

Patient: **SAMPLE**
PATIENT

DOB:

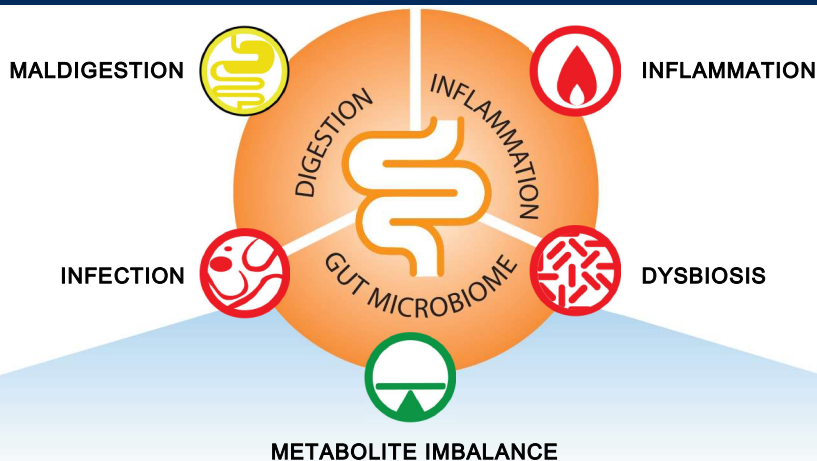
Sex:

MRN:

2200 GI Effects™ Comprehensive Profile - Stool

Powered by **Genova AI**

Results Overview



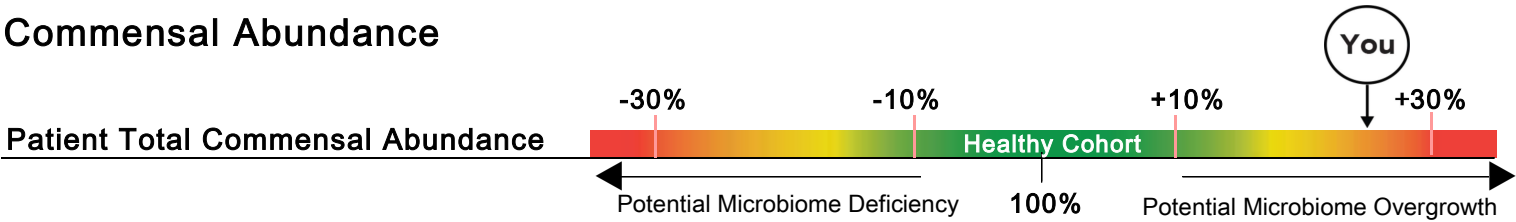
Functional Imbalance Scores

Key **< 2** : Low Need for Support **2-3** : Optional Need for Support **4-6** : Moderate Need for Support **7-10** : High Need for Support

	Need for Digestive Support	Need for Inflammation Modulation	Need for Microbiome Support	Need for Prebiotic Support	Need for Antimicrobial Support
	MALDIGESTION	INFLAMMATION	DYSBIOSIS	METABOLIC IMBALANCE	INFECTION
	5	10	10	0	10
Biomarkers	Pancreatic Elastase ▼ Products of Protein Breakdown ● Fecal Fats ●	Calprotectin ▲ Eosinophil Protein X ▲ Secretory IgA ● Occult Blood ●	IAD/Methane Score ▲ PP Bacteria/Yeast ▲ Reference Variance ▲ Total Abundance ▲	Total SCFA's ● n-Butyrate Conc. ● SCFA (%) ● Beta-glucuronidase ●	Parasitic Infection ▲ PP Bacteria/Yeast ▲ Total Abundance ▲ Pathogenic Bacteria ●
Therapeutic Support Options	• Digestive Enzymes • Betaine HCl • Bile Salts • Apple Cider Vinegar • Mindful Eating Habits • Digestive Bitters	• Elimination Diet/ Food Sensitivity Testing • Mucosa Support: Slippery Elm, Althea, Aloe, DGL, etc. • Zinc Carnosine • L-Glutamine • Quercetin • Turmeric • Omega-3's • GI Referral (If Calpro is Elevated)	• Pre-/Probiotics • Increase Dietary Fiber Intake • Consider SIBO Testing • Increase Resistant Starches • Increase Fermented Foods • Meal Timing	• Pre-/Probiotics • Increased Dietary Fiber Intake • Increase Resistant Starches • increase Fermented Foods • Calcium D-Glucarate (for high beta-glucuronidase)	• Antibiotics (if warranted) • Antimicrobial Herbal Therapy • Antiparasitic Herbal Therapy (if warranted) • <i>Saccharomyces boulardii</i>

