

UPCOMING EVENTS

**ADHD in Perimenopause:
The Estrogen-Dopamine
Connection and Clinical
Implications**

Presented by Ruth Hobson, ND
July 1, 2026 at 12 PM Pacific

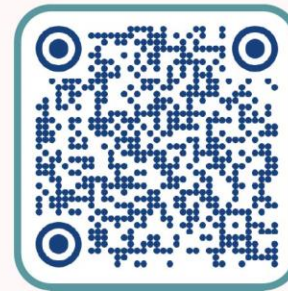
**The Estrobolome:
How Gut Dysbiosis and Liver
Detoxification Shape Estrogen
Balance**

Presented by Dr. Dan Kalish, DC
July 7, 2026 at 12 PM Pacific

Visit doctorsdata.com/Register-for-Webinars



WILL BEGIN SHORTLY

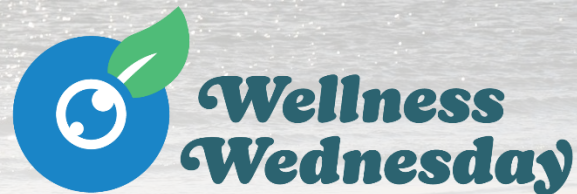


MORE WEB EVENTS



Harnessing the Microbiome to Boost GLP-1: Insights from the GI360™

Jeannie Gorman, MS, CCN





Qualifications-and-Licensing

For 50+ years, DDI has been recognized and respected by many American and European regulating and governing agencies.

- ✔ Doctor's Data is a **federally licensed CLIA laboratory** with appropriate state certifications and licenses.
- ✔ We participate in quality assurance and proficiency testing programs including those offered by the **College of American Pathology (CAP), Centers for Disease Control (CDC), New York State Department of Health, Le Centre de Toxicologie du Quebec and others.**
- ✔ DDI is an approved provider for the **Joint Research Centre of the European Commission: Reference Material Unit**
 - ✔ We assist with the certification of reference materials
 - ✔ We do the same for the NY State Department of Health

Licenses and Certifications

American Proficiency Institute Certificate	
Clinical Laboratory Improvement Act (CLIA) Certificate #14D0646470. Categories: Routine Chemistry, Toxicology, Bacteriology, Mycology, Parasitology and General Immunology.	
College of American Pathologists	
DEQAS Vitamin D Certificate	
EQUIP Certificate	
European Commission Joint Research Center Validated Supplier for Trace Elements	
New York State Department of Health PFI #5449. Categories: Clinical Chemistry (routine), Toxicology (Blood Lead), Mycology, Parasitology and Hematology.	
Maryland Department of Health Laboratory Permit #795. Categories: Clinical Chemistry (routine), Toxicology (Blood Lead, Heavy Metals), Microbiology, Bacteriology, Mycology and Parasitology.	
Ohio Department of Health Laboratory Approval #C10074.	
Pennsylvania Department of Health Clinical Laboratory Permit, Lab ID Number 031847.	
State of California Clinical Laboratory License, CLIA Number 14D0646470.	
State of Rhode Island and Providence Plantations - DEPARTMENT OF HEALTH - License #LC000421.	



Qualifications-and-Licensing

Today's Session Objectives:

- 🌱 Describe the GI360's™ comprehensive assessment of microbiome composition
- 🌱 Identify patients on, or considering, GLP-1 agonist or incretin-based therapy with metabolic dysfunction, appetite dysregulation, or suboptimal clinical response for stool testing
- 🌱 Interpret GI360™ results in the context of imbalances leading to impaired endogenous GLP-1 signaling and metabolic response
- 🌱 Implement targeted interventions to support GLP-1 signaling and treatment outcomes
- 🌱 Explore a variety of testing and retesting to monitor microbiome changes and metabolic signaling in patients on GLP-1/incretin-based therapies

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Extensive Assessment of the
GI MICROBIOME

LEARN MORE



About

ABOUT THE TEST

SAMPLE REPORT

RESOURCE GUIDE

COLLECTION
INSTRUCTIONS

PUBLICATIONS

POSTERS AND
ABSTRACTS

VIDEOS AND
PODCASTS

FREQUENTLY ASKED
QUESTIONS

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RESOURCE GUIDE





GI360™ Stool Test Profile Options

	GI360™	GI360™ ESSENTIALS	GI360™ MICROBIOME
Microbiome Diversity and Abundance; PCR	✓	✓	✓
Viruses, Pathogens, and Parasites; PCR	✓	✓	
Expanded Parasitology; Microscopy	✓	✓	
Bacterial and Fungal Culturomics w/ Direct Susceptibilities; MALDI-TOF MS	✓	✓	
Stool Chemistries	✓		
Beta-Glucuronidase	✓		



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COLLECTION INSTRUCTIONS

PPIs H2 blockers are contraindicated for H. pylori Antigen testing to avoid false negative.



3 IMPORTANT PREP INFO

BEFORE YOU START: Please read all of the instructions carefully before beginning. Consult your physician for specific instructions and before stopping any medications.

DISCONTINUE THE FOLLOWING

2 weeks before test

Antibiotics, antiparasitics, antifungals, or probiotic supplements, proton pump inhibitors (PPIs) and Bismuth

2 days before test

Aspirin and other NSAIDs, digestive enzymes, laxatives (particularly mineral oil, castor oil, and glycerin enemas/suppositories), activated charcoal, betaine HCl, antacids or bentonite clay

OTHER INFORMATION

Do not collect samples when there is active bleeding from hemorrhoids or menstruation

Wait at least 4 weeks from a colonoscopy or barium enema before collecting

Do not contaminate the stool with urine or water

Patient Stool Testing Indications

🌱 Known GI diagnoses with symptoms:

- IBD, IBS, Enteropathogens

🌱 Chronic Metabolic Conditions:

- Diabetes, Obesity, Metabolic Syndrome

🌱 Immune Dysfunction:

- Autoimmunity, MCASynd, prolonged SARS-Cov-2

🌱 Chronic Inflammatory Diseases:

- CVD, Alzheimer's, arthritis, cancer

🌱 Mental Health:

- Chronic stress, depression, anxiety, cognition
- Other gut-brain axis conditions

🌱 Low Soluble Fiber Diets:

- Processed foods, Low FODMAP, Keto, Vegan/Vegetarian, Carnivore, incretin-based therapy use

🌱 General Health Concerns:

- Fertility and hormonal health
- Obesity and/or use of incretin-based agonists
- Liver, adrenal and thyroid dysfunction
- Iron malabsorption

🌱 Optimal health and longevity

Pharmacomicrobiomic Effects

- 🌿 **Incretin-based receptor agonists:** Increases in *Akkermansia spp.*, *Faecalibacterium prausnitzii*, *Eubacterium*, *Bifidobacterium spp.*
- 🌿 **Proton Pump Inhibitors (PPIs):** Raise gastric/intestinal pH and alter bile acid metabolism, promoting overgrowth of *Clostridioides difficile* and *Enterococcus spp.*
- 🌿 **Metformin (Glucophage):** Enriches short-chain fatty acid–producing taxa (e.g., *Akkermansia muciniphila*, *Bifidobacterium spp.*), while also increasing *Escherichia coli*, which may contribute to GI intolerance. This shift has been described as a potential “beneficial dysbiosis” associated with cardiometabolic improvement (Farup et al., 2018).
- 🌿 **Non-steroidal anti-inflammatory drugs (NSAIDs):** Disrupt mucosal integrity, reduce microbial diversity, and increase pro-inflammatory signaling.
- 🌿 **Antipsychotics (e.g., olanzapine, risperidone):** Shift microbiota toward increased Firmicutes and reduced *Bifidobacterium* and *Lactobacillus spp.*, patterns associated with metabolic dysregulation.

