



Patient: **RYAN**
MAIDENBERG
DOB: January 23, 1990
Sex: M
MRN: 1232482631

Order Number: I4300581
Completed: May 15, 2015
Received: May 05, 2015
Collected: April 28, 2015

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4126 Southwest Freeway
Suite 1030
Houston, TX 77027

GI Effects™ Comprehensive Profile - Stool

Interpretation At-a-Glance

INFECTION



INFLAMMATION

EPX ▲



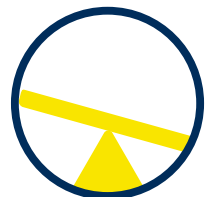
INSUFFICIENCY



IMBALANCE

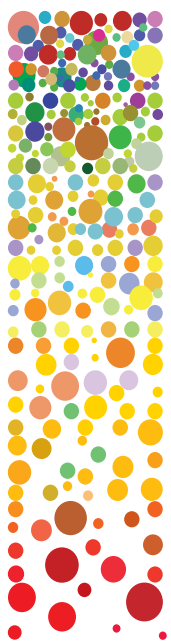
n-Butyrate ▼

Total SCFA ▼



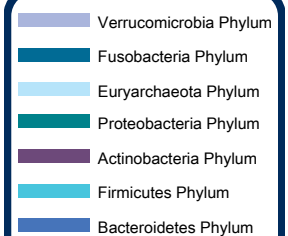
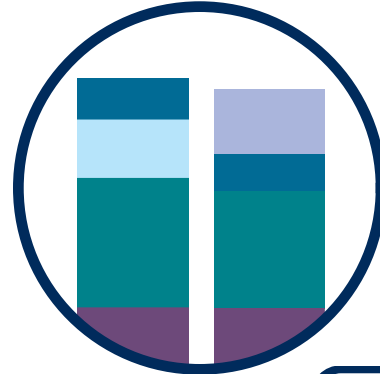
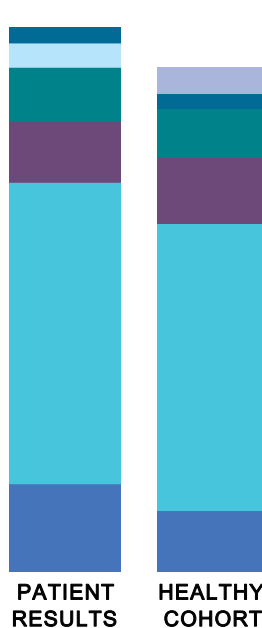
DIVERSITY ASSOCIATION

HIGHER



LOWER

RELATIVE ABUNDANCE



GI Effects™ Comprehensive Profile - Stool

Methodology: GC/MS, Automated Chemistry, EIA

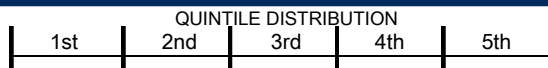
Effects™ Comprehensive Profile - Stool		QUINTILE DISTRIBUTION					Reference Range	
Methodology: GC/MS, Automated Chemistry, EIA		Results	1st	2nd	3rd	4th		5th
Digestion and Absorption								
Pancreatic Elastase 1 † ♦	>500		>200 mcg/g					
Products of Protein Breakdown (Total*) (Valerate, Isobutyrate, Isovalerate)	6.3		1.8-9.9 micromol/g					
Fecal Fat (Total*)	14.7		3.2-38.6 mg/g					
Triglycerides	0.8		0.3-2.8 mg/g					
Long-Chain Fatty Acids	6.1		1.2-29.1 mg/g					
Cholesterol	6.8 H		0.4-4.8 mg/g					
Phospholipids	1.0		0.2-6.9 mg/g					
Inflammation and Immunology								
Calprotectin † ♦	42		<=50 mcg/g					
Eosinophil Protein X (EPX)†	3.7		<=7.0 mcg/g					
Fecal secretory IgA	219		<=885 mcg/g					
Gastrointestinal Microbiome								
Metabolic								
Short-Chain Fatty Acids (SCFA) (Total*) (Acetate, n-Butyrate, Propionate)	30.7		>=23.3 micromol/g					
n-Butyrate Concentration	6.4		>=3.6 micromol/g					
n-Butyrate %	20.8		11.8-33.3 %					
Acetate %	44.7 L		48.1-69.2 %					
Propionate %	34.4 H		<=29.3 %					
Beta-glucuronidase	<DL L		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.

