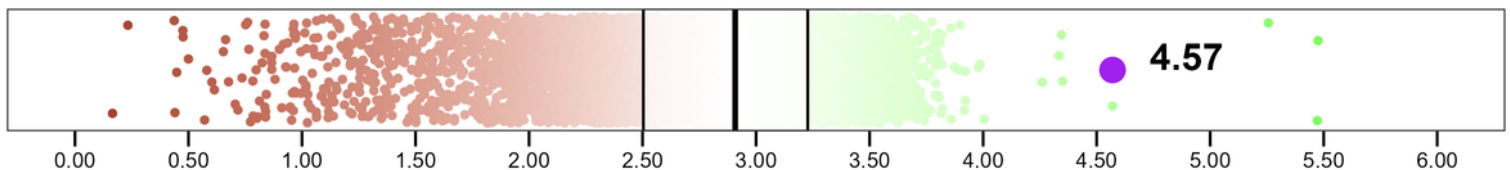
Richness



Simpson Index



Shannon Index



Poor ← → Optimal

Scientist Notes:

- The sample demonstrates a diverse and balanced microbial ecosystem with high richness, normative Simpson index, and high Shannon index, reflecting robust microbial evenness and functional potential.
- High Richness: Indicates a wide variety of species, enhancing functional redundancy and resilience to environmental or dietary changes.
- Normative Simpson Index: Suggests balanced species dominance, with no single taxa disproportionately affecting overall community stability.
- High Shannon Index: Reflects both richness and evenness, supporting diverse metabolic pathways and adaptability.

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



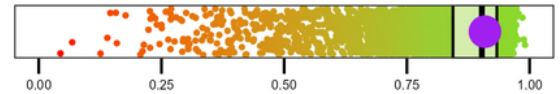
Resilience Score



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.

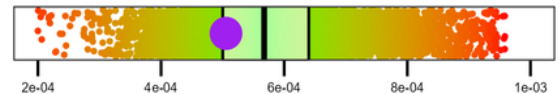
Microbial Diversity

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



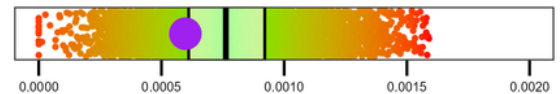
Functional Stability

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



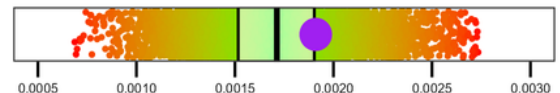
Functional Redundancy

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



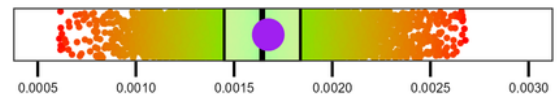
Stress Response and Adaptation

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



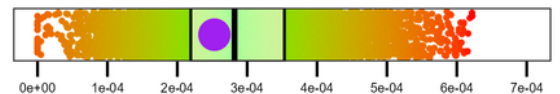
Microbial Interaction Networks

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.

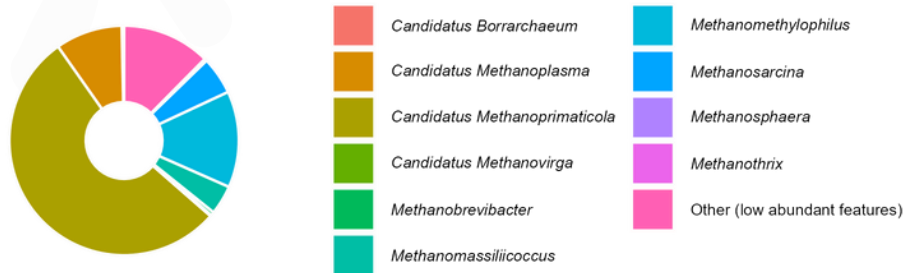


Archaeome



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:

- Key Insights
 - Methane Production: Low-normative methane levels suggest moderate methanogenic activity, which helps regulate gut hydrogen levels but has been linked to slower transit times, constipation, and potential low-grade inflammation in cases of overproduction.
 - Diverse Methanogen Presence: Multiple methanogenic genera enhance functional redundancy and resilience against disruptions.
 - Low-Abundance Features: Genera like *Methanobrevibacter* and *Methanomassiliicoccus* contribute minimally to overall activity but expand archaeal diversity.
- Clinical Implications
 - Strengths: Balanced methane output supports microbial stability and reduces the likelihood of excessive bloating or dysbiosis.
 - Weaknesses: Persistent low abundance of key genera may limit optimal methanogenic functionality, potentially contributing to suboptimal hydrogen recycling and slight inflammation risk if imbalances occur.

