

YOUR PERSONALIZED REPORT

PATHOGENS

The testing includes pathogens (bacterial, parasitic and viral) commonly known to cause gastroenteritis. Note that not all individuals with positive findings will present with symptoms. Many factors, including the health of the individual (such as immune health, digestive function, and microbiome balance), the transient nature of most pathogens, and the presence and expression of virulence factors, all contribute to pathogen virulence and individual symptoms.

BACTERIAL PATHOGENS	Result	Reference
<i>Campylobacter</i>	<dl	< 1.00e3
<i>C. difficile</i> Toxin A	<dl	< 1.00e3
<i>C. difficile</i> Toxin B	<dl	< 1.00e3
Enterohemorrhagic <i>E. coli</i>	<dl	< 1.00e3
<i>E. coli</i> O157	<dl	< 1.00e3
Enteroinvasive <i>E. coli</i> / <i>Shigella</i>	<dl	< 1.00e3
Enterotoxigenic <i>E. coli</i> LT/ST	<dl	< 1.00e3
Shiga-like Toxin <i>E. coli</i> stx1	<dl	< 1.00e3
Shiga-like Toxin <i>E. coli</i> stx2	<dl	< 1.00e3
<i>Salmonella</i>	<dl	< 1.00e4
<i>Vibrio cholerae</i>	<dl	< 1.00e5
<i>Yersinia enterocolitica</i>	<dl	< 1.00e5
PARASITIC PATHOGENS		
<i>Cryptosporidium</i>	<dl	< 1.00e6
<i>Entamoeba histolytica</i>	<dl	< 1.00e4
<i>Giardia</i>	<dl	< 5.00e3
VIRAL PATHOGENS		
Adenovirus 40/41	<dl	< 1.00e10
Norovirus GI/II	<dl	< 1.00e7

KEY: Results are reported as genome equivalents per gram of stool, which is a standard method for estimating the number of microbes measured per gram of stool, based on qPCR analysis of DNA samples.

Results are expressed in standard scientific notation. For example, a reported result of 3.5e7 is equivalent to 3.5×10^7 microbes per gram, which equals 35,000,000 (35 million) microbes per gram of stool.

< dl represents results below detectable limit.

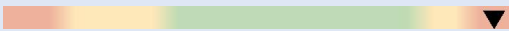
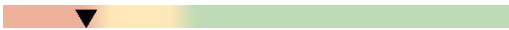
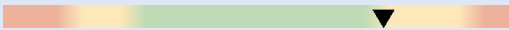
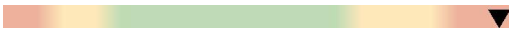
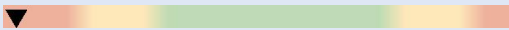

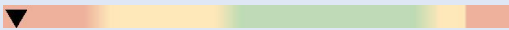

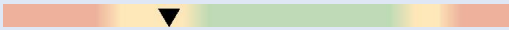
HELICOBACTER PYLORI

H. PYLORI & VIRULENCE FACTORS



	Result	Reference
<i>Helicobacter pylori</i>	2.22e2	< 1.00e3
Virulence Factor, babA	N/A	Negative
Virulence Factor, cagA	N/A	Negative
Virulence Factor, dupA	N/A	Negative
Virulence Factor, iceA	N/A	Negative
Virulence Factor, oipA	N/A	Negative
Virulence Factor, vacA	N/A	Negative
Virulence Factor, virB	N/A	Negative
Virulence Factor, virD	N/A	Negative

COMMENSAL/KEYSTONE BACTERIA

COMMENSAL BACTERIA

	Result	Reference
<i>Bacteroides fragilis</i>	3.21e11 H 	1.6e9 - 2.5e11
<i>Bifidobacterium</i> spp.	5.26e7 L 	> 6.7e7
<i>Enterococcus</i> spp.	4.06e7 	1.9e5 - 2.0e8
<i>Escherichia</i> spp.	1.51e10 H 	3.7e6 - 3.8e9
<i>Lactobacillus</i> spp.	9.12e2 L 	8.6e5 - 6.2e8
<i>Enterobacter</i> spp.	2.62e7 	1.0e6 - 5.0e7
<i>Akkermansia muciniphila</i>	<dl L 	1.0e1 - 8.2e6
<i>Faecalibacterium prausnitzii</i>	1.62e5 	1.0e3 - 5.0e8
<i>Roseburia</i> spp.	1.56e8 	5.0e7 - 2.0e10

