Theriome
The Science of You

Élie® Report

Gut Microbiome - Test Results

[redacted]

Barcode: [redacted]

Report Date:
October 21, 2025

Sample Collection Method:
OMNIgene®•GUT

Analytical Platform:
Illumina NovaSeq 2000

Sequencing and Annotation:
Shotgun whole genome sequencing

Report Reviewed By:
Alex Mohr, PhD

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.*

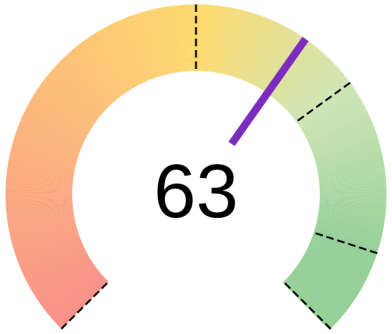
Table of Contents

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, 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. 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.

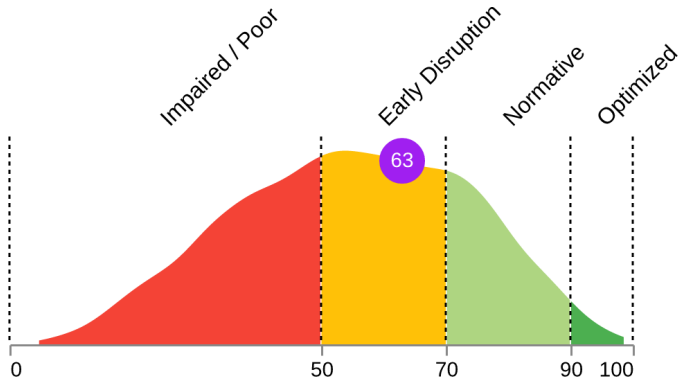
Summary of Results

This page gives you a quick snapshot of your gut health. Overall Score rolls all domains into a single 0–100 result (higher is better), with dashed cutoffs indicating interpretation zones. Where You Fall vs Others shows your position (purple dot) within our reference population. Individual Domain Scores breaks results down by area on the same 0–100 scale using zone-colored dots; risk panels are marked "lower is better." Use this as your at-a-glance overview before exploring the detailed sections that follow.

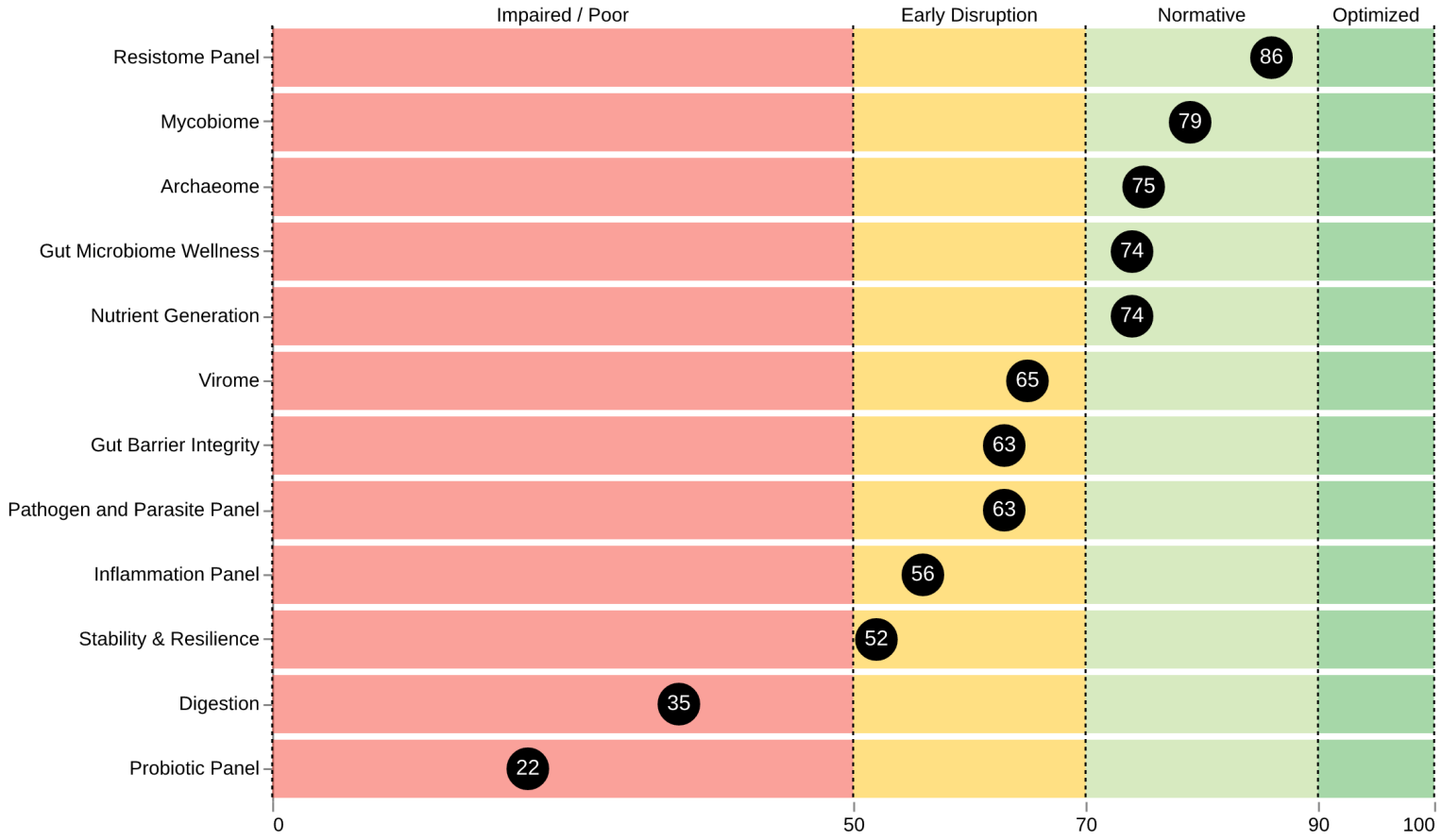
Overall Score



Where You Fall vs Others



Individual Domain Scores



Digital Twin Protocol: Personalized Plan

Next Steps Re-test in: **6** Months

Digital twinning is a data-driven simulation of you. We combine your microbiome results with your survey context to model how diet, lifestyle, and supplement changes may shift key report domains such as Stability & Resilience, SCFA, Barrier, and Digestion. The engine explores many "what if" scenarios and then ranks the most helpful actions for you, presenting clear doses, concise watchouts, and focus tags that match the report pages. This is a clinician-guided decision support tool rather than medical advice on its own, and the plan can be adjusted over time as your needs change. If you experience major health events, for example a course of antibiotics or an acute GI illness, please contact your clinician because your plan and retest timing may need to change.

Recommendation	Dosage/Amount	Focus	Score
Acetate restoration via soluble-fiber base (PHGG first-line) — PHGG reliably raises acetate/total SCFAs with good gas tolerance; addresses impaired acetate (25) and SCFA balance (47.9) and supports bloating relief.	*PHGG 2 g/day × 3 days → 3 g/day × 3 days → 5–6 g/day as tolerated; in water or yogurt.*	SCFA; Motility; Bloating	**5**
Strain-specific probiotic program — low Global Probiotic (22%) + acetate deficit and barrier stress; choose strains with motility, SCFA, and tolerance signals.	*Daily: B. lactis HN019 (1–10B CFU), B. longum BB536 (1–5B), L. plantarum 299v (10^10), L. rhamnosus GG (10^10). Start at ½-dose; add one strain every 4–7 days. Separate from PHGG by 3–4 h.*	Probiotic; SCFA; Motility; Fertility-safe	**5**
Pre-conception one-carbon upgrade — One-carbon 50.1 (early disruption) despite "normative" microbe B-vitamins; support TTC.	*Prenatal with methylfolate 400–800 µg, B12 (methylcobalamin) 250–500 µg, choline 450–550 mg/day (diet+supp).*	Methylation; Fertility-safe	**5**
Urogenital Lactobacillus add-on (TTC-focused) — optional support to encourage vaginal Lactobacillus dominance and immune tolerance during pre-conception; complements main probiotic stack without antimicrobials.	*L. rhamnosus GR-1 + L. reuteri RC-14 (≥2B CFU/day), oral. Separate from PHGG by 3–4 h.*	Urogenital; Probiotic; Fertility-safe	**5**
Redox cofactor repletion — Redox = 0; bolster NADPH/antioxidant tone without TTC-contraindicated botanicals.	*Riboflavin 25–50 mg, Niacinamide 250 mg with meals; Vitamin C 500 mg/day.*	Redox; Inflammation	**5**

