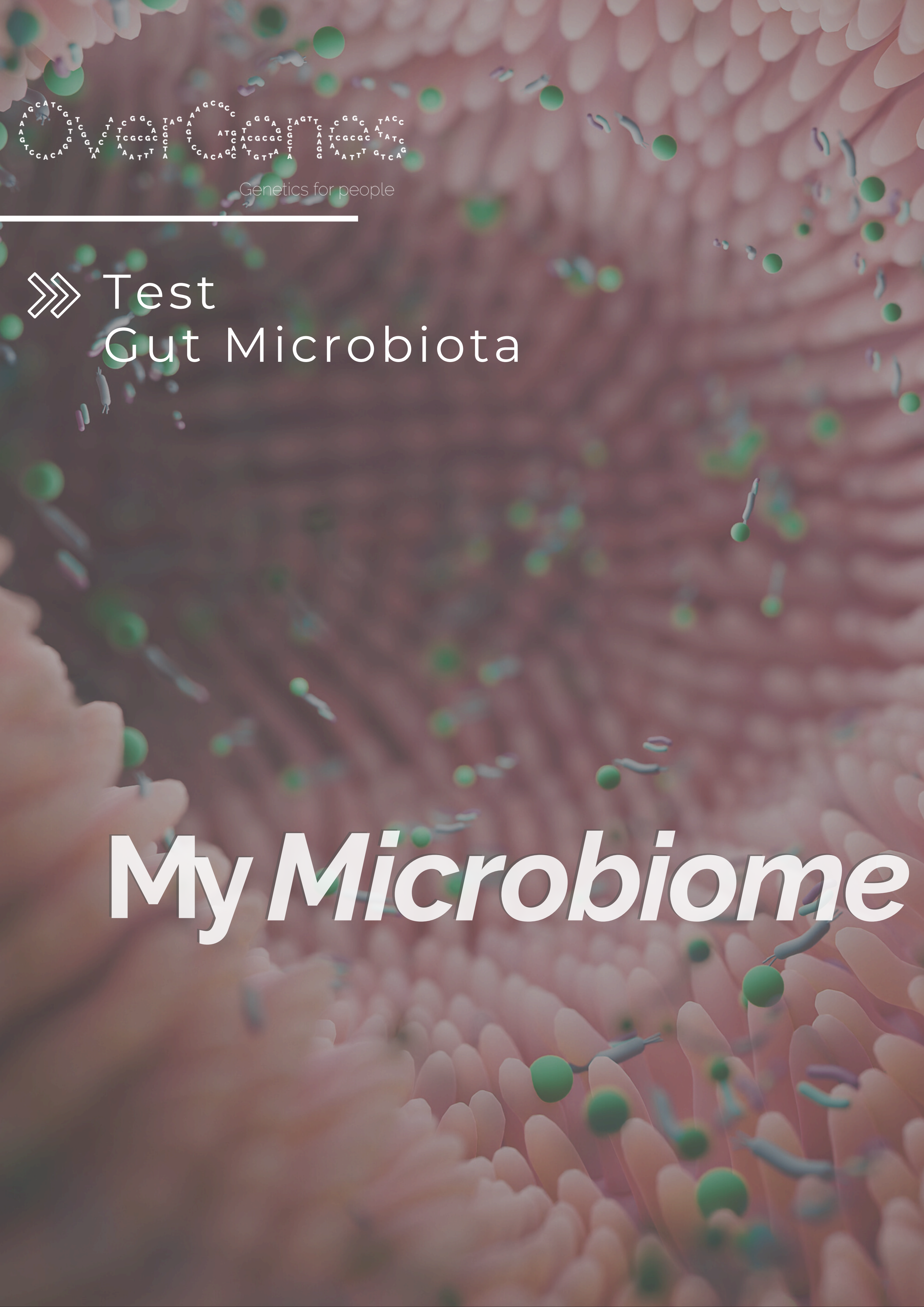


OverGenes

Genetics for people

Test
Gut Microbiota

My Microbiome

1 Introduction

MyMicrobiome provides a global view of the state of the user's microbiota in relation to the CLOM (CLustering Of Microbiomes) database. This database is the result of the research of the project *Global clustering of microbiome profiles and community search tool* funded by the *Spanish Ministry of Science and Innovation - R+D+i Projects Proof of Concept 2022*. The CLOM database collects phenotypic data and gastrointestinal microbiota profiles from thousands of published gastrointestinal microbiota samples. The results are based on the study of the patient's phenotypes and their microbial profiles in the CLOM database.