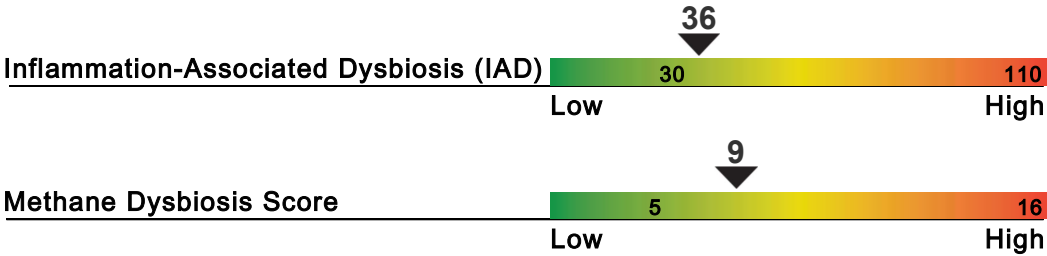
Commensal Microbiome Analysis

Commensal Abundance



Total Commenal Balance: The total commensal abundance is a sum-total of the reported commensal bacteria compared to a healthy cohort. Low levels of commensal bacteria are often observed after antimicrobial therapy, or in diets lacking fiber and/or prebiotic-rich foods and may indicate the need for microbiome support. Conversely, higher total commensal abundance may indicate potential bacteria overgrowth or probiotic supplementation.

Dysbiosis Patterns



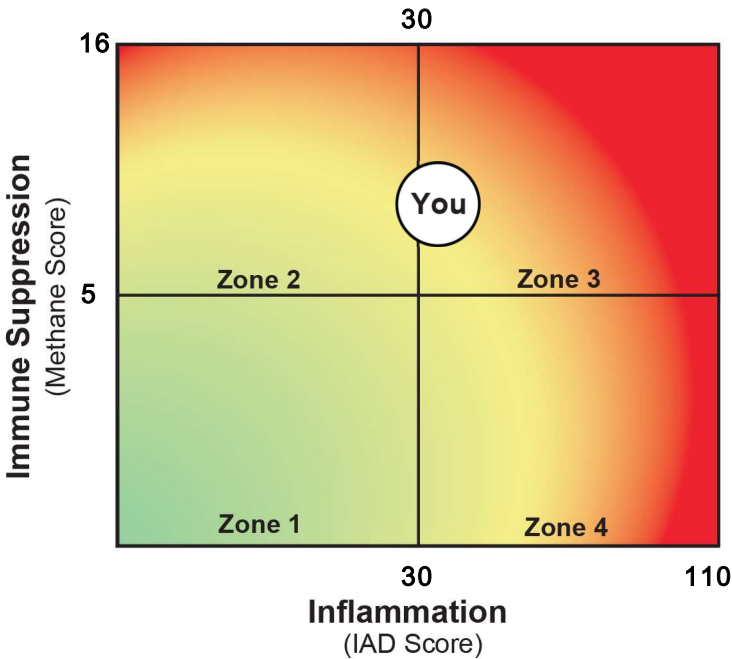
Dysbiosis Patterns: Genova's data analysis has led to the development of unique dysbiosis patterns, related to key physiologic disruptions, such as immunosuppression and inflammation. These patterns may represent dysbiotic changes that could pose clinical significance. Please see Genova's published literature for more details: <https://rdcu.be/bRhzv>

Zone 1: The commensal profile in this zone does not align with profiles associated with intestinal inflammation or immunosuppression. If inflammatory biomarkers are present, other causes need to be excluded, such as infection, food allergy, or more serious pathology.