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

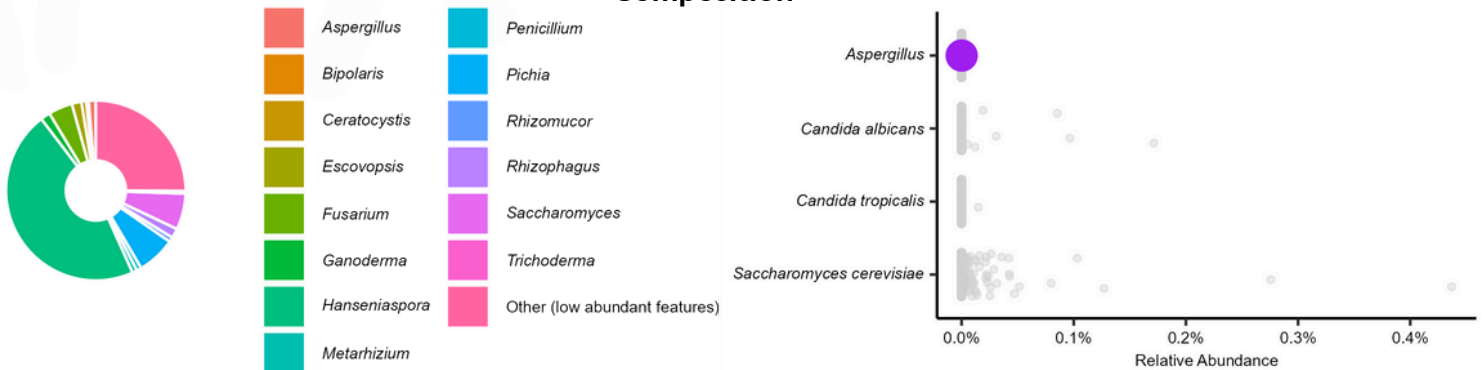


Mycobiome

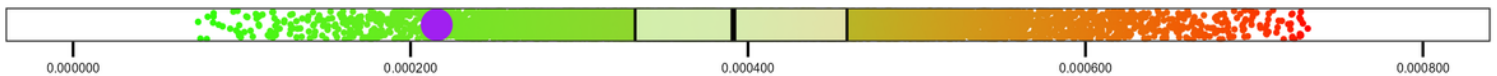


The Mycobiome represents the community of fungi within the gut microbiome. Although present in much lower abundance compared to bacteria, fungi play a significant role in health, maintaining microbial balance, supporting digestion, and regulating immune responses (21, 22). Common fungal species such 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.

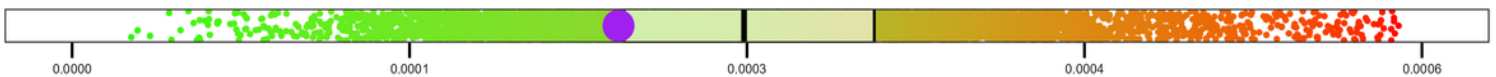
Composition



Yeast Carbohydrate Metabolism



Fungal Virulence



Scientist Notes:

- Strengths:
 - Absence of *Candida albicans*: Reduces the risk of fungal infections or dysbiosis.
 - Low Fungal Virulence: Indicates a stable mycobiome with minimal inflammatory or pathogenic activity.
 - Presence of Beneficial Genera: Genera like *Saccharomyces* and *Pichia* contribute to gut health and microbial balance.
- Weaknesses:
 - Low Overall Fungal Abundance: Limits the mycobiome's functional impact and adaptability.
 - Moderate Diversity: While present, the variety of fungal genera is not optimal for robust ecosystem resilience.



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.	4.42 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.	2.86 CPM	3 to 20 CPM
	4.2.1.1: Carbonic anhydrase	Participates in detoxification processes through hydration reactions.	45.97 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.	Absent	5 to 50 CPM
	4.1.1: Decarboxylase	Facilitates the removal of carboxyl groups in mycotoxins, neutralizing their effects.	128.83 CPM	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.	0.80 CPM	5 to 50 CPM
	2.1.1.45: Methyltransferase	Adds methyl groups to alter toxic functional groups in mycotoxins, reducing their activity.	93.68 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
Fumonisin	3.1.4.3: Phospholipase C	Involved in breaking down sphingolipid analogs produced by fumonisins, mitigating their effects.	Absent	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.	1.98 CPM	0 to 50 CPM

Scientist Notes:

- This sample shows a moderate capacity for mycotoxin detoxification with key strengths and areas for improvement.
- Strengths:
 - High decarboxylase activity supports significant detoxification of deoxynivalenol.
 - Elevated methyltransferase and carbonic anhydrase activity provide broad metabolic flexibility for detoxification.
- Weaknesses:
 - The absence of critical enzymes, including peroxidase, monooxygenase, and fumonisin-targeting enzymes, severely limits bioremediation capacity for aflatoxins, fumonisins, and zearalenone.
 - Low amidase and aldose reductase activity constrain general detoxification processes.

