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Deutsche Akkreditierungsstelle
D-ML-13188-01-00

External ID 101188560000

Name		Date of Birth		Order ID	
First Name		Sex	Female	Order Date	07.06.2024
Sampling Date	06.06.2024 08:15	Validation by	Dr. Herbert Schmidt	Findings Status	**Final Report**
Sample Material	FE, T909	Validation Date	17.06.2024	Findings Date	17.06.2024

Stool Diagnostics

Molekulargenetische Mikrobiomanalyse Maxi NEU

Molecular genetic microbiome analysis 3.0

Stool Properties

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Colour	brown				FE NA) VISU
Consistency	mushy				FE NA) VISU
pH	7,2		5,8 - 6,5		FE NA) TESTS

Biodiversity

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Diversity	5,69		> 5,5		FE NA) MGSEQ

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.

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Enterotype

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Enterotyp	1=2				FE NA) MGSEQ

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

Enterotyp

Dysbiosis index

FE
NA) RECHN

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

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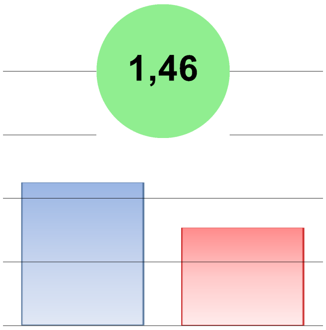
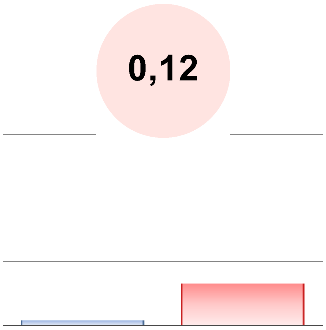
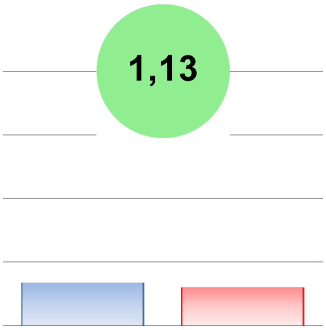
Ratio



Firmicutes / Bacteroidetes
Standard Range: < 3,0



Actinobacteria / Proteobacteria
Standard Range: > 1,0



Prevotella / Bacteroides
Standard Range: > 0,1

FE=stool, T909=stool

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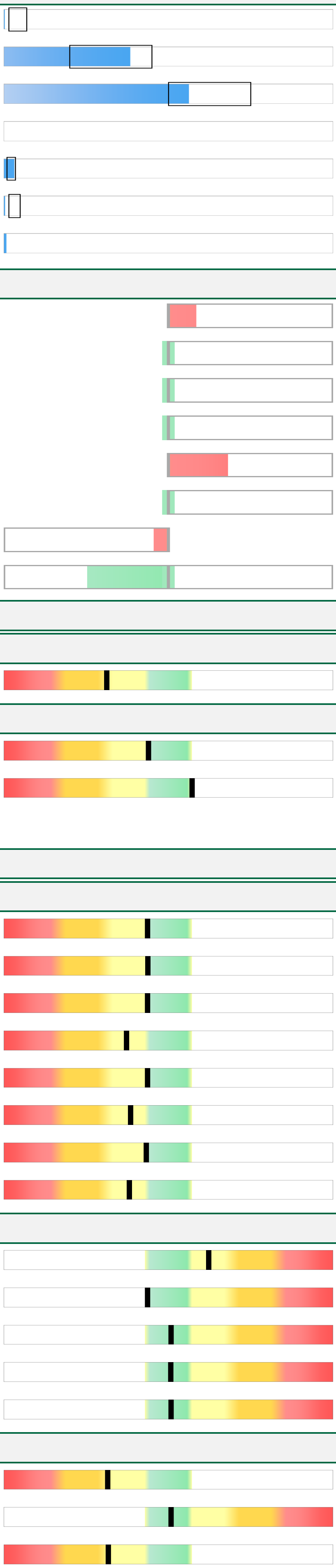