The microbial profiles of thousands of human fecal samples stored in the CLOM database, together with the application of mathematical methods, have allowed the development of a unique MICROBIOTA PROFILE'S CLASSIFIER, which places the person in one of the types of existing bacterial community. The current version of the CLOM database is based on up to 14 community profiles.

Using biomedical literature, each profile is correlated as possible RISK or PROTECTION FACTORS against diseases such as various types of cancer, intestinal diseases, microbial infections or other comorbidities including diabetes, obesity, cholesterol and hypertension.

The MyMicrobiome results report informs on:

- the person's microbial community profile among the 14 CLOM profiles;

- the main phenotypic data of the person;

- the diversity of the person's specific microbiota, also indicating the potential functions of the microbial groups found.

The microbiota profile defined in this analysis has been obtained by applying strict statistics methods and quality filters to guarantee the maximum reliability of the results.

Three types of results are provided:

- summary data relating to the microbial community to which the person's profile fits;

- values related to the person microbiome profile;

- reference values: **as there is no consensus on the reference values**, in this report the reference values are calculated considering the distributions of the profiles from healthy individuals stored in the CLOM database.

Test identification data

ID TEST : **REF.0001**
DATE : **24 September 2024**
Age (Years) : **45**
Sex (M/F) : **Male**
Height (cm) : **154**
Weitght(Kg) : **78**
BMI : **32.9** (obesity)

YOUR MICROBIOME PROFILE

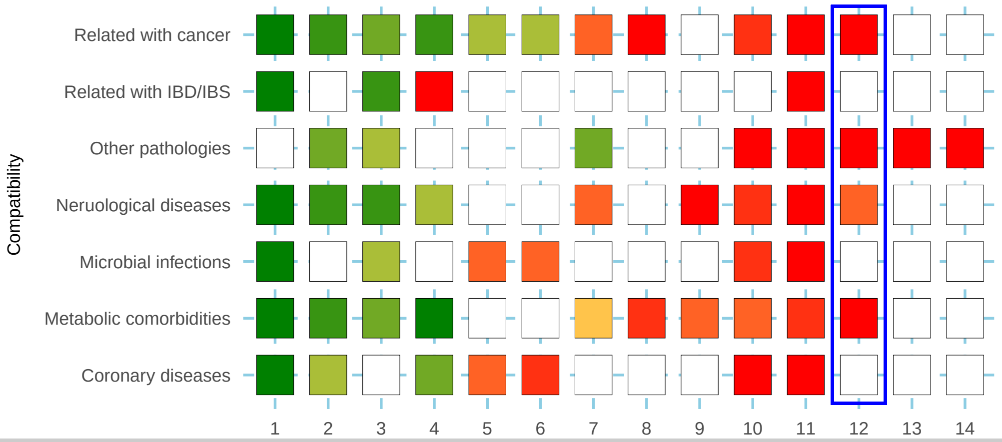
IMPORTANT: This result represents an informative guide based on probabilistic association data for each profile and disease.

- THEREFORE IT IS NOT A CLINICAL DIAGNOSIS -

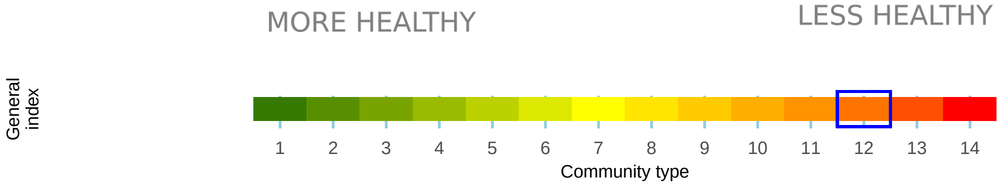
Your community is the **12**.

CORRELATION **Profile / Pathology (CLOM database)**

Protection ↔ Risk
🟢 🟢 🟡 🟠 🔴



CORRELATION **Healthy state as defined by the CLOM database**



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DIVERSITY INDEXES. Diversity indexes offer a measure of the microbial population structure of the analyzed sample.

YOUR RESULTS Diversity indexes

	Reference CLOM Healthy samples	YOUR VALUES	
Espected species (CHAO1)	(70.25 - 74.56)	93.00	⇑
Observed species	(70.25 - 74.56)	93.00	⇑
Shannon diversity	(2.74 - 2.79)	3.20	⇑
Dominance (Inverse Simpson)	(9.95 - 10.5)	12.68	⇑
Firmicutes/Bacteroidota Ratio	(9.11 - 19.7)	7.93	⇓

Reference values. Reference values have been established based on all samples from healthy individuals stored in the CLOM database. This result is indicative to understand the structure of your microbiota and has no direct association with an eventual pathological state.