**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.

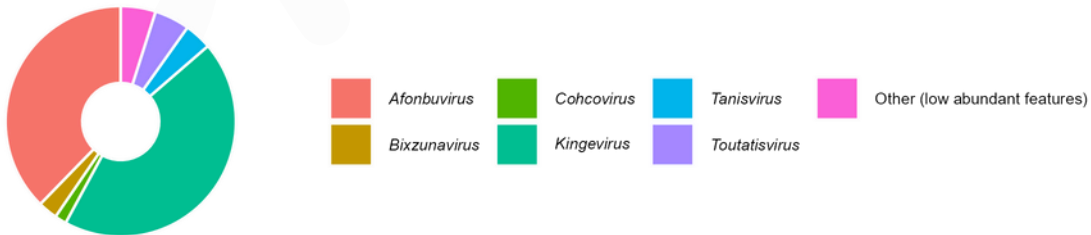


Virome

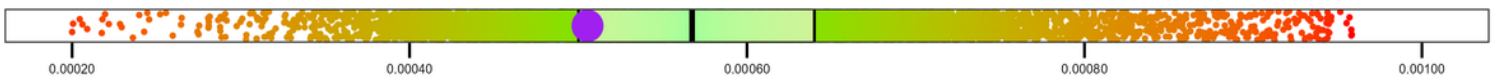


The Virome refers to the collection of viruses within the gut microbiome, including bacteriophages (viruses that infect bacteria) and eukaryotic viruses that interact with human cells (28). Bacteriophages play a crucial role in regulating bacterial populations, shaping microbial diversity, and maintaining 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



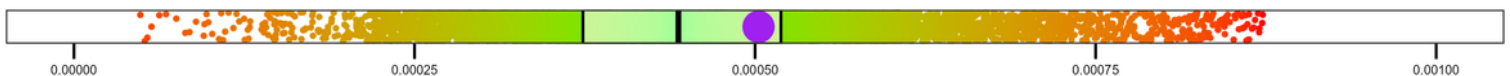
Viral Replication and Life Cycle



Host-Phage Interactions



Phage-Mediated Horizontal Gene Transfer



Scientist Notes:

- This sample reflects a low-abundance virome with moderate functional activity, characterized by high phage-mediated horizontal gene transfer but reduced viral replication and host-phage interactions.
- Strengths:
 - High horizontal gene transfer supports microbial adaptability and metabolic diversity.
 - The presence of *Kingeivirus* and *Afonbuvirus* indicates functional virome contributions, despite low overall abundance.
- Weaknesses:
 - Reduced replication and host-phage interactions limit the virome's ability to regulate bacterial populations and stabilize microbial ecosystems.
 - Low virome abundance reduces its overall functional impact and resilience.

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



Probiotic Panel



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*
<i>Akkermansia muciniphila</i>	1532.19 CPM	10 to 5,000 CPM
<i>Bacillus cereus</i>	< detection limit	<1 to 10 CPM
<i>Bacillus clausii</i>	< detection limit	<10 to 100 CPM
<i>Bacillus coagulans</i>	< detection limit	<10 to 50 CPM
<i>Bacillus licheniformis</i>	< detection limit	<10 to 50 CPM
<i>Bacillus megaterium</i>	< detection limit	<10 to 50 CPM
<i>Bacillus pumilus</i>	< detection limit	<1 to 10 CPM
<i>Bacillus subtilis</i>	2.41 CPM	<10 to 100 CPM
<i>Bifidobacterium animalis (subsp. animalis)</i>	< detection limit	10 to 500 CPM
<i>Bifidobacterium animalis (subsp. lactis)</i>	< detection limit	50 to 1,000 CPM
<i>Bifidobacterium bifidum</i>	< detection limit	20 to 1,000 CPM
<i>Bifidobacterium breve</i>	2.41 CPM	50 to 1,000 CPM
<i>Bifidobacterium longum (subsp. infantis)</i>	< detection limit	50 to 1,500 CPM
<i>Bifidobacterium longum (subsp. longum)</i>	< detection limit	100 to 5,000 CPM



