

External ID 101070461900

Name	[REDACTED]	Date of Birth	[REDACTED]	Order ID	11857447
First Name	[REDACTED]	Sex	Female	Order Date	17.09.2019
Sampling Date	12.09.2019 08:30	Validation Date	Thomas Gugerel	Findings Status	Final Report
Sample Material	FE	Validation on	24.09.2019	Findings Date	26.09.2019

Test	Result	Unit	Standard Range	Previous Result
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Stool Diagnostics

Moleculargenetic Microbiomeanalysis MIDI

Stool Properties

Colour	brown			FE NA) VISU
Consistency	mushy			FE NA) VISU
pH	6,0		5,8 - 6,5	FE NA) TESTS

Biodiversity

Diversity	5,01		> 5,0	FE NA) MGSEQ
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The bacterial diversity in the intestinal tract may vary considerably from person to person. Antibiotic therapies, infections, increasing age, unbalanced diets or smoking are causes of declining diversity.

Grad



Bacteria Phyla (Distribution)

Actinobacteria	1,2	%	1,0 - 5	FE NA) MGSEQ
Bacteroidetes	53,4	%	30 - 60	FE NA) MGSEQ
Firmicutes	41,6	%	30 - 60	FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0	FE NA) MGSEQ
Proteobacteria	3,3	%	1,5 - 5,0	FE NA) MGSEQ
Verrucomicrobia	0,0	%	1,5 - 5	FE NA) MGSEQ
Other	0,4	%		FE NA) MGSEQ

Ratio

Firmicutes/Bacteroidetes	0,78	Quotient	< 1,5	FE NA) RECHN
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Enterotype

Enterotype	1=2			FE NA) MGSEQ
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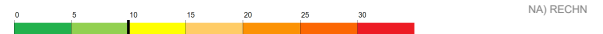
Human intestinal microbiomes can be differentiated into three Enterotypes. Enterotypes are defined by dominant bacterial clusters with distinct metabolic properties.

Enterotyp



Dysbiosis index

The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.



Index



Test	Result	Unit	Standard Range	Visual Scale	Previous Result
Bacteria Phyla - most important genera and species					
Actinobacteria					
Bifidobacteria	5,7 x 10 ⁹ CFU/g faeces		> 5,0 x 10 ⁹		FE NA) MGSEQ
Bifidobacterium adolescentis	47	%			FE NA) MGSEQ
Bifidobacterium longum	42	%			FE NA) MGSEQ
Equol producing bacteria	6,3 x 10 ⁹ CFU/g faeces		> 5,0 x 10 ⁹		FE NA) MGSEQ
Bacteroidetes					
Bacteroides	2,3 x 10 ¹¹ CFU/g faeces		> 1,5 x 10 ¹¹		FE NA) MGSEQ
Prevotella	2,5 x 10 ¹¹ CFU/g faeces		> 1,0 x 10 ¹⁰		FE NA) MGSEQ
Prevotella copri	25	%			FE NA) MGSEQ
Firmicutes					
Butyrate producing bacteria					
Faecalibacterium prausnitzii	7,4 x 10 ¹⁰ CFU/g faeces		> 5,0 x 10 ¹⁰		FE NA) MGSEQ
Eubacterium rectale	9,4 x 10⁹ CFU/g faeces		> 1,0 x 10 ¹⁰		FE NA) MGSEQ
Eubacterium hallii	4,2 x 10⁹ CFU/g faeces		> 5,0 x 10 ⁹		FE NA) MGSEQ
Roseburia species	7,3 x 10 ¹⁰ CFU/g faeces		> 2,0 x 10 ¹⁰		FE NA) MGSEQ
Ruminococcus species	1,8 x 10¹⁰ CFU/g faeces		> 3,0 x 10 ¹⁰		FE NA) MGSEQ
Coprococcus	3,6 x 10 ¹⁰ CFU/g faeces		> 2,0 x 10 ¹⁰		FE NA) MGSEQ
Total bacterial count	2,0 x 10 ¹¹ CFU/g faeces		> 1,3 x 10 ¹¹		FE NA) MGSEQ
Clostridia					
Clostridia total bacterial count	4,7 x 10⁹ CFU/g faeces		< 4,0 x 10 ⁹		FE NA) MGSEQ
Clostridia cluster I	4,6 x 10 ⁸ CFU/g faeces		< 2,0 x 10 ⁹		FE NA) MGSEQ
Fusobacteria					
Fusobacterium species	< 1,0 x 10 ⁶ CFU/g faeces		< 1,0 x 10 ⁷		FE NA) MGSEQ
Verrucomicrobia					
Akkermansia muciniphila	1,3 x 10⁷ CFU/g faeces		> 5,0 x 10 ⁹		FE NA) MGSEQ
Proteobacteria					
Pathogenic or potentially pathogenic bacteria					
Haemophilus	8,7 x 10 ⁸ CFU/g faeces		< 1,0 x 10 ⁹		FE NA) MGSEQ
Acinetobacter	< 1,0 x 10 ⁶ CFU/g faeces		< 1,0 x 10 ⁶		FE NA) MGSEQ
Escherichia coli Biovare	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE A) KULTAZ
Proteus species	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE A) KULTAZ
Klebsiella species	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE A) KULTAZ
Enterobacter species	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE A) KULTAZ
Serratia species	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE A) KULTAZ
Hafnia species	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE A) KULTAZ
Morganella species	< 1,0 x 10 ⁴ CFU/g faeces		< 1,0 x 10 ⁴		FE NA) MIB
Histamine producing bacteria					
Histamine producing bacteria	< 1,0 x 10 ⁶ CFU/g faeces		< 5,0 x 10 ⁸		FE NA) MGSEQ
H2S production					
Sulphate reducing bacteria	1,4 x 10 ⁹ CFU/g faeces		< 2,0 x 10 ⁹		FE NA) MGSEQ