⇑: Values above the reference maximum.

⇔: Values within reference range.

⇓: Values below the reference minimum.

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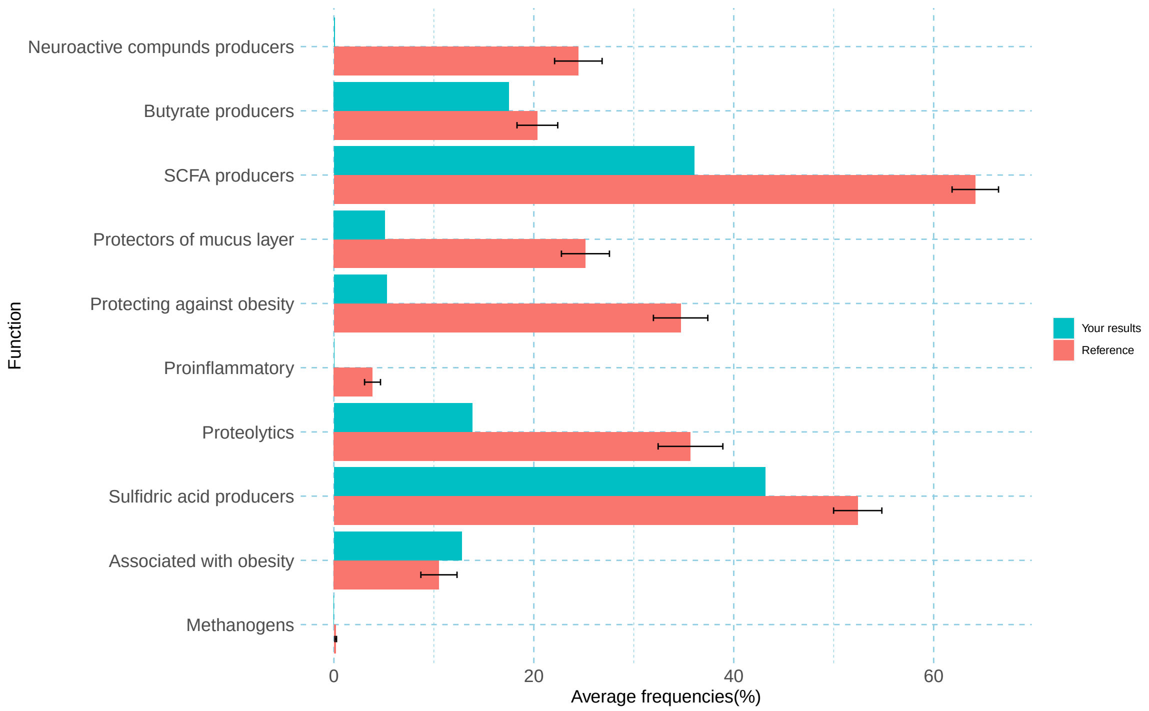
MAIN FUNCTIONS

The potential functions covered by the user's microbiota are presented and compared to the average values of healthy individuals from the CLOM database. This result is indicative to understand the structure of your microbiota and **has no direct association with an eventual pathological state**.

YOUR RESULTS Profile / Function (CLOM database)



Legend. The length of each bar represents the cumulative frequencies of each function in:

- the user's sample,

- the average of healthy individuals from the CLOM database,

The confidence intervals of the average data (Reference) are also reported.

Test identification data

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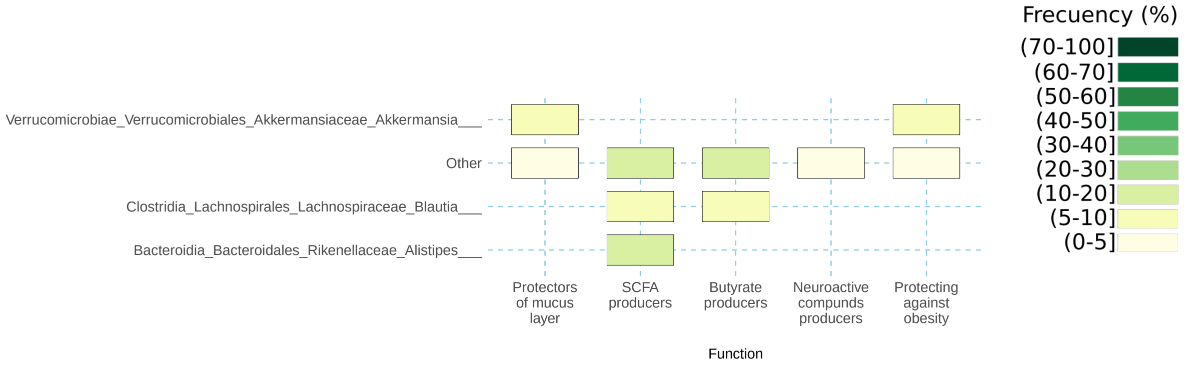
FUNCTIONAL PROFILE. Potential functions covered by the user's microbiota.