Pharmacobiomic Effects (cont'd)

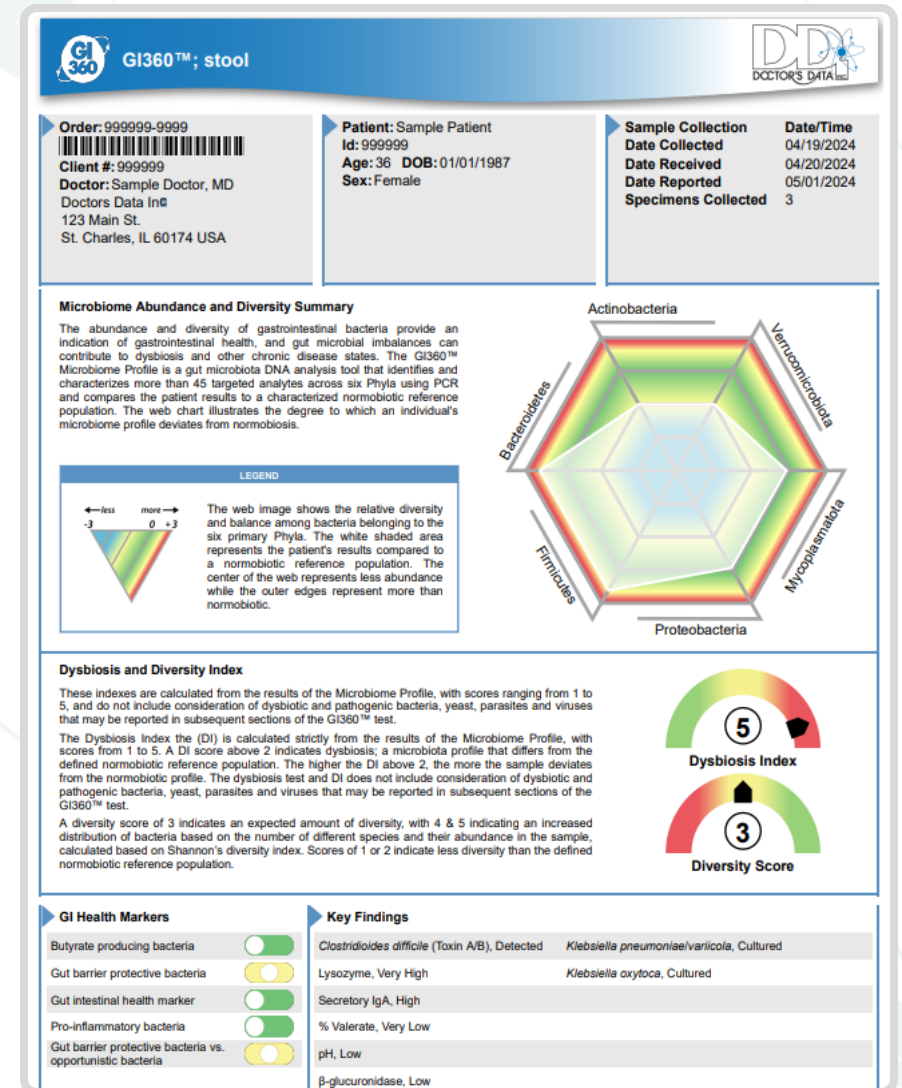
- 🌿 **Statins (HMG-CoA reductase inhibitors):** Modulate bile acid metabolism and microbial enzymatic activity, influencing drug metabolism and trimethylamine N-oxide (TMAO) production.
- 🌿 **Selective serotonin reuptake inhibitors (SSRIs):** Exhibit antimicrobial activity and can disrupt microbial membrane integrity, leading to shifts in community structure and oxidative stress responses.
- 🌿 **Hormonal contraceptives (BCPs):** Emerging evidence suggests gut microbiome composition and timing of exposure may influence susceptibility to mood-related and metabolic effects.
- 🌿 **Cannibus (CBD), Tetrahydrocannabinol (THC):** Strongly bidirectional; may increase *Akkermansia spp.*, *Faecalibacterium prausnitzii spp.*



GI360™

Bridging the diagnostic gap

- PCR analysis for the abundance and diversity of key bacterial populations of the microbiome
- Standardized testing and scoring system to differentiate normobiotic vs. dysbiotic
- Reliable PCR detection of clinically relevant pathogenic bacteria, viruses and parasites
- Microbiology culture using MALDI-ToF ID allows Standardized susceptibility testing of dysbiotic bacteria and yeast
- Comprehensive parasitology by microscopy
- Advanced stool chemistry analysis to assess gastrointestinal function





PCR for Clinical Microbiology

Validated, targeted, and clinically actionable



- Amplifies specific DNA targets ("barcodes")
- Requires DNA extraction; results depend on validated primer/probe sets
- High analytical sensitivity and specificity
- FDA-cleared platforms provide standardized, reliable, reproducible detection
- Ideal for quickly identifying pathogenic bacteria, parasites, and viruses



Multiplex PCR, Laboratory Validations

Technical verification

Parameter	Results
Repeatability	2.6% CV
Reproducibility	4.2% CV

DDI's PCR Platform Reliability & Standards

- 🔍 Rapid, reproducible results within and across labs
- 🔍 **FDA-approved & CE-marked probes** ensure clinical validity
- 🔍 <5% variability between runs, confirmed in international labs
- 🔍 Minimizes **false positives and false negatives** for reliable interpretation



Evidence-Based Microbiome Testing

- PCR-based microbial detection methods vary in **accuracy** across the industry.
- DDI provides **validated** assay performance, including sensitivity, specificity, reproducibility, and clinical relevance. Published validation and independent peer review ensure scientific rigor, defensible targets, and reliable reporting algorithms.
- Peer-reviewed validation **elevates** microbiome testing from informational to clinically actionable, supporting more precise care and therapeutic planning



EVALUATION OF GUT BACTERIA: SEQUENCING VS. qPCR

Sequencing

- Broad view of all DNA
- **Answers “Who’s all there?”**
- Sequences random DNA fragments to assemble entire genomes
- Ideal for discovering new genes or genetic potential
- *Not diagnostic*
- *Lack established reference ranges*

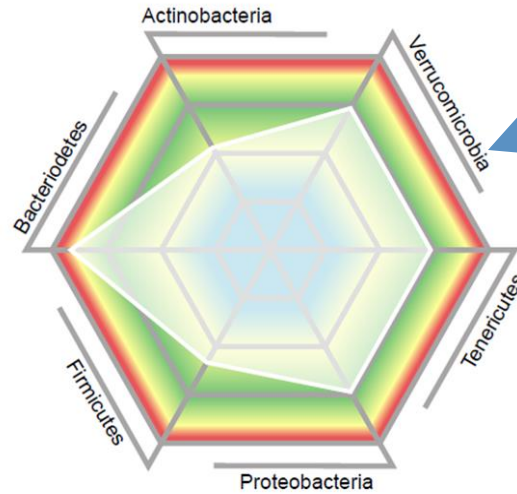
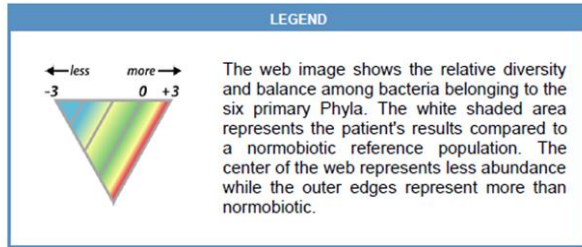
qPCR

- Targeted amplification of specific DNA
- **Answers “Is it there?”**
- High sensitivity, **specificity**
 - Pathogen identification
- Validated PCR methods support precision care and improve confidence in clinical planning

GI360™ Microbiome Abundance and Diversity

Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.



Patients results at a glance compared to the normobiotic reference population. Deviation from a hexagonal shape indicates variant abundance and diversity within the microbial community.

Dysbiosis and Diversity Index

These indexes are calculated from the results of the Microbiome Profile, with scores ranging from 1 to 5, and do not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

A dysbiosis score above 2 indicates dysbiosis; a microbiota profile that differs from the defined normobiotic reference population. The higher the score above 2, the more the sample deviates from the normobiotic profile.

A diversity score of 3 indicates an expected amount of diversity, with 4 & 5 indicating an increased distribution of bacteria based on the number of different species and their abundance in the sample, calculated based on Shannon's diversity index. Scores of 1 or 2 indicate less diversity than the defined normobiotic reference population.



There are different types of dysbiosis. The Dysbiosis Index is calculated strictly from the Microbiota Abundance analytes, and does not include specific pathogenic and dysbiotic bacteria, yeast, parasites and viruses that may be identified in subsequent sections of the GI360™.

PCR Detection of Clinically Relevant Species



Actinobacteria Phyla

- 🌱 Bifidobacteria family

Bacteroidetes Phyla

- 🌱 Pro-inflammatory
- 🌱 Diet driven

Firmicutes Phyla

- 🌱 Butyrogenic species
- 🌱 Lactobacillus family
- 🌱 Phascolarctobacteria spp.

