



Patient: **SAMPLE PATIENT**

Order Number:

DOB:

Completed:

Sex:

Received:

MRN:

Collected:

GI Effects™ Comprehensive Profile - Stool

Interpretation At-a-Glance

INFECTION



INFLAMMATION

Calprotectin ▲
Fecal Lactoferrin ▲
EPX ▲
Fecal secretory IgA ▲



INSUFFICIENCY

Fecal Fats (Total) ▲



IMBALANCE

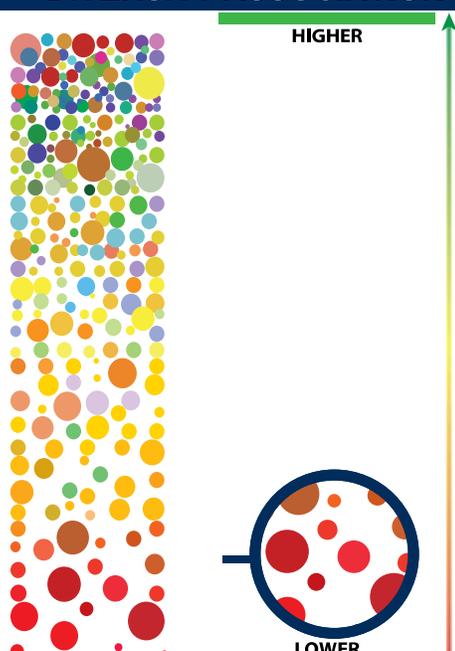
PP Bacteria ▲
Beneficial Bacteria ▼
n-Butyrate ▼
Beta-glucuronidase ▲



DIVERSITY ASSOCIATION

HIGHER

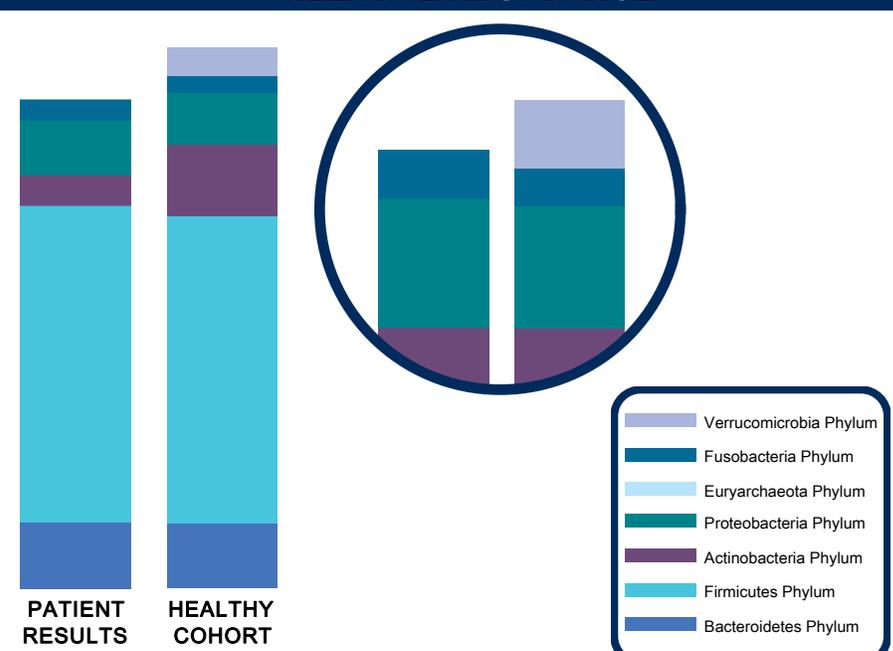
LOWER



RELATIVE ABUNDANCE

PATIENT RESULTS

HEALTHY COHORT



- Verrucomicrobia Phylum
- Fusobacteria Phylum
- Euryarchaeota Phylum
- Proteobacteria Phylum
- Actinobacteria Phylum
- Firmicutes Phylum
- Bacteroidetes Phylum