BACTERIAL PHYLA

<i>Bacteroidetes</i>	7.12e12 H 	8.6e11 - 3.3e12
<i>Firmicutes</i>	2.11e10 L 	5.7e10 - 3.0e11
<i>Firmicutes:Bacteroidetes Ratio</i>	0.00 	< 1.0

OPPORTUNISTIC/OVERGROWTH MICROBES

DYSBIOTIC & OVERGROWTH BACTERIA	Result	Reference
<i>Bacillus</i> spp.	1.46e5	< 1.76e6
<i>Enterococcus faecalis</i>	2.98e3	< 1.00e4
<i>Enterococcus faecium</i>	1.23e2	< 1.00e4
<i>Morganella</i> spp.	<dl	< 1.00e3
<i>Pseudomonas</i> spp.	2.06e8 High ↑	< 1.00e4
<i>Pseudomonas aeruginosa</i>	5.46e5 High ↑	< 5.00e2
<i>Staphylococcus</i> spp.	1.11e4 High ↑	< 1.00e4
<i>Staphylococcus aureus</i>	9.93e1	< 5.00e2
<i>Streptococcus</i> spp.	3.95e2	< 1.00e3
COMMENSAL OVERGROWTH MICROBES		
<i>Desulfovibrio</i> spp.	1.76e7	< 7.98e8
<i>Methanobacteriaceae</i> (family)	1.02e8	< 3.38e8
INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA		
<i>Citrobacter</i> spp.	8.05e6 High ↑	< 5.00e6
<i>Citrobacter freundii</i>	4.50e4	< 5.00e5
<i>Klebsiella</i> spp.	7.18e4 High ↑	< 5.00e3
<i>Klebsiella pneumoniae</i>	1.19e3	< 5.00e4
<i>M. avium</i> subsp. <i>paratuberculosis</i>	<dl	< 5.00e3
<i>Proteus</i> spp.	6.01e5 High ↑	< 5.00e4
<i>Proteus mirabilis</i>	6.97e2	< 1.00e3
COMMENSAL INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA		
<i>Enterobacter</i> spp.	2.62e7	< 5.00e7
<i>Escherichia</i> spp.	1.51e10 High ↑	< 3.80e9
<i>Fusobacterium</i> spp.	3.25e6	< 1.00e8
<i>Prevotella</i> spp.	1.70e7	< 1.00e8

FUNGI/YEAST

FUNGI/YEAST	Result	Reference
<i>Candida</i> spp.	<dl	< 5.00e3
<i>Candida albicans</i>	<dl	< 5.00e2
<i>Geotrichum</i> spp.	<dl	< 3.00e2
<i>Microsporidium</i> spp.	<dl	< 5.00e3
<i>Rhodotorula</i> spp.	<dl	< 1.00e3

VIRUSES

VIRUSES	Result	Reference
Cytomegalovirus	<dl	< 1.00e5
Epstein-Barr Virus	<dl	< 1.00e7

PARASITES

PROTOZOA	Result	Reference
<i>Blastocystis hominis</i>	<dl	< 2.00e3
<i>Chilomastix mesnili</i>	<dl	< 1.00e5
<i>Cyclospora</i> spp.	<dl	< 5.00e4
<i>Dientamoeba fragilis</i>	<dl	< 1.00e5
<i>Endolimax nana</i>	<dl	< 1.00e4
<i>Entamoeba coli</i>	<dl	< 5.00e6
<i>Pentatrichomonas hominis</i>	<dl	< 1.00e2
WORMS		
<i>Ancylostoma duodenale</i>	Not Detected	Not Detected
<i>Ascaris lumbricoides</i>	Not Detected	Not Detected
<i>Necator americanus</i>	Not Detected	Not Detected
<i>Trichuris trichiura</i>	Not Detected	Not Detected
<i>Taenia</i> spp.	Not Detected	Not Detected