Proteobacteria Phyla

- 🌱 Pro-inflammatory
- 🌱 Diet driven

Mycoplasmata Phyla

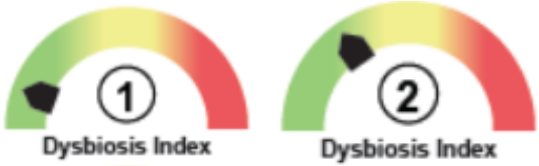



Verrucomicrobiota Phyla

- 🌱 *Akkermansia spp.*



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Dysbiosis Index (DI) Score: Clinical Interpretation

DI Score	Interpretation	Clinical Significance	Clinical Action
	Normobiotic	Microbiome composition consistent with a healthy reference population; balanced diversity and abundance	Expected adaptation or minimal support
	Borderline	Minor deviations from normobiosis	Probiotic, soluble fiber, diet intervention
	Moderate Dysbiosis	Significant deviation from normobiosis; functional collapse; increased inflammation markers	Address inflammation, probiotic, soluble fiber, diet intervention
	Severe Dysbiosis	Major deviation from normobiosis; likelihood of pathogenic or opportunistic overgrowth; mucosal risk	All the above, escalate evaluation

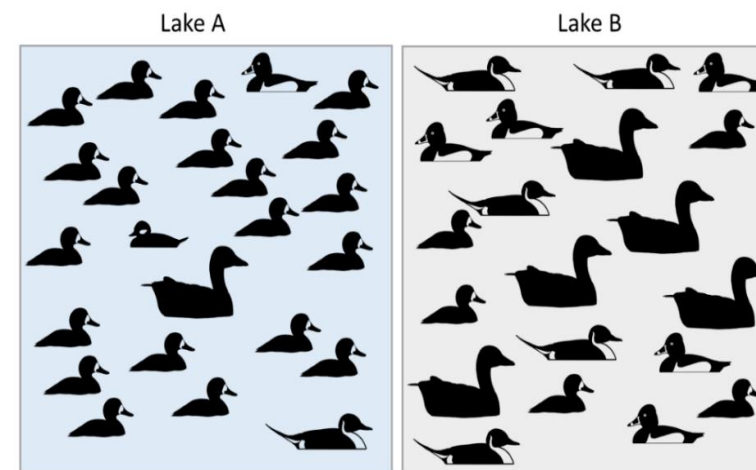


Diversity Score: Clinical Interpretation

Measures (Microbiome) Diversity: Combines richness (number of species) and **evenness** (distribution of individuals across species).

Sensitive to Rare Species: Particularly responsive to changes in the abundance of **low-prevalence species**, making it a sensitive indicator of microbial shifts.

Clinical Benchmark: Normobiotic: High Diversity Score (4–5) indicates a balanced and resilient gut microbiome.



Functional Interpretation

Dysbiosis Index: Measures divergence from a healthy normobiotic profile



Diversity Score: Reflects overall microbiome resilience, richness, and ecosystem depletion



A dysbiotic or non-diverse microbiome may explain a struggle with tolerability, plateaus early, or an incomplete metabolic response.



GI360™

FUNCTIONAL GUILD CRITERIA

GI Health Markers

Butyrate producing bacteria



Gut barrier protective bacteria



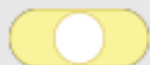
Gut intestinal health marker



Pro-inflammatory bacteria



Gut barrier protective bacteria vs. opportunistic bacteria



= Expected

= Imbalanced

Functional Marker	Bacteria	Profile criteria for imbalance	Description
Butyrate producing bacteria	<i>Evobacterium hallii</i>	At least two of the butyrate producers below healthy range	Insufficient levels of butyrate are associated with an impaired gastrointestinal health. Butyrate is a short-chain fatty acid produced by microbial fermentation in the large intestine of humans. It is important for regulating multiple functions of gut cells, may be important for regulating inflammatory and immunological responses and plays a role in the maintenance of intestinal barrier function. Beneficial bacteria belonging to the phylum Firmicutes are major butyrate producers.
	<i>Evobacterium rectale</i>		
	<i>Faecalibacterium prausnitzii</i>		
Gut mucosa protective bacteria	<i>Faecalibacterium prausnitzii</i>	Both mucosa protective below healthy range	Mucus and mucosa-associated bacteria form a specific protective environment in the gut. A disruption of the mucosa layer may promote specific bacterial colonization and immunological responses and enhance the development of gastrointestinal diseases. Imbalance of gut mucosa protective bacteria has been associated with various gastrointestinal disorders.
	<i>Akkermansia muciniphila</i>		
Gut intestinal health marker	<i>Faecalibacterium prausnitzii</i>	<i>F. prausnitzii</i> below healthy range with at least two [-2]	<i>Faecalibacterium prausnitzii</i> is one of the most prevalent bacteria within the human gastrointestinal tract. It is recognized as a major butyrate producer and can promote anti-inflammatory processes and intestinal barrier function. Lower levels of <i>Faecalibacterium prausnitzii</i> in the stool may have been associated with gastrointestinal and metabolic disorders.
Gut barrier protective vs. opportunistic bacteria	<i>Faecalibacterium prausnitzii</i>	<i>F. prausnitzii</i> below healthy range and at least one of the opportunists above healthy range.	The intestinal epithelial barrier is not a static physical barrier but one that can interact with the gut microbes and cells of the immune system. An imbalance between the gut barrier protective bacteria and potentially harmful bacteria may lead to gut barrier disruption and is associated with an increased susceptibility to certain diseases.
	<i>Ruminococcus gnavus</i>		
	Proteobacteria		
	<i>Shigella</i> spp. & <i>Escherichia</i> spp.		
Pro-inflammatory bacteria	Proteobacteria	Both pro-inflammatory above healthy range, and of which at least one +2 above	Diverse Proteobacteria species are associated with inflammation in various - mainly gastrointestinal - disorders. In a healthy gut microbiota, their increase may promote intestinal inflammation due to molecules present on their surface which are potent triggers of inflammatory responses. Inflammation in itself may also promote the growth of Proteobacteria species. Pro-inflammatory bacteria levels may thus give indications of the susceptibility of the patient to intestinal inflammation and to the possible development of gastrointestinal disorders.
	<i>Shigella</i> spp. & <i>Escherichia</i> spp.		



[DOCTORSDATA.COM/GI360-STOOL](https://doctorsdata.com/GI360-STOOL)

GI 360 Microbiome Bacterial Abundance; Multiplex PCR



Order: SAMPLE REPORT

Client #: 12345
 Doctor: Sample Doctor
 Doctor's Data, Inc.
 3755 Illinois Ave.
 St. Charles, IL 60174

Patient: Sample Patient
 Age: 35
 Sex: Female

Sample Collection Date/Time

	-3	-2	-1	0	+1	+2	+3	Result
	Very Low	Low	Within Reference Interval	High	Very High			Norm. micro predo

Acetivacteria	Result	-3	-2	-1
<i>Actinobacteria</i>	-3			
<i>Acintomyetales</i>	-1			
<i>Bifidobacterium</i> spp.	-3			
Bacteroidetes	Result	-3	-2	-1
<i>Alistipes</i> spp.	+1			
<i>Alistipes onderdonkii</i>	0			
<i>Bacteroides fragilis</i>	+2			
<i>Bacteroides</i> spp. & <i>Prevotella</i> spp.	+3			
<i>Bacteroides</i> spp.	+2			
<i>Bacteroides pectinophilus</i>	+1			
<i>Bacteroides stercoris</i>	+3			
<i>Bacteroides zoogloeiformans</i>	+1			
<i>Parabacteroides johnsonii</i>	0			
<i>Parabacteroides</i> spp.	+1			
Firmicutes	Result	-3	-2	-1
<i>Firmicutes</i>	-1			
Bacilli Class	0			

*This test was developed and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements. The U.S. Food and Drug Administration (FDA) has not approved or cleared this test; however, FDA clearance is not currently required for means for clinical diagnosis or patient management decisions.