Probiotic Panel

Bacterial Probiotics	Result*	Reference*
<i>Faecalibacterium prausnitzii</i>	7896.02 CPM	1,000 to 5,000 CPM
<i>Lactobacillus acidophilus</i>	< detection limit	10 to 1,000 CPM
<i>Levilactobacillus brevis</i>	< detection limit	10 to 500 CPM
<i>Lactobacillus casei</i>	< detection limit	50 to 1,000 CPM
<i>Lactobacillus delbrueckii (subsp. bulgaricus)</i>	< detection limit	<10 to 50 CPM
<i>Lactobacillus delbrueckii (subsp. delbrueckii)</i>	< detection limit	<10 to 50 CPM
<i>Limosilactobacillus fermentum</i>	< detection limit	10 to 500 CPM
<i>Lactobacillus gasseri</i>	< detection limit	10 to 200 CPM
<i>Lactobacillus helveticus</i>	< detection limit	10 to 500 CPM
<i>Lactocaseibacillus paracasei</i>	2.14 CPM	50 to 1,000 CPM
<i>Lactiplantibacillus plantarum</i>	< detection limit	50 to 1,000 CPM
<i>Limosilactobacillus reuteri</i>	< detection limit	10 to 500 CPM
<i>Lactocaseibacillus rhamnosus</i>	< detection limit	10 to 1,000 CPM
<i>Lactobacillus salivarius</i>	< detection limit	10 to 500 CPM
<i>Lactococcus lactis</i>	< detection limit	10 to 1,000 CPM
<i>Propionibacterium freudenreichii</i>	< detection limit	10 to 500 CPM
<i>Streptococcus salivarius</i>	83.44 CPM	50 to 1,500 CPM



Probiotic Panel

Bacterial Probiotics	Result*	Reference*
<i>Streptococcus thermophilus</i>	5.35 CPM	100 to 1,000 CPM
<i>Veillonella atypica</i>	17.39 CPM	10 to 500 CPM

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

Scientist Notes:

- Strengths:
 - *Akkermansia muciniphila*: Detected at 1532.19 CPM, well within the reference range (10–5,000 CPM), supporting gut barrier integrity and mucin regulation.
 - *Faecalibacterium prausnitzii*: Elevated at 7896.02 CPM (reference: 1,000–5,000 CPM), indicative of strong anti-inflammatory capacity and SCFA (butyrate) production.
 - *Streptococcus salivarius*: Detected at 83.44 CPM, within the range (50–1,500 CPM), contributing to oral and gut health.
 - *Veillonella atypica*: Present at 17.39 CPM (10–500 CPM), supporting lactate metabolism and SCFA production.
- Weaknesses:
 - *Bifidobacterium* species: Most strains, including *B. animalis*, *B. bifidum*, and *B. breve*, are below detection limits, reducing SCFA and acetate production potential.
 - *Lactobacillus* species: Key strains such as *L. acidophilus*, *L. casei*, and *L. plantarum* are absent, limiting lactic acid production and resilience to pathogens.
 - *Bacillus* species: Several strains (e.g., *B. cereus*, *B. clausii*, *B. coagulans*) are below detection thresholds, reducing spore-forming probiotic benefits.
 - Fungal probiotics: *Saccharomyces boulardii* and *S. cerevisiae* are undetected, limiting fungal-mediated gut support and defense against pathogens.

***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



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*
<i>Camphylobacter spp.</i>	< detection limit	<10 CPM
<i>Clostridioides difficile</i> (formerly <i>Clostridium difficile</i>)	< detection limit	10 to 1,000 CPM
<i>Enterotoxigenic Bacteroides fragilis</i> (ETBF)	23.81 CPM	10 to 1,000 CPM
<i>Escherichia coli</i> O157	< detection limit	10 to 1,000 CPM
<i>Helicobacter pylori</i>	< detection limit	<10 CPM
<i>Mycobacterium avium subsp. paratuberculosis</i> (MAP)	< detection limit	<10 CPM
<i>Salmonella enterica</i>	4.82 CPM	<10 CPM
<i>Shigella spp.</i>	< detection limit	<10 CPM
<i>Vibrio cholerae</i>	< detection limit	Typically undetected
<i>Yersinia enterocolitica</i>	< detection limit	<10 CPM

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





Pathogen and Parasite Panel

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

Scientist Notes:

- This panel indicates overall excellent pathogen control with isolated low-level detections. While the presence of ETBF and *Salmonella enterica* is notable, their levels are low and manageable with targeted strategies.
 - Low Pathogen Burden: Most bacterial, fungal, viral, protist, and parasitic pathogens are undetectable, reflecting minimal immediate infection risk.
 - Detection of *Enterotoxigenic Bacteroides fragilis* (ETBF): Present at 23.81 CPM (reference: 10–1,000 CPM). ETBF is associated with inflammatory bowel conditions and warrants monitoring or intervention.
 - Trace Detection of *Salmonella enterica*: Low level (4.82 CPM, <10 CPM reference) suggests potential subclinical colonization or environmental exposure, although not immediately concerning.