Digital Twin Protocol: Personalized Plan

Next Steps Re-test in: **6** Months

Recommendation	Dosage/Amount	Focus	Score
Meal-timing for MMC — 8–10 h sitting + mild constipation pattern; fasting windows support migrating motor complex and reduce gas.	*12-h eating window; 4–5 h between meals (no snacks); 10-min walk post-meal.*	Motility; Bloating	**5**
Kiwifruit (whole or powder) — improves stool form/frequency with low gas burden; supports motility & SCFA.	*2 green kiwifruit/day or powder 5–7 g/day.*	Motility; SCFA; Bloating	**4**
Resistant starch type-2 (RS2) — slow build — augments butyrate while keeping gas manageable; fits Butyrate 64 (ED) & SCFA balance aims.	*Start ¼ tsp raw potato starch nightly; ↑ by ¼ tsp every 5–7 days to 1–2 tsp.*	SCFA; Butyrate; Bloating	**4**
Polyphenol pattern for mucus-niche competition — counter pressure from R. gnavus/B. fragilis; favor saccharolytics.	*Daily berries (1 cup); green tea 1–2 cups (decaf OK); pomegranate arils ½ cup 3×/wk.*	Ecology-shift; Barrier; Inflammation	**4**
Swap solid fats/high-fat meats → EVOO + fish 2×/wk — addresses diet driver; supports bile balance & anti-inflammatory profile.	*Replace butter/tallow with extra-virgin olive oil; salmon/sardines 2×/wk; lean meats otherwise.*	Inflammation; Diet-shift; Bile	**4**
Gentle barrier support (glutamine + zinc foods) — Barrier 63 with good TJ score; nudge mucin synthesis.	*L-glutamine 5 g in water 1–2×/day; zinc-rich foods (pumpkin seeds, beef, oysters 1×/wk).*	Barrier; Mucin	4
Digestive capacity training — Sugar digestion 0, Detox 13, Phytate 38; "one new fiber at a time."	*Introduce 1 new plant/week (½ serving for 3 days → full); keep gas/bloat log.*	Diet-diversity; Digestion	**4**
Ginger for post-prandial bloat — pro-kinetic and TTC-compatible.	*Ginger tea or 550 mg cap with largest meal; up to 1 g/day.*	Motility; Bloating; Fertility-safe	**3**
Magnesium (motility support) — clarify survey units; use gut-friendly salt to improve stool form.	*Magnesium citrate 100–200 mg at night; titrate; cap ~400 mg elemental/day total.*	Motility; Constipation	**3**

Digital Twin Protocol: Personalized Plan

Next Steps Re-test in: **6** Months

Recommendation	Dosage/Amount	Focus	Score
Lactose & excess-fructose trial — aligns with reported triggers; reduce osmotic load while enzymes uptrain.	*2–3 week reduction; re-challenge one at a time; prefer lactose-free/fermented dairy.*	Bloating; Digestion	**3**
S. boulardii guard-rail (optional) — hedge against C. difficile/pathobiont wobble during fiber ramp.	*5–10B CFU/day with meals for 4–8 weeks, then stop.*	Pathobiont-check; Probiotic	**2**
Creatine monohydrate (energy/redox adjunct) — may aid exercise adherence for weight goal under TTC.	*3 g/day; no loading; hydrate.*	Redox; Metabolism; Fitness	**2**
Sleep & stress guardrails — preserve optimized GABA signaling.	*7–8 h/night; 10-min PM wind-down; screen hygiene.*	Neuro-gut; Lifestyle	**2**

Notes: *Priority score indicates clinical importance and expected benefit: 5 cornerstone, 4 strong adjunct, 3 helpful, 2 optional, 1 conditional. Focus tags match the report domains to show why each item matters. Dose uses plain units and Duration reflects a typical trial window before reassessment. This table supports clinical decision-making and is not medical advice on its own; your clinician will adapt it to medical history, medications, allergies, preferences, and cost. Retest timing follows the report's guidance, usually within 2 to 12 months, and may change after major health events such as antibiotics or acute GI illness. If significant side effects occur, pause the item and contact your clinician.*

P.I.L.L.A.R. Approach

The P.I.L.L.A.R. Approach* is a six-phase framework designed to turn complex microbiome findings into a practical, personalized plan. Rooted in systems biology and integrative medicine, it supports phased gut-directed therapy that moves from targeted disruption removal to long-term microbial resilience. Each phase addresses a specific functional layer of the gastrointestinal system. Precision focuses on reducing microbial disruptors and inflammation. Integration supports digestive capacity and nutrient absorption. Lining strengthens the gut barrier and modulates immune reactivity. Load promotes reinoculation with beneficial microbes and restoration of microbial balance. Adaptation targets lifestyle, stress, and circadian influences on the gut. Resilience guides long-term maintenance, microbial diversity, and dietary reintroduction. Within each domain, the report outlines key issues identified from clinical and microbiome data, followed by targeted recommendations. Timing and duration are included to support phased implementation, reduce reactivity, and improve outcomes. The protocol is dynamic and designed to evolve based on progress and retesting.

1. Precision (Targeted Removal & Modulation of Gut Disruptors)	
Issues:	• *Early-disruption resilience (52%) with pressure from R. gnavus, B. fragilis, low-level C. difficile, Pseudomonas.* • *Bloating/gas tied to sugar digestion = 0%, SCFA balance 47.9%, acetate 25%.* • *Suspected triggers: lactose, excess fructose, fructans.*
Recommendations:	• *Polyphenol pattern for mucus-niche competition (berries daily; green tea 1–2 cups; pomegranate ½ cup 3×/wk).* • *Lactose & excess-fructose trial (2–3 weeks, then single-item re-challenges; keep calcium via lactose-free/fermented dairy).* • *(Optional) S. boulardii 5–10B CFU/d for 4–8 weeks during fiber escalation as a guard-rail against pathobiont wobble.* • *Avoid broad antimicrobials during TTC unless clinically indicated.*
Timing & Duration:	• *Start Week 1. Polyphenols 12 weeks; keep during the full program.* • *Micro-elimination sequence Weeks 1–4, then personalize thresholds.* • *S. boulardii Weeks 2–9 if needed only.*

2. Integration (Rebuild Digestive Capacity & Nutrient Absorption)	
Issues:	• *Global Digestion 35% (impaired); sugar digestion 0%, detox 13%, phytate 38%; gas 50% (early disruption).*
Recommendations:	• *PHGG: 2 g/day ×3 days → 3 g/day ×3 days → 5–6 g/day as tolerated (night dosing works well).* • *Resistant starch type-2 (RS2): ¼ tsp nightly; increase by ¼ tsp every 5–7 days to 1–2 tsp.* • *Kiwifruit strategy: 2 green kiwifruit/day or powder 5–7 g/day (motility + SCFA).* • *Digestive capacity training: add one new plant/week (½ serving for 3 days → full), maintain a gas/bloat log.*
Timing & Duration:	• *Begin Week 1 with PHGG; layer RS2 from Week 2; kiwifruit from Week 1.* • *Maintain these 8–12 weeks, then continue the best-tolerated fiber(s) through Month 6.*

P.I.L.L.A.R. Approach

3. Lining (Strengthen Gut Barrier & Reduce Inflammation)

Issues:	• *Barrier 63% (early disruption) with weak SCFA balance; redox 0%; H_2S 25%.*
Recommendations:	• *Glutamine + zinc-rich foods (glutamine 5 g 1–2×/day; pumpkin seeds/beef; oysters 1×/wk).* • *Redox cofactor repletion: riboflavin 25–50 mg, niacinamide 250 mg with meals, vitamin C 500 mg/d.* • *Keep olive-oil-forward, low-solid-fat pattern (see Load/Adaptation for details) to reduce bile-tension signals.*
Timing & Duration:	• *Start Week 1. Reassess symptoms at Week 6; continue through Month 3, then maintain the food pattern to Month 6.*

4. Load (Reinoculate with Beneficial Microbes & Microbial Balance)

Issues:	• *Global Probiotic 22% (impaired); many lactobacilli absent; need acetate and motility support.*

Recommendations:	• *Strain-specific probiotic stack (daily)*
	  ◦ *B. lactis HN019 (1–10B CFU) → transit/motility.*
	  ◦ *B. longum BB536 (1–5B) → acetate-leaning SCFA support.*
	  ◦ *L. plantarum 299v (10^{10}) → bloat/gas modulation.*
	  ◦ *L. rhamnosus GG (10^{10}) → barrier/immune tolerance.*
	  ◦ *Start at ½ dose and add one strain every 4–7 days; separate from PHGG by 3–4 h.*
	• *Urogenital Lactobacillus add-on (optional, TTC-focused): L. rhamnosus GR-1 + L. reuteri RC-14 (≥2B CFU/d), separate from PHGG by 3–4 h.*
	• *Dietary load shift to favor saccharolytics: swap butter/tallow → EVOO, and add fish 2×/wk (sardine/salmon), lean meats otherwise.*

Timing & Duration:	• *Begin stack Week 1 (HN019 first), layer weekly until all four by Week 4; continue to Month 6.* • *Urogenital add-on Weeks 2–12 if chosen.* • *Diet shift starts Week 1, maintain through Month 6.*