Notes:
 RI= Reference Interval, L (blue)= Low (below RI), WRI (green)= Within RI (optimal), WRI (yellow)= Within RI (not optimal), H (red)= High (above RI)
 Methodology: Multiplex PCR

Analyzed by DOCTOR'S DATA, INC. • 3755 Illinois Avenue, St. Charles, IL 60174

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 Age: 35
 Sex: Female

Sample Collection Date/Time

Firmicutes	Result	-3	-2	-1	0
<i>Catenibacterium mitsuokai</i>	0				
Clostridia Class	-2				
<i>Clostridium methypentosum</i>	0				
<i>Clostridium</i> L2-50	0				
<i>Coprobacillus cateniformis</i>	0				
<i>Dialister invisus</i>	0				
<i>Dialister invisus</i> & <i>Megasphaera micronuciformis</i>	0				
<i>Dorea</i> spp.	0				
<i>Eubacterium bifforme</i>	0				
<i>Eubacterium hallii</i>	-1				
<i>Eubacterium rectale</i>	0				
<i>Eubacterium siraeum</i>	-2				
<i>Faecalibacterium prausnitzii</i>	-3				
Lachnospiraceae	+1				
<i>Lactobacillus ruminis</i> & <i>Pediococcus acidilactici</i>	-1				
<i>Lactobacillus</i> spp.	-3				
<i>Phascolarctobacterium</i> spp.	0				
<i>Ruminococcus albus</i> & <i>R. bromii</i>	0				
<i>Ruminococcus gnavus</i>	+3				
<i>Streptococcus agalactiae</i> & <i>Eubacterium rectale</i>	0				

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 St. Charles, IL 60174

Patient: Sample Patient
 Age: 35
 Sex: Female

Sample Collection Date/Time
 Date Collected: 08/29/2019
 Date Received: 08/30/2019
 Date Reported: 08/31/2019
 Specimens Collected: 1

Firmicutes	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i> & <i>S. sanguinis</i>	0								-1 to +1
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i>	-1								-1 to +1
<i>Streptococcus</i> spp.	0								-1 to +1
<i>Veillonella</i> spp.	0								-1 to +1
Proteobacteria	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Proteobacteria</i>	-1								-1 to +1
<i>Enterobacteriaceae</i>	-1								-1 to +1
<i>Escherichia</i> spp.	-2								-1 to +1
<i>Acinetobacter junii</i>	0								-1 to +1
Tenericutes	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Mycoplasma hominis</i>	+1								-1 to +1
Verrucomicrobia	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Akkermansia muciniphila</i>	-2								-1 to +1

GI 360 Microbiome Abundance Information:

GI 360 technology represents a unique approach to microbiome analysis. By combining information from a well-defined set of pre-determined markers, it enables highly reproducible and standardized information to be derived from the complex human microbiota profile. Genomic bacterial DNA is extracted from the samples using an in-house developed method comprising both mechanical and enzymatic degradation of bacterial cells followed by a clean-up process proven to yield high quality gDNA. The data is then checked for quality control and converted to an abundance score relative to a normobiotic reference standard.

*This test was developed and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements. The U.S. Food and Drug Administration (FDA) has not approved or cleared this test; however, FDA clearance is not currently required for clinical use. The results are not intended to be used as a sole means for clinical diagnosis or patient management decisions.

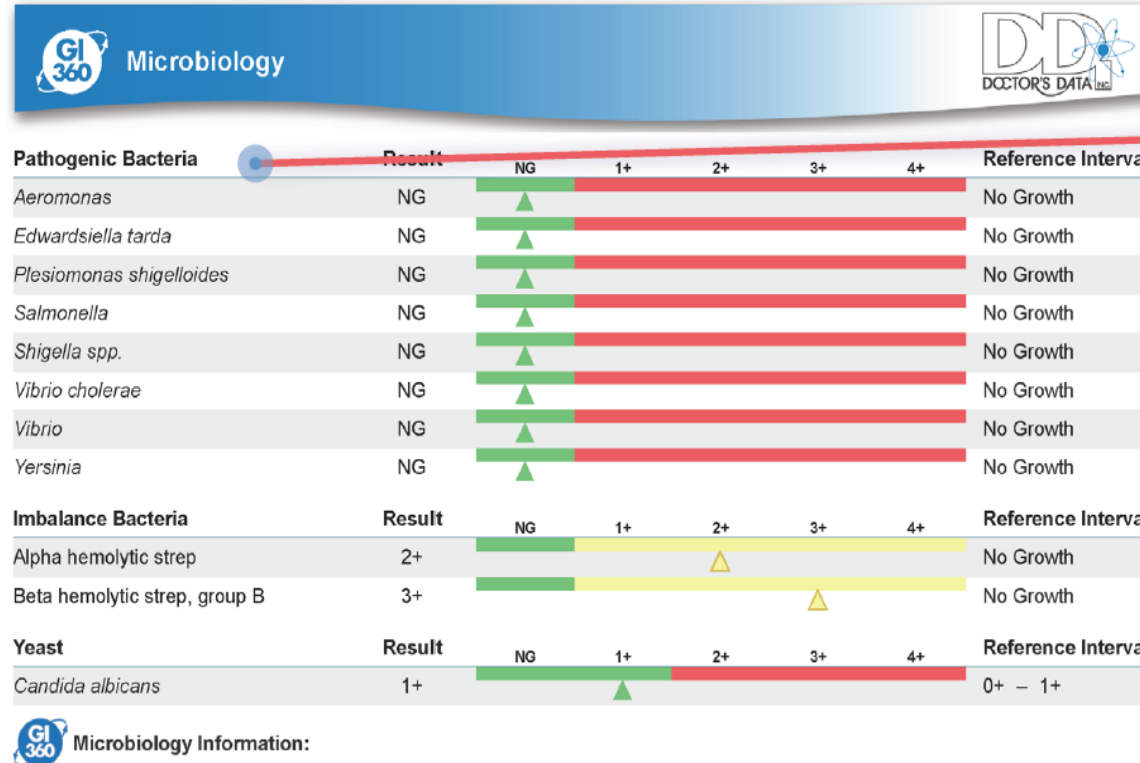
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 Methodology: Multiplex PCR

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Beyond the initial summary page

State of the Art Culturomics: MALDI-TOF

- 🌱 Aerobic and Anaerobic culturing
- 🌱 Ability to identify organisms outside of molecular DNA primer set
- 🌱 Reports are specific to the individual, expandable fields





















Culture complements PCR detection of dysbiotic and pathogenic bacteria and yeast. All sections within Microbiology are expandable fields. The greater the number of detected bacteria and yeast, the more expansive the reporting.

Inhibition Results: Natural Agents/Rx

Citrobacter farmeri / amalonaticus

Natural Agents	Low Inhibition	High Inhibition
Caprylic Acid*		
Uva Ursi*		
Olive Leaf Extract*		
Oregano*		
Goldenseal*		
Ionic Silver*		
Colloidal Silver*		

Prescriptive Agents	Resistant	Intermediate	Susceptible
Amoxicillin-Clavulanic Acid			
Ampicillin			
Cefazolin			
Ceftazidime			
Ciprofloxacin			
Sulfamethoxazole / Trimethoprim			



Susceptibility Information:

- **Natural antibacterial** agents may be useful for treatment of patients when organisms display in-vitro sensitivity to these agents. The test is performed by using standardized techniques and filter paper disks impregnated with the listed agent. Relative sensitivity is reported for each natural agent based upon the diameter of the zone of inhibition surrounding the disk. Data based on over 5000 individual observations were used to relate the zone size to the activity level of the agent. A scale of relative sensitivity is defined for the natural agents tested.
- **Susceptible** results imply that an infection due to the bacteria may be appropriately treated when the recommended dosage of the tested antimicrobial agent is used. **Intermediate** results imply that response rates may be lower than for susceptible bacteria when the tested antimicrobial agent is used. **Resistant** results imply that the bacteria will not be inhibited by normal dosage levels of the tested antimicrobial agent.



GI Pathogens Profile: multiplex PCR detection



Viruses	Result
Adenovirus F40/41	Negative <input type="checkbox"/>
Norovirus GI/GII	Negative <input type="checkbox"/>
Rotavirus A	Negative <input type="checkbox"/>
Pathogenic Bacteria	Result
<i>Campylobacter</i> (<i>C. jejuni</i> , <i>C. coli</i> and <i>C. lari</i>)	Negative <input type="checkbox"/>
<i>Clostridioides difficile</i> (Toxin A/B)	Positive <input checked="" type="checkbox"/>
<i>Escherichia coli</i> O157	Negative <input type="checkbox"/>
Enterotoxigenic <i>Escherichia coli</i> (ETEC) lt/st	Negative <input type="checkbox"/>
<i>Salmonella</i> spp.	Negative <input type="checkbox"/>
Shiga-like toxin-producing <i>Escherichia coli</i> (STEC) stx1/stx2	Negative <input type="checkbox"/>
<i>Shigella</i> (<i>S. boydii</i> , <i>S. sonnei</i> , <i>S. flexneri</i> & <i>S. dysenteriae</i>)	Negative <input type="checkbox"/>
<i>Vibrio cholerae</i>	Negative <input type="checkbox"/>
Parasites	Result
<i>Cryptosporidium</i> (<i>C. parvum</i> and <i>C. hominis</i>)	Negative <input type="checkbox"/>
<i>Entamoeba histolytica</i>	Negative <input type="checkbox"/>
<i>Giardia duodenalis</i> (AKA <i>intestinalis</i> & <i>lamblia</i>)	Negative <input type="checkbox"/>

PCR testing is very sensitive and allows for the detection of extremely low levels of pathogens. Decisions regarding clinical intervention should take the patient's complete clinical history and presentation into account.