***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



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% / 12.56x / 99.89%
Bacitracin	-	-	Absent	-
Beta-lactams	cfxA	U75371	Probable	100.00% / 37.79x / 92.05%
Bleomycin	-	-	Absent	-
Chloramphenicol	-	-	Absent	-
Fosfomycin	-	-	Absent	-
Fusaric acid	-	-	Absent	-
Fusidic acid	-	-	Absent	-
Integrase	-	-	Absent	-
Lincosamides	lnuC	AY928180	Present	100.00% / 45.65x / 99.89%
MLs (macrolides, lincosamides, streptogramins)	-	-	Absent	-
Macrolides	ermB	M11180	Present	100.00% / 16.35x / 99.94%
	ermF	M14730	Present	100.00% / 22.59x / 98.86%
	ermG	M15332	Present	100.00% / 3.48x / 98.57%



Antimicrobial Resistance Panel

Drug Class	Gene	Accession	Status*	Coverage Depth ID
	mefA	AF227520	Present	98.58% / 9.72x / 98.63%
	msrD_or_mel	AF227521	Present	100.00% / 18.02x / 98.22%
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% / 41.76x / 99.92%
	tetO	M18896	Present	100.00% / 41.85x / 99.92%
	tetQ	X58717	Present	100.00% / 74.10x / 97.64%
	tetW	AJ222769	Present	100.00% / 7.79x / 99.53%
	tetX	M37699	Probable	98.19% / 13.76x / 92.31%



Antimicrobial Resistance Panel

Drug Class	Gene	Accession	Status*	Coverage Depth ID
Trimethoprim	-	-	Absent	-
Vancomycin	-	-	Absent	-

Scientist Notes:

This sample exhibits 11 confirmed and 2 probable AMR genes across 5 antibiotic classes, highlighting robust resistance mechanisms.

- Key Resistance Genes and Mechanisms:
 - Aminoglycosides: aadS indicates enzymatic resistance.
 - Beta-lactams: cfxA (probable) confers partial penicillin and cephalosporin resistance.
 - Lincosamides: lnuC suggests clindamycin resistance.
 - Macrolides: ermB, ermF, ermG, mefA, msrD mediate methylation and efflux-based resistance.
 - Tetracyclines: tet32, tetO, tetQ, tetW, tetX reflect ribosomal protection and enzymatic inactivation.
- Clinical Implications:
 - Broad-spectrum resistance: Confirmed resistance to aminoglycosides, beta-lactams, macrolides, lincosamides, and tetracyclines significantly limits treatment options.
 - Risk of treatment failure: High gene coverage and identity suggest functional resistance with clinical relevance.
 - Potential for cross-resistance: Overlapping mechanisms in macrolides and lincosamides enhance the risk of multidrug resistance.
- Potential for Horizontal Gene Transfer:
 - Genes such as ermF and tetQ are commonly associated with mobile genetic elements, amplifying the likelihood of horizontal transfer within microbial communities.

***Note:** For each gene, the status is called as 'Present' if coverage is $\geq 85\%$ and identity is $\geq 95\%$, 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

Poor

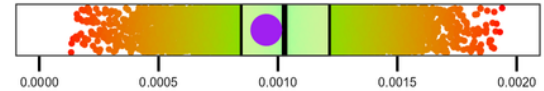
Optimal

70%

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.

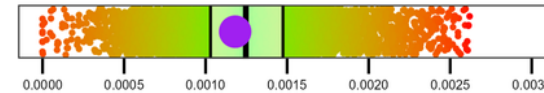
Fiber Degradation Capacity

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.



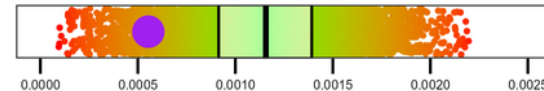
Protein Fermentation

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.



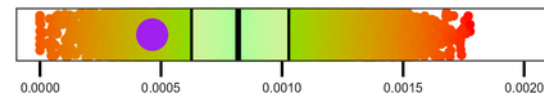
Gas Production

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.