Test	Result	Unit	Standard Range	Previous Result	Method
Immunogenicity / Mucus production					
Immunogenically effective bacteria					
Escherichia coli	1,0 x 10⁸	CFU/g faeces	10 ⁶ - 10 ⁷		FE A) KULTAZ
Enterococcus species	2,0 x 10 ⁶	CFU/g faeces	10 ⁶ - 10 ⁷		FE A) KULTAZ
Lactobacillus species	6,0 x 10 ⁵	CFU/g faeces	10 ⁵ - 10 ⁷		FE A) KULTAZ
Mucin production / Mucosa barrier					
Akkermansia muciniphila	1,3 x 10⁷	CFU/g faeces	> 5,0 x 10 ⁹		FE NA) MGSEQ
Faecalibacterium prausnitzii	7,4 x 10 ¹⁰	CFU/g faeces	> 5,0 x 10 ¹⁰		FE NA) MGSEQ
Yeasts / Molds					
Candida albicans	< 1,0 x 10 ³	CFU/g faeces	< 1,0 x 10 ³		FE A) KULTAZ
Candida species	< 1,0 x 10 ³	CFU/g faeces	< 1,0 x 10 ³		FE A) KULTAZ
Geotrichum candidum	< 1,0 x 10 ³	CFU/g faeces	< 1,0 x 10 ³		FE A) KULTAZ
Moulds	negative		negative		FE A) KULTAZ
Parasites					
Pathobionts					
Blastocystis hominis	negative		negative		FE NA) MOLEK
Dientamoeba fragilis	negative		negative		FE NA) MOLEK
Pathogenic intestinal protozoa					
Giardia lamblia	negative		negative		FE NA) MOLEK
Entamoeba histolytica	negative		negative		FE NA) MOLEK
Cryptosporidium species	negative		negative		FE NA) MOLEK
Cyclospora cayetanensis	negative		negative		FE NA) MOLEK

Overview - Results and Therapy Options



pH		
Enterotype		
Biodiversity		
Ratio Firmicutes/Bacteroidetes		
Equol producing bacteria		
Butyrate producing bacteria		prebiotics on the basis of resistant starch* or scFOS/scGOS*
Mucus production		prebiotics (scFOS/scGOS)*
Mucosa integrity		
Milieu stabilising bacteria		
Immunogenic bacteria		immunogenic effective probiotics*
Clostridia - total bacteria count		
Clostridia cluster I		
Fusobacteria		
Histamine producing bacteria		
H2S producing bacteria (SRB)		
Potentially pathogenic bacteria		
Candida (facultive pathogenic)		