invivo®

The Human Microbiome Company

GI ECOLOGIX

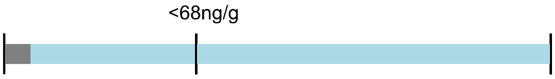
invivo

REPORT ID:

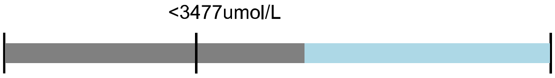
TEST REPORTED: 17/06/2021
TEST RECEIVED: 08/06/2021
PATIENT NAME: SAMPLE PATIENT
PATIENT DOB:
GENDER: FEMALE

REPORT STATUS: COMPLETED
CLINICIAN NAME: SAMPLE CLINICIAN
ACCESSION NO:
SAMPLE TYPE: STOOL

Care Quality Commission
Registered

Immune	RESULTS:			RANGE:
Beta Defensin 2	5ng/g	NORMAL		<68ng/g
Secretory IgA	159ug/g	NORMAL		<188ug/g

Inflammation	RESULTS:			RANGE:
Calprotectin	127ug/g	HIGH		<100ug/g

Digestion	RESULTS:			RANGE:
Bile Acids	5466umol/L	HIGH		<3477umol/L
Pancreatic Elastase	162ug/g	LOW		>200ug/g

Other	RESULTS:			RANGE:
FIT (Occult Blood)	0ug/g	NORMAL		<10ug/g
Zonulin	2ng/g	NORMAL		<100ng/g

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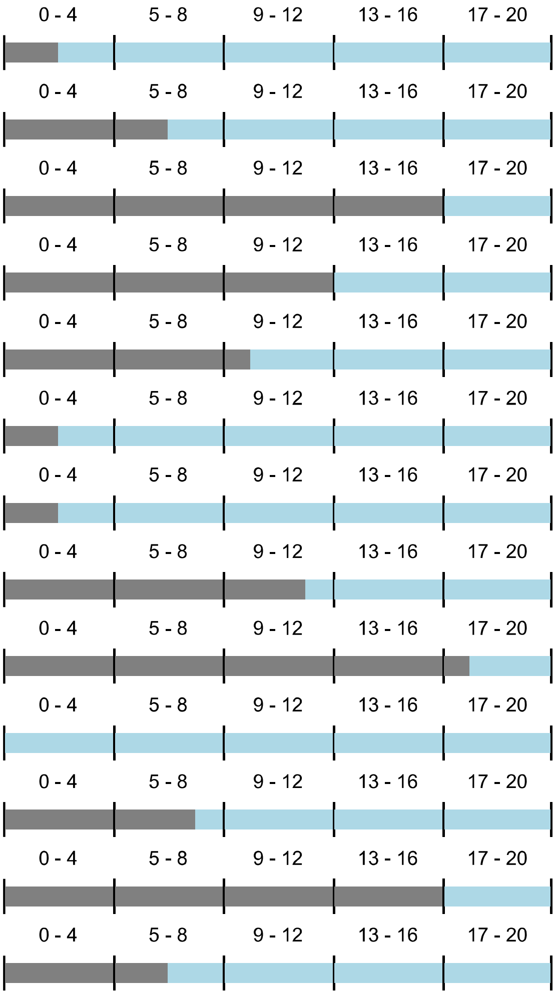
***Disclaimer**: This test was developed, and its performance characteristics determined by Invivo Diagnostics. This test is not intended for use by consumers or physicians as a means to cure, treat, prevent, diagnose or mitigate any disease or other medical condition. The information contained in this document is in no way to be taken as prescriptive nor to replace the physicians duty of care and personalised care practices.*

