



**Patient: Jane Doe**

**Order Number:**

DOB: September 16, 1960

Completed: October 05, 2017

Sex: F

Received: September 21, 2017

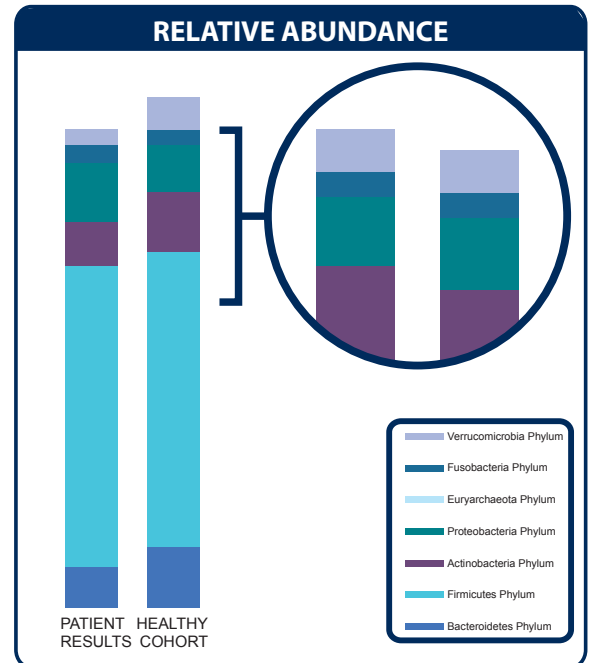
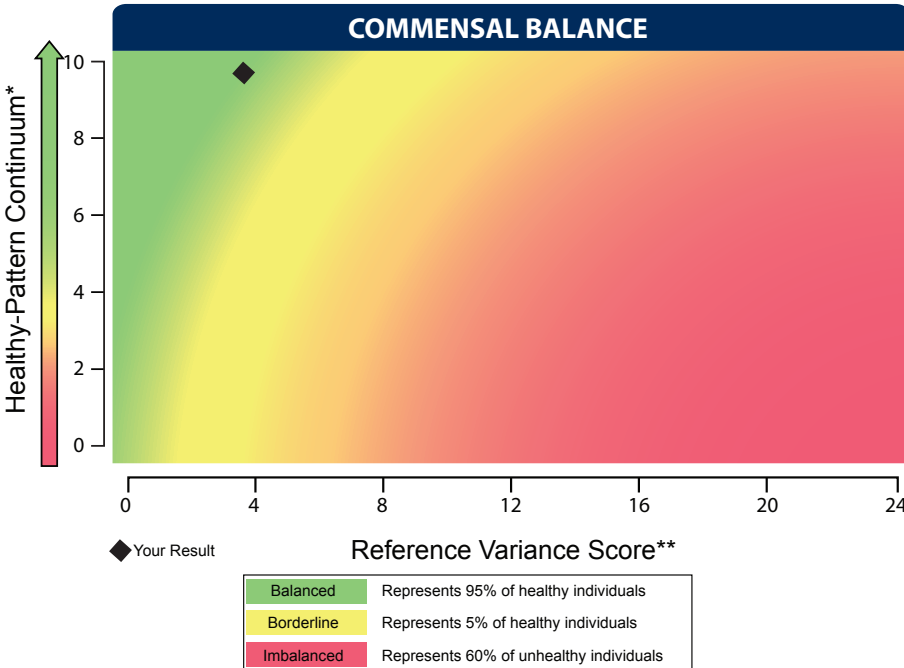
MRN:

Collected: September 20, 2017

# SAMPLE REPORT

## 2205 GI Effects™ Microbial Ecology Profile – Stool

### Interpretation At-a-Glance



\* A progressive ranking scale based on a Genova proprietary algorithm that differentiates healthy and unhealthy commensal patterns.