P.I.L.L.A.R. Approach

5. Adaptation (Lifestyle & Metabolic Optimization)

Issues:	• *Mild constipation tendency (Bristol ≈3, q1–2 d); 8–10 h/day seated; TTC requires gentle energy/redox support.*
Recommendations:	• *Meal timing for MMC: 12-h eating window; 4–5 h between meals; 10-min walk post-meal.* • *Morning motility routine: warm water → 5 diaphragmatic breaths → 5–10 min walk/hip hinges.* • *Ginger up to 1 g/d with largest meal for post-prandial bloat (PRN).* • *Magnesium citrate 100–200 mg QHS, titrate (cap ~400 mg elemental/d total).* • *Creatine 3 g/d to support training adherence (optional TTC-compatible adjunct).* • *Sleep & stress guardrails: 7–8 h/night; 10-min PM wind-down; screen hygiene.*
Timing & Duration:	• *Start Week 1; ingrain routines by Week 6; maintain through Month 6.*

6. Resilience (Maintain Long-Term Gut Stability)

Issues:	• *Need to consolidate gains in SCFA balance, digestion, barrier, and probiotic tone.*
Recommendations:	• *Keep the best-tolerated two probiotic strains (often HN019 + BB536) beyond Month 3.* • *Maintain PHGG at the lowest effective dose; keep RS2 if well-tolerated.* • *Plant-diversity rotation: 20–30 different plants/week target by Month 6 (use your fiber log to pick winners).* • *Trigger thresholding: re-test lactose/fructans/fructose individually every 4–6 weeks to find your personal dose, not bans.*
Timing & Duration:	• *Months 4–6 focus on consolidation; carry forward into maintenance after the retest.*

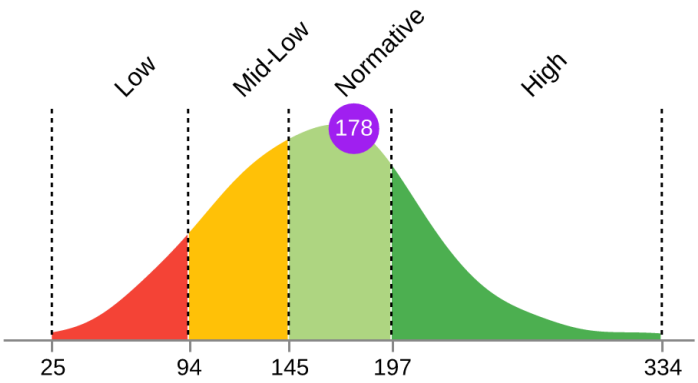
Overview of Gut Microbiome Sample

The Overall Microbiome domain provides a snapshot of your gut microbial ecosystem. First, we display the total number of detected microbial features. Next, a kingdom-level breakdown shows the broad composition of your gut microbiome, typically dominated by Bacteria but also including Archaea, Fungi, and Viruses. Each group plays a distinct role: Bacteria support digestion and immune function; Archaea contribute to gas metabolism; Fungi help regulate gut balance; and Viruses modulate microbial populations. Finally, the top 20 most abundant species—your core microbiome—are highlighted. These are the most dominant taxa in your sample and are likely key contributors to health-related functions such as nutrient metabolism, gut barrier integrity, and immune modulation.

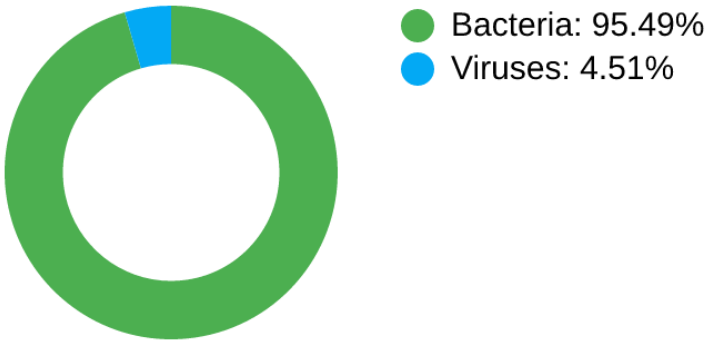
Classification Overview

This is a mixed/metagenomic sample **75.55%** of **8,774,292** reads were classified. An additional **0.01%** of reads were classified, but are non-specific or host reads.

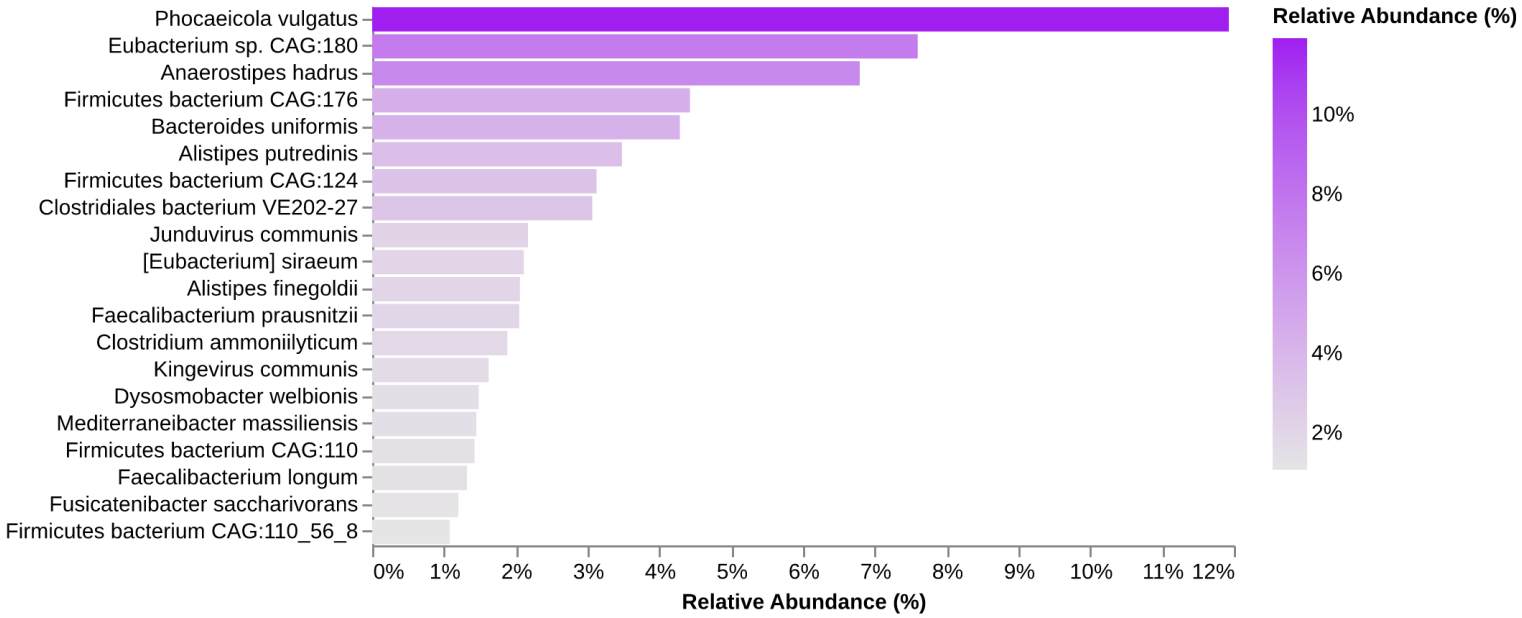
Total number of detected microbial features



Composition snapshot

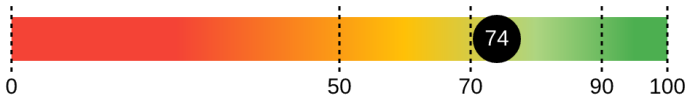


Core microbiome



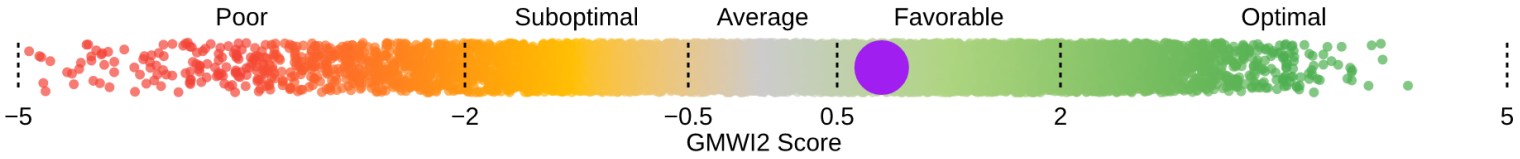
Note: *The density plot for Total Number of Detected Microbial Features represents the distribution of all samples in the reference cohort. The core microbiome includes the most abundant taxa identified and may shift in response to changes in diet, health status, medication use, etc.*