INTESTINAL HEALTH MARKERS

DIGESTION	Result	Reference
Steatocrit	<dl 	< 15 %
Elastase-1	>750 	> 200 ug/g
GI MARKERS		
β-Glucuronidase	1198 	< 2486 U/mL
Occult Blood - FIT	<dl 	< 10 ug/g
IMMUNE RESPONSE		
Secretory IgA	1435 	510 - 2010 ug/g
Anti-gliadin IgA	108 	< 175 U/L
Eosinophil Activation Protein (EDN, EPX)	1.10 	< 2.34 ug/g
INFLAMMATION		
Calprotectin	21 	< 173 ug/g

The assays were developed and/or the performance characteristics determined by Diagnostic Solutions Laboratory.

H. PYLORI ANTIBIOTIC RESISTANCE GENES

	Result	Reference
Amoxicillin	N/A	Negative
<i>Genes associated with amoxicillin resistance</i>		
PBP1A S414R	N/A	
PBP1A T556S	N/A	
PBP1A N562Y	N/A	

	Result	Reference
Clarithromycin	N/A	Negative
<i>Genes associated with clarithromycin resistance</i>		
A2142C	N/A	
A2142G	N/A	
A2143G	N/A	

	Result	Reference
Fluoroquinolones	N/A	Negative
<i>Genes associated with fluoroquinolone resistance</i>		
gyrA N87K	N/A	
gyrA D91N	N/A	
gyrA D91G	N/A	
gyrB S479N	N/A	
gyrB R484K	N/A	

	Result	Reference
Tetracycline	N/A	Negative
<i>Genes associated with tetracycline resistance</i>		
A926G	N/A	
AGA926-928TTC	N/A	

UNIVERSAL ANTIBIOTIC RESISTANCE GENES

	Result	Reference		Result	Reference		Result	Reference
b-Lactams	Negative	Negative	Macrolides	Negative	Negative	Trimethoprim	Negative	Negative
blaNDM-1	Absent		acrA	Absent		dfrA1	Absent	
CTX-M 1	Absent		acrB	Absent		dfrA12	Absent	
CTX-M 2	Absent		emrE	Absent		dfrA14	Absent	
CTX-M 8/25	Absent		ermA	Absent		dfrA15	Absent	
CTX-M 9	Absent		ermB	Absent		dfrA17	Absent	
GES	Absent		ermC	Absent		dfrA5	Absent	
OXA-1	Absent		macA	Absent		dfrA7	Absent	
PER-1	Absent		macB	Absent		dfrB1	Absent	
PER-2	Absent		mefA	Absent		dfrB2	Absent	
SHV	Absent		mphA	Absent		dfrB3	Absent	
TEM	Absent		msrA	Absent				
VEB	Absent		tolC	Absent				
Fluoroquinolones	Positive	Negative	Ciprofloxacin	Negative	Negative	Sulfonamides	Positive	Negative
qnrA	Present		emea	Absent		sul1	Present	
qnrB	Absent		pmra	Absent		sul2	Present	
qnrS1	Absent					sul3	Present	
Vancomycin	Negative	Negative	Nitroimidazoles	Negative	Negative	Methacillin	Negative	Negative
vanA	Absent		nimA	Absent		mecA	Absent	
vanA2	Absent		nimB	Absent		Chloramphenicol	Negative	Negative
vanB	Absent		nimC	Absent		cata13	Absent	
vanC1	Absent		nimD	Absent				
vanC2-1	Absent		nimE	Absent				
vanC2-2	Absent							

Detection of resistance-associated genes may not confer phenotypic drug resistance. Detected genes cannot be associated with specific microbes.