\*\*The total number of Commensal Bacteria (PCR) that are out of reference range for this individual



## 2205 GI Effects™ Microbial Ecology Profile – Stool

### Interpretation At-a-Glance

Commensal Bacteria	Patient Results Out of Reference Range	Genova Diagnostics Commensal Bacteria Clinical Associations*							
		IBS	IBD	Metabolic Syndrome	Chronic Fatigue	Auto-immune	Type 2 Diabetes	High Blood Pressure	Mood Disorders
<b>Bacteroidetes Phylum</b>									
<i>Bacteroides-Prevotella</i> group		↑	↑	↑	↑	↑	↑	↑	↑
<i>Bacteroides vulgatus</i>		↑			↑	↑		↑	↑
<i>Barnesiella</i> spp.									
<i>Odoribacter</i> spp.	<b>H</b>								
<i>Prevotella</i> spp.		↑		↑	↑	↑		↑	↑
<b>Firmicutes Phylum</b>									
<i>Anaerotruncus colihominis</i>		↑	↑	↑	↑	↑	↑	↑	↑
<i>Butyrivibrio crossotus</i>	<b>L</b>								
<i>Clostridium</i> spp.									
<i>Coprococcus eutactus</i>		↑			↑	↑		↑	↑
<i>Faecalibacterium prausnitzii</i>		↑				↑			↑
<i>Lactobacillus</i> spp.									
<i>Pseudoflavonifractor</i> spp.		↑	↑	↑	↑	↑	↑	↑	↑
<i>Roseburia</i> spp.			↓						
<i>Ruminococcus</i> spp.		↓↑	↓	↓	↓	↓↑	↓↑	↓↑	↓↑
<i>Veillonella</i> spp.		↑	↑	↑	↑	↑	↑		↑
<b>Actinobacteria Phylum</b>									
<i>Bifidobacterium</i> spp.									
<i>Bifidobacterium longum</i>									
<i>Collinsella aerofaciens</i>		↓↑	↓↑	↓	↓↑	↓↑	↓↑	↓↑	↓↑
<b>Proteobacteria Phylum</b>									
<i>Desulfovibrio piger</i>									↑
<i>Escherichia coli</i>		↑	↑	↑	↑	↑	↑	↑	↑
<i>Oxalobacter formigenes</i>		↑		↑	↑				↑
<b>Euryarchaeota Phylum</b>									
<i>Methanobrevibacter smithii</i>	<b>H</b>	↑				↑			↑
<b>Fusobacteria Phylum</b>									
<i>Fusobacterium</i> spp.		↑	↑	↑	↑	↑	↑	↑	↑
<b>Verrucomicrobia Phylum</b>									
<i>Akkermansia muciniphila</i>		↓	↓	↓	↓	↓	↓	↓	↓

\*Information derived from GDx results data comparing a healthy cohort to various clinical condition cohorts. The chart above showing a comparison of patient results to clinical conditions is meant for informational purposes only; it is not diagnostic, nor does it imply that the patient has a specific clinical diagnosis or condition.

The arrows indicate Genova's clinical condition cohort test results falling below ↓ or above ↑ the reference range that is greater than that of Genova's healthy cohort.

↓↑ Indicates Genova's clinical condition cohort test results falling below and above the reference range that are greater than that of Genova's healthy cohort.

Cells with bolded arrows indicate Genova's clinical condition cohort had more test results falling above versus below ↓↑ or more below versus above ↑↓ the reference range compared to that of Genova's healthy cohort.