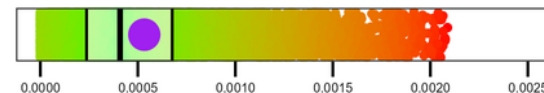
Lactose and Simple Sugar Digestion

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



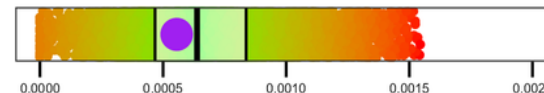
Fat Metabolism

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



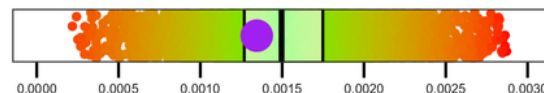
Phytate Metabolism

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

Poor

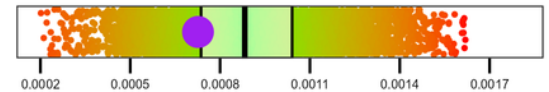
Optimal

60%

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.

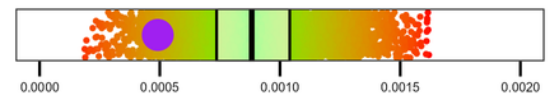
Butyrate Production

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.



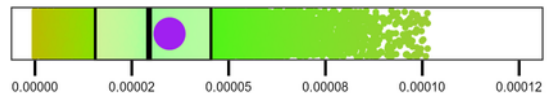
Acetate Production

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.



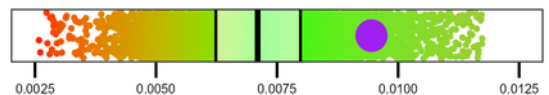
Lactate Production

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.



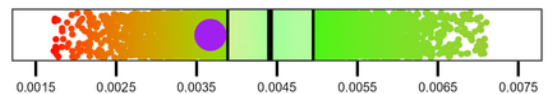
Amino Acid Synthesis

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

Poor

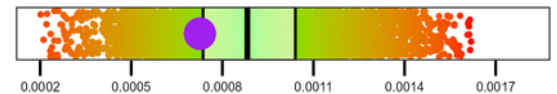
Optimal

60%

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.

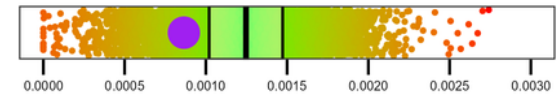
Butyrate Production

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."



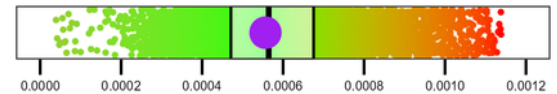
Mucus Degradation

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.



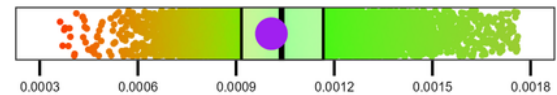
LPS-Production (Endotoxemia Risk)

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.



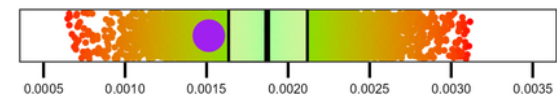
Tight Junction Regulation

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

Poor

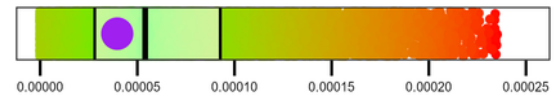
Optimal

70%

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.

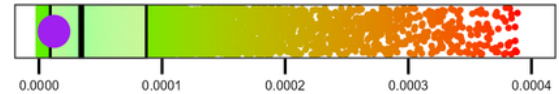
Bile Acid Metabolism

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.



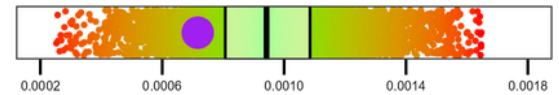
Hydrogen Sulfide (H2S) Production

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.



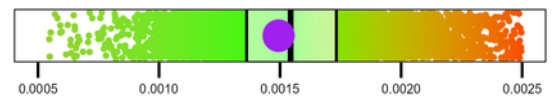
Tryptophan Metabolism

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).



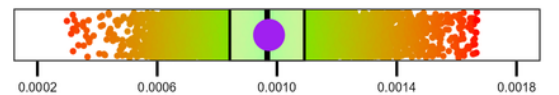
Cytokine Production

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:

6
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 **6 months**.

