



Patient: **SAMPLE**
PATIENT

GI Effects™ Microbial Ecology Profile - Stool

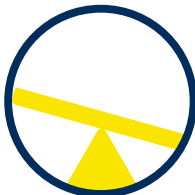
Interpretation At-a-Glance

INFECTION



IMBALANCE

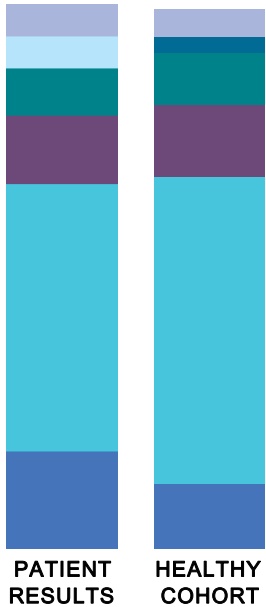
Beneficial Bacteria ▼



DIVERSITY ASSOCIATION



RELATIVE ABUNDANCE



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



Patient: **SAMPLE**
PATIENT

GI Effects™ Microbial Ecology Profile - Stool

Methodology: DNA by PCR

Gastrointestinal Microbiome

Commensal Bacteria (PCR)

Result
CFU/g stool

QUINTILE DISTRIBUTION

1st

2nd

3rd

4th

5th

Reference Range
CFU/g stool

Bacteroidetes Phylum

Bacteroides-Prevotella group

8.4E7



3.4E6 - 1.5E9

Bacteroides vulgatus

1.3E8



<=2.2E9

Barnesiella spp.

1.6E8



<=1.6E8

Odoribacter spp.

8.8E7 H



<=8.0E7

Prevotella spp.

4.2E6



1.4E5 - 1.6E7

Firmicutes Phylum

Anaerotruncus colihominis

9.5E6



<=3.2E7

Butyrivibrio crossotus

<DL L



5.5E3 - 5.9E5

Clostridium spp.

2.9E9



1.7E8 - 1.5E10

Coprococcus eutactus

<DL



<=1.2E8

Faecalibacterium prausnitzii

9.0E8



5.8E7 - 4.7E9

Lactobacillus spp.

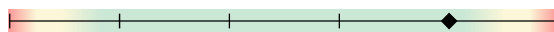
7.4E8



8.3E6 - 5.2E9

Pseudoflavonifractor spp.

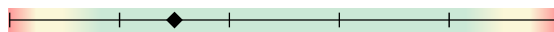
6.0E7



4.2E5 - 1.3E8

Roseburia spp.

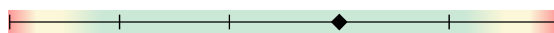
2.1E9



1.3E8 - 1.2E10

Ruminococcus spp.

1.0E9



9.5E7 - 1.6E9

Veillonella spp.

8.5E6

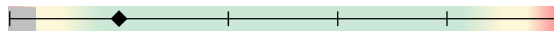


1.2E5 - 5.5E7

Actinobacteria Phylum

Bifidobacterium spp.

3.3E8



<=6.4E9

Bifidobacterium longum

<DL



<=7.2E8

Collinsella aerofaciens

5.1E8



1.4E7 - 1.9E9

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).

Methodology: DNA by PCR

Gastrointestinal Microbiome							
Commensal Bacteria (PCR)	Result CFU/g stool	QUINTILE DISTRIBUTION					Reference Range CFU/g stool
		1st	2nd	3rd	4th	5th	
Proteobacteria Phylum							
<i>Desulfovibrio piger</i>	<DL						<=1.8E7
<i>Escherichia coli</i>	1.6E6						9.0E4-4.6E7
<i>Oxalobacter formigenes</i>	4.8E5						<=1.5E7
Euryarchaeota Phylum							
<i>Methanobrevibacter smithii</i>	1.2E8 H						<=8.6E7
Fusobacteria Phylum							
<i>Fusobacterium</i> spp.	<DL						<=2.4E5
Verrucomicrobia Phylum							
<i>Akkermansia muciniphila</i>	2.6E8						>=1.2E6
Firmicutes/Bacteroidetes Ratio							
<i>Firmicutes/Bacteroidetes</i> (F/B Ratio)	24						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.

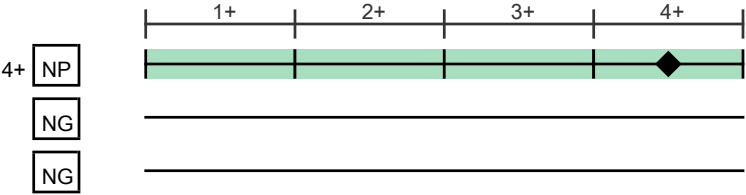
Gastrointestinal Microbiome

Bacteriology (Culture)

Lactobacillus spp.

Escherichia coli

Bifidobacterium



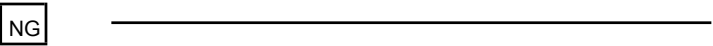
Additional Bacteria

alpha haemolytic Streptococcus

gamma haemolytic Streptococcus



Mycology (Culture)



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.

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

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.

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	

** Indicates testing 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

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.

Methodology: EIA, Fecal Immunochemical Testing (FIT)

Additional Results

	Result	Expected Value
Color††	Brown	
Consistency††	Formed/Normal	

Lab Comments (if applicable)

††Results provided from patient input.

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