Gut Microbiome Wellness

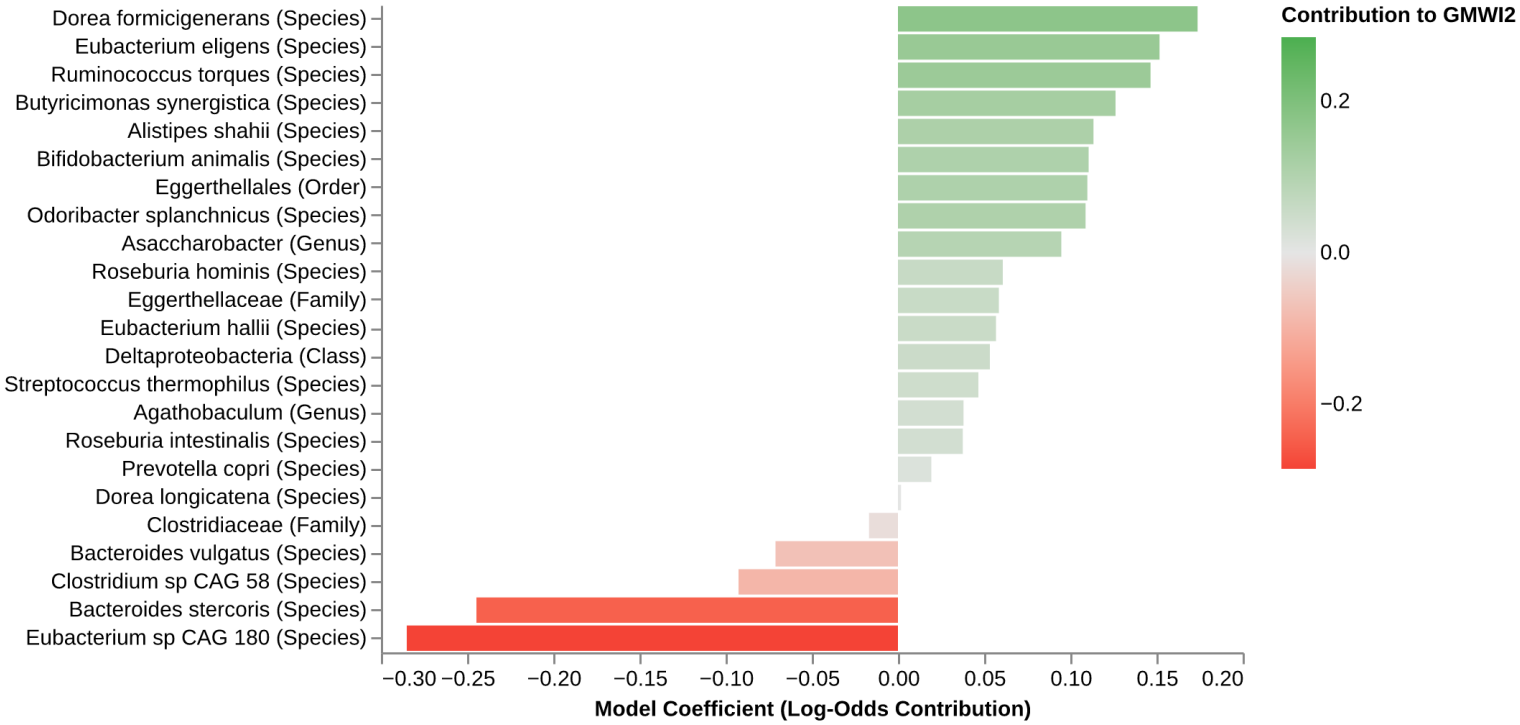


The Gut Microbiome Wellness Index 2 (GMWI2) provides a scientifically-validated holistic assessment of gut health by analyzing the composition of your microbiome to estimate your likelihood of having a clinically dysbiotic community. This indicator is disease-agnostic, meaning it assesses general health 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.

GMWI2 Index Score (Raw Model Output)

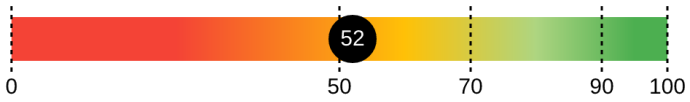


Gut Microbial Signatures Underlying the GMWI2 Index Score



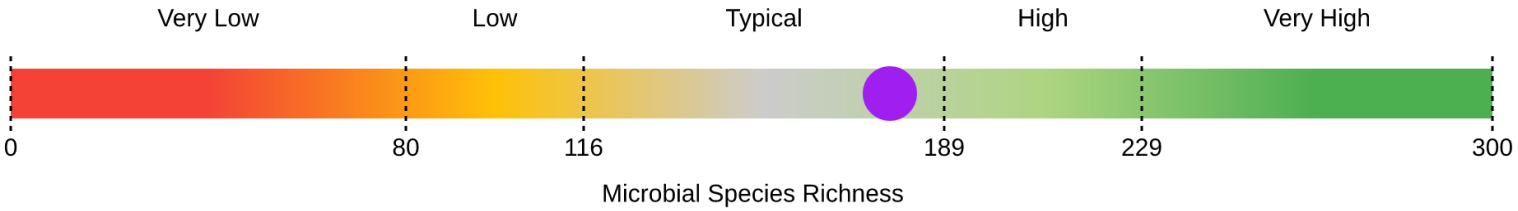
Note: *Bar color indicates the direction of each taxon's contribution to the GMWI2 score. Green bars represent taxa associated with healthier gut profiles (positive contributors), while red bars indicate taxa linked to dysbiosis or disease-associated states (negative contributors).*

Stability & Resilience

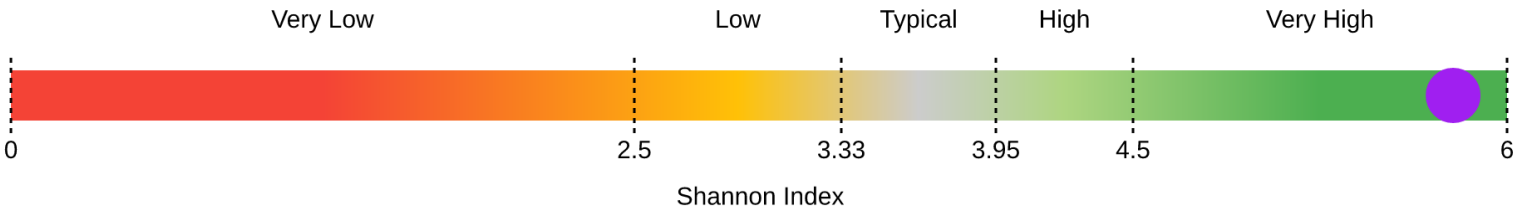


The Microbiome Stability & Resilience Score reflects how well your gut microbiome maintains balance and adapts in response to stress, illness, or dietary change. A stable and resilient microbiome is one that is both diverse (rich in different species and evenly distributed), functionally redundant (with multiple microbes capable of performing essential roles), and ecologically robust (demonstrating strong structural cohesion and adaptability to stressors). This score combines five key features: (1) Richness (number of unique microbial species), (2) Evenness (balance in species abundance), (3) Functional Redundancy (backup capability for microbial functions), (4) Ecological Stability (resistance to disruption), and (5) Adaptive Capacity (presence of stress response pathways). Together, these elements provide a holistic view of how well your microbiome can sustain health, recover from disruption, and support a stable internal environment. A higher score suggests a gut ecosystem that is better equipped to maintain homeostasis and resist dysbiosis.

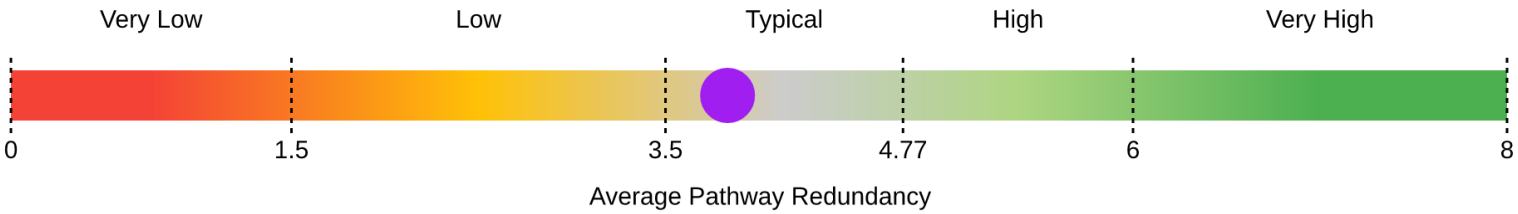
Diversity Richness



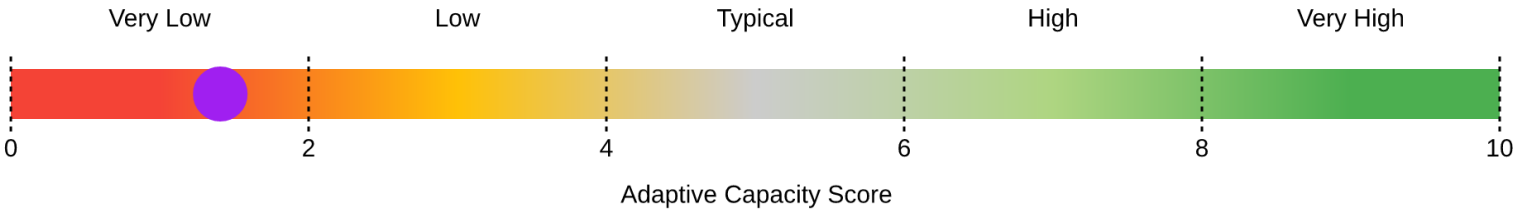
Diversity Balance



Functional Redundancy

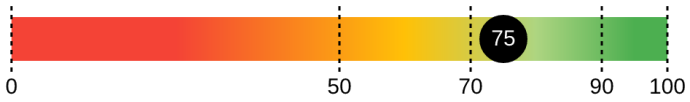


Adaptive Capacity



Note: *The overall score is derived from metagenomic sequencing data and reflects five core features, each rescaled and averaged to generate a 0–100 Stability & Resilience Score. Diversity Richness and Balance are weighted by abundance. Scores should be interpreted in the context of overall health and lifestyle factors.*

Archaeome



The Archaeome encompasses the archaeal members of the gut microbiome. Though generally under 2% of total microbes, these organisms are essential for maintaining fermentation balance and gas metabolism through methane production. In this report we quantify key dimensions; total archaeal abundance, methanogen dominance, methanogenesis pathway activity, and taxonomic evenness. By examining each component alongside the integrated score, you can see not only how many archaea are present, but how effectively they function, how balanced the methanogen population is, and how diverse the community is.