GI Effects™ Comprehensive Profile - Stool

Methodology: GC/MS, Automated Chemistry, EIA

	Results	QUINTILE DISTRIBUTION					Reference Range
		1st	2nd	3rd	4th	5th	
Digestion and Absorption							
Pancreatic Elastase 1 †	>500						>200 mcg/g
Products of Protein Breakdown (Total*) (Valerate, Isobutyrate, Isovalerate)	6.6						1.8-9.9 micromol/g
Fecal Fat (Total*)	41.8 H						3.2-38.6 mg/g
Triglycerides	3.5 H						0.3-2.8 mg/g
Long-Chain Fatty Acids	26.3						1.2-29.1 mg/g
Cholesterol	7.7 H						0.4-4.8 mg/g
Phospholipids	4.3						0.2-6.9 mg/g
Inflammation and Immunology							
Calprotectin †	693 H						<=50 mcg/g
Eosinophil Protein X (EPX) †	10.3 H						<=4.6 mcg/g
Fecal secretory IgA	>UL H						<=885 mcg/g
Gastrointestinal Microbiome							
Metabolic							
Short-Chain Fatty Acids (SCFA) (Total*) (Acetate, n-Butyrate, Propionate)	45.6						>=23.3 micromol/g
n-Butyrate Concentration	6.6						>=3.6 micromol/g
n-Butyrate %	14.5						11.8-33.3 %
Acetate %	62.4						48.1-69.2 %
Propionate %	23.0						<=29.3 %
Beta-glucuronidase	6,237						368-6,266 U/g

*Total value is equal to the sum of all measurable parts.

†These results are not represented by quintile values.

A. L. Peace-Brewer, PhD, D(ABMLI), Lab Director · CLIA Lic. #34D0655571 · Medicare Lic. #34-8475

Tests were developed and their performance characteristics determined by Genova Diagnostics. Unless otherwise noted with *, the assays have not been cleared or approved by the U.S. Food and Drug Administration.



Gastrointestinal Microbiome

Commensal Bacteria (PCR)	Result CFU/g stool	QUINTILE DISTRIBUTION					Reference Range CFU/g stool
		1st	2nd	3rd	4th	5th	
Bacteroidetes Phylum							
<i>Bacteroides-Prevotella</i> group	2.9E9 H						3.4E6-1.5E9
<i>Bacteroides vulgatus</i>	3.8E9 H						<=2.2E9
<i>Barnesiella</i> spp.	<DL						<=1.6E8
<i>Odoribacter</i> spp.	6.6E6						<=8.0E7
<i>Prevotella</i> spp.	1.8E7 H						1.4E5-1.6E7
Firmicutes Phylum							
<i>Anaerotruncus colihominis</i>	7.2E7 H						<=3.2E7
<i>Butyrivibrio crossotus</i>	3.2E4						5.5E3-5.9E5
<i>Clostridium</i> spp.	7.0E9						1.7E8-1.5E10
<i>Coprococcus eutactus</i>	7.0E5						<=1.2E8
<i>Faecalibacterium prausnitzii</i>	1.2E10 H						5.8E7-4.7E9
<i>Lactobacillus</i> spp.	3.7E8						8.3E6-5.2E9
<i>Pseudoflavonifractor</i> spp.	3.2E8 H						4.2E5-1.3E8
<i>Roseburia</i> spp.	1.0E9						1.3E8-1.2E10
<i>Ruminococcus</i> spp.	8.9E7 L						9.5E7-1.6E9
<i>Veillonella</i> spp.	2.4E7						1.2E5-5.5E7
Actinobacteria Phylum							
<i>Bifidobacterium</i> spp.	4.1E7						<=6.4E9
<i>Bifidobacterium longum</i>	8.7E6						<=7.2E8
<i>Collinsella aerofaciens</i>	<DL L						1.4E7-1.9E9
Proteobacteria Phylum							
<i>Desulfovibrio piger</i>	<DL						<=1.8E7
<i>Escherichia coli</i>	8.7E7 H						9.0E4-4.6E7
<i>Oxalobacter formigenes</i>	8.2E5						<=1.5E7
Euryarchaeota Phylum							
<i>Methanobrevibacter smithii</i>	<DL						<=8.6E7
Fusobacteria Phylum							
<i>Fusobacterium</i> spp.	1.8E5						<=2.4E5
Verrucomicrobia Phylum							
<i>Akkermansia muciniphila</i>	<DL						>=1.2E6
Firmicutes/Bacteroidetes Ratio							
<i>Firmicutes/Bacteroidetes</i> (F/B Ratio)	7 L						12-620