Zone 2: This pattern of bacteria is associated with impaired intestinal barrier function (low fecal sIgA and EPX). Patients in this zone have higher rates of opportunistic infections (e.g. *Blastocystis spp.* & *Dientamoeba fragilis*) as well as fecal fat malabsorption. Commensal abundance is higher in this group suggesting potential bacterial overgrowth.

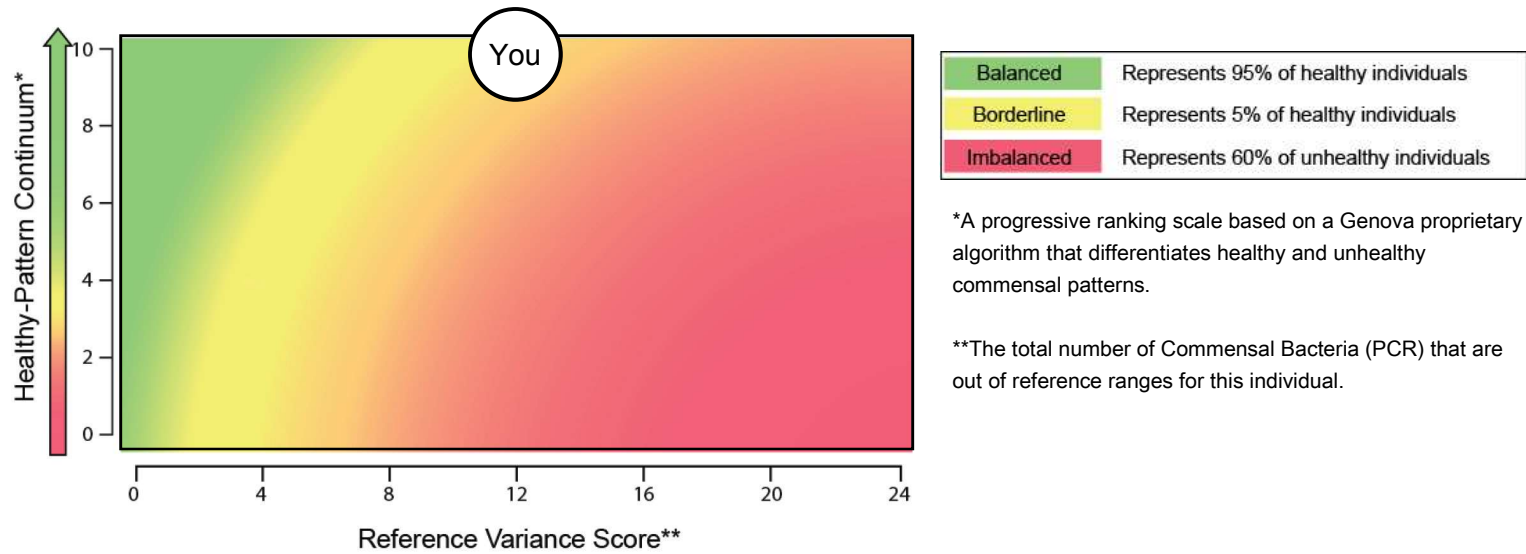
Zone 3: Patients in this zone may have more inflammation compared to those in zone 4. However, commensal abundance is usually higher making use of antimicrobial therapy relatively safer. Patients in this zone may have higher rates of pathogenic infections.

Zone 4: This commensal profile is associated with increased intestinal inflammation. IBD patients are more likely to have this pattern of bacteria. Commensal abundance is lower in this zone; therefore, antibiotic use for GI potential pathogens should be used with caution. In addition to standard treatment for intestinal inflammation, modulation of the commensal gut profile is encouraged.

