



Order:999999-9999



Client #:99999

Doctor:Sample Doctor

Sample Clinic

1234 Main St

Saint Charles, IL 60174 U.S.A.

Patient:SAMPLE PATIENT

Id:99999999

Age:62 DOB:01/12/1957

Sex: Male

Sample Collection

Date/Time

Date Collected

09/23/2019

Date Received

09/26/2019

Date Reported

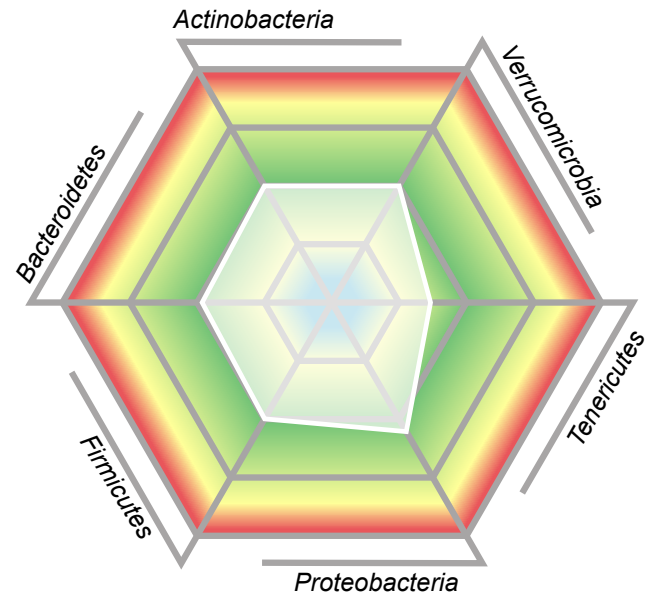
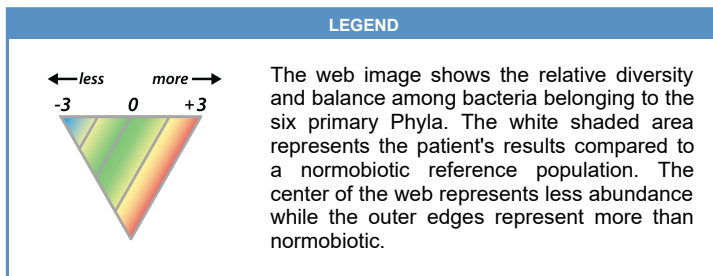
10/10/2019

Specimens Collected

2

Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.



Dysbiosis Index

The Dysbiosis Index (DI) is a calculation with scores from 1 to 5 based on the overall bacterial abundance and profile within the patient's sample as compared to a reference population. Values above 2 indicate a microbiota profile that differs from the defined normobiotic reference population (i.e., dysbiosis). The higher the DI above 2, the more the sample is considered to deviate from normobiosis.

DI Score

5



Expected Flora Summary

Clostridia Class, WRI	◆
Bacteroides fragilis, WRI	◆
Bacteroides spp. & Prevotella spp., WRI	◆
Bifidobacterium spp., WRI	◆
Escherichia spp., WRI	◆
Lactobacillus spp., WRI	◆

Key Findings

Salmonella spp., Detected
Lactoferrin, Very High
Calprotectin, Very High
Morganella morganii, Detected
Salmonella group, Detected
Yeast, Detected
Candida albicans, Detected

Notes:

WRI = Within Reference Interval



Microbiome Bacterial Abundance; Multiplex PCR



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LEGEND



Results are graphed as deviations from a normobiotic population. Normobiosis or a normobiotic state characterizes a composition of the microbiota profile in which microorganisms with potential health benefits predominate in abundance and diversity over potentially harmful ones.