Parasitology via Microscopy, O&P



Parasitology; Microscopy



Protozoa	Result	
<i>Balantidium coli</i>	Not Detected	<input type="checkbox"/>
<i>Blastocystis</i> spp.	Not Detected	<input type="checkbox"/>
<i>Chilomastix mesnili</i>	Not Detected	<input type="checkbox"/>
<i>Dientamoeba fragilis</i>	Not Detected	<input type="checkbox"/>
<i>Endolimax nana</i>	Not Detected	<input type="checkbox"/>
<i>Entamoeba coli</i>	Not Detected	<input type="checkbox"/>
<i>Entamoeba hartmanni</i>	Not Detected	<input type="checkbox"/>
<i>Entamoeba histolytica/Entamoeba dispar</i>	Not Detected	<input type="checkbox"/>
<i>Entamoeba polecki</i>	Not Detected	<input type="checkbox"/>
<i>Enteromonas hominis</i>	Not Detected	<input type="checkbox"/>
<i>Giardia duodenalis</i>	Not Detected	<input type="checkbox"/>
<i>Iodamoeba bütschlii</i>	Not Detected	<input type="checkbox"/>
<i>Isospora belli</i>	Not Detected	<input type="checkbox"/>
<i>Pentatrichomonas hominis</i>	Not Detected	<input type="checkbox"/>
<i>Retortamonas intestinalis</i>	Not Detected	<input type="checkbox"/>
Cestodes - Tapeworms	Result	
<i>Diphyllobothrium latum</i>	Not Detected	<input type="checkbox"/>
<i>Dipylidium caninum</i>	Not Detected	<input type="checkbox"/>
<i>Hymenolepis diminuta</i>	Not Detected	<input type="checkbox"/>
<i>Hymenolepis nana</i>	Not Detected	<input type="checkbox"/>
<i>Taenia</i>	Not Detected	<input type="checkbox"/>
Trematodes - Flukes	Result	

Microscopy (O&P) permits detection of many additional parasites not detected using PCR.

- 🎯 CDC standard of care for parasitology
- 🎯 Three stool collections on three separate days
- 🎯 Identification of O&P (>30 common parasites);
- 🎯 Macroscopy ID profile can be ordered separately

Parasitology via Microscopy, Other Markers



Parasitology; Microscopy



Other Markers	Result		Reference Interval
Yeast	Few	<input checked="" type="checkbox"/>	Not Detected – Rare
RBC	Not Detected	<input type="checkbox"/>	Not Detected – Rare
WBC	Not Detected	<input type="checkbox"/>	Not Detected – Rare
Muscle fibers	Not Detected	<input type="checkbox"/>	Not Detected – Rare
Vegetable fibers	Moderate	<input checked="" type="checkbox"/>	Not Detected – Few
Charcot-Leyden Crystals	Not Detected	<input type="checkbox"/>	Not Detected
Pollen	Not Detected	<input type="checkbox"/>	Not Detected
Macroscopic Appearance	Result		Reference Interval
Color	Brown	<input type="checkbox"/>	Brown
Consistency	Soft	<input type="checkbox"/>	Soft
Mucus	Negative	<input type="checkbox"/>	Negative

Visualization of moderate to many yeast microscopically in the absence of cultured yeast may be consistent with small intestinal fungal overgrowth. Consider symptomology for the patient.






Stool Chemistries



Digestion / Absorption	Result	Unit	L	WRI	H	Reference Interval
Elastase	>500	µg/g				> 200
Fat Stain	Few					None – Moderate
Carbohydrates†	Negative					Negative
Inflammation	Result	Unit	L	WRI	H	Reference Interval
Lactoferrin	1.2	µg/mL				< 7.3
Lysozyme*	221	ng/mL				≤ 500
Calprotectin	<10	µg/g				< 80
Immunology	Result	Unit	L	WRI	H	Reference Interval
Secretory IgA*	25.5	mg/dL				30 – 275
Short Chain Fatty Acids	Result	Unit	L	WRI	H	Reference Interval
% Acetate‡	61	%				50 – 72
% Propionate‡	17	%				11 – 25
% Butyrate‡	18	%				11 – 32
% Valerate‡	3.7	%				0.8 – 5.0
Butyrate‡	1.5	mg/mL				0.8 – 4.0
Total SCFA's†	8.3	mg/mL				5.0 – 16.0
Intestinal Health Markers	Result	Unit	L	WRI	H	Reference Interval
pH	6.5					5.8 – 7.0
β-glucuronidase*	5020	U/h*g				4000 – 9400
Occult Blood	Negative					Negative

Commentary Section


Commentary


<p>Order: 999999-9999</p>  <p>Client #: 999999</p> <p>Doctor: Sample Doctor, MD Doctors Data Inc 123 Main St. St. Charles, IL 60174 USA</p>	<p>Patient: Sample Patient Id: 999999 Age: 64 DOB: 00/00/1959 Sex: Female</p>	<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th>Sample Collection Date/Time</th> <th>Date/Time</th> </tr> </thead> <tbody> <tr> <td>Date Collected</td> <td>08/19/2023</td> </tr> <tr> <td>Date Received</td> <td>08/21/2023</td> </tr> <tr> <td>Date Reported</td> <td>08/31/2023</td> </tr> <tr> <td>Specimens Collected</td> <td>3</td> </tr> </tbody> </table>	Sample Collection Date/Time	Date/Time	Date Collected	08/19/2023	Date Received	08/21/2023	Date Reported	08/31/2023	Specimens Collected	3
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Introduction



This analysis of the stool specimen provides fundamental information about the overall gastrointestinal health of the patient. When abnormal microflora or significant aberrations in intestinal health markers are detected, specific commentaries are presented. If no significant abnormalities are found, commentaries are not presented.

Microbiome Abundance Information

Actinobacteria (phylum)
Actinobacteria is one of the largest bacterial phyla, comprised of Gram-positive bacteria. This phylum includes a wide range of species, with different morphological and physiological characteristics. Significant groups in the human colon include Actinomycetales and Bifidobacteriales. Actinomycetales were inversely associated with clinically significant depression in IBS patients, suggesting these bacteria may be depleted in depressed IBS patients. A strict vegetarian diet may increase the total count of *Actinomyces* spp. compared to following a Western diet.

↓ **Actinomycetales (order)**
Actinomycetales are considered low abundance colonizers of the gastrointestinal tract with primary residence on the skin. Intake of proton-pump inhibitor drugs has been shown to increase the abundance of Actinomycetales in the gut, possibly by reducing gastric acidity and enabling intestinal colonization by oral microbes. Actinomycetales may be depleted in depressed irritable bowel syndrome patients. The abundance of *Actinomyces* spp. was shown to be higher with a strict vegetarian diet compared to a common Western diet.

↓ **Bifidobacterium (genus)**
Considered amongst the most beneficial commensal bacteria in the human gut, *Bifidobacterium* spp. are able to degrade monosaccharides, galacto-, manno-, and fructo-oligosaccharides, as well as some complex carbohydrates. Many of the non-digestible oligosaccharides, found as natural components in mother's milk, select for colonization of these species which dominate the infant gut shortly after birth. Bifidobacteria may provide health benefits directly through interactions with the host, and indirectly through interactions with other microorganisms. *Bifidobacterium* spp. take part in production and adsorption of vitamins, such as vitamins K and B12, biotin, folate, thiamine, riboflavin, and pyridoxine. They are also involved in lipid absorption and metabolism, glucose and energy homeostasis, and regulating intestinal barrier function. Although *Bifidobacterium* produce acetate over butyrate, healthy levels of *Bifidobacterium* spp. facilitate colonization of *Faecalibacterium. prausnitzii*. Polyphenols derived from chocolate, green tea, blackcurrant, red wine and grape seed extracts have been shown to increase *Bifidobacterium* species. The increased abundance of *Bifidobacterium* species has been associated with amelioration of inflammation. Multiple published studies have suggested that there is an association between obesity and a lower abundance of bifidobacteria. They may also be less abundant in elderly populations, patients with rheumatoid arthritis, and in individuals diagnosed with Alzheimer's disease. Patients with active inflammatory bowel disease (IBD) have a lower abundance of *Bifidobacterium* spp. than patients whose IBD is in remission. Taking a probiotic containing bifidobacteria, lactobacilli, and streptococci might help in controlling ulcerative colitis symptoms and preventing their recurrence. Some *Bifidobacterium* strains have been shown to have beneficial effects in irritable bowel syndrome (IBS). *Bifidobacterium* spp. abundance has been shown to be diminished with IBD and with long term use of macrolide antibiotics. Luminal bifidobacteria is reduced with restriction of fermentable carbohydrates, i.e. a low FODMAP diet. High fat dietary feeding is also associated with reduced abundance of bifidobacteria. Consumption of maize and barley-based whole grain products and red berries, which are comprised of anthocyanins, are known to increase levels of bifidobacteria.