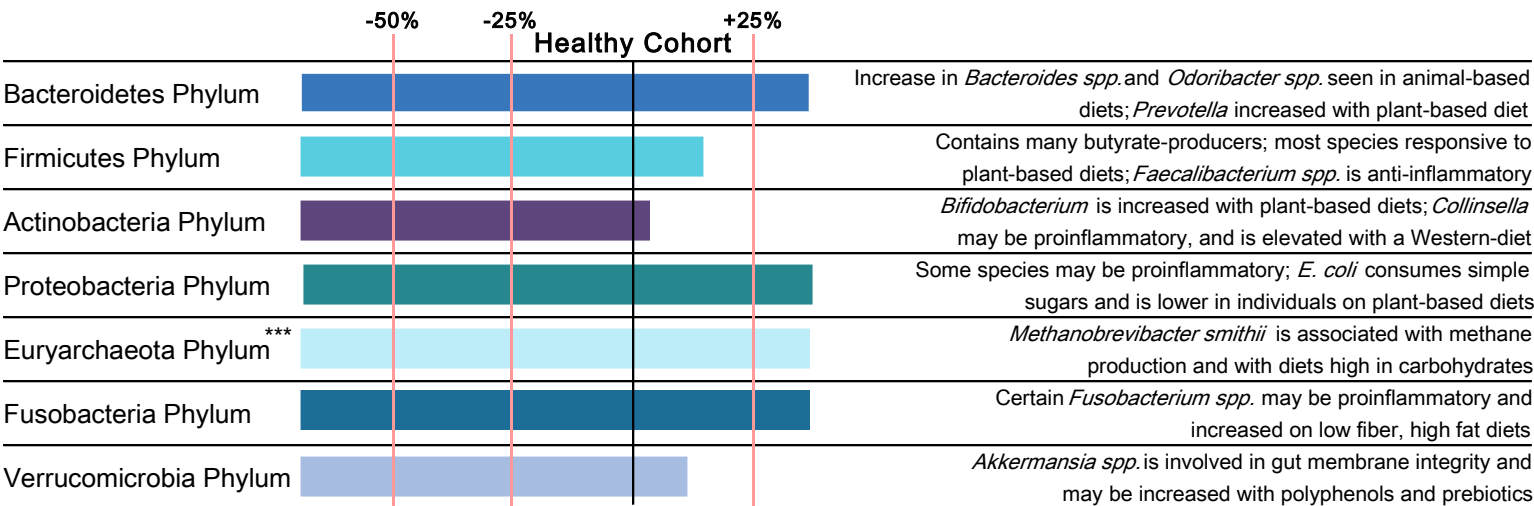


Commensal Microbiome Analysis

Commensal Balance



Relative Commensal Abundance


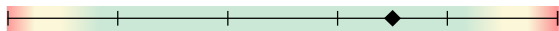

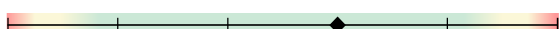
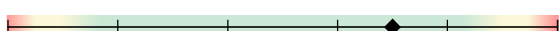


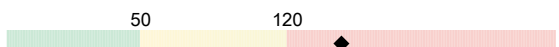

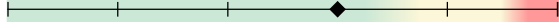
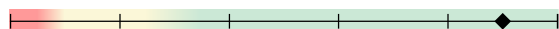
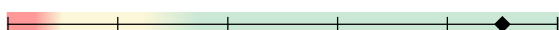


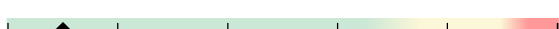
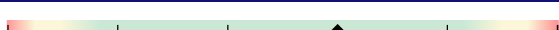


Relative Abundance: The relative abundance compares the quantity of each of 7 major bacterial phyla to a healthy cohort. This can indicate broader variances in the patient's gut microbiome profile. Certain interventions may promote or limit individual phyla when clinically appropriate. Please refer to Genova's Stool Testing Support Guide for more information on modulation of commensal bacteria through diet & nutrient interventions. ***Roughly 75% of the healthy cohort had below detectable levels of *Methanobrevibacter smithii*.