Archaea % of Total Quality Reads

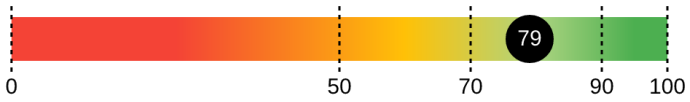
Archaea Composition

No abundance data available

Methane Production Capacity

Note: *"Methanogen status" is determined based on either (a) archaeal reads from known methanogenic genera exceeding 2% of total microbial reads or (b) elevated abundance of the hydrogenotrophic methanogenesis pathway (≥50 RPK). "Methane Production Capacity" reflects a composite of multiple metabolic routes—including H_2 + CO_2, methylated amines (e.g., TMA, MMA, DMA), methanol, acetate, and thiols—using functional pathway data derived from MetaCyc annotations.*

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. Common fungal species such as Candida albicans and Saccharomyces are critical for gut health, with Saccharomyces acting as a beneficial probiotic and Candida becoming pathogenic if overgrown. The balance of the mycobiome is crucial, as disruptions can contribute to conditions such as inflammatory bowel disease (IBD) and other gastrointestinal disorders.

Fungi % of Total Quality Reads

Fungi Composition

No abundance data available

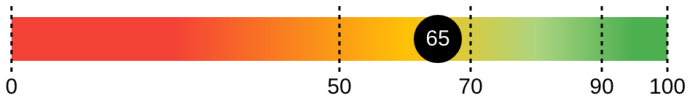
Fungal Carbohydrate Metabolism

Fungal Pathogenic Potential

Note: *The Fungal Overgrowth status badge is determined by evaluating both the total relative abundance of fungal reads (≥0.5%) and the proportional dominance of Candida within the fungal community (≥60%). This classification is based on thresholds derived from population- level data and clinical correlation with dysbiosis symptoms.*

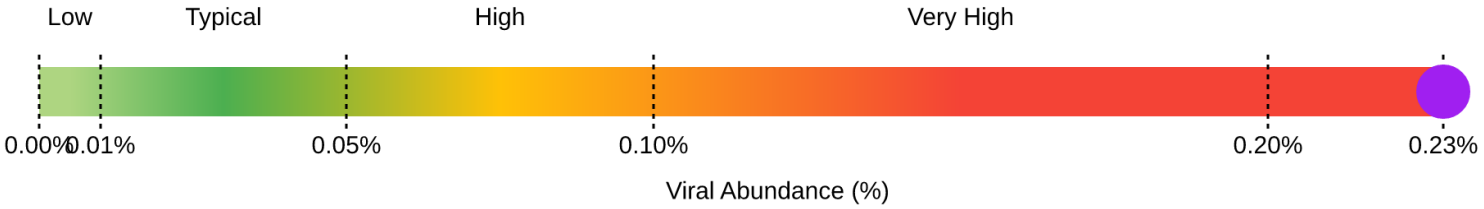
The domains Fungal Carbohydrate Metabolism and Fungal Pathogenic Potential represent composite scores based on the combined relative abundance of multiple MetaCyc pathways. These were selected for their relevance to fungal energy metabolism, host adaptation, redox stress resilience, and ecological behavior in the gut. For scoring and visualization purposes, each composite is plotted against normative distributions and interpreted using traffic-light reference zones.

Virome

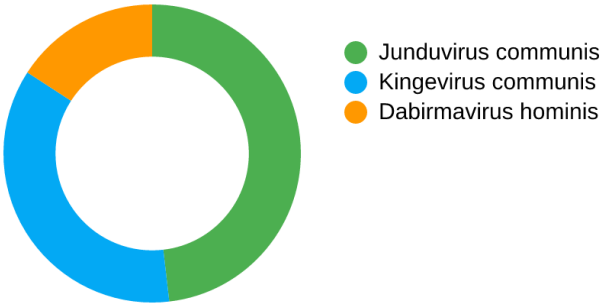


The Virome refers to the collection of viruses within the gut microbiome, including bacteriophages (viruses that infect bacteria) and eukaryotic viruses that interact with human cells. Bacteriophages play a crucial role in regulating bacterial populations, shaping microbial diversity, and maintaining a balanced gut ecosystem. They help control harmful bacterial overgrowth, contributing to gut stability and resilience. The presence of specific enteric viruses can influence gut health and immune function, with some associated with infections or inflammatory conditions.

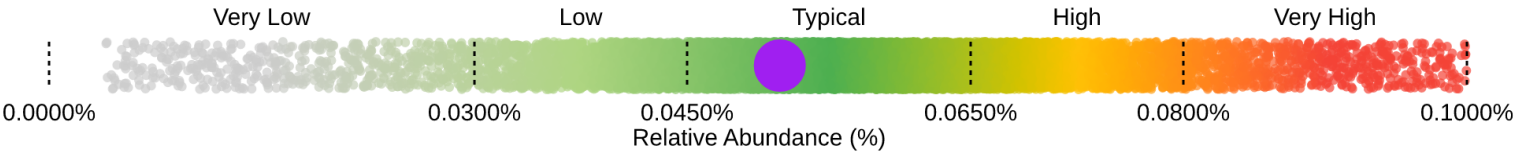
Virome % of Total Quality Reads



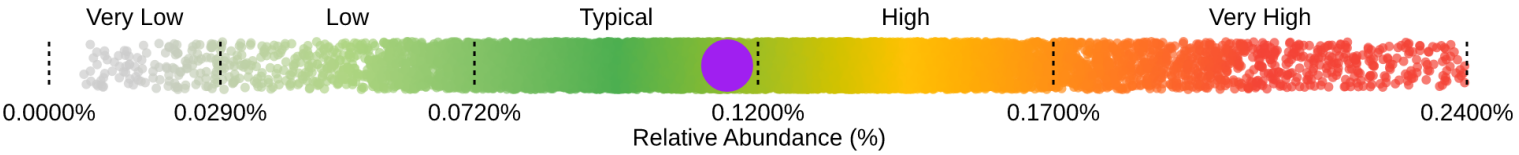
Viral Composition



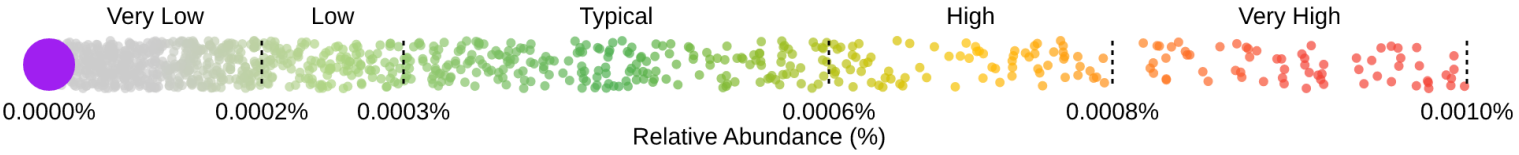
Viral Biosynthetic Activity



Phage-Driven Microbiome Disruption

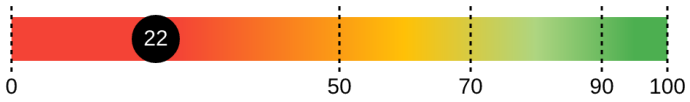


Phage-Driven Gene Exchange



Note: *"CrAss-like Phage Dominant" reflects >50% CrAss-type phage abundance. Functional scores are composites based on viral metabolic pathways involved in biosynthesis, host disruption, and gene exchange.*

Probiotic Panel



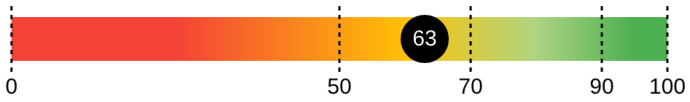
This panel identifies and quantifies beneficial microbial taxa within your gut microbiome that are known for their health-promoting properties. Probiotics, defined as live microorganisms that confer a health benefit to the host when administered in adequate amounts, play a crucial role in maintaining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

