



PATIENT: XXXXXXXXXXXXXXXXXXXX

TEST REF: TST-NL-XXXXX

TEST NUMBER: T-NL-XXXXXX

COLLECTED: 2025-XX-XX

GENDER: XXXXX

PRACTITIONER:

AGE: XX

XXXXXXXXXXXXXXXXXXXXXX

XXXXXXXXXXXXXXXXXXXXXX

TEST NAME: Stoolomx-gi-map-sample-report

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
<i>Enterohemorrhagic E. coli</i>	2.43e4 High ↑	< 1.00e3
<i>E. coli</i> O157	<dl	< 1.00e3
Enteroinvasive <i>E. coli/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.

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

TEST NAME: Stoolomx-gi-map-sample-report

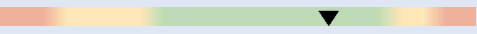

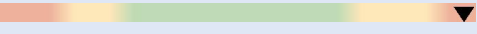

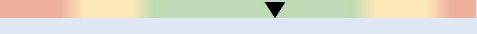
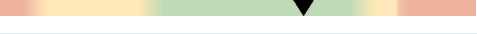
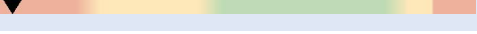
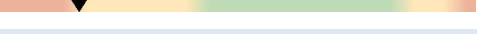
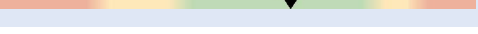
HELICOBACTER PYLORI

H. PYLORI & VIRULENCE FACTORS




	Result	Reference
<i>Helicobacter pylori</i>	3.05e2	< 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>	5.85e10		1.6e9 - 2.5e11
<i>Bifidobacterium</i> spp.	1.06e11		> 6.7e7
<i>Enterococcus</i> spp.	8.37e8 H		1.9e5 - 2.0e8
<i>Escherichia</i> spp.	8.73e9 H		3.7e6 - 3.8e9
<i>Lactobacillus</i> spp.	3.24e7		8.6e5 - 6.2e8
<i>Enterobacter</i> spp.	1.74e7		1.0e6 - 5.0e7
<i>Akkermansia muciniphila</i>	<dl L		1.0e1 - 8.2e6
<i>Faecalibacterium prausnitzii</i>	1.38e3		1.0e3 - 5.0e8
<i>Roseburia</i> spp.	1.81e9		5.0e7 - 2.0e10

BACTERIAL PHYLA

<i>Bacteroidetes</i>	4.92e12 H		8.6e11 - 3.3e12
<i>Firmicutes</i>	4.70e11 H		5.7e10 - 3.0e11
<i>Firmicutes:Bacteroidetes Ratio</i>	0.10		< 1.0

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OPPORTUNISTIC/OVERGROWTH MICROBES

DYSBIOTIC & OVERGROWTH BACTERIA

	Result	Reference
<i>Bacillus</i> spp.	7.97e6 High ↑	< 1.76e6
<i>Enterococcus faecalis</i>	3.89e6 High ↑	< 1.00e4
<i>Enterococcus faecium</i>	2.12e4 High ↑	< 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>	4.05e3 High ↑	< 5.00e2
<i>Streptococcus</i> spp.	2.29e4 High ↑	< 1.00e3

COMMENSAL OVERGROWTH MICROBES

<i>Desulfovibrio</i> spp.	1.72e8	< 7.98e8
<i>Methanobacteriaceae</i> (family)	9.06e7	< 3.38e8

INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA

<i>Citrobacter</i> spp.	<dl	< 5.00e6
<i>Citrobacter freundii</i>	7.75e4	< 5.00e5
<i>Klebsiella</i> spp.	<dl	< 5.00e3
<i>Klebsiella pneumoniae</i>	5.31e2	< 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.	1.74e7	< 5.00e7
<i>Escherichia</i> spp.	8.73e9 High ↑	< 3.80e9
<i>Fusobacterium</i> spp.	1.26e6	< 1.00e8
<i>Prevotella</i> spp.	1.96e7	< 1.00e8

FUNGI/YEAST

FUNGI/YEAST

	Result	Reference
<i>Candida</i> spp.	9.57e4 High ↑	< 5.00e3
<i>Candida albicans</i>	6.22e1	< 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

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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

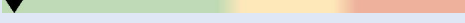

<i>Ancylostoma duodenale</i>	Not Detected	Not Detected
<i>Ascaris lumbricoides</i>	Not Detected	Not Detected
<i>Necator americanus</i>	Not Detected	Not Detected
<i>Trichuris trichiura</i>	Not Detected	Not Detected
<i>Taenia</i> spp.	Not Detected	Not Detected

INTESTINAL HEALTH MARKERS

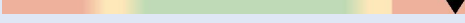
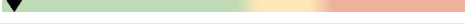
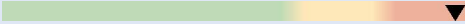
DIGESTION