Physician Notes/Recommendations

2200 GI Effects™ Comprehensive Profile - Stool

Methodology: GC/MS, Automated Chemistry, EIA

2200 GI Effects™ Comprehensive Profile - Stool		QUINTILE DISTRIBUTION					Reference Range
	Result	1st	2nd	3rd	4th	5th	
Methodology: GC/MS, Automated Chemistry, EIA							
Digestion and Absorption							
Pancreatic Elastase 1 †	158 L						>200 mcg/g
Products of Protein Breakdown (Total*) (Valerate, Isobutyrate, Isovalerate)	6.0						1.8-9.9 micromol/g
Fecal Fat (Total*)	19.5						3.2-38.6 mg/g
Triglycerides	1.1						0.3-2.8 mg/g
Long-Chain Fatty Acids	12.9						1.2-29.1 mg/g
Cholesterol	0.5						0.4-4.8 mg/g
Phospholipids	5.0						0.2-6.9 mg/g
Inflammation and Immunology							
Calprotectin †	145 H						<=50 mcg/g
Eosinophil Protein X (EPX)†	4.9 H						<=4.6 mcg/g
Fecal secretory IgA	206						<=885 mcg/g
Gut Microbiome Metabolites							
Metabolic							
Short-Chain Fatty Acids (SCFA) (Total*) (Acetate, n-Butyrate, Propionate)	81.3						>=23.3 micromol/g
n-Butyrate Concentration	18.1						>=3.6 micromol/g
n-Butyrate %	22.3						11.8-33.3 %
Acetate %	63.1						48.1-69.2 %
Propionate %	14.6						<=29.3 %
Beta-glucuronidase	2,297						368-6,266 U/g

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

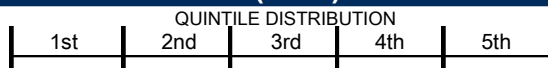
†These results are not represented by quintile values.

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

Methodology: DNA by PCR

Gastrointestinal Microbiome (PCR)

Commensal Bacteria (PCR)

Result
CFU/g stoolReference Range
CFU/g stool

Bacteroidetes Phylum

<i>Bacteroides-Prevotella</i> group	2.4E8		3.4E6-1.5E9
<i>Bacteroides vulgatus</i>	1.2E9		<=2.2E9
<i>Barnesiella</i> spp.	3.6E7		<=1.6E8
<i>Odoribacter</i> spp.	7.1E7		<=8.0E7
<i>Prevotella</i> spp.	1.4E8 H		1.4E5-1.6E7

Firmicutes Phylum

<i>Anaerotruncus colihominis</i>	3.4E7 H		<=3.2E7
<i>Butyrivibrio crossotus</i>	5.0E7 H		5.5E3-5.9E5
<i>Clostridium</i> spp.	2.1E8		1.7E8-1.5E10
<i>Coprococcus eutactus</i>	1.0E8		<=1.2E8
<i>Faecalibacterium prausnitzii</i>	7.5E8		5.8E7-4.7E9
<i>Lactobacillus</i> spp.	1.6E8		8.3E6-5.2E9
<i>Pseudoflavonifractor</i> spp.	3.0E8 H		4.2E5-1.3E8
<i>Roseburia</i> spp.	7.6E7 L		1.3E8-1.2E10
<i>Ruminococcus</i> spp.	1.9E9 H		9.5E7-1.6E9
<i>Veillonella</i> spp.	1.5E8 H		1.2E5-5.5E7

Actinobacteria Phylum

<i>Bifidobacterium</i> spp.	1.5E8		<=6.4E9
<i>Bifidobacterium longum</i>	1.4E8		<=7.2E8
<i>Collinsella aerofaciens</i>	5.1E8		1.4E7-1.9E9