		Detected (CPM)	Ref. Min	Ref. Max	% of Ref. Range
Bacterial Taxa	*Akkermansia muciniphila*	0.00	10	5,000	0.00%
	Alkalihalobacillus clausii	0.00	10	100	0.00%
	Bacillus licheniformis	0.00	10	50	0.00%
	Bacillus pumilus	0.00	10	50	0.00%
	Bacillus subtilis	0.00	10	100	0.00%
	Bifidobacterium adolescentis	0.00	10	500	0.00%
	Bifidobacterium animalis subsp. animalis	0.00	10	500	0.00%
	Bifidobacterium animalis subsp. lactis	246.62	50	1,000	20.70%
	Bifidobacterium bifidum	0.00	20	1,000	0.00%
	Bifidobacterium breve	0.00	50	1,000	0.00%
	Bifidobacterium longum subsp. infantis	0.00	50	1,500	0.00%
	Bifidobacterium longum subsp. longum	1.96	100	5,000	0.00%
	Clostridium butyricum	0.00	10	100	0.00%
	Enterococcus faecium	0.00	10	100	0.00%
	Escherichia coli Nissle 1917	0.00	10	100	0.00%
	Faecalibacterium prausnitzii	4,660.17	1,000	10,000	40.67%
	Heyndrickxia coagulans	0.00	10	100	0.00%
	Lacticaseibacillus casei	0.00	10	1,000	0.00%
	Lacticaseibacillus paracasei	0.00	10	1,000	0.00%
	Lacticaseibacillus rhamnosus	0.00	10	1,000	0.00%
	Lactiplantibacillus plantarum	0.00	10	1,000	0.00%
	Lactobacillus acidophilus	0.00	10	1,000	0.00%
	Lactobacillus delbrueckii subsp. bulgaricus	0.00	10	500	0.00%
	Lactobacillus delbrueckii subsp. delbrueckii	0.00	10	500	0.00%

		Detected (CPM)	Ref. Min	Ref. Max	% of Ref. Range
	Lactobacillus gasseri	0.00	10	200	0.00%
	Lactobacillus helveticus	0.00	10	500	0.00%
	Lactobacillus johnsonii	0.00	10	500	0.00%
	Lactobacillus salivarius	0.00	10	500	0.00%
	Lactococcus lactis	65.31	10	1,000	5.59%
	Leuconostoc mesenteroides	1.66	5	100	0.00%
	Levilactobacillus brevis	0.00	10	500	0.00%
	Limosilactobacillus fermentum	0.00	10	500	0.00%
	Limosilactobacillus reuteri	0.00	10	1,000	0.00%
	Oxalobacter formigenes	0.00	10	100	0.00%
	Pediococcus	0.00	5	100	0.00%
	Priestia megaterium	0.00	10	100	0.00%
	Propionibacterium freudenreichii	0.00	10	500	0.00%
	Streptococcus salivarius	16.89	10	1,000	0.70%
	Streptococcus thermophilus	127.16	10	2,000	5.89%
	Veillonella atypica	0.00	10	500	0.00%
Fungal Taxa	*Saccharomyces cerevisiae*	0.00	100	2,000	0.00%
	Kluyveromyces marxianus	0.00	10	500	0.00%

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.

		Detected (CPM)	Ref. Min	Ref. Max	% of Ref. Range
Bacterial pathogens	*Campylobacter*	1.66	0	10	16.59%
	Campylobacter jejuni	0.00	0	10	0.00%
	Citrobacter	0.15	0	10	1.51%
	Citrobacter braakii	0.00	0	10	0.00%
	Citrobacter freundii	0.00	0	10	0.00%
	Clostridioides difficile	12.82	10	1,000	0.28%
	Bacteroides fragilis	17.80	10	1,000	0.79%
	Escherichia coli O157	0.00	10	1,000	0.00%
	Escherichia coli ETEC H10407	0.00	10	1,000	0.00%
	Escherichia coli 042	0.00	10	1,000	0.00%
	Escherichia coli O127	0.00	10	1,000	0.00%
	Klebsiella	1.51	10	1,000	0.00%
	Klebsiella oxytoca	0.00	10	1,000	0.00%
	Klebsiella pneumoniae	0.00	10	1,000	0.00%
	Mycobacterium	4.53	0	10	45.25%
	Mycobacterium avium subsp. Para-tuberculosis	0.00	0	10	0.00%
	Proteus	0.75	0	10	7.54%
	Proteus mirabilis	0.00	0	10	0.00%
	Pseudomonas	11.61	0	10	100.00%
	Pseudomonas aeruginosa	0.00	0	10	0.00%
	Stenotrophomonas maltophilia	0.00	0	10	0.00%
	[Ruminococcus] gnavus	27.45	0	10	100.00%
	Salmonella enterica	0.00	0	10	0.00%

		Detected (CPM)	Ref. Min	Ref. Max	% of Ref. Range
	Shigella	0.00	0	10	0.00%
	Staphylococcus aureus	1.51	0	10	15.08%
	Vibrio cholerae	0.00	0	10	0.00%
	Vibrio parahaemolyticus	0.00	0	10	0.00%
	Yersinia enterocolitica	0.00	0	10	0.00%
Fungal pathogens	*Aspergillus*	0.00	0	10	0.00%
	Candida albicans	0.00	0	10	0.00%
Viral pathogens	*Astrovirus*	0.00	0	10	0.00%
	Cytomegalovirus	0.00	0	10	0.00%
	Adenovirus sp. F41	0.00	0	10	0.00%
	Human herpesvirus 4 type 2	0.00	0	10	0.00%
	Human bocavirus 1	0.00	0	10	0.00%
	Human betaherpesvirus 6	0.00	0	10	0.00%
	Human betaherpesvirus 7	0.00	0	10	0.00%
	Human gammaherpesvirus 8	0.00	0	10	0.00%
	Human parvovirus B19	0.00	0	10	0.00%
	Norovirus	0.00	0	10	0.00%
	Rotavirus	0.00	0	10	0.00%
	Sapovirus	0.00	0	10	0.00%
Protist pathogens	*Neobalantidium coli*	0.00	0	10	0.00%
	Blastocystis hominis	0.00	0	10	0.00%
	Cryptosporidium	0.00	0	10	0.00%
	Cyclospora cayetanensis	0.00	0	10	0.00%
	Entamoeba histolytica	0.00	0	10	0.00%
	Giardia lamblia	0.00	0	10	0.00%
	Cystoisospora belli	0.00	0	10	0.00%
Atypical & Extraintestinal (0–10 CPM)	*Borrelia*	0.00	0	10	0.00%
	Anaplasma phagocytophilum	0.00	0	10	0.00%
	Chlamydia pneumoniae	0.00	0	10	0.00%

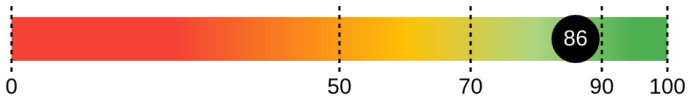
		Detected (CPM)	Ref. Min	Ref. Max	% of Ref. Range
	Coxsackievirus	0.00	0	10	0.00%
	Mycoplasma	52.19	0	10	100.00%
Helminth Parasites	*Ascaris lumbricoides*	0.00	0	10	0.00%
	Enterobius vermicularis	0.00	0	10	0.00%
	Fasciola hepatica	0.00	0	10	0.00%
	Strongyloides stercoralis	0.00	0	10	0.00%
	Schistosoma mansoni	0.00	0	10	0.00%
	Taenia	0.00	0	10	0.00%
	Toxocara	0.00	0	10	0.00%
	Trichuris trichiura	0.00	0	1	0.00%

Note: *This panel leverages shotgun metagenomic sequencing to sensitively detect and quantify pathogenic bacteria, fungi, viruses, protists, atypical organisms, and helminths in stool. Reported values are Counts Per Million (CPM), reflecting the estimated pathogen or parasite genome copies per million total microbial reads. Each feature is compared against a Reference Range derived from healthy-control data: For most pathogens, healthy microbiomes exhibit < 10 CPM or are "Typically undetectable." Sustained detection above these thresholds may indicate active colonization, infection, or gut barrier compromise.*

Key Considerations:

- *Infection Threshold: CPM values above the upper limit of the reference range (e.g., > 1,000 CPM for select opportunistic bacteria) suggest a higher likelihood of clinically significant infection or overgrowth.*
- *Clinical Correlation: Always interpret pathogen load in light of patient symptoms, immune status, and other laboratory findings (e.g., toxin gene assays, serologies, inflammatory markers).*
- *Caveats & Limitations: (1)Low-level detections (< Ref_Min) often reflect background or transient exposure—not necessarily infection; (2) Cross-contamination, index bleed, and database misassignments can produce false positives at very low CPM; (3) This panel is not a stand-alone diagnostic; positive findings should prompt confirmatory testing using targeted assays (e.g., PCR, culture, antigen tests).*

Resistome Panel

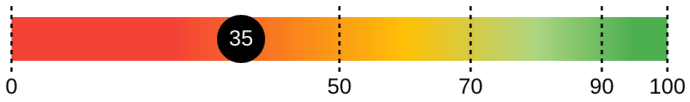


This section summarizes the results of the Antimicrobial Resistance (AMR) Panel. This panel is comprised of a total of 8733 sequences to assess the presence of 1448 antimicrobial resistance gene groups across 59 antibiotic classes. AMR occurs when bacteria and fungi develop the ability to defeat drugs 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.