Methodology: DNA by PCR

Gastrointestinal Microbiome

Commensal Bacteria (PCR)

Result
CFU/g stoolReference Range
CFU/g stool

Bacteroidetes Phylum

<i>Bacteroides-Prevotella</i> group	1.3E9		3.4E6-1.5E9
<i>Bacteroides vulgatus</i>	7.3E9 H		<=2.2E9
<i>Barnesiella</i> spp.	3.7E7		<=1.6E8
<i>Odoribacter</i> spp.	2.8E6		<=8.0E7
<i>Prevotella</i> spp.	2.6E7 H		1.4E5-1.6E7

Firmicutes Phylum

<i>Anaerotruncus colihominis</i>	5.3E7 H		<=3.2E7
<i>Butyrivibrio crossotus</i>	3.2E4		5.5E3-5.9E5
<i>Clostridium</i> spp.	1.5E10		1.7E8-1.5E10
<i>Coprococcus eutactus</i>	3.2E6		<=1.2E8
<i>Faecalibacterium prausnitzii</i>	5.8E8		5.8E7-4.7E9
<i>Lactobacillus</i> spp.	5.6E9 H		8.3E6-5.2E9
<i>Pseudoflavonifractor</i> spp.	2.4E8 H		4.2E5-1.3E8
<i>Roseburia</i> spp.	3.4E9		1.3E8-1.2E10
<i>Ruminococcus</i> spp.	3.7E8		9.5E7-1.6E9
<i>Veillonella</i> spp.	2.4E7		1.2E5-5.5E7

Actinobacteria Phylum

<i>Bifidobacterium</i> spp.	2.4E9		<=6.4E9
<i>Bifidobacterium longum</i>	1.7E8		<=7.2E8
<i>Collinsella aerofaciens</i>	1.4E7		1.4E7-1.9E9

Proteobacteria Phylum

<i>Desulfovibrio piger</i>	<DL		<=1.8E7
<i>Escherichia coli</i>	5.8E7 H		9.0E4-4.6E7
<i>Oxalobacter formigenes</i>	5.3E6		<=1.5E7

Euryarchaeota Phylum

<i>Methanobrevibacter smithii</i>	3.5E6		<=8.6E7
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Fusobacteria Phylum

<i>Fusobacterium</i> spp.	5.2E4		<=2.4E5
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Verrucomicrobia Phylum

<i>Akkermansia muciniphila</i>	<DL		>=1.2E6
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Firmicutes/Bacteroidetes Ratio

<i>Firmicutes/Bacteroidetes</i> (F/B Ratio)	18		12-620
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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 7.3×10^6 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.

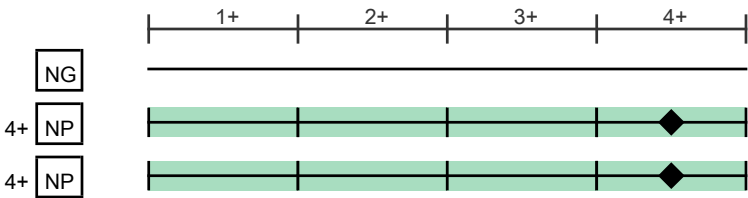
Gastrointestinal Microbiome

Bacteriology (Culture)

Lactobacillus spp.

Escherichia coli

Bifidobacterium

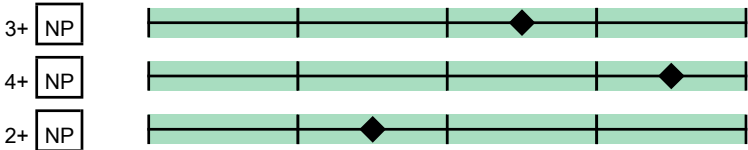


Additional Bacteria

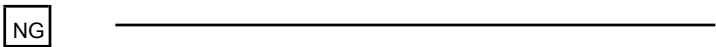
alpha haemolytic Streptococcus

Haemolytic Escherichia coli

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
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New York Clinical Lab PFI #4578 · Florida Clinical Lab Lic. #800008124

Additional Results

	Result	Expected Value
Fecal Occult Blood♦	Negative	Negative
Consistency††	Formed/Normal	

Lab Comments (if applicable)

††Results provided from patient input.

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