Proteobacteria Phylum

<i>Desulfovibrio piger</i>	8.7E7 H		<=1.8E7
<i>Escherichia coli</i>	1.3E8 H		9.0E4-4.6E7
<i>Oxalobacter formigenes</i>	5.0E7 H		<=1.5E7

Euryarchaeota Phylum

<i>Methanobrevibacter smithii</i>	1.4E8 H		<=8.6E7
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Fusobacteria Phylum

<i>Fusobacterium</i> spp.	2.3E7 H		<=2.4E5
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Verrucomicrobia Phylum

<i>Akkermansia muciniphila</i>	3.1E7		>=1.2E6
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Firmicutes/Bacteroidetes Ratio

<i>Firmicutes/Bacteroidetes</i> (F/B Ratio)	11 L		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 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 (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.

Bacteriology (Culture)

Lactobacillus spp.

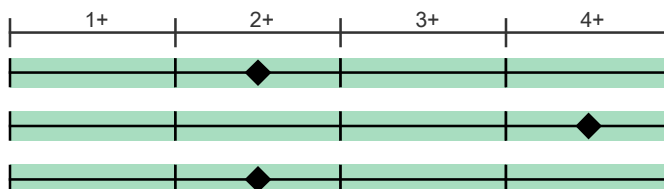
2+ NP

Escherichia coli

4+ NP

Bifidobacterium

2+ NP



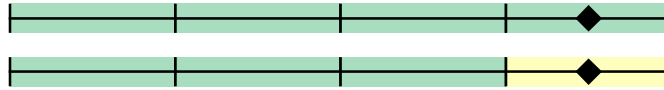
Additional Bacteria

alpha haemolytic Streptococcus

4+ NP

Klebsiella pneumoniae

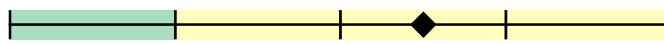
4+ PP



Mycology (Culture)

Candida species

3+ PP



KOH Preparation for Yeast**

Methodology: Potassium Hydroxide (KOH) Preparation for Yeast

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.

Result

KOH Preparation, stool

Few Yeast Present

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

** 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



Parasitology**

Microscopic O&P Results

Microscopic O&P is capable of detecting all described gastrointestinal parasites. The organisms listed in the box represent those commonly found in microscopic stool analysis. Should an organism be detected that is not included in the list below, it will be reported in the Additional Results section. For an extensive reference of all potentially detectable organisms, please visit www.gdx.net/product/gi-effects-comprehensive-stool-test

Genus/species	Result
Nematodes - roundworms	
<i>Ancylostoma/Necator</i> (Hookworm)	Not Detected
<i>Ascaris lumbricoides</i>	Not Detected
<i>Capillaria philippinensis</i>	Not Detected
<i>Enterobius vermicularis</i>	Not Detected
<i>Strongyloides stercoralis</i>	Not Detected
<i>Trichuris trichiura</i>	Not Detected
Cestodes - tapeworms	
<i>Diphyllobothrium latum</i>	Not Detected
<i>Dipylidium caninum</i>	Not Detected
<i>Hymenolepis diminuta</i>	Not Detected
<i>Hymenolepis nana</i>	Not Detected
<i>Taenia</i> spp.	Not Detected
Trematodes - flukes	
<i>Clonorchis/Opisthorchis</i> spp.	Not Detected
<i>Fasciola</i> spp./ <i>Fasciolopsis buski</i>	Not Detected
<i>Heterophyes/Metagonimus</i>	Not Detected
<i>Paragonimus</i> spp.	Not Detected
<i>Schistosoma</i> spp.	Not Detected
Protozoa	
<i>Balantidium coli</i>	Not Detected
<i>Blastocystis</i> spp.	Rare Detected
<i>Chilomastix mesnili</i>	Not Detected
<i>Cryptosporidium</i> spp.	Not Detected
<i>Cyclospora cayetanensis</i>	Not Detected
<i>Dientamoeba fragilis</i>	Moderate Detected
<i>Entamoeba coli</i>	Not Detected
<i>Entamoeba histolytica/dispar</i>	Not Detected
<i>Entamoeba hartmanii</i>	Not Detected
<i>Entamoeba polecki</i>	Not Detected
<i>Endolimax nana</i>	Not Detected
<i>Giardia</i>	Not Detected
<i>Iodamoeba buetschlii</i>	Not Detected
<i>Cystoisospora</i> spp.	Not Detected
<i>Trichomonads</i> (e.g. <i>Pentatrichomonas</i>)	Not Detected
Additional Findings	
White Blood Cells	Not Detected
Charcot-Leyden Crystals	Not Detected
Other Infectious Findings	