		Status*	Accession	Coverage / Depth / ID
Drug Class	**Gene**			
Aminoglycosides	*A16S*	Probable	CP020418:383737-385288	81.95% / 1372.86× / 93.97%
	ANT6	Probable	NG_047378:28-894	91.58% / 195.96× / 92.20%
Beta-lactams	*CFX*	Present	U38243:149-1115	97.31% / 594.41× / 97.44%
	CBLA	Probable	NG_047624:101-991	99.33% / 286.08× / 94.25%
MLS	*LNUA*	Present	NG_047920:101-613	100.00% / 1410.33× / 97.99%
	MEFE	Present	AF251288.1:794-2000	100.00% / 1748.67× / 98.92%
	MLS23S	Probable	NR_076234.1:0-2900	85.52% / 2843.45× / 93.96%
Tetracyclines	*TETQ*	Present	L33696.1:825-2750	100.00% / 2467.55× / 99.09%
	TETW	Present	EU434751.1:642-2578	97.83% / 658.96× / 98.59%
Trimethoprim	*DFRF*	Probable	AF028812:392-887	84.24% / 344.65× / 92.80%

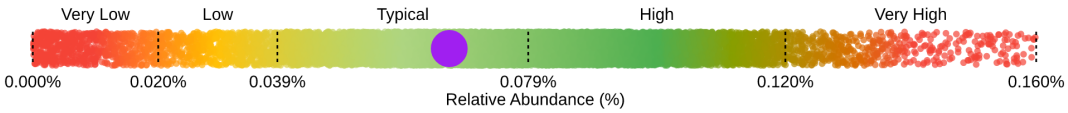
Note: *For each gene, the status is called as 'Present' if coverage is >=85% and identity is >=95%, and 'Probable' if coverage is >80% and identity is >90%. The coverage, depth, and identity statistics for each resistance gene are calculated as a weighted average of the corresponding markers with the highest detection status. These statistics are calculated from a sequence alignment to a curated reference database. This Resistome Panel is for research use only and is not intended for clinical diagnosis or treatment decisions.*

Digestion

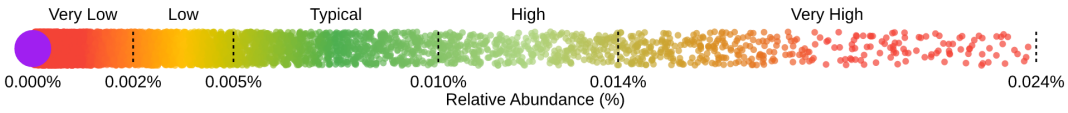


The Digestion section integrates seven key microbial functions—polysaccharide degradation, protein fermentation, gas production, sugar and lactose digestion, fat metabolism, phytate breakdown, and detoxification—to provide a comprehensive view of your gut community's capacity to process and absorb nutrients. By quantifying the relative abundance of these pathways and translating them into subdomain scores (0–100), we can pinpoint strengths (e.g., robust fiber-degrading enzymes or efficient sugar utilization) and weaknesses (e.g., excessive proteolysis or gas-generating potential) that may underlie common symptoms like bloating, malabsorption, or nutrient deficiencies. These individual scores are then combined into a Global Digestion Score, which offers a single, intuitive metric of overall digestive resilience. Together, these data empower targeted dietary and therapeutic strategies to restore balance, enhance energy harvest, and support long-term gut and systemic well-being.

Complex Carbohydrate Degradation Capacity



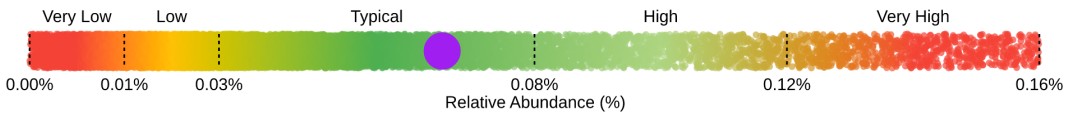
Protein Fermentation Capacity



Gas Production

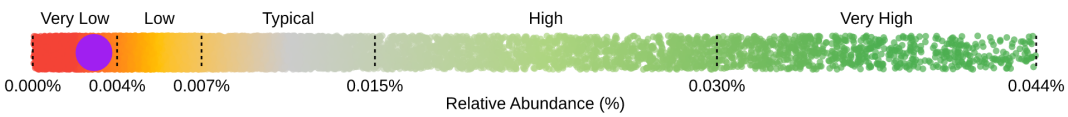
Lactose and Simple Sugar Digestion

Fat Metabolism



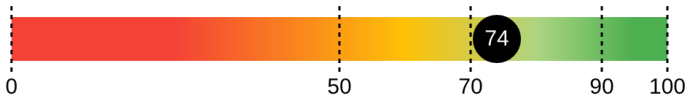
Phytate Metabolism

Detoxification Capacity



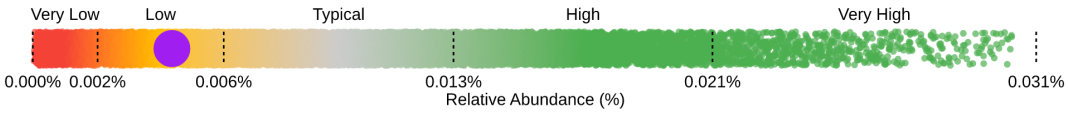
Note: *These subdomain scores are intended to guide clinical interpretation in conjunction with patient history, dietary intake, and other laboratory findings. Extreme values warrant further investigation or specialist referral.*

Nutrient Generation

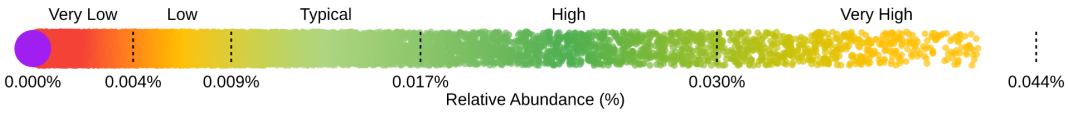


The Nutrient Generation section quantifies eight core biosynthetic functions of your gut microbiome - SCFA production (butyrate, acetate, propionate, lactate) that fuels colonocytes, modulates lipid/glucose metabolism, and dampens inflammation; Amino-acid synthesis supplying both essential and non-essential amino acids for protein turnover, tissue repair, and neurotransmitter precursors; B-vitamin synthesis (B_1–B_{12}, folate, biotin) providing cofactors for energy metabolism, red-blood-cell formation, and DNA repair; Vitamin K production supporting clotting and bone health; and Polyamine synthesis (putrescine, spermidine, spermine) which drives epithelial proliferation and mucosal resilience. By measuring the relative abundance of these pathways, this section reveals how effectively your microbiome contributes to nutrient availability, barrier integrity, and systemic physiology—and helps pinpoint which functions may benefit from targeted dietary, prebiotic, or probiotic interventions.

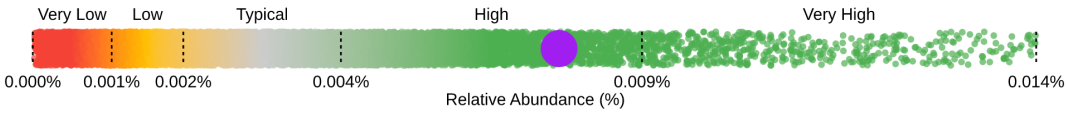
Butyrate Production



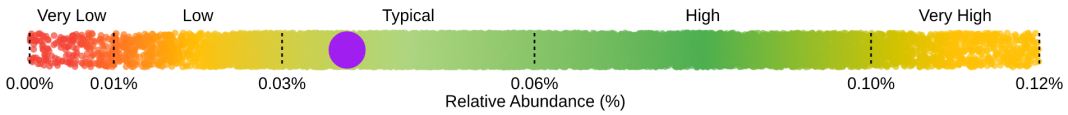
Acetate Production



Propionate Production

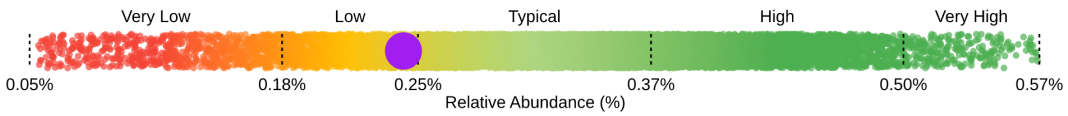


Lactate Production

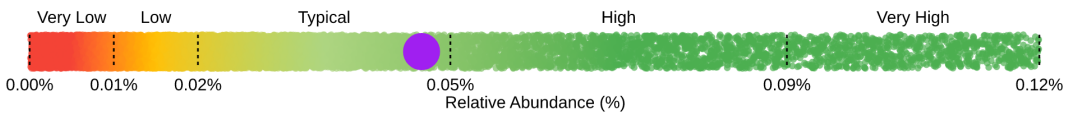


Amino Acid Synthesis

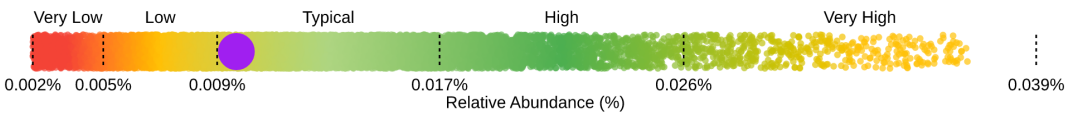
B-Vitamin Synthesis Capacity



Vitamin K Production

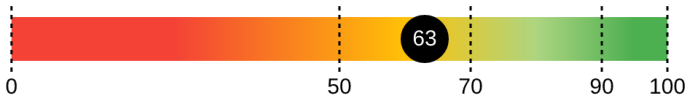


Polyamine Synthesis



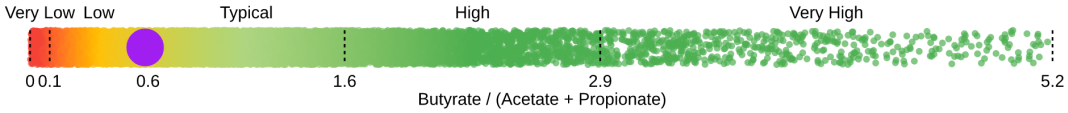
Note: *These subdomain scores are intended to guide clinical interpretation in conjunction with patient history, dietary intake, and other laboratory findings. Extreme values warrant further investigation or specialist referral.*