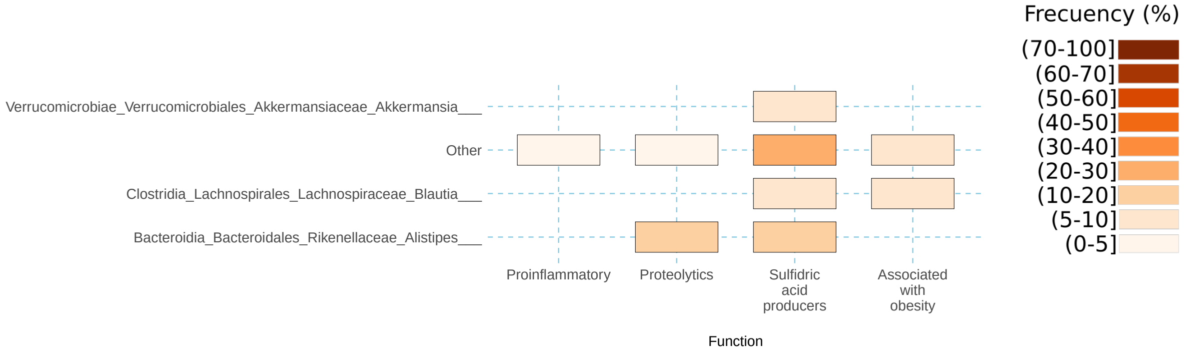
Legends. The color scales represent the frequencies of each organism covering a certain function.

YOUR RESULTS Profile / Function (CLOM database)

Beneficial



Problematics



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BMI : **32.9** (obesity)

Functions. Here the bacterial species and their representation in the most important functions of your microbiota are shown. A star (second column) indicates that the species belongs to the TOP 30.

Neuroactive compunds producers

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris		(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___		(5.79-6.85)	0.056	⇓

Butyrate producers

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Clostridia_Clostridiales_Clostridiaceae_Clostridium_sensu_stricto_1___	*	(0-0.33)	1.321	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes_Anaerostipes_caccae		(0.03-0.12)	0.112	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes___	*	(1.18-1.49)	4.552	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Blautia___	*	(5.21-6.02)	6.510	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Clostridium_scindens		(0.03-0.1)	0.084	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Eubacterium_sp.		(0.01-0.12)	0.276	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium___		(0.37-0.5)	0.070	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia___	*	(1-1.33)	1.316	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia_gut_metagenome	*	(0.01-0.09)	1.330	⇑
Clostridia_Oscillospirales_Butyricicoccaceae_Butyricicoccus___		(0.5-0.57)	0.112	⇓
Clostridia_Oscillospirales_Oscillospiraceae_Flavonifractor___		(0.09-0.13)	0.061	⇓
Clostridia_Oscillospirales_Oscillospiraceae_Oscillibacter___		(0.09-0.13)	0.206	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Faecalibacterium___		(6.44-7.23)	0.173	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Subdoligranulum___	*	(1.4-1.67)	1.297	⇓
Clostridia_Oscillospirales_Ruminococcaceae_UBA1819_uncultured_organism		(0.02-0.06)	0.084	⇑

SCFA producers

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium_Clostridium_spiroforme	*	(0.02-0.05)	0.492	⇑
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium___	*	(0-0.13)	1.012	⇑
Bacilli_Lactobacillales_Streptococcaceae_Streptococcus_Streptococcus_salivarius		(0.04-0.37)	0.066	⇔
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris		(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___		(5.79-6.85)	0.056	⇓
Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes___	*	(0.62-0.93)	10.473	⇑
Clostridia_Clostridiales_Clostridiaceae_Clostridium_sensu_stricto_1___	*	(0-0.33)	1.321	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes_Anaerostipes_caccae		(0.03-0.12)	0.112	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes___	*	(1.18-1.49)	4.552	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Blautia___	*	(5.21-6.02)	6.510	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Clostridium_scindens		(0.03-0.1)	0.084	⇔

(continued)