Recommendation	Dosage/Amount	Domain(s)	Score*
Enhance microbial diversity with resistant starch sources like green bananas, cooked/cooled potatoes, or legumes.	Include 1–2 servings/day to encourage SCFA-producing bacteria like <i>Faecalibacterium</i> .	GMWI, Community Diversity, Resilience, Virome	5
Rotate timing of current probiotics to maximize colonization without competition. Composition shows support for <i>Akkermansia muciniphila</i> and <i>Veillonella atypica</i> grafting.	Take Just Thrive in the morning and the multi-strain SEED blend in the evening. Consider readjusting probiotic regimen upon retesting.	Probiotic Panel, GMWI, Gut Barrier Integrity	5
Supplement with tributyrin to improve butyrate levels and gut barrier integrity.	300–500 mg/day, taken with meals.	Nutrient Generation, Gut Barrier Integrity	5
Incorporate prebiotic-rich foods like onions, garlic, and leeks to support <i>Lactobacillus</i> and <i>Bifidobacterium</i> growth.	Add 1/2 cup/day, distributed across meals.	GMWI, Probiotic Panel, Digestion	5
Add <i>Saccharomyces boulardii</i> to complement bacterial strains and reduce pathogen colonization.	5 billion CFU/day for 4–6 weeks; take separately from SEED to avoid competition.	Pathogen and Parasite Panel, Resilience	5
Address ETBF activity with Berberine or Allicin.	500 mg Berberine or 600 mg Allicin daily, 2-week cycles with breaks.	Digestion, Archaeome, Pathogen and Parasite Panel	5
Limit red meat to reduce <i>Clostridiaceae</i> - and ETBF-driven inflammation while ensuring adequate protein intake from lean sources.	Replace with fish, eggs, or plant proteins; max 3 servings of red meat per week.	GMWI, Inflammatory Panel, Pathogen and Parasite Panel	4
Increase Tryptophan-Rich Foods: Provides precursors for serotonin synthesis and gut-brain signaling.	Turkey, salmon, eggs, nuts, seeds, tofu (1–2 servings/day).	Nutrient Generation, Inflammatory Panel	4

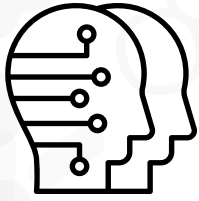


Digital Twinning Personal Protocol

Next Steps
Re-test in:

6
Months

Recommendation	Dosage/Amount	Domain(s)	Score*
<i>Incorporate intermittent fasting (16:8 protocol) to enhance microbial stability and resilience.</i>	<i>Practice 3–5 days/week; ensure hydration and nutrient adequacy during eating periods.</i>	Resilience, Gut Barrier Integrity, Virome	4
<i>Introduce polyphenol-rich foods such as pomegranate, green tea, and cranberries to inhibit ETBF growth and reduce inflammation.</i>	<i>Consume 1–2 servings of polyphenol-rich foods daily (e.g., 1 cup green tea or 1/2 cup cranberries).</i>	Inflammatory Panel, Gut Barrier Integrity	2
<i>Rotate Ultra Binder every 3 months for detox support, focusing on endotoxin clearance. Take binders (e.g., Ultra Binder) 2 hours apart from nutrient-dense supplements (e.g., fish oil, greens) to avoid nutrient sequestration.</i>	<i>Use binders 3x/week, preferably between meals, for 4–6 weeks.</i>	Gut Barrier, AMR Panel	3
<i>Supplement with N-Acetylcysteine (NAC) to promote glutathione production and reduce inflammation.</i>	<i>600–1200 mg/day, taken with meals.</i>	Inflammatory Panel, Resilience	3
<i>Optimize virome functionality by incorporating fermented foods like kimchi, kefir, or sauerkraut.</i>	<i>1–2 servings/day.</i>	Virome, Community Diversity	3
<i>Address AMR concerns by limiting unnecessary antibiotic use and enhancing gut resilience.</i>	<i>Avoid antibiotics unless clinically necessary; consult healthcare provider.</i>	AMR Panel, GMWI	2
<i>Incorporate dietary zinc to enhance tight junction regulation and support gut integrity.</i>	<i>15 mg/day from dietary sources or supplements.</i>	Gut Barrier Integrity	2
<i>Increase Protein Diversity: Add lean protein sources like fish and legumes, distributing intake evenly across meals.</i>	<i>Weekly rotation.</i>	GMWI, Digestion, Nutrient Generation	2



Digital Twinning Personal Protocol

Next Steps
Re-test in:

