PATIENT: XXXXXXXXXXXXXXXXXXXX
TEST REF: **TST-NL-XXXXX**
TEST NUMBER: T-NL-XXXXXX
GENDER: XXXXX
AGE: XX
COLLECTED: 2025-XX-XX
PRACTITIONER: XXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXX

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**
Campylobacter	<dl		< 1.00e3
C. difficile Toxin A	<dl		< 1.00e3
C. difficile Toxin B	<dl		< 1.00e3
Enterohemorrhagic E. coli	**2.43e4**	**High ↑**	< 1.00e3
E. coli O157	<dl		< 1.00e3
Enteroinvasive *E. coli/Shigella*	<dl		< 1.00e3
Enterotoxigenic *E. coli* LT/ST	<dl		< 1.00e3
Shiga-like Toxin *E. coli* stx1	<dl		< 1.00e3
Shiga-like Toxin *E. coli* stx2	<dl		< 1.00e3
Salmonella	<dl		< 1.00e4
Vibrio cholerae	<dl		< 1.00e5
Yersinia enterocolitica	<dl		< 1.00e5
PARASITIC PATHOGENS			
Cryptosporidium	<dl		< 1.00e6
Entamoeba histolytica	<dl		< 1.00e4
Giardia	<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.

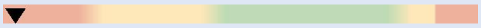
The assays were developed and/or the performance characteristics determined by Diagnostic Solutions Laboratory.

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

HELICOBACTER PYLORI

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

BACTERIAL PHYLA			
Bacteroidetes	4.92e12 H		8.6e11 - 3.3e12
Firmicutes	4.70e11 H		5.7e10 - 3.0e11
Firmicutes:Bacteroidetes Ratio	0.10		< 1.0

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

OPPORTUNISTIC/OVERGROWTH MICROBES

DYSBIOTIC & OVERGROWTH BACTERIA	Result		Reference
Bacillus spp.	**7.97e6**	**High ↑**	< 1.76e6
Enterococcus faecalis	**3.89e6**	**High ↑**	< 1.00e4
Enterococcus faecium	**2.12e4**	**High ↑**	< 1.00e4
Morganella spp.	<dl		< 1.00e3
Pseudomonas spp.	<dl		< 1.00e4
Pseudomonas aeruginosa	<dl		< 5.00e2
Staphylococcus spp.	<dl		< 1.00e4
Staphylococcus aureus	**4.05e3**	**High ↑**	< 5.00e2
Streptococcus spp.	**2.29e4**	**High ↑**	< 1.00e3

COMMENSAL OVERGROWTH MICROBES			
Desulfovibrio spp.	1.72e8		< 7.98e8
Methanobacteriaceae (family)	9.06e7		< 3.38e8

INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA			
Citrobacter spp.	<dl		< 5.00e6
Citrobacter freundii	7.75e4		< 5.00e5
Klebsiella spp.	<dl		< 5.00e3
Klebsiella pneumoniae	5.31e2		< 5.00e4
M. avium subsp. paratuberculosis	<dl		< 5.00e3
Proteus spp.	<dl		< 5.00e4
Proteus mirabilis	<dl		< 1.00e3

COMMENSAL INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA			
Enterobacter spp.	1.74e7		< 5.00e7
Escherichia spp.	**8.73e9**	**High ↑**	< 3.80e9
Fusobacterium spp.	1.26e6		< 1.00e8
Prevotella spp.	1.96e7		< 1.00e8

FUNGI/YEAST

FUNGI/YEAST	Result		Reference
Candida spp.	**9.57e4**	**High ↑**	< 5.00e3
Candida albicans	6.22e1		< 5.00e2
Geotrichum spp.	<dl		< 3.00e2
Microsporidium spp.	<dl		< 5.00e3
Rhodotorula spp.	<dl		< 1.00e3

VIRUSES

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

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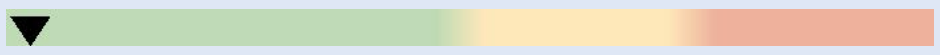
PARASITES

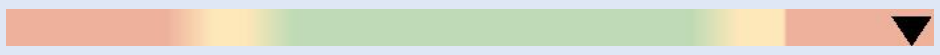
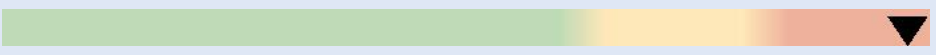
PROTOZOA	Result	Reference
Blastocystis hominis	<dl	< 2.00e3
Chilomastix mesnili	<dl	< 1.00e5
Cyclospora spp.	<dl	< 5.00e4
Dientamoeba fragilis	<dl	< 1.00e5
Endolimax nana	<dl	< 1.00e4
Entamoeba coli	<dl	< 5.00e6
Pentatrichomonas hominis	<dl	< 1.00e2

WORMS		
Ancylostoma duodenale	Not Detected	Not Detected
Ascaris lumbricoides	Not Detected	Not Detected
Necator americanus	Not Detected	Not Detected
Trichuris trichiura	Not Detected	Not Detected
Taenia 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

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**
Genes associated with amoxicillin resistance		
PBP1A S414R	**N/A**	
PBP1A T556S	**N/A**	
PBP1A N562Y	**N/A**	