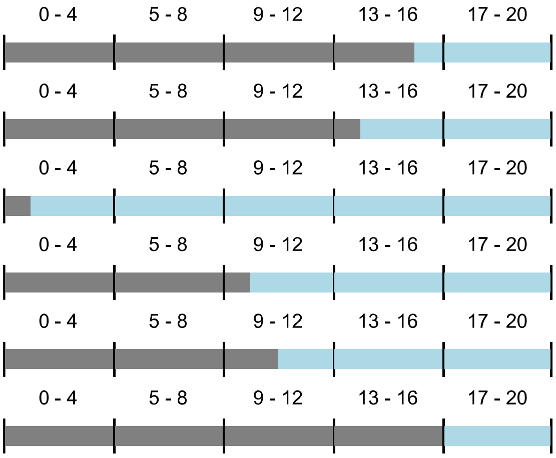
Commensal Bacteria

	RESULTS:		RANGE:
Akkermansia muciniphila	2.2		1.7-7.1
Anaerostipes caccae	5.9		3.0-7.3
Bacteroides spp.	16.4		14.8-17.5
Bifidobacterium spp.	12		7.3-16.3
Blautia obeum	9.4	LOW	15.5-17.9
Coprococcus eutactus	2.1	LOW	10.4-16.5
Escherichia coli	2.4	LOW	4.5-12.0
Eubacterium rectale	11.4		7.7-14.8
Faecalibacterium prausnitzii	17		14.2-18.3
Lactobacillus spp.	<DL	LOW	2.7-8.9
Roseburia homini	7		5.7-10.2
Ruminococcus bromii	15.6		14.2-17.7
Subdoligranulum variabile	6.3		6.3-12.5



Bacteroides Sub Group

	RESULTS:		RANGE:
Bacteroides dorei	15.3		6.1-17.0
Bacteroides fragilis	13.3		10.7-14.8
Bacteroides ovatus	1.1	LOW	3.5-9.2
Bacteroides thetaiotaomicron	8.8		6.2-12.5
Bacteroides uniformis	10.1	LOW	10.9-16.5
Bacteroides vulgatus	16.1		14.6-17.4



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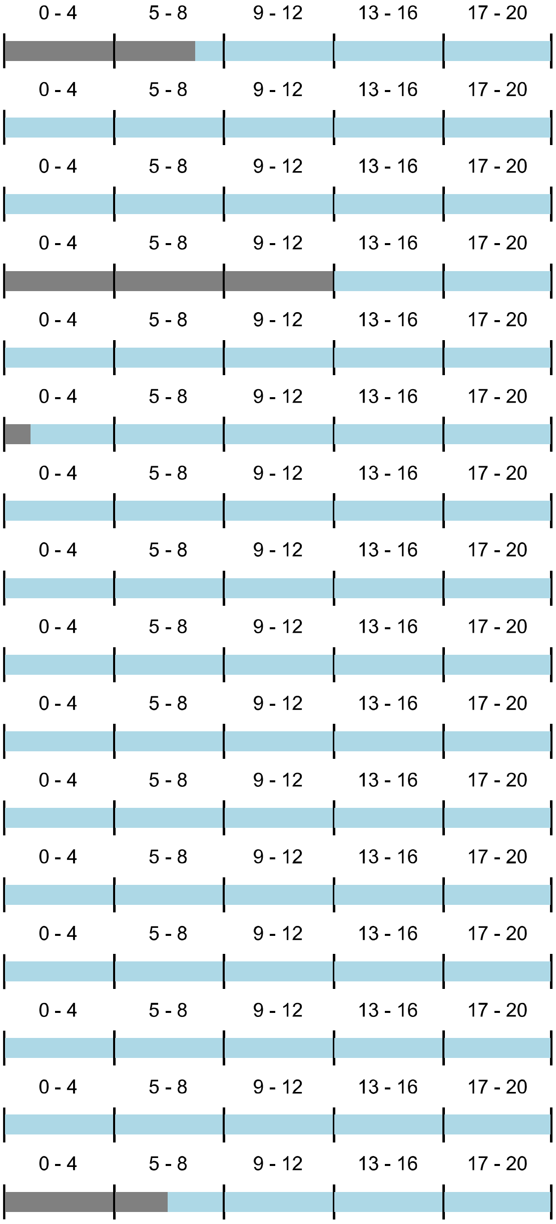
Gram Negative (-) Bacteria

