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DNA STOOL ANALYSIS BY QUANTITATIVE PCR

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 x 10⁷ 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>	1.16e2	< 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>	9.53e9		1.6e9 - 2.5e11
<i>Bifidobacterium</i> spp.	1.77e9		> 6.7e7
<i>Enterococcus</i> spp.	4.15e7		1.9e5 - 2.0e8
<i>Escherichia</i> spp.	1.90e7		3.7e6 - 3.8e9
<i>Lactobacillus</i> spp.	2.56e6		8.6e5 - 6.2e8
<i>Enterobacter</i> spp.	1.63e6		1.0e6 - 5.0e7
<i>Akkermansia muciniphila</i>	<dl L		1.0e1 - 8.2e6
<i>Faecalibacterium prausnitzii</i>	<dl L		1.0e3 - 5.0e8
<i>Roseburia</i> spp.	2.04e8		5.0e7 - 2.0e10

BACTERIAL PHYLA

<i>Bacteroidetes</i>	3.25e11 L		8.6e11 - 3.3e12
<i>Firmicutes</i>	3.00e10 L		5.7e10 - 3.0e11
<i>Firmicutes:Bacteroidetes Ratio</i>	0.09		< 1.0

OPPORTUNISTIC/OVERGROWTH MICROBES

DYSBIOTIC & OVERGROWTH BACTERIA	Result	Reference
<i>Bacillus</i> spp.	2.75e4	< 1.76e6
<i>Enterococcus faecalis</i>	<dl	< 1.00e4
<i>Enterococcus faecium</i>	<dl	< 1.00e4
<i>Morganella</i> spp.	<dl	< 1.00e3
<i>Pseudomonas</i> spp.	<dl	< 1.00e4
<i>Pseudomonas aeruginosa</i>	<dl	< 5.00e2
<i>Staphylococcus</i> spp.	<dl	< 1.00e4
<i>Staphylococcus aureus</i>	4.19e1	< 5.00e2
<i>Streptococcus</i> spp.	1.88e3 High ↑	< 1.00e3
COMMENSAL OVERGROWTH MICROBES		
<i>Desulfovibrio</i> spp.	<dl	< 7.98e8
Methanobacteriaceae (family)	3.04e6	< 3.38e8
INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA		
<i>Citrobacter</i> spp.	<dl	< 5.00e6
<i>Citrobacter freundii</i>	<dl	< 5.00e5
<i>Klebsiella</i> spp.	1.95e4 High ↑	< 5.00e3
<i>Klebsiella pneumoniae</i>	1.28e2	< 5.00e4
<i>M. avium</i> subsp. <i>paratuberculosis</i>	<dl	< 5.00e3
<i>Proteus</i> spp.	<dl	< 5.00e4
<i>Proteus mirabilis</i>	<dl	< 1.00e3
COMMENSAL INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA		
<i>Enterobacter</i> spp.	1.63e6	< 5.00e7
<i>Escherichia</i> spp.	1.90e7	< 3.80e9
<i>Fusobacterium</i> spp.	1.42e6	< 1.00e8
<i>Prevotella</i> spp.	4.24e6	< 1.00e8

FUNGI/YEAST

FUNGI/YEAST	Result	Reference
<i>Candida</i> spp.	1.57e4 High ↑	< 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

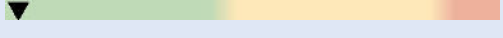

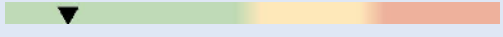



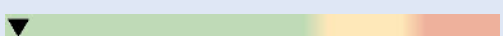

VIRUSES

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	1171 	< 2486 U/mL
Occult Blood - FIT	<dl 	< 10 ug/g
IMMUNE RESPONSE		
Secretory IgA	969 	510 - 2010 ug/g
Anti-gliadin IgA	64 	< 175 U/L
Eosinophil Activation Protein (EDN, EPX)	0.48 	< 2.34 ug/g
INFLAMMATION		
Calprotectin	<dl 	< 173 ug/g

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	