The gray-shaded portion of a quintile reporting bar represents the proportion of the reference population with results below detection limit.

Commensal results and reference range values are displayed in a computer version of scientific notation, where the capital letter "E" indicates the exponent value (e.g., 7.3E6 equates to 7.3 x 10⁶ or 7,300,000).

The Firmicutes/Bacteroidetes ratio (F/B Ratio) is estimated by utilizing the lowest and highest values of the reference range for individual organisms when patient results are reported as <DL or >UL.



Gastrointestinal Microbiome

Bacteriology (Culture)

Lactobacillus spp.

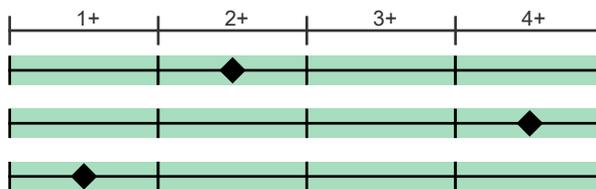
2+ NP

Escherichia coli

4+ NP

Bifidobacterium

1+ NP



Additional Bacteria

alpha haemolytic Streptococcus

3+ NP

Streptococcus agalactiae gp B

4+ NP

gamma haemolytic Streptococcus

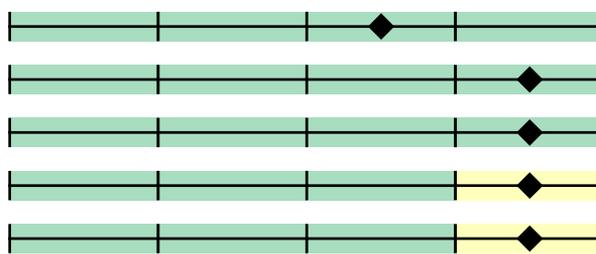
4+ NP

Pseudomonas aeruginosa

4+ PP

Proteus mirabilis

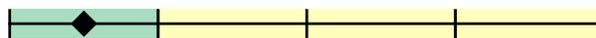
4+ PP



Mycology (Culture)

Candida albicans/dubliniensis

1+ NP



** Microbiology culture performed by Genova Diagnostics, Inc. 63 Zillicoa St., Asheville, NC 28801-0174
 A. L. Peace-Brewer, PhD, D(ABMLI), Lab Director - CLIA Lic. #34D0655571 - Medicare Lic. #34-8475

Human microflora is influenced by environmental factors and the competitive ecosystem of the organisms in the GI tract. Pathogenic significance should be based upon clinical symptoms.

Additional Bacteria

Non-Pathogen: Organisms that fall under this category are those that constitute normal, commensal flora, or have not been recognized as etiological agents of disease.

Potential Pathogen: Organisms that fall under this category are considered potential or opportunistic pathogens when present in heavy growth.

Pathogen: The organisms that fall under this category have a well-recognized mechanism of pathogenicity in clinical literature and are considered significant regardless of the quantity that appears in the culture.

Microbiology Legend

NG	NP	PP	P
No Growth	Non-Pathogen	Potential Pathogen	Pathogen



Methodology: Direct Microscopic Examination, EIA

Parasitology

Microscopic Exam Results**

No Ova or Parasites seen

Parasitology

Parasite Recovery: Literature suggests that >90% of enteric parasitic infections may be detected in a sample from a single stool collection. Increased sensitivity results from the collection of additional specimens on separate days.