	Result	Reference
Steatocrit	<dl 	< 15 %
Elastase-1	>750 	> 200 ug/g

GI MARKERS

β-Glucuronidase	202 	< 2486 U/mL
Occult Blood - FIT	9 	< 10 ug/g


IMMUNE RESPONSE

Secretory IgA	>6000 H 	510 - 2010 ug/g
Anti-gliadin IgA	82 	< 175 U/L
Eosinophil Activation Protein (EDN, EPX)	7.94 H 	< 2.34 ug/g

INFLAMMATION

Calprotectin	1385 H 	< 173 ug/g
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ADD-ON TESTS

Zonulin	531.5 H 	< 175 ng/g
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TEST NAME: Stoolomx-gi-map-sample-report

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	

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BILE ACIDS - SUMMARY

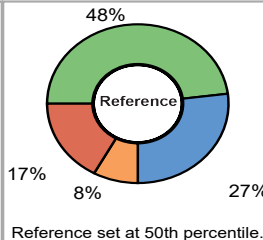
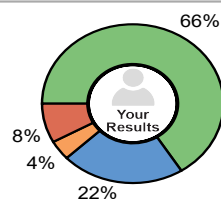
The Bile Acids Panel assesses fecal concentrations of primary and secondary bile acids and provides insights into microbiome diversity, digestive function, motility, and various gut-related conditions.

SUMMARY INFO

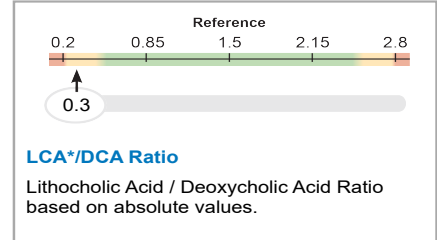
Total Bile Acids - ng/g	2.61e6	<div><div></div></div>	2.37e5 - 6.29e6
Secondary Bile Acids- %	98.1	<div><div></div></div>	> 90.5
Primary Bile Acids - %	1.9	<div><div></div></div>	< 7.8

Bile Acid Percentages

- Deoxycholic Acid-DCA
- Lithocholic Acid-LCA*
- Iso-LCA
- Other



Reference set at 50th percentile.



*LCA value is the summation of LCA + Allo-LCA



SHORT CHAIN FATTY ACIDS - SUMMARY

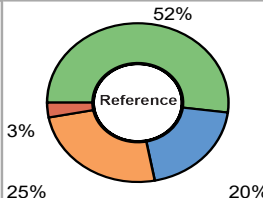
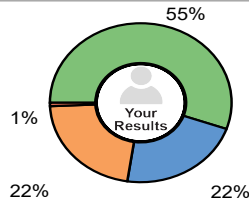
The Postbiotic Fatty Acid Metabolite Panel assesses fecal concentrations of straight chain and branched chain fatty acids. These metabolites provide a variety of beneficial effects for intestinal health, anti-inflammation, metabolism and immunity, and give dietary insight.

SUMMARY INFO

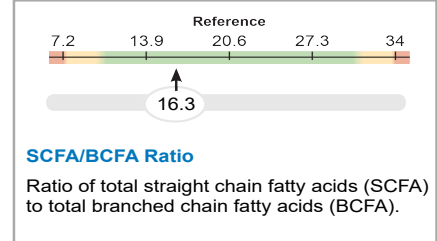
Major Straight Chain Fatty Acids - µg/g	2.16e4 H	<div><div></div></div>	3.63e3 - 1.95e4
Acetate - %	55.3	<div><div></div></div>	38.3 - 68.0
Butyrate - %	22.0	<div><div></div></div>	7.7 - 32.6
Propionate - %	21.9	<div><div></div></div>	14.1 - 33.6
Valerate - %	0.7	<div><div></div></div>	0.5 - 6.2

Major SCFA Percent

- Acetate
- Butyrate
- Propionate
- Valerate



Reference set at 50th percentile.