Test		Result	Unit	Standard Range	Previous Result	Sample Material Method
Phyla						
Actinobacteria		0,4	%	1,5 - 7		FE NA) MGSEQ
Bacteroidetes		38,5	%	20 - 45		FE NA) MGSEQ
Firmicutes		56,3	%	50 - 75		FE NA) MGSEQ
Fusobacteria		0,0	%	0,0 - 1,0		FE NA) MGSEQ
Proteobacteria		3,3	%	1,0 - 3,5		FE NA) MGSEQ
Verrucomicrobia		0,5	%	1,5 - 5,0		FE NA) MGSEQ
Other		0,9	%			FE NA) MGSEQ
Metabolome (functional groups)						
Secondary bile acids		25,4	%			
TMA / TMAO		-40,5	%			
Indoxyl sulfate		-50,0	%			
Phenols		-33,7	%			
Ammonia		54,2	%			
Histamine		-50,0	%			
Equol		-9,0	%			
Beta glucuronidases		-49,5	%			
Bacteria Phyla - most important genera and species						
Actinobacteria						
Bifidobacterium		2,2 x 10^9	CFU/g faeces	> 1,0 x 10^10		FE NA) MGSEQ
Bacteroidetes						
Bacteroides		1,5 x 10^11	CFU/g faeces	> 5,0 x10^10		FE NA) MGSEQ
Prevotella		1,7 x 10^11	CFU/g faeces	> 1,0 x 10^10		FE NA) MGSEQ
Prevotella	copri	16	%			FE NA) MGSEQ
Firmicutes						
Butyrate producing bacteria						
Total bacteria count		3,0 x 10^11	CFU/g faeces	> 2,4 x 10^11		FE NA) MGSEQ
Faecalibacterium prausnitzii		1,5 x 10^11	CFU/g faeces	>1,0 x10^11		FE NA) MGSEQ
Eubacterium rectale		2,3 x 10^10	CFU/g faeces	> 2,0 x 10^10		FE NA) MGSEQ
Eubacterium hallii		9,0 x 10^9	CFU/g faeces	> 1,5 x 10^10		FE NA) MGSEQ
Roseburia spp.		3,0 x 10^10	CFU/g faeces	> 3,0 x10^10		FE NA) MGSEQ
Ruminococcus spp.		3,4 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEQ
Coprococcus spp.		4,9 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEQ
Butyrivibrio spp.		9,8 x 10^9	CFU/g faeces	>1,5 x 10^10		FE NA) MGSEQ
Clostridia						
Clostridia total bacteria count		5,8 x 10^9	CFU/g faeces	< 4,0 x 10^9		FE NA) MGSEQ
Clostridia Cluster I		1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Clostridium histolyticum		< 1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Clostridium perfringens		< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8		FE NA) MGSEQ
Clostridium sporogenes		< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8		FE NA) MGSEQ
Other Firmicutes						
Christensenellaceae		1,2 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Dialister spp.		< 1,0 x 10^5	CFU/g faeces	< 4,0 x 10^10		FE NA) MGSEQ
Cl. butyricum		2,5 x 10^7	CFU/g faeces	> 1,0 x 10^8		FE NA) MGSEQ