Methodology: DNA by PCR

## Gastrointestinal Microbiome

	Result CFU/g stool	QUINTILE DISTRIBUTION					Reference Range CFU/g stool
		1st	2nd	3rd	4th	5th	
<b>Commensal Bacteria (PCR)</b>							
<b>Bacteroidetes Phylum</b>							
<i>Bacteroides-Prevotella</i> group	8.4E7						3.4E6 - 1.5E9
<i>Bacteroides vulgatus</i>	1.3E8						<=2.2E9
<i>Barnesiella</i> spp.	1.6E8						<=1.6E8
<i>Odoribacter</i> spp.	8.8E7 <b>H</b>						<=8.0E7
<i>Prevotella</i> spp.	4.2E6						1.4E5 - 1.6E7
<b>Firmicutes Phylum</b>							
<i>Anaerotruncus colihominis</i>	9.5E6						<=3.2E7
<i>Butyrivibrio crossotus</i>	<DL <b>L</b>						5.5E3 - 5.9E5
<i>Clostridium</i> spp.	2.9E9						1.7E8 - 1.5E10
<i>Coprococcus eutactus</i>	<DL						<=1.2E8
<i>Faecalibacterium prausnitzii</i>	9.0E8						5.8E7 - 4.7E9
<i>Lactobacillus</i> spp.	7.4E8						8.3E6 - 5.2E9
<i>Pseudoflavonifractor</i> spp.	6.0E7						4.2E5 - 1.3E8
<i>Roseburia</i> spp.	2.1E9						1.3E8 - 1.2E10
<i>Ruminococcus</i> spp.	1.0E9						9.5E7 - 1.6E9
<i>Veillonella</i> spp.	8.5E6						1.2E5 - 5.5E7
<b>Actinobacteria Phylum</b>							
<i>Bifidobacterium</i> spp.	3.3E8						<=6.4E9
<i>Bifidobacterium longum</i>	<DL						<=7.2E8
<i>Collinsella aerofaciens</i>	5.1E8						1.4E7 - 1.9E9
<b>Proteobacteria Phylum</b>							
<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
<b>Euryarchaeota Phylum</b>							
<i>Methanobrevibacter smithii</i>	1.2E8 <b>H</b>						<=8.6E7
<b>Fusobacteria Phylum</b>							
<i>Fusobacterium</i> spp.	<DL						<=2.4E5
<b>Verrucomicrobia Phylum</b>							
<i>Akkermansia muciniphila</i>	2.6E8						>=1.2E6
<b>Firmicutes/Bacteroidetes Ratio</b>							
<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 10<sup>6</sup> 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.



Methodology: culture/MALDI-TOF MS, Automated and Manual Biochemical Methods, Vitek 2® System Microbial identification and Antibiotic susceptibility

## Gastrointestinal Microbiome

### Bacteriology (Culture)

*Lactobacillus* spp.

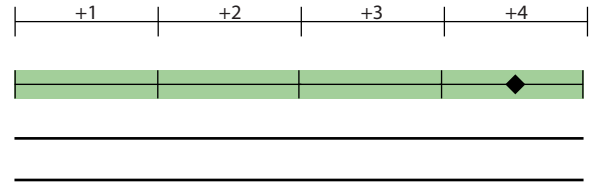
4+ NP

*Escherichia coli*

NG

*Bifidobacterium*

NG



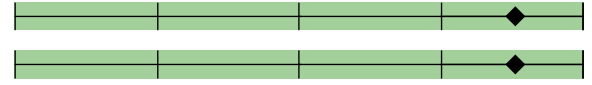
### Additional Bacteria

*alpha haemolytic Streptococcus*

4+ NP

*gamma haemolytic Streptococcus*

4+ NP



### Mycology (Culture)

NG



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 are well-recognized pathogens in clinical literature that have a clearly recognized mechanism of pathogenicity and are considered significant regardless of the quantity that appears in culture.



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	



Methodology: EIA, Fecal Immunochemical Testing (FIT)

## Additional Results

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

†† Results provided from patient input.

\*\* 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: Microscopy*

## Potassium Hydroxide (KOH) Preparation for Yeast

**Result**

KOH Preparation, stool

Rare Yeast Present

**Potassium Hydroxide (KOH) Preparation for Yeast**

These yeast usually represent the organisms isolated by culture. In the presence of a negative yeast culture, microscopic yeast may reflect organisms not viable enough to grow in culture. The presence of yeast on KOH prep should be correlated with the patient's symptoms. However, moderate to many yeast suggests yeast overgrowth.

The result is reported as the amount of yeast seen microscopically.

Rare: 1-2 per slide

Few: 2-5 per high power field (HPF)

Moderate: 5-10 per HPF

Many: >10 per HPF