Parasitology EIA Tests:

	In Range	Out of Range
<i>Cryptosporidium</i> ♦	Negative	
<i>Giardia lamblia</i> ♦	Negative	
<i>Entamoeba histolytica</i> ♦	Negative	

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Additional Results

	Result	Expected Value
Fecal Occult Blood♦	Negative	Negative
Consistency††	Not Given	
HpSA - <i>H. pylori</i>	Negative	Negative
<i>Campylobacter</i> spp♦	Negative	Negative
<i>Clostridium difficile</i> ♦**	Negative	Negative
Shiga toxin <i>E. coli</i> ♦**	Negative	Negative
Fecal Lactoferrin♦**	Positive	Negative

HpSA (Helicobacter pylori stool antigen) Helicobacter pylori is a bacterium which causes peptic ulcer disease and plays a role in the development of gastric cancer. Direct stool testing of the antigen (HpSA) is highly accurate and is appropriate for diagnosis and follow-up of infection.

Campylobacter Campylobacter jejuni is the most frequent cause of bacterial-induced diarrhea. While transmission can occur via the fecal-oral route, infection is primarily associated with the ingestion of contaminated and poorly cooked foods of animal origin, notably, red meat and milk.

Clostridium difficile is an anaerobic, spore-forming gram-positive bacterium. After a disturbance of the gut flora (usually with antibiotics), colonization with Clostridium difficile can take place. Clostridium difficile infection is much more common than once thought.

Shiga toxin E. coli Shiga toxin-producing Escherichia coli (STEC) is a group of bacterial strains that have been identified as worldwide causes of serious human gastrointestinal disease. The subgroup enterohemorrhagic E. coli includes over 100 different serotypes, with O157:H7 being the most significant, as it occurs in over 80% of all cases. Contaminated food continues to be the principal vehicle for transmission; foods associated with outbreaks include alfalfa sprouts, fresh produce, beef, and unpasteurized juices.

Lab Comments (if applicable)

††Results provided from patient input.

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Bacteria Sensitivity

Prescriptive Agents

<i>Pseudomonas aeruginosa</i>	R	I	S-DD	S	NI
Ciprofloxacin				S	
Tetracycline	R				
Trimethoprim/Sulfa	R				

Natural Agents

<i>Pseudomonas aeruginosa</i>	LOW INHIBITION	HIGH INHIBITION
Berberine		
Oregano		
Plant Tannins		
Uva-Ursi		

Prescriptive Agents:

The R (Resistant) category implies isolate is not inhibited by obtainable levels of pharmaceutical agent.

The I (Intermediate) category includes isolates for which the minimum inhibition concentration (MIC) values usually approach obtainable pharmaceutical agent levels and for which response rates may be lower than for susceptible isolates.

The S-DD (Susceptible-Dose Dependent) category implies clinical efficacy when higher than normal dosage of a drug can be used and maximal concentration achieved.

The S (Susceptible) column implies that isolates are inhibited by the usually achievable concentrations of the pharmaceutical agent.

NI (No Interpretive guidelines established) category is used for organisms that currently do not have established guidelines for MIC interpretation.

Refer to published pharmaceutical guidelines for appropriate dosage therapy.

Natural Agents:

In this assay, inhibition is defined as the reduction level on organism growth as a direct result of inhibition by a substance. The level of inhibition is an indicator of how effective the substance was at limiting the growth of an organism in an in vitro environment. High inhibition indicates a greater ability by the substance to limit growth, while Low Inhibition a lesser ability to limit growth. The designated natural products should be considered investigational in nature and not be viewed as standard clinical treatment substances.



Bacteria Sensitivity

Prescriptive Agents

	R	I	S-DD	S	NI
<i>Proteus mirabilis</i>					
Ampicillin				S	
Amox./Clavulanic Acid				S	
Cephalothin				S	
Ciprofloxacin				S	
Tetracycline	R				
Trimethoprim/Sulfa				S	

Natural Agents

	LOW INHIBITION	HIGH INHIBITION
<i>Proteus mirabilis</i>		
Berberine		
Oregano		
Plant Tannins		
Uva-Ursi		

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