Gut Barrier Integrity

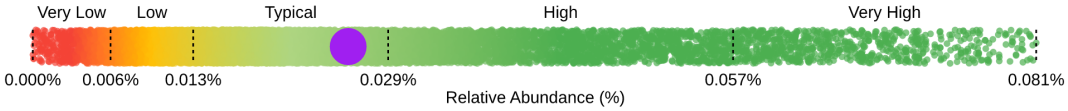


The Gut Barrier Integrity section brings together eight critical microbial functions to assess how the gut lining is supported or compromised: SCFA Balance (the ratio of butyrate versus acetate + propionate, which promotes tight-junction health); Mucin Synthesis (production of the mucus layer and its biochemical precursors, key for physically protecting epithelial cells); Mucin Degradation (microbial breakdown of mucin glycoproteins, which can thin the mucus barrier); Pathogen-Associated Molecular Pattern–Mediated Tight-Junction Disruption (increasing paracellular permeability); Ammonia Production (toxic deamination byproducts that injure enterocytes); Cadaverine Biosynthesis (loosens junctions); β-Glucuronidase Capacity (exposing the mucosa to toxins); and p-Cresol Production (tyrosine-derived cytotoxin that damages epithelial integrity). By scoring each of these domains and combining them into a single Barrier Integrity Index, we capture the balance between protective activities and damaging processes, providing a comprehensive portrait of "leakiness" risk versus barrier resilience.

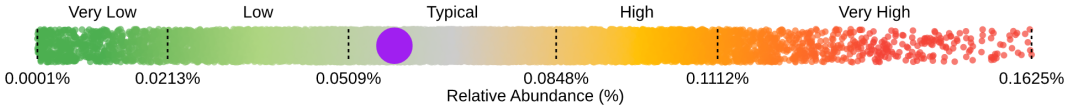
SCFA Balance



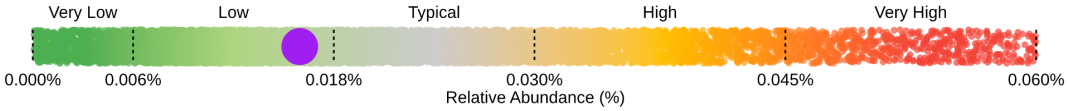
Mucin Synthesis



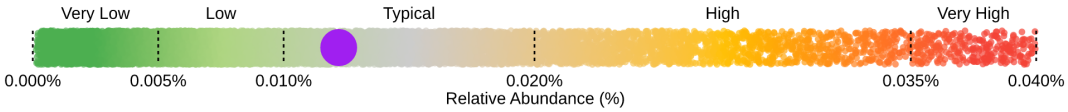
Mucin Degradation



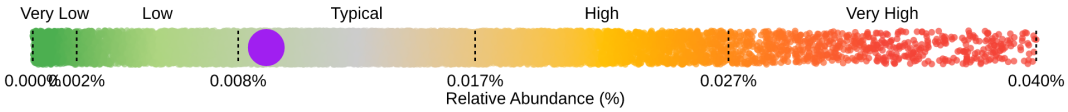
Ammonia Production



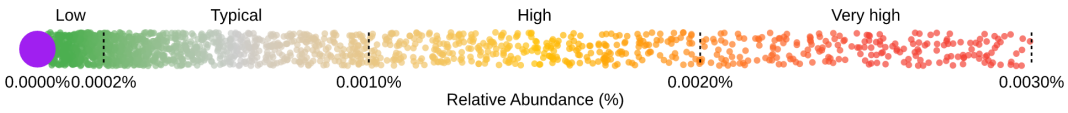
Cadaverine Biosynthesis



β-Glucuronidase Capacity



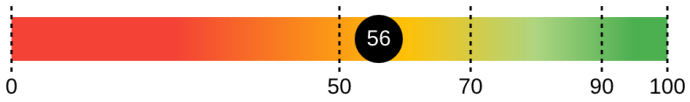
p-Cresol Production



PAMP-mediated TJ Disruption

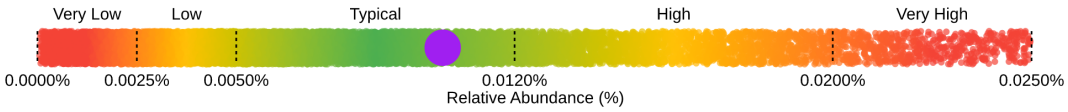
Note: *These subdomain scores are intended to guide clinical interpretation in conjunction with patient history, dietary intake, and other laboratory findings. Extreme values warrant further investigation or specialist referral.*

Inflammation Panel

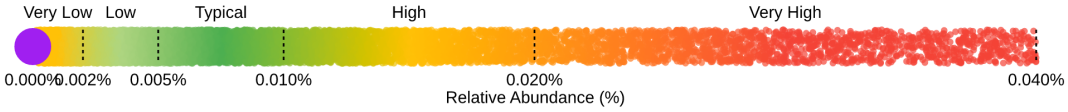


The Inflammation Panel evaluates gut microbiome functions and metabolites that influence the body's inflammatory balance. It focuses on six key pathways: bile acid metabolism, hydrogen sulfide (H_2S) production, lipopolysaccharide (LPS) production, redox cofactor balance, GABA production, and one-carbon/methyl donor metabolism. These pathways collectively affect immune signaling, oxidative stress, gut barrier function, and systemic inflammatory tone. Chronic low-grade inflammation, often fueled by imbalances in these microbial processes, has been linked to conditions such as autoimmune disease, metabolic syndrome, cardiovascular disease, and gut disorders like inflammatory bowel disease. By profiling both pro-inflammatory and anti-inflammatory activities, this panel highlights potential microbial contributions to inflammation, supporting targeted strategies to restore balance and promote immune resilience.

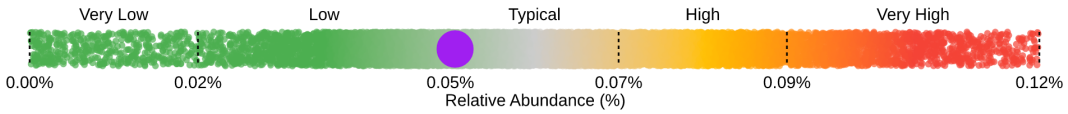
Bile Acid Metabolism



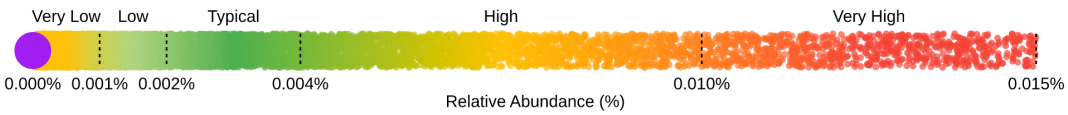
Hydrogen Sulfide (H2S) Production



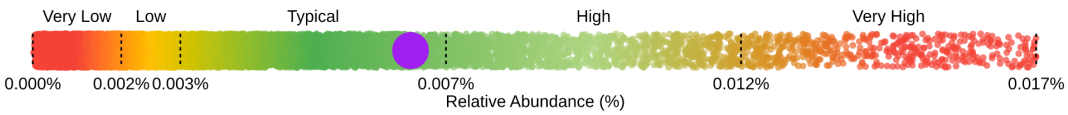
LPS Production



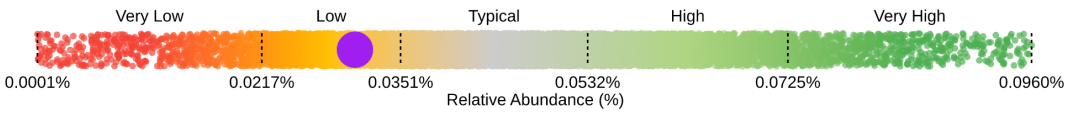
Redox Cofactor Balance



GABA Production



One-Carbon / Methyl Donors



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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 Kapa HyperPlus Library Preparation Kit, followed by amplification and purification.
4. **Sequencing Platform and Parameters:** Shotgun metagenomic sequencing was performed on the Illumina NextSeq 2000 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 2-3 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, a highly sensitive and rapid k-mer classification algorithm is utilized to map sequencing reads back to its database, which includes more than 148,000 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. 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 diversity, were calculated to assess community richness and composition. Statistical analysis and visualization were performed using Python. 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.