Sample Collection Date/Time	Date/Time
Date Collected	08/19/2023
Date Received	08/21/2023
Date Reported	08/31/2023
Specimens Collected	3

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DDI Retesting Stool Profiles

Post GI Therapy

- GI360™ Microbiome, GI360™ Essentials
- GI Pathogens Profile
- Microbiology, Bacteriology, Yeast
- Parasitology
- Stool Chemistries Profile
- H. pylori* Antigen Profile

Separate Stool Chemistry marker profiles:

- Elastase
- Calprotectin
- Lysozyme
- Lactoferrin
- Secretory IgA
- β -glucuronidase

2-3 months “feed and seed”
Targeted probiotic + soluble fiber





Moving From Assessment to Application

Applying GI360™ Findings to Incretin-based Therapy



- Interpreting microbiome influences on metabolic signaling
- Identifying barriers to treatment response
- Implementing targeted interventions
- Monitoring outcomes through testing and retesting

Incretin-Based Therapies Overview

GLP-1 receptor agonists

- **Liraglutide** (injectable)
- **Dulaglutide** (injectable)
- **Semaglutide** (injectable, oral)

Dual incretin (GIP/GLP-1) receptor agonist

- **Tirzepatide** (injectable)

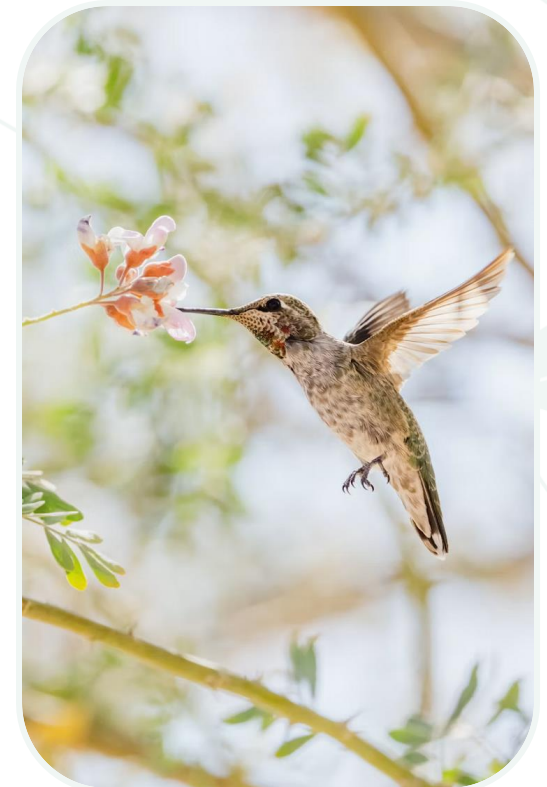
Clinical use considerations:

- Current use: Type 2 diabetes, obesity / weight management
- Expanding cardiometabolic indications
- Emerging multi-system interest (neurologic, hepatic, renal, behavioral)
- Transition from injectable to emerging oral formulations, with evolving understanding of direct gastrointestinal exposure effects

Endogenous GLP-1 Physiology

Gut–Brain Axis

- 🌱 **Secreted by L-cells** (distal ileum & colon) in response to nutrients
- 🌱 **Gut–brain signaling**
 - Enteric and vagal pathways **signal to the hypothalamus**, supporting satiety and appetite regulation.
- 🌱 **GI effects**
 - Slows gastric emptying and intestinal transit
- 🌱 **Influences glycemic, bile acid, and gut hormone signaling pathways**
 - Increased Glucose-dependent insulin secretion
 - Decreased Glucagon & hepatic gluconeogenesis



Microbiome + Incretin-based therapy

Metabolic Outcomes

SCFAs (butyrate, propionate, acetate)

- Fiber fermentation products
- Less stimulation of intestinal L-cells leading to increased incretin therapy agents

Dysbiosis effect

- Lower SCFA-producing bacteria leads to lower GLP-1 response
- Increased permeability + LPS leads to inflammation, insulin resistance

Gut–brain signaling

- Microbial metabolites modulate satiety/vagal pathways
- Impacts appetite and glycemic control

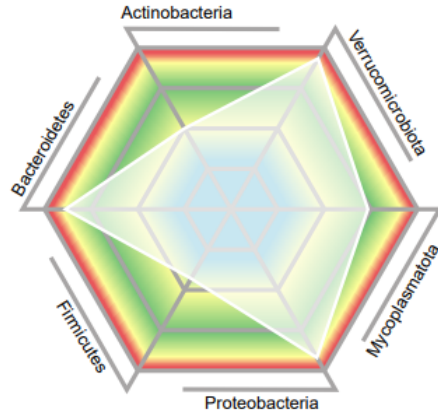
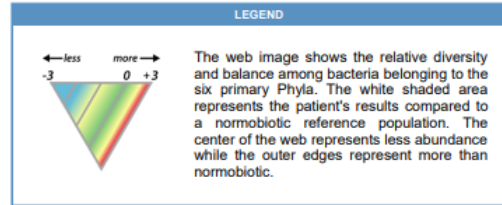
Clinical relevance

- Microbiome may influence GLP-1 receptor agonist response
- Targeting diet/prebiotics may enhance outcomes

Microbiome Bacterial Abundance; Multiplex PCR

Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.



Dysbiosis and Diversity Index

These indexes are calculated from the results of the Microbiome Profile, with scores ranging from 1 to 5, and do not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

The Dysbiosis Index (DI) is calculated strictly from the results of the Microbiome Profile, with scores from 1 to 5. A DI score above 2 indicates dysbiosis; a microbiota profile that differs from the defined normobiotic reference population. The higher the DI above 2, the more the sample deviates from the normobiotic profile. The dysbiosis test and DI does not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

A diversity score of 3 indicates an expected amount of diversity, with 4 & 5 indicating an increased distribution of bacteria based on the number of different species and their abundance in the sample, calculated based on Shannon's diversity index. Scores of 1 or 2 indicate less diversity than the defined normobiotic reference population.



GI Health Markers

Butyrate producing bacteria	<input type="checkbox"/>
Gut barrier protective bacteria	<input checked="" type="checkbox"/>
Gut intestinal health marker	<input type="checkbox"/>
Pro-inflammatory bacteria	<input type="checkbox"/>
Gut barrier protective bacteria vs. opportunistic bacteria	<input type="checkbox"/>

= Expected = Imbalanced

Key Findings

Butyrate, Low
Total SCFA's, Low

Patterns in the Incretin-based therapy Gut Microbiome

Web: Microbiome Abundance & Diversity

- Low Actinobacteria phylum (i.e. Bifidobacterium family)
- Higher Proteobacteria, Verrucomicrobiota, and Bacteroidetes phyla
 - Due to imbalanced, inflammatory diet, metabolic disease

Dysbiosis Index: 5

- Severe imbalanced membership associated with IBS, IBD, Obesity, Diabetes Mellitus

Diversity Score: 1

- Low diversity may suggest a reduced “support system” for endogenous GLP-1 signaling, even when pharmacologic GLP-1 agonists are used

Patterns in Incretin-based Agonist Gut Microbiome

Need support for members and soluble fiber 8-15g QD

Low *F. prausnitzii*, key butyrogenic species, indicates microbiome is in poor health & inflammation risk

Associated with excess protein & fat dietary pattern, low fiber and inflammation

Fiber & mucosal barrier protocol needed, consider zonulin test & systemic inflammation (hsCRP)

GI Health Markers		Key Findings
Butyrate producing bacteria	<input type="checkbox"/>	Butyrate, Low
Gut barrier protective bacteria	<input checked="" type="checkbox"/>	Total SCFA's, Low
Gut intestinal health marker	<input type="checkbox"/>	
Pro-inflammatory bacteria	<input type="checkbox"/>	
Gut barrier protective bacteria vs. opportunistic bacteria	<input type="checkbox"/>	

= Expected = Imbalanced



Microbiome Bacterial Abundance; Multiplex PCR



LEGEND						
-3	-2	-1	0	+1	+2	+3
Very Low	Low	Within Reference Interval	High	Very High		

Results are graphed as deviations from a normobiotic population. Normobiosis or a normobiotic state characterizes a composition of the microbiota profile in which microorganisms with potential health benefits predominate in abundance and diversity over potentially harmful ones.

