

The Human Microbiome Company

GI ECOLOGIX

REPORT ID: S017212

TEST REPORTED: 02/11/2022 **TEST RECEIVED:** 02/11/2022

CLINICIAN NAME: CLINICIAN

Lab Director: Emma Beamish, PhD

PATIENT NAME: FIRST LAST **PATIENT DOB:** 02/11/2022

SAMPLE TYPE: STOOL SEX: FEMALE

Care Quality Commission Registered



Helicobacter pylori Stool Antigen	NEGATIVE			
Immune	RESULTS:			RANGE:
Beta Defensin 2 Secretory IgA	4.0ng/g 9.0ug/g	NORMAL NORMAL	<68ng/g 	<68ng/g <188ug/g
Inflammation	RESULTS:			RANGE:
Calprotectin	0.0ug/g	NORMAL	<100ug/g	<100ug/g
Digestion	RESULTS:			RANGE:
Bile Acids Pancreatic Elastase	611.0umol/l 521.0ug/g	NORMAL	<3477umol/L 	<3477umol/L >200ug/g
Other	RESULTS:			RANGE:
FIT (Occult Blood)	0.0ug/g	NORMAL	<10ug/g 	<10ug/g
Zonulin	0.0ng/g	NORMAL		<100ng/g

Commensal Bacteria	RESULTS:							RANGE:
1			0 - 4	5 - 8 I	9 - 12	13 - 16 I	17 - 20	1
Akkermansia muciniphila	3.9		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	1.7-7.1
Anaerostipes caccae	8.4	HIGH	0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	3.0-7.3
Bacteroides spp.	15.6		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	14.8-17.5
Bifidobacterium spp.	8.7							7.3-16.3
Blautia obeum	17.4		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	15.5-17.9
Coprococcus eutactus	15.3		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	10.4-16.5
Escherichia coli	4.9		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	4.5-12.0
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Eubacterium rectale	9.4		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	7.7-14.8
Faecalibacterium prausnitzii	16.8		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	14.2-18.3
Lactobacillus spp.	8.0		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	2.7-8.9
Roseburia homini	7.6		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	5.7-10.2
Ruminococcus bromii	16.5							14.2-17.7
Subdoligranulum variabile	11.9		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	6.3-12.5

Bacteroides Sub Group	RESULTS:							RANGE:
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bacteroides dorei	<dl< td=""><td>LOW</td><td></td><td></td><td></td><td></td><td></td><td>6.1-17.0</td></dl<>	LOW						6.1-17.0
'			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bacteroides fragilis	12.3							10.7-14.8
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bacteroides ovatus	8.9							3.5-9.2
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bacteroides thetaiotaomicron	8.6							6.2-12.5
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bacteroides uniformis	9.3	LOW						10.9-16.5
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bacteroides vulgatus	15.3							14.6-17.4



Gram Negative (-) Bacteria

RESULTS:

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			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Bilophila wadsworthia	5.0		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	2.4-9.5
Citrobacter freundii	<dl< td=""><td></td><td>0.4</td><td>5.0</td><td>0.10</td><td>10.10</td><td>17.00</td><td><1.0</td></dl<>		0.4	5.0	0.10	10.10	17.00	<1.0
Citrobacter koseri	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><dl< td=""></dl<></td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<dl< td=""></dl<>
Desulfovibrio spp.	0.5		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<6.9
			0 - 4	5 - 8	9 - 12	13 - 16 I	17 - 20	
Enterobacter cloacae	0.0		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<2.8
Fusobacterium nucleatum	4.8	HIGH	0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<2.8
Hafnia alvei	3.7							0.8-9.0
Klebsiella oxytoca	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><1.5</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<1.5
Klebsiella pneumoniae	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><2.5</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<2.5
	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td>. <2.5</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	. <2.5
Morganella morganii	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><0.5</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<0.5
Oxalobacter formigenes	<dl< td=""><td></td><td>0.4</td><td>5.0</td><td>0.10</td><td>10.10</td><td>17.00</td><td><1.6</td></dl<>		0.4	5.0	0.10	10.10	17.00	<1.6
Prevotella copri	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><11.4</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<11.4
Proteus mirabilis	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><0.4</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<0.4
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Pseudomonas aeruginosa	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><0.7</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<0.7
Serratia marcescens	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><0.4</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<0.4
Veillonella spp.	8.3				J 12	10 10	1, 20	4.0-10.0