6
Months

Recommendation	Dosage/Amount	Domain(s)	Score*
<i>Aim to reduce nicotine intake by 20-30% per week to allow the body and microbiome to gradually adjust.</i>	<i>Chronic nicotine exposure has been shown to decrease overall microbial diversity, which is critical for a resilient gut ecosystem. Limit to 2 mg/day</i>	General	2
<i>Limit Alcohol Consumption</i>	<i>Alcohol disrupts B-vitamin synthesis pathways and microbial activity. Limit intake to 1-2 drinks/week.</i>	General	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*
<i>Akkermansia muciniphila</i>	Degrades mucin and supports gut barrier integrity and metabolic health (42-44).	0.88%	0.5-3%
<i>Alistipes putredinis</i>	Ferments amino acids and is involved in immune regulation and inflammation (45).	1.92%	1-3%
<i>Bacteroides fragilis</i>	Breaks down complex carbohydrates and aids in immune regulation (46).	< 0.01%	5-10%
<i>Bacteroides ovatus</i>	Aids in digestion of plant-derived polysaccharides, essential for fiber breakdown (47).	< 0.01%	2-6%
<i>Bacteroides vulgatus</i>	Breaks down polysaccharides and plays a role in immune modulation (48, 49).	< 0.01%	3-7%
<i>Bifidobacterium bifidum</i>	Digests human milk oligosaccharides and supporting gut health (50).	< 0.01%	0.5-3%
<i>Bifidobacterium breve</i>	Plays a role in digesting dietary fiber and producing vitamins (51).	< 0.01%	0.5-4%
<i>Bifidobacterium longum</i>	Supports digestion and immune function, commonly found in infants and adults (52).	< 0.01%	1-5%
<i>Blautia obeum</i>	Produces SCFAs, helps maintain gut pH and suppress pathogens (53).	0.18%	1-4%
<i>Clostridium leptum</i>	Helps in the fermentation of dietary fiber, producing short-chain fatty acids (54).	< 0.01%	3-6%
<i>Coprococcus comes</i>	Produces short-chain fatty acids, playing a role in maintaining gut homeostasis (55).	0.67%	2-5%
<i>Desulfovibrio piger</i>	Produces hydrogen sulfide and is involved in sulfate reduction in the gut (56).	0.54%	0.1-1%
<i>Enterococcus faecalis</i>	Common, but can become pathogenic if overgrown, linked to dysbiosis (57).	< 0.01%	0-1%
<i>Escherichia coli</i>	Common gut resident, but pathogenic strains like O157 can cause disease (58).	0.02%	0-1%
<i>Eubacterium rectale</i>	Butyrate producer important for maintaining gut barrier and reducing inflammation (59).	< 0.01%	3-7%
<i>Faecalibacterium prausnitzii</i>	Major producer of butyrate, a SCFA with anti-inflammatory properties (60).	1.10%	3-7%



Keystone Microbes

Microbe	Description	Result*	Reference*
<i>Fusobacterium nucleatum</i>	Linked to inflammation and gut disease; naturally present in low levels (61).	< 0.01%	0-0.5%
<i>Lactobacillus acidophilus</i>	Common probiotic that supports lactose digestion and gut health (62).	< 0.01%	0.1-5%
<i>Lactiplantibacillus plantarum</i>	Produces lactic acid, supports gut barrier function and has probiotic effects (63).	< 0.01%	0.1-5%
<i>Lactcaseibacillus rhamnosus</i>	Probiotic species known for supporting gut health and immune modulation (64).	0.01%	0.1-3%
<i>Lactococcus lactis</i>	Ferments lactose, often found in fermented dairy, supports gut health (65).	< 0.01%	0.1-2%
<i>Methanobrevibacter smithii</i>	Archaea that produces methane and aids in reducing intestinal hydrogen levels (66).	< 0.01%	0.1-2%
<i>Parabacteroides distasonis</i>	Role in bile acid metabolism and breaking down complex carbohydrates (67).	0.20%	1-3%
<i>Peptostreptococcus anaerobius</i>	Involved in the fermentation of proteins and can become pathogenic in dysbiosis (68, 69).	< 0.01%	0-1%
<i>Prevotella copri</i>	Associated with high-fiber diets and involved in carbohydrate fermentation (70).	< 0.01%	2-6%
<i>Roseburia inulinivorans</i>	Ferments dietary fibers to produce butyrate, supporting gut health (71).	0.17%	2-7%
<i>Ruminococcus bromii</i>	Specializes in breaking down resistant starches, aiding digestion and fermentation (72).	0.12%	1-5%
<i>Ruminococcus gnavus</i>	Ferments sugars and contributes to inflammation in some cases of dysbiosis (73).	< 0.01%	0.1-4%
<i>Streptococcus thermophilus</i>	Ferments lactose, commonly found in dairy products, supports digestion (74).	< 0.01%	0.1-2%
<i>Veillonella parvula</i>	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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