	Result	Reference
Clarithromycin	**N/A**	**Negative**
Genes associated with clarithromycin resistance		
A2142C	**N/A**	
A2142G	**N/A**	
A2143G	**N/A**	

	Result	Reference
Fluoroquinolones	**N/A**	**Negative**
Genes associated with fluoroquinolone resistance		
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**
Genes associated with tetracycline resistance		
A926G	**N/A**	
AGA926-928TTC	**N/A**	

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

BILE ACIDS - SUMMARY

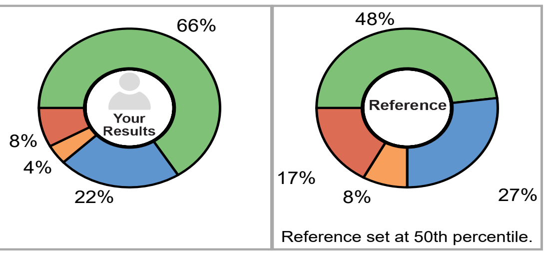
The Bile Acids Panel assesses fecal concentrations of primary and secondary bile acids and provides insights into microbiome diversity, digestive function, motility, and various gut-related conditions.

SUMMARY INFO

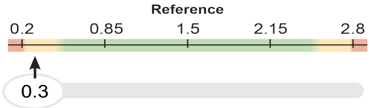
Total Bile Acids - ng/g	2.61e6	2.37e5 - 6.29e6
Secondary Bile Acids- %	98.1	> 90.5
Primary Bile Acids - %	1.9	< 7.8

Bile Acid Percentages

- 🟩 Deoxycholic Acid-DCA
- 🟦 Lithocholic Acid-LCA*
- 🟧 Iso-LCA
- 🟥 Other



Reference set at 50th percentile.



LCA*/DCA Ratio

Lithocholic Acid / Deoxycholic Acid Ratio based on absolute values.

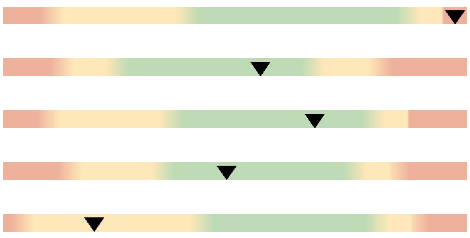
*LCA value is the summation of LCA + Allo-LCA

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.

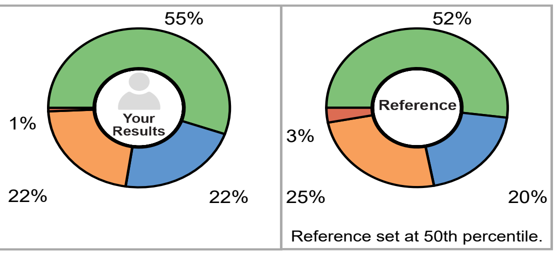
SUMMARY INFO

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

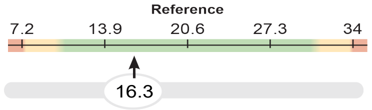


Major SCFA Percent

- 🟩 Acetate
- 🟦 Butyrate
- 🟧 Propionate
- 🟥 Valerate



Reference set at 50th percentile.



SCFA/BCFA Ratio

Ratio of total straight chain fatty acids (SCFA) to total branched chain fatty acids (BCFA).

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

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

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

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

SHORT CHAIN FATTY ACIDS - RESULTS

Total Short Chain Fatty Acids - µg/g **2.30e4 H** 4.23e3 - 2.10e4

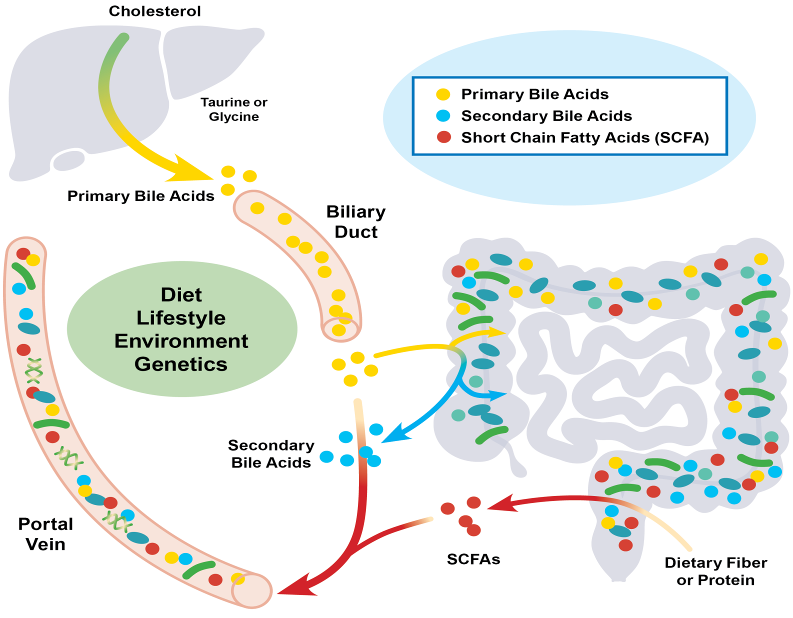
SACCHAROLYTIC STRAIGHT CHAIN FATTY ACIDS (SCFA)

	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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