Gram Positive (+) Bacteria

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Clostridium perfringens	4.8	HIGH						<4.0
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Clostridium sporogenes	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td><dl< td=""></dl<></td></dl<>							<dl< td=""></dl<>
Enternance formalia	DI		0 - 4	5 - 8 I	9 - 12	13 - 16 I	17 - 20 I	
Enterococcus faecalis	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><3.0</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<3.0
Enterococcus faecium	<dl< td=""><td></td><td></td><td></td><td>J</td><td>.0 .0</td><td>., =0</td><td><2.6</td></dl<>				J	.0 .0	., =0	<2.6
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Enterococcus gallinarum	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td><0.9</td></dl<>							<0.9
A.	DI		0 - 4 I	5 - 8 I	9 - 12	13 - 16 I	17 - 20	
Methanobrevibacter smithii	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><8.3</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<8.3
Mycobacterium avium	<dl< td=""><td></td><td></td><td></td><td> </td><td>10 10</td><td>17 20</td><td><0.2</td></dl<>					10 10	17 20	<0.2
·			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	!
Ruminococcus gnavus	9.4							4.1-10.7
5 .	4.0	LUOLI	0 - 4	5 - 8 I	9 - 12	13 - 16 I	17 - 20	1 00
Ruminococcus torques	4.3	HIGH	0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<2.3
Staphylococcus aureus	3.5	HIGH			J 12	10 10	17 20	<3.5
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	1
Streptococcus agalactiae	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td><0.9</td></dl<>							<0.9
	5.		0 - 4	5 - 8 I	9 - 12	13 - 16 I	17 - 20	١
Streptococcus pneumoniae	<dl< td=""><td></td><td>0 - 4</td><td>5 - 8</td><td>9 - 12</td><td>13 - 16</td><td>17 - 20</td><td><0.1</td></dl<>		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	<0.1
Streptococcus pyogenes	<dl< td=""><td></td><td>0 - 4</td><td>5-0</td><td>9-12</td><td>13 - 16</td><td>17 - 20</td><td><dl< td=""></dl<></td></dl<>		0 - 4	5-0	9-12	13 - 16	17 - 20	<dl< td=""></dl<>

Mycology	RESULTS:						RANGE:
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Aspergillus fumigatus	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td><0.1</td></dl<>						<0.1
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	•
Candida albicans	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td><0.6</td></dl<>						<0.6
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	•
Candida tropicalis	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td><0.3</td></dl<>						<0.3
,		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	•
Malassezia restricta	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td><0.5</td></dl<>						<0.5

Parasitology	RESULTS:							
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Blastocystis hominis	9.5	HIGH						< 6.4
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Dientamoeba fragilis	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>< 12.5</td></dl<>							< 12.5
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Entamoeba histolytica	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>							< DL
			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Giardia lamblia	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>							< DL
1			ı	ı	I	I	ı	1

Bacterial Pathogens	RESULTS:						RANGE:
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
B. fragilis Enterotoxigenic	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>						< DL
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	•
Clostridium difficile	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>						< DL
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
Clostridium difficile (tox A)	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>						< DL
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	•
Clostridium difficile (tox B)	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>						< DL
		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	1
Yersinia enterocolitica	<dl< td=""><td></td><td></td><td></td><td></td><td></td><td>< DL</td></dl<>						< DL

The GI EcologiXTM profile utilises the highly sensitive quantitative PCR (qPCR) TaqMan technology for analysis of the gastrointestinal microbiota. Microbial genes of interest are quantified within a sample and their abundances are normalised to an endogenous and highly conserved gene. The qPCR results are therefore reported as the relative abundance of a microorganism as proportional to the whole microbial community.