<i>Actinobacteria</i>	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Actinobacteria</i>	0			▲					-1 to +1
<i>Actinomycetales</i>	0			▲					0 to +1
<i>Bifidobacterium</i> spp.	0			▲					-1 to +1
<i>Bacteroidetes</i>	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Alistipes</i> spp.	-1			▲					-1 to +1
<i>Alistipes onderdonkii</i>	-1			▲					-1 to +1
<i>Bacteroides fragilis</i>	+1					▲			0 to +1
<i>Bacteroides</i> spp. & <i>Prevotella</i> spp.	0			▲					-1 to +1
<i>Bacteroides stercoris</i>	0			▲					0 to +1
<i>Bacteroides zoogloformans</i>	0			▲					0 to +1
<i>Parabacteroides johnsonii</i>	0			▲					0 to +1
<i>Parabacteroides</i> spp.	0			▲					-1 to +1
<i>Firmicutes</i>	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Firmicutes</i>	0			▲					-1 to +1
Bacilli Class	-1			▲					-1 to +1
<i>Catenibacterium mitsuokai</i>	0			▲					-1 to +1
Clostridia Class	+1					▲			-1 to +1
<i>Clostridium</i> L2-50	0			▲					-1 to +1

The gray-shaded area of the bar graph represents reference values outside the reporting limits for this test.

*This test was developed and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements. The U. S. Food and Drug Administration (FDA) has not approved or cleared this test; however, FDA clearance is not currently required for clinical use. The results are not intended to be used as a sole means for clinical diagnosis or patient management decisions.

Notes:

Methodology: Multiplex PCR



Microbiome Bacterial Abundance; Multiplex PCR



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<i>Firmicutes</i>	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Dialister invisus</i>	0				▲				0 to +1
<i>Dialister invisus</i> & <i>Megasphaera micronuciformis</i>	0				▲				0 to +1
<i>Dorea</i> spp.	0				▲				0 to +1
<i>Eubacterium bifforme</i>	0				▲				0 to +1
<i>Eubacterium hallii</i>	0				▲				-1 to +1
<i>Eubacterium rectale</i>	0				▲				0 to +1
<i>Eubacterium siraeum</i>	0				▲				-1 to +1
<i>Faecalibacterium prausnitzii</i>	-2		▲						-1 to +1
Lachnospiraceae	0				▲				-1 to +1
<i>Lactobacillus ruminis</i> & <i>Pediococcus acidilactici</i>	0				▲				0 to +1
<i>Lactobacillus</i> spp.	0				▲				0 to +1
<i>Phascolarctobacterium</i> spp.	0				▲				0 to +1
<i>Ruminococcus albus</i> & <i>R. bromii</i>	0				▲				0 to +1
<i>Ruminococcus gnavus</i>	+3							▲	0 to +1
<i>Streptococcus agalactiae</i> & <i>Eubacterium rectale</i>	0				▲				0 to +1
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i> & <i>S. sanguinis</i>	0				▲				-1 to +1
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i>	0				▲				0 to +1
<i>Streptococcus</i> spp.	0				▲				0 to +1
<i>Veillonella</i> spp.	0				▲				-1 to +1