Actinobacteria	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
Actinobacteria	-1			▲					0
Actinomycetales	0				▲				0
Bifidobacterium family	-1			▲					0
Proteobacteria	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
Proteobacteria	+2						▲		0
Enterobacteriaceae	+1					▲			0
Escherichia spp.	0				▲				0
Mycoplasmata	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
Metamycoplasma hominis	0				▲				0

Associated with longevity, metabolism, overall health, immune function, intrinsic K2, B-Vitamin production

Elevated in dysbiosis, high fat/protein diet. Inflammation and IBS



Microbiome Bacterial Abundance; Multiplex PCR



Lower levels associated with poor soluble fiber, inflammation

Associated with longevity, metabolism, overall health, immune function

Associated with mucosal barrier, intestinal permeability



Akkermansia muciniphila spp.

Elevated *Akkermansia*

Verrucomicrobiota	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Akkermansia muciniphila</i>	+2						▲		0

- Links microbial activity with **barrier integrity and host metabolic signaling**
- Mucin-degrading organism involved in **mucus layer turnover and barrier dynamics**
- Implicated in:
 - Immune modulation** via mucosal signaling pathways
 - Metabolic signaling**, including associations with GLP-1–related physiology (endogenous)
 - Gut–metabolic cross-talk** influencing inflammatory and energy balance states
- Context dependent, influenced by diet, microbial balance, and overall gut ecosystem function



Digestion / Absorption	Result	Unit	L	WRI	H	Reference Interval
Elastase	131	µg/g				> 200
Fat Stain	Few					None – Moderate
Carbohydrates [†]	Negative					Negative
Inflammation	Result	Unit	L	WRI	H	Reference Interval
Lactoferrin	0.7	µg/mL				< 7.3
Lysozyme*	205	ng/mL				≤ 500
Calprotectin	<10	µg/g				< 80
Immunology	Result	Unit	L	WRI	H	Reference Interval
Secretory IgA*	32.1	mg/dL				30 – 275
Short Chain Fatty Acids	Result	Unit	L	WRI	H	Reference Interval
% Acetate [‡]	68	%				50 – 72
% Propionate [‡]	15	%				11 – 25
% Butyrate [‡]	14	%				11 – 32
% Valerate [‡]	3.0	%				0.8 – 5.0
Butyrate [‡]	0.71	mg/mL				0.8 – 4.0
Total SCFA's [‡]	5.1	mg/mL				5.0 – 16.0
Intestinal Health Markers	Result	Unit	L	WRI	H	Reference Interval
pH	6.5					5.8 – 7.0
β-glucuronidase*	3200	U/h*g				4000 – 9400
Occult Blood	Negative					Negative

Low Elastase

- Exocrine pancreatic sufficiency marker
- Support with pancreatin
- Repeat marker in 4-6 weeks
- Refer out for diagnostics if still low

Fat Malabsorption

- Possible gallbladder implications to investigate

Incretin-based therapy - Fecal Elastase Interpretation

Incretin-based therapy may indirectly influence fecal elastase results. Mechanisms may include:

- 🌿 Delayed gastric emptying
- 🌿 Reduced caloric intake
- 🌿 Chronis stress/sympathetic dominance
- 🌿 Altered entero-pancreatic signaling
- 🌿 Changes in GI transit time

Interpretation should be correlated with:

- 🌿 Stool consistency
- 🌿 Malabsorption symptoms
- 🌿 Nutrient deficiencies
- 🌿 Weight loss pattern
- 🌿 Clinical history

Mildly low elastase does not always indicate true pancreatic insufficiency



Digestion / Absorption	Result	Unit	L	WRI	H	Reference Interval
Elastase	131	µg/g				> 200
Fat Stain	Few					None – Moderate
Carbohydrates [†]	Negative					Negative
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pH	6.5					5.8 – 7.0
β-glucuronidase*	3200	U/h*g				4000 – 9400
Occult Blood	Negative					Negative

Low Butyrate & Total SCFAs

- Reduced colonic energy supply and impaired mucosal integrity
- Increases gut inflammation due to reduced epithelial fuel and impaired barrier integrity
- Weakens metabolic signaling, including GLP-1/PYY and AMPK pathways
 - Reflects dysbiosis + low diversity, often worsened by incretin therapy induced low-fiber intake (poor weight loss response)

Butyrate, SCFAS, and Fiber

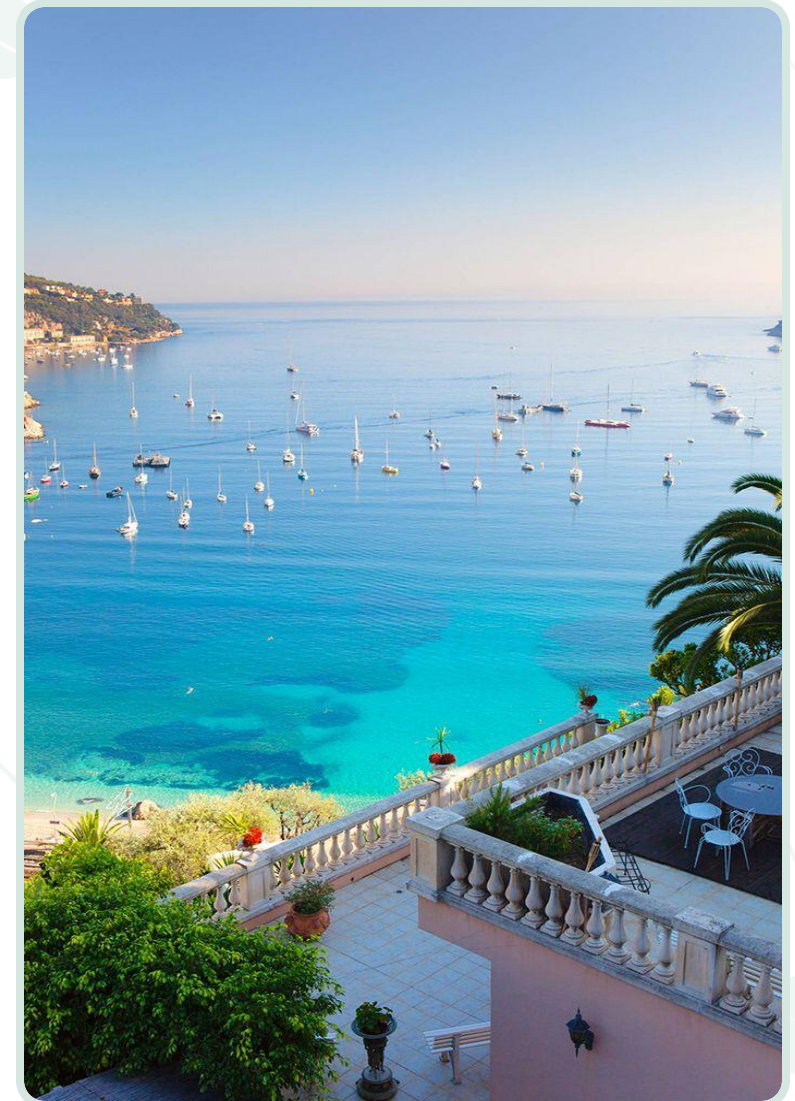
Types of Fiber:

- 🌱 **Soluble Fiber (fermentable):** primary driver of SCFA and butyrate production
 - 🌱 Therapeutic Dose: 8-15g/QD
 - 🌱 Inulin, psyllium husk, legumes, bananas, artichoke, chia seeds
- 🌱 **Resistant Starch:** fermented by specific colonic microbial communities
- 🌱 **Insoluble Fiber (non-fermentable):** supports stool bulk and transit; indirect gut health benefits
 - 🌱 Vegetables, fruits, flax, bran



Incretin-based therapy + Low Food Volume

- 🕒 **Goal:** Preserve diversity + SCFA production despite reduced intake
- 🕒 **Soluble fiber (8-15g QD)**
 - 🕒 Inulin, psyllium husk, PHGG, oats, cooled starches, legumes
 - 🕒 Supports Bifidobacterium, F. prausnitzii, A. muciniphila to increase SCFAs
- 🕒 **Polyphenols**
 - 🕒 Berries, pomegranate, green/red teas, colorful plants
 - 🕒 Support diversity + barrier integrity
- 🕒 **Fermented foods**
 - 🕒 Yogurt, kefir, kimchi, sauerkraut
 - 🕒 Increases microbial diversity, immune modulation
- 🕒 **Clinical intent**
 - 🕒 Counter dysbiosis + SCFA decline during appetite suppression
 - 🕒 Trend towards a Mediterranean-style diet