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Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Fusobacteria					
Fusobacterium	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^7		FE NA) MGSEQ
Verrucomicrobia					
Akkermansia muciniphila	4,5 x 10^8	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Proteobacteria					
Pathogenic or potentially pathogenic bacteria					
Haemophilus spp.	3,1 x 10^8	CFU/g faeces	< 5,0 x 10^8		FE NA) MGSEQ
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 10^7		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 10^7		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	1,6 x 10^9	CFU/g faeces	< 2,5 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 wadsworthii	< 1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Oxalate degrading bacteria					
Oxalobacter formigenes	< 1,0 x 10^5	CFU/g faeces	> 1,0 x 10^8		FE NA) MGSEQ
Immunogenicity / Mucus production					
Immunogenically effective bacteria					
Escherichia coli	1,0 x 10^6	CFU/g faeces	10^6 - 10^7		FE NA) MGSEQ
Enterococcus spp.	4,24 x 10^6	CFU/g faeces	10^6 - 10^7		FE NA) MGSEQ
Lactobacillus spp.	1,2 x 10^6	CFU/g faeces	10^5 - 10^7		FE NA) MGSEQ
Mucin production / Mucosal barrier					
Akkermansia muciniphila	4,5 x 10^8	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Faecalibacterium prausnitzii	1,5 x 10^11	CFU/g faeces	>1,0 x10^11		FE NA) MGSEQ
Archaea					
Methanogens					
Methanobrevibacter spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^8		FE NA) MGSEQ

ATTENTION: The new OmicSnap tube and the matrix enable even more effective sample disruption, especially with gram-positive bacteria. This results in slight shifts in the standard ranges. We ask you to take this into account.

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Mycobiome: relevant yeasts					
Candida albicans (CA)	<1,0 x 10^3	CFU/g faeces	<1,0 x 10^3		FE NA) QPCR
Candida krusei (CK)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida glabrata (CG)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida dubliniensis (CD)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida parapsilosis (CP)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida tropicalis (CTp)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR

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Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Candida lusitaniae (CL)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Parasites					
Pathobionts					
Blastocystis hominis	positive		negative		FE A) MOLEK
Dientamoeba fragilis	negative		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
Maldigestion, malabsorption, MIS					
Digestive Residues					
Quantitative determination of fat	4,20	g/100g	< 3,5		FE NA) PHOT
Quantitative determination of nitrogen	0,50	g/100g	< 1,0		FE NA) PHOT
Quantitative determination of sugar	3,10	g/100g	< 2,5		FE NA) PHOT
Quantitative determination of water	80,40	g/100g	75 - 85		FE NA) PHOT
Determination of Maldigestion					
Pancreatic elastase	239,91	µg/g	> 200		FE A) ELISA
Bile acids in stool	13,17	µmol/l	< 70		FE NA) PHOTO
Detection of Malabsorption					
Calprotectin	<17,90	mg/l	< 50		FE A) ELISA
Alpha1-Antitrypsin	6,4	mg/dl	< 27,5		FE A) ELISA
Special Request					
Secretory IgA	<167,0	µg/ml	510 - 2040		FE A) ELISA
Leaky gut: Zonulin, Histamine					
Zonulin	79,42	ng/ml	< 55		FE A) ELISA
Histamine in stool	2390,3	ng/ml	< 959		T909 A) ELISA
Special gastro-enterological diagnostics					
Gastro diagnostics					
Helicobacter AG	negative		negative		FE A) CLIA

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Overview - Results and Therapy Options

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pH	⇧	milieu stabilizing probiotics *
Enterotype		
Biodiversitiy	●	
Ratio Firmicutes/Bacteroidetes	●	
Butyrate producing bacteria	⇩	prebiotics on the basis of resistant starch* or scFOS/scGOS*
Mucus production	⇩	prebiotics (scFOS/scGOS)*
Mucosa integrity	●	
Milieu stabilising bacteria	⇩	milieu stabilizing probiotics*, prebiotics (scFOS/scGOS)*
Immunogenic bacteria	⇩	immunogenic effective probiotics*
Clostridia - total bacteria count	⇧	milieu stabilizing probiotics*, prebiotics (scFOS/scGOS)*
Clostridia cluster I	●	
Fusobacteria	●	
H2S producing bacteria (SRB)	●	
Potentially pathogenic bacteria	●	
Candida (facultive pathogenic)	●	
Oxalate degrading bacteria	⇩	low-oxalate diet

Metabolome (functional groups)

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

Equol ⬇