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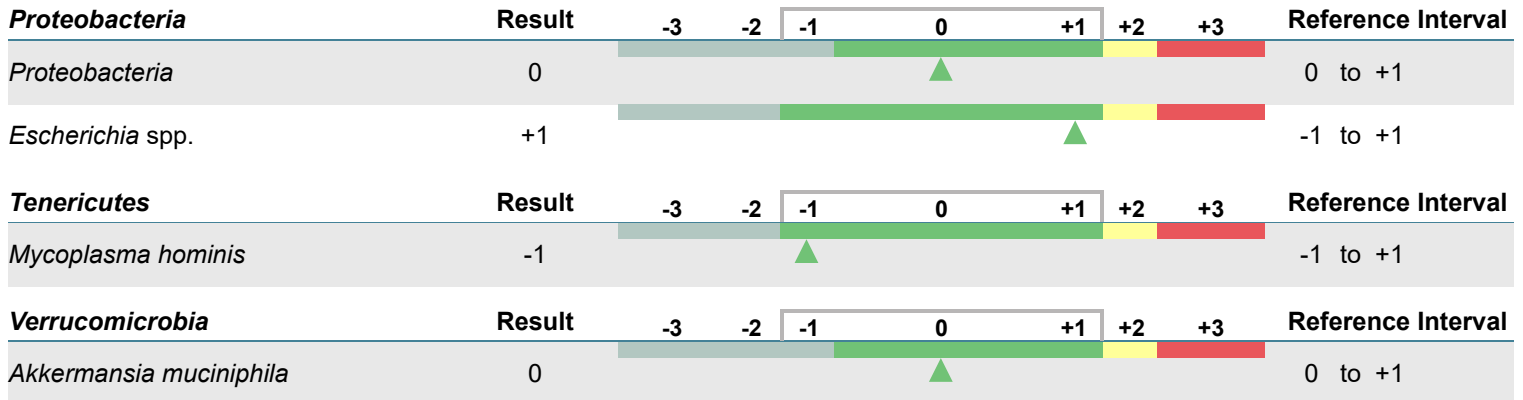
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Microbiome Abundance Information:

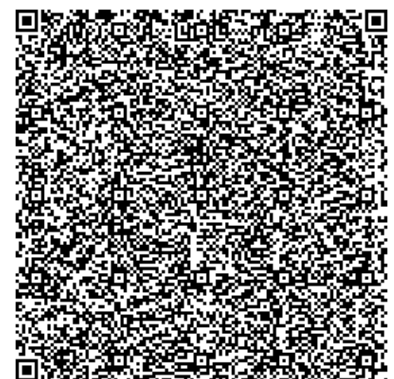
The GI360™ Microbiome Profile is a gut microbiota profiling test that characterizes patient results by determining deviation from a well-defined state of normobiosis using PCR. The profiling approach contrasts to direct diagnosis of a particular disease by detecting one organism. Characteristic sets of bacteria are required in a healthy normobiotic gut, and deviation will represent a potentially dysbiotic state. Measurement of deviation in bacterial microbiota makes it possible to characterize differences in the patient's results based on an established algorithm that defines normobiosis. By combining information from a well-defined set of predetermined PCR probes, this test enables highly reproducible and standardized information to be derived from the complex human microbiota. A summary web graphic chart is provided to represent bacterial abundance and diversity within a stool sample.

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Viruses	Result
Adenovirus F40/41	Negative <input checked="" type="checkbox"/>
Norovirus GI/GII	Negative <input checked="" type="checkbox"/>
Rotavirus A	Negative <input checked="" type="checkbox"/>

Pathogenic Bacteria	Result
<i>Campylobacter (C. jejuni, C. coli and C. lari)</i>	Negative <input checked="" type="checkbox"/>
<i>Clostridium difficile (Toxin A/B)</i>	Negative <input checked="" type="checkbox"/>
<i>Escherichia coli O157</i>	Negative <input checked="" type="checkbox"/>
Enterotoxigenic <i>Escherichia coli</i> (EPEC) It/st	Negative <input checked="" type="checkbox"/>
<i>Salmonella</i> spp.	Positive <input type="checkbox"/>
Shiga-like toxin-producing <i>Escherichia coli</i> (STEC) stx1/stx2	Negative <input checked="" type="checkbox"/>
<i>Shigella (S. boydii, S. sonnei, S. flexneri & S. dysenteriae)</i>	Negative <input checked="" type="checkbox"/>
<i>Vibrio cholerae</i>	Negative <input checked="" type="checkbox"/>

Parasites	Result
<i>Cryptosporidium (C. parvum and C. hominis)</i>	Negative <input checked="" type="checkbox"/>
<i>Entamoeba histolytica</i>	Negative <input checked="" type="checkbox"/>
<i>Giardia duodenalis (AKA intestinalis & lamblia)</i>	Negative <input checked="" type="checkbox"/>

Notes:

Methodology: Multiplex PCR