Microbiome requirements are non-negotiable biology

DDI Complementary Profiles

Gastrointestinal Health testing

- 🌿 *H. pylori* Antigen, stool
- 🌿 Celiac & Gluten Sensitivity, bloodspot, serum
- 🌿 Zonulin Family Protein, stool, serum

Endocrinology testing

- 🌿 HuMap, urine
- 🌿 Neurotransmitters, urine
- 🌿 Cortisol, saliva, urine

Environmental Exposure & Detox testing

- 🌿 Hepatic Detox, blood

Nutritional Status testing

- 🌿 **NAD, whole blood**
- 🌿 **Fatty Acid, while blood**
- 🌿 Vitamin D, blood spot, serum
- 🌿 **Amino Acids, blood, urine**
- 🌿 Iodine/Halides, urine

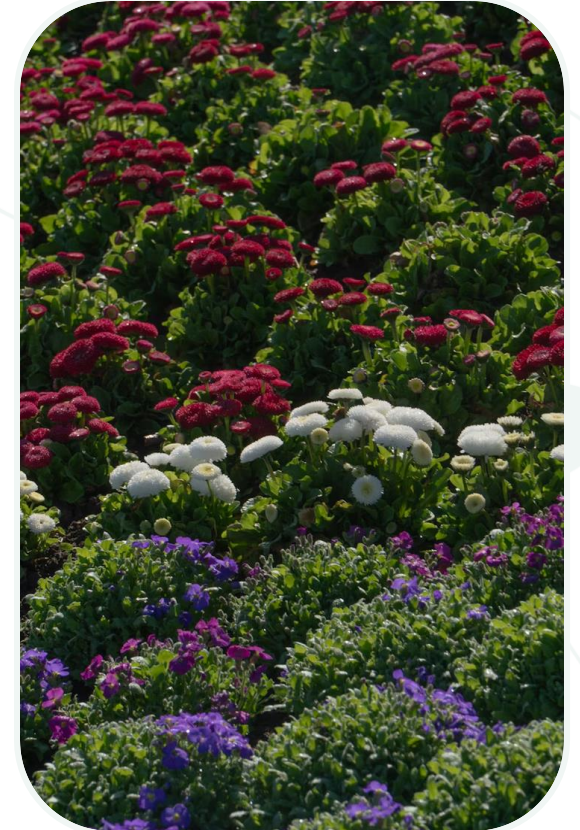
Toxic and Essential Elements testing

- 🌿 Toxic and Essential Elements, hair, urine
- 🌿 Oxidative Stress, urine

Methylation Testing

- 🌿 **DNA Weight Control (SNPS), buccal swab**
- 🌿 **Methylation Profile, plasma**

Cardiometabolic profile, serum

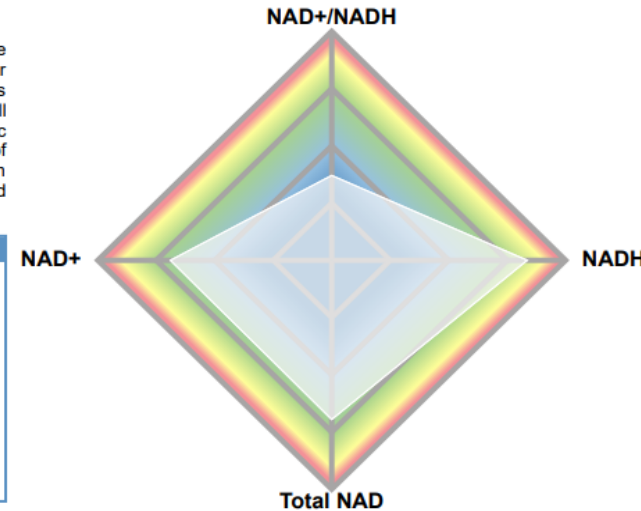
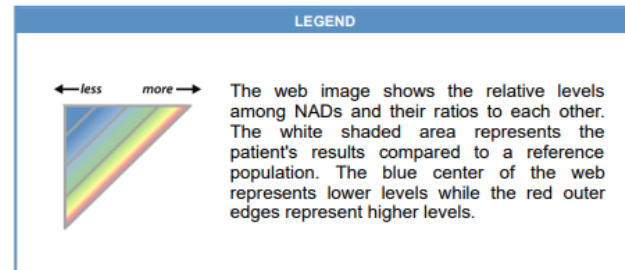


Collection Type



NADs: Metabolic Powerhouses

In the body, B3 vitamins manifest as NADs (nicotinamide adenine dinucleotides). NADs are crucial molecules central to diverse cellular processes, notably energy metabolism. Additionally, NADs are key players in regulatory pathways, influencing processes such as DNA repair and cell survival. For the clearest assessment of mitochondrial and metabolic function, it is essential to measure both the reduced and oxidized forms of NAD: NAD+ and NADH. Their significance in cellular activities makes them targets for research and interventions related to health, longevity, and disease.



Analytes	Result	Unit	L	WRI	H	Reference Interval
NAD+*	28	µmol	20.5	28	36	20 – 36
NADH*	1.7	µmol	0.6	1.7	1.8	0.6 – 1.8
Calculations	Result	Unit	L	WRI	H	Reference Interval
Total NAD	29.7	µmol	20.5	29.7	38.0	20.5 – 38.0
NAD+/NADH	16.5		16.3	16.5	46.0	16.3 – 46.0

- 🌱 Cellular energy status
- 🌱 Redox balance
- 🌱 Metabolic efficiency

🌱 Incretin therapy relevance:

- Weight loss, caloric reduction, and metabolic shift affect changes in NAD demand/turnover



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Extensive Assessment of the
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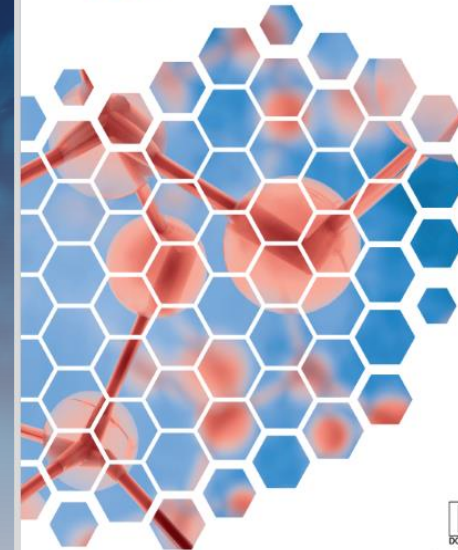
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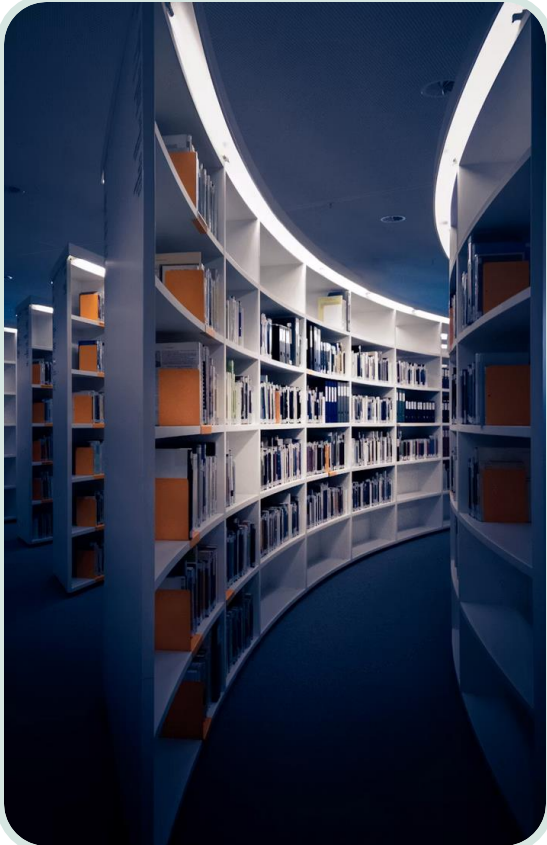
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- 🌐 Human microbiome intervention literature emphasizing functional vs taxonomic interpretation (multiple studies summarized in *Surg Obes Relat Dis.* and *Obes Rev.*)
- 🌐 Human dietary and metabolic intervention studies demonstrating dynamic microbiome adaptation (*Obesity Surgery, Nature Reviews Gastroenterology & Hepatology*, multiple reviews)