

External ID

Name	Date of Birth	Female	Order ID	
First Name	Sex		Order Date	21.01.2021
Sampling Date	21.01.2021 00:00	Validation by	Findings Status	Final Report
Sample Material	FE	Validation Date	Findings Date	09.02.2021

Test	Result	Unit	Standard Range	Previous Result
Stool Diagnostics				
Mikrobiomanalyse Midi PLUS (Microbiom Center)				
Molecular genetic microbiome analysis 3.0				
Biodiversity				
Diversity	6,07		> 5	

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.



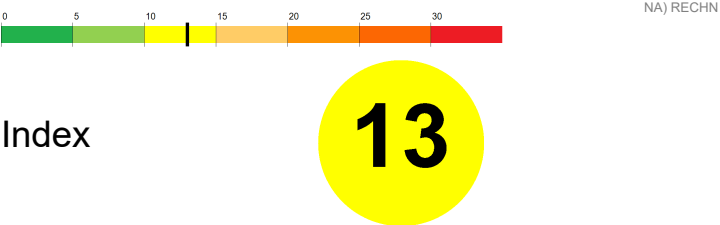
Enterotype				
Enterotyp	1=2			

Human intestinal microbiomes can be differentiated into three Enterotypes. Enterotypes are defined by dominant bacterial clusters with distinct metabolic properties.

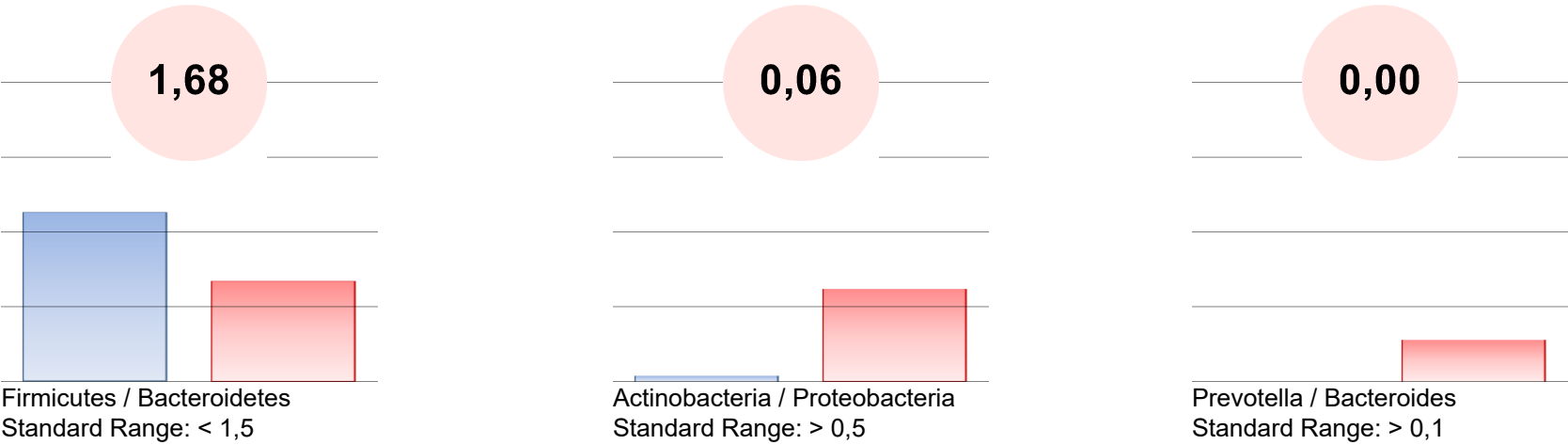


Dysbiosis index				
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The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.



Ratio				
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Phyla				
Actinobacteria	0,4	%	1,0 - 5,0	
Bacteroidetes	33,6	%	30 - 60	

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Test	Result	Unit	Standard Range	Previous Result	
Firmicutes	56,6	%	30 - 60		FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0		FE NA) MGSEQ
Proteobacteria	6,2	%	1,5 - 5,0		FE NA) MGSEQ
Verrucomicrobia	2,2	%	1,5 - 5,0		FE NA) MGSEQ
Other	1,1	%			FE NA) MGSEQ
Metabolome (functional groups)					
Secondary bile acids	-1,5	%			
TMA / TMAO	-44,5	%			
Indoxyl sulfate	-50,0	%			
Phenols	-44,6	%			
Ammonia	-33,9	%			
Histamine	-50,0	%			
Equol	-39,2	%			
Beta glucuronidases	-48,3	%			
Bacteria Phyla - most important genera and species					
Actinobacteria					
Bifidobacterium	1,9 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Bifidobacterium	longum	69	%		FE NA) MGSEQ
Bifidobacterium	adolescentis	27	%		FE NA) MGSEQ
Bacteroidetes					
Bacteroides	1,4 x 10^11	CFU/g faeces	> 1,5 x 10^11		FE NA) MGSEQ
Bacteroides	uniformis	12	%		FE NA) MGSEQ
Bacteroides	ovatus	7	%		FE NA) MGSEQ
Prevotella	1,1 x 10^8	CFU/g faeces	> 1,0 x 10^10		FE NA) MGSEQ
Prevotella	copri	0	%		FE NA) MGSEQ
Histamine producing bacteria					
Butyrate producing bacteria					
Total bacteria count	2,1 x 10^11	CFU/g faeces	> 1,2 x 10^11		FE NA) MGSEQ
Faecalibacterium prausnitzii	9,7 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEQ
Eubacterium rectale	6,7 x 10^9	CFU/g faeces	> 1,0 x 10^10		FE NA) MGSEQ
Eubacterium hallii	2,3 x 10^10	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Roseburia spp.	1,0 x 10^10	CFU/g faeces	> 2,0 x 10^10		FE NA) MGSEQ
Ruminococcus spp.	2,4 x 10^10	CFU/g faeces	> 3,0 x 10^10		FE NA) MGSEQ
Coprococcus spp.	3,6 x 10^10	CFU/g faeces	> 2,0 x 10^10		FE NA) MGSEQ
Butyrivibrio spp.	9,7 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Clostridia					
Clostridia total bacteria count	4,6 x 10^9	CFU/g faeces	< 4,0 x 10^9		FE NA) MGSEQ
Clostridia Cluster I	4,6 x 10^7	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Fusobacteria					
Fusobacterium	<1,0 x 10^5	CFU/g faeces	< 1,0 x 10^7		FE NA) MGSEQ
Verrucomicrobia					
Akkermansia muciniphila	2,2 x 10^10	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Proteobacteria					
Pathogenic or potentially pathogenic bacteria					
Haemophilus spp.	2,8 x 10^8	CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ

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Acinetobacter spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Proteus spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Klebsiella spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Enterobacter spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Serratia spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Hafnia spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Morganella spp.	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^6	FE NA) MGSEQ
Citrobacter spp.	<1,0 x 10^5 CFU/g faeces		< 5,0 x 10^8	FE NA) MGSEQ
Pseudomonas spp.	<1,0 x 10^5 CFU/g faeces		< 5,0 x 10^7	FE NA) MGSEQ
Providencia spp.	<1,0 x 10^5 CFU/g faeces		< 5,0 x 10^7	FE NA) MGSEQ
H2S production				
Sulphate reducing bacteria	1,0 x 10^9 CFU/g faeces		< 2,0 x 10^9	FE NA) MGSEQ
Desulfovibrio piger	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^9	FE NA) MGSEQ
Desulfomonas pigra	<1,0 x 10^5 CFU/g faeces		< 1,0 x 10^9	FE NA) MGSEQ
Bilophila wadsworthia	<1,0 x 10^5 CFU/g faeces		< 2,0 x 10^9	FE NA) MGSEQ
Immunogenicity / Mucus production				
Immunogenically effective bacteria				
Escherichia coli	1,7 x 10^7 CFU/g faeces		10^6 - 10^7	FE NA) MGSEQ
Enterococcus spp.	1,0 x 0 CFU/g faeces		10^6 - 10^7	FE NA) MGSEQ
Lactobacillus spp.	2,3 x 10^6 CFU/g faeces		10^5 - 10^7	FE NA) MGSEQ
Mucin production / Mucosal barrier				
Akkermansia muciniphila	2,2 x 10^10 CFU/g faeces		> 5,0 x 10^9	FE NA) MGSEQ
Faecalibacterium prausnitzii	9,7 x 10^10 CFU/g faeces		> 5,0 x 10^10	FE NA) MGSEQ
Archaea				
Methanogens				
Methanobrevibacter spp.	2,1 x 10^8 CFU/g faeces		< 1,0 x 10^8	FE NA) MGSEQ
Mycobiome: relevant yeasts				
Candida albicans (CA)	4,2 x 10^4 KBE /g Stuhl		<1,0 x 10^3	FE NA) QPCR
Candida krusei (CK)	<1,0 x 10^3 KBE /g Stuhl		< 1,0 x 10^3	FE NA) QPCR
Candida glabrata (CG)	<1,0 x 10^3 KBE /g Stuhl		< 1,0 x 10^3	FE NA) QPCR
Candida dubliniensis (CD)	<1,0 x 10^3 KBE /g Stuhl		< 1,0 x 10^3	FE NA) QPCR
Candida parapsilosis (CP)	<1,0 x 10^3 KBE /g Stuhl		< 1,0 x 10^3	FE NA) QPCR
Candida tropicalis (CTp)	<1,0 x 10^3 KBE /g Stuhl		< 1,0 x 10^3	FE NA) QPCR
Candida lusitaniae (CL)	<1,0 x 10^3 KBE /g Stuhl		< 1,0 x 10^3	FE NA) QPCR
Parasites				
Pathobionts				
Blastocystis hominis	borderline		negative	FE A) MOLEK
Dientamoeba fragilis	positive		negative	FE A) MOLEK
Pathogenic intestinal protozoa				
Giardia lamblia	negative		negative	FE A) MOLEK
Entamoeba histolytica	negative		negative	FE A) MOLEK
Cryptosporidium species	negative		negative	FE A) MOLEK
Cyclospora cayetanensis	negative		negative	FE A) MOLEK

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Overview - Results and Therapy Options



pH	
Enterotype	
Biodiversitiy	
Ratio Firmicutes/Bacteroidetes	
Butyrate producing bacteria	
Mucus production	
Mucosa integrity	
Milieu stabilising bacteria	
Immunogenic bacteria	
Clostridia - total bacteria count	
Clostridia cluster I	
Fusobacteria	
H2S producing bacteria (SRB)	
Potentially pathogenic bacteria	
Candida (facultive pathogenic)	

Metabolome (functional groups)

Secondary bile acids	
TMA / TMAO	
Beta glucuronidases	
Indoxyl sulfate	
Phenols	
Ammonia	
Histamine	
Equol	