	RESULTS:		RANGE:
Bilophila wadsworthia	7.4		2.4-9.5
Citrobacter freundii	<DL		<1.0
Citrobacter koseri	<DL		<DL
Desulfovibrio spp.	12.1	HIGH	<6.9
Enterobacter cloacae	<DL		<2.8
Fusobacterium nucleatum	0.9		<2.8
Hafnia alvei	<DL	LOW	0.8-9.0
Klebsiella oxytoca	<DL		<1.5
Klebsiella pneumoniae	<DL		<2.5
Morganella morganii	<DL		<0.5
Oxalobacter formigenes	<DL		<1.6
Prevotella copri	<DL		<11.4
Proteus mirabilis	<DL		<0.4
Pseudomonas aeruginosa	<DL		<0.7
Serratia marcescens	<DL		<0.4
Veillonella spp.	5.7		4.0-10.0



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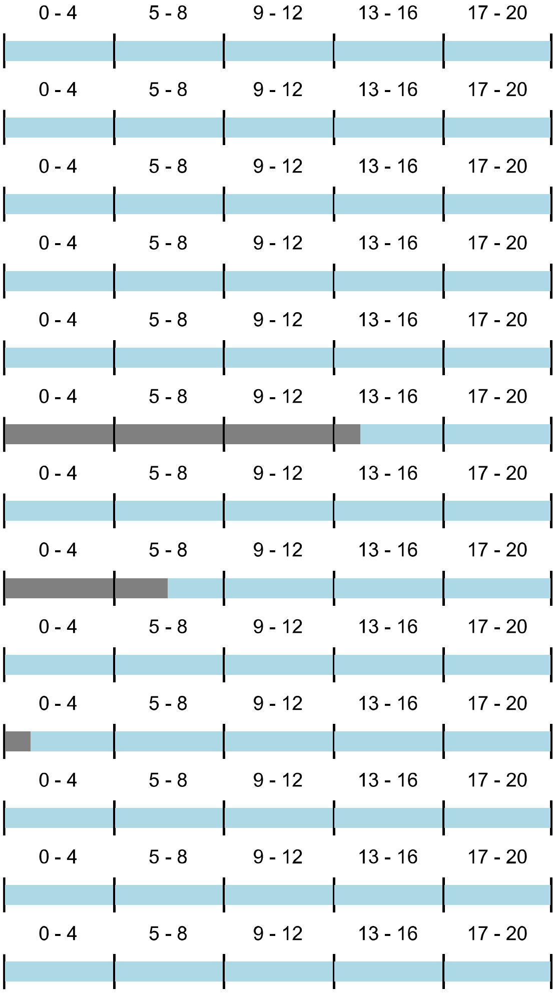
Gram Positive (+) Bacteria

	RESULTS:		RANGE:
Clostridium perfringens	<DL		<4.0
Clostridium sporogenes	<DL		<DL
Enterococcus faecalis	<DL		<3.0
Enterococcus faecium	<DL		<2.6
Enterococcus gallinarum	<DL		<0.9
Methanobrevibacter smithii	12.6	HIGH	<8.3
Mycobacterium avium	<DL		<0.2
Ruminococcus gnavus	5.8		4.1-10.7
Ruminococcus torques	<DL		<2.3
Staphylococcus aureus	1.3		<3.5
Streptococcus agalactiae	<DL		<0.9
Streptococcus pneumoniae	<DL		<0.1
Streptococcus pyogenes	<DL		<DL



Helicobacter pylori

	RESULTS:	RANGE:
Helicobacter pylori Stool Antigen	NEGATIVE	NEGATIVE

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Mycology	RESULTS:		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	RANGE:
Aspergillus fumigatus	<DL							<0.1
Candida albicans	<DL							<0.6
Candida tropicalis	<DL							<0.3
Malassezia restricta	<DL							<0.5

Parasitology	RESULTS:		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	RANGE:
Blastocystis hominis	9.7	HIGH	▨	▨	▨			< 6.4
Dientamoeba fragilis	<DL							< 12.5
Entamoeba histolytica	<DL							< DL
Giardia lamblia	<DL							< DL

Bacterial Pathogens	RESULTS:		0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	RANGE:
B. fragilis Enterotoxigenic	<DL							< DL
Clostridium difficile	<DL							< DL
Clostridium difficile (tox A)	<DL							< DL
Clostridium difficile (tox B)	<DL							< DL
Yersinia enterocolitica	<DL							< DL

The GI EcologiX™ 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.

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