One negative specimen does not rule out the possibility of a parasitic infection.

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Parasitology

PCR Parasitology - Protozoa**

Methodologies: DNA by PCR, Next Generation Sequencing

Organism	Result	Units		Expected Result
Blastocystis spp.	6.00e2	femtograms/microliter C&S stool	Detected	Not Detected
Cryptosporidium parvum/hominis	<1.76e2	genome copies/microliter C&S stool	Not Detected	Not Detected
Cyclospora cayetanensis	<2.65e2	genome copies/microliter C&S stool	Not Detected	Not Detected
Dientamoeba fragilis	6.40e2	genome copies/microliter C&S stool	Detected	Not Detected
Entamoeba histolytica	<9.64e1	genome copies/microliter C&S stool	Not Detected	Not Detected
Giardia	<1.36e1	genome copies/microliter C&S stool	Not Detected	Not Detected

Blastocystis spp. Reflex Subtyping

Type 1:	Not Detected	Type 4:	Not Detected	Type 7:	Not Detected
Type 2:	Detected	Type 5:	Not Detected	Type 8:	Not Detected
Type 3:	Not Detected	Type 6:	Not Detected	Type 9:	Not Detected

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Additional Results

Methodology: Fecal Immunochemical Testing (FIT)

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

††Results provided from patient input.
Tests were developed and their performance characteristics determined by Genova Diagnostics. Unless otherwise noted with ♦, the assays have not been cleared by the U.S. Food and Drug Administration.

Zonulin Family Peptide

Methodology: EIA	Result	Reference Range	Zonulin Family Peptide
Zonulin Family Peptide, Stool	100.0	22.3-161.1 ng/mL	<p>This test is for research use only. Genova will not provide support on interpreting the test results. This test does not detect zonulin.¹ The Scheffler paper suggests that the IDK kit may detect a zonulin family peptide, such as properdin. Genova's unpublished data demonstrated that the current IDK kit results were associated with stool inflammation biomarkers and an inflammation-associated dysbiosis profile.</p> <p>The performance characteristics of Zonulin Family Peptide have been verified by Genova Diagnostics, Inc. The assay has not been cleared by the U.S. Food and Drug Administration.</p>

Reference:

1. Scheffler L, et al. Widely Used Commercial ELISA Does Not Detect Precursor of Haptoglobin2, but Recognizes Properdin as a Potential Second Member of the Zonulin Family. *Front Endocrinol.* 2018;9:22.



Macroscopic/Direct Exam for Parasites **

Methodology: Macroscopic Evaluation

No human parasite detected in sample.

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



Mycology Sensitivity

Azole Antifungals

<i>Candida species</i>	R	I	S-DD	S	NI
Fluconazole				0.5	
Voriconazole				<=0.008	
Nystatin	=50				

Natural Agents

<i>Candida species</i>	LOW INHIBITION	HIGH INHIBITION
Berberine		
Caprylic Acid		
Garlic		
Undecylenic Acid		
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.

Nystatin and Natural Agents:

Results for Nystatin are being reported with natural antifungals in this category in accordance with laboratory guidelines for reporting sensitivities. In this assay, inhibition is defined as the reduction level on organism growth as a direct result of inhibition by a natural 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

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

Natural Agents

<i>Klebsiella pneumoniae</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.