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BILE ACIDS - RESULTS

PRIMARY BILE ACIDS	Abbreviation	Conjugation**	Result ng/g	Reference ng/g
Total Primary Bile Acids			4.87e4 L	2.37e5 - 4.85e6
Cholic Acid	CA	U	4.04e3	< 5.92e4
Chenodeoxycholic Acid	CDCA	U	3.08e4	2.16e3 - 6.87e4
Taurochenodeoxycholic Acid	TCDCA	C	7.39e2 H	< 4.14e2
Taurocholic Acid	TCA	C	1.51e3 H	< 5.19e2
Glycochenodeoxycholic Acid	GCDCA	C	3.59e2	1.18e1 - 8.11e2
Glycocholic Acid	GCA	C	3.04e2	< 7.55e2
Hyocholic Acid	HCA	U	1.10e4 H	< 5.50e3
SECONDARY BILE ACIDS	Abbreviation	Conjugation**	Result ng/g	Reference ng/g
Total Secondary Bile Acids			2.56e6	1.97e5 - 6.23e6
Deoxycholic Acid	DCA	U	1.73e6	2.24e3 - 2.33e6
Lithocholic Acid*	LCA	U	5.71e5	6.12e3 - 1.37e6
Isolithocholic Acid	ISO-LCA	U	9.78e4	2.21e3 - 5.36e5
12-Ketolithocholic Acid	12-KLCA	U	9.46e4	1.87e3 - 5.30e5
3-oxoDeoxycholic Acid	3-oxoDCA	U	4.74e3	3.53e2 - 1.12e5
Ursodeoxycholic Acid	UDCA	U	<dl	< 5.77e4
7-Ketolithocholic Acid	7-KLCA	U	2.10e3	< 8.94e3
7-Ketodeoxycholic Acid	7-KDCA	U	1.10e3	< 1.01e4
Dehydrolithocholic Acid	DHLCA	U	1.33e3	< 4.52e4
Hyodeoxycholic Acid	HDCA	U	6.28e4 H	< 5.27e4
Alloisolithocholic Acid	AlloIso-LCA	U	8.44e2	< 7.53e4
3-Dehydrocholic Acid	3-DHCA	U	1.12e2	< 5.85e2
Glycolithocholic Acid	GLCA	C	<dl	< 2.20e2
Glycoursodeoxycholic Acid	GUDCA	C	3.81e1	< 3.08e2
Glycodeoxycholic Acid	GDCA	C	<dl	< 5.40e2
Taurolithocholic Acid	TLCA	C	<dl	< 2.68e2
Tauroursodeoxycholic Acid	TUDCA	C	<dl	< 1.28e2
Taurodeoxycholic Acid	TDCA	C	6.36e1	< 8.56e2

*LCA value is the summation of LCA + Allo-LCA | ** C = Conjugated | U = Unconjugated

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SHORT CHAIN FATTY ACIDS - RESULTS

Total Short Chain Fatty Acids - µg/g

2.30e4 H



4.23e3 - 2.10e4

SACCHAROLYTIC STRAIGHT CHAIN FATTY ACIDS (SCFA)

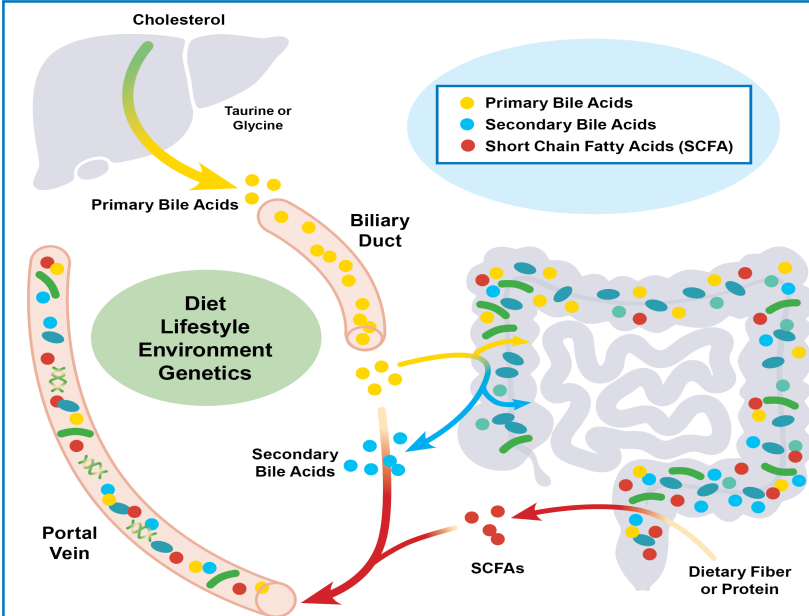
	Result µg/g	Reference µg/g
Total SCFA	2.17e4 H	3.65e3 - 1.95e4
Acetate	1.20e4 H	2.09e3 - 9.72e3
Butyrate	4.76e3	3.94e2 - 5.79e3
Propionate	4.75e3	5.91e2 - 5.45e3
Valerate	1.59e2	4.33e1 - 7.73e2
Caproate	4.62e0	7.15e-1 - 1.44e2

PROTEOLYTIC BRANCHED CHAIN FATTY ACIDS (BCFA)

	Result µg/g	Reference µg/g
Total BCFA	1.33e3	1.65e2 - 1.67e3
Iso-butyrate	4.60e2	5.65e1 - 5.64e2
Iso-valerate	4.93e2	4.45e1 - 6.58e2
2-Methylbutyrate	3.73e2	3.82e1 - 4.61e2
Iso-caproate	<dl	< 9.93e0



BILE ACIDS AND FATTY ACIDS OVERVIEW



Primary bile acids are synthesized from cholesterol in the liver and conjugated with either taurine or glycerin. They are stored in the gallbladder and released during digestion to assist with the absorption of fat and fat-soluble vitamins.

95% of primary bile acids are reabsorbed via the portal vein, while 5% are metabolized by gut bacteria to produce secondary bile acids.

Saccharolytic short chain fatty acids (SCFAs) are primarily metabolites of dietary fiber fermentation in the gut while proteolytic branched chain fatty acids (BCFAs) are metabolites of protein fermentation.

Acetate, propionate, and butyrate are three major SCFAs, which account for 90% of the SCFAs produced by gut microbiota. SCFAs are known to have numerous health effects and can enhance fecal excretion of bile acids.

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