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Eubacterium_sp.		(0.01-0.12)	0.276	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium___		(0.37-0.5)	0.070	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia___	*	(1-1.33)	1.316	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia_gut_metagenome	*	(0.01-0.09)	1.330	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_gnavus_group___		(0.28-0.83)	0.281	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_torques_group___		(0.52-0.8)	0.267	⇓
Clostridia_Oscillospirales_Butyricicoccaceae_Butyricicoccus___		(0.5-0.57)	0.112	⇓
Clostridia_Oscillospirales_Oscillospiraceae_Flavonifractor___		(0.09-0.13)	0.061	⇓
Clostridia_Oscillospirales_Oscillospiraceae_Oscillibacter___		(0.09-0.13)	0.206	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Faecalibacterium___		(6.44-7.23)	0.173	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus_Ruminococcus_bicirculans	*	(0.29-0.52)	4.187	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus___	*	(0.1-0.49)	1.489	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Subdoligranulum___	*	(1.4-1.67)	1.297	⇓
Clostridia_Oscillospirales_Ruminococcaceae_UBA1819_uncultured_organism		(0.02-0.06)	0.084	⇑
Negativicutes_Veillonellales-Selenomonadales_Veillonellaceae_Dialister___		(0.43-0.62)	0.201	⇓

Protectors of mucus layer

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris		(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___		(5.79-6.85)	0.056	⇓
Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia___	*	(0-0.76)	5.021	⇑

Protecting against obesity

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris		(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___		(5.79-6.85)	0.056	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Faecalibacterium___		(6.44-7.23)	0.173	⇓
Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia___	*	(0-0.76)	5.021	⇑

Proinflammatory

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella___		(0-0.62)	0.042	⇔

Proteolytics

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium_Clostridium_spiroforme	*	(0.02-0.05)	0.492	⇑
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium___	*	(0-0.13)	1.012	⇑
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris		(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___		(5.79-6.85)	0.056	⇓
Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes___	*	(0.62-0.93)	10.473	⇑
Clostridia_Clostridiales_Clostridiaceae_Clostridium_sensu_stricto_1___	*	(0-0.33)	1.321	⇑

(continued)

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Clostridium_scindens		(0.03-0.1)	0.084	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Eubacterium_sp.		(0.01-0.12)	0.276	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium___		(0.37-0.5)	0.070	⇓
Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella___		(0-0.62)	0.042	⇔

Sulfidric acid producers

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium_Clostridium_spiroforme	*	(0.02-0.05)	0.492	⇑
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium___	*	(0-0.13)	1.012	⇑
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea_Absiella_argi		(0-0.29)	0.211	⇔
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea___	*	(0-0.17)	1.030	⇑
Bacilli_Lactobacillales_Streptococcaceae_Streptococcus_Streptococcus_salivarius		(0.04-0.37)	0.066	⇔
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris		(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___		(5.79-6.85)	0.056	⇓
Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes___	*	(0.62-0.93)	10.473	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes_Anaerostipes_caccae		(0.03-0.12)	0.112	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes___	*	(1.18-1.49)	4.552	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Blautia___	*	(5.21-6.02)	6.510	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Clostridium_scindens		(0.03-0.1)	0.084	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Eubacterium_sp.		(0.01-0.12)	0.276	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium___		(0.37-0.5)	0.070	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia___	*	(1-1.33)	1.316	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia_gut_metagenome	*	(0.01-0.09)	1.330	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_gnavus_group___		(0.28-0.83)	0.281	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_torques_group___		(0.52-0.8)	0.267	⇓
Clostridia_Oscillospirales_Oscillospiraceae_Flavonifractor___		(0.09-0.13)	0.061	⇓
Clostridia_Oscillospirales_Oscillospiraceae_Oscillibacter___		(0.09-0.13)	0.206	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus_Ruminococcus_bicirculans	*	(0.29-0.52)	4.187	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus___	*	(0.1-0.49)	1.489	⇑
Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Intestinibacter___	*	(0-0.25)	3.311	⇑
Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Romboutsia___		(0-0.28)	0.300	⇑
Coriobacteriia_Coriobacteriales_Eggerthellaceae_Adlercreutzia___		(0.04-0.08)	0.375	⇑
Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella___		(0-0.62)	0.042	⇔
Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia___	*	(0-0.76)	5.021	⇑

Associated with obesity

Domain Phylum Class Order Family Genus Species	Top30	Reference	YOUR VALUES %	
Clostridia_Lachnospirales_Lachnospiraceae_Blautia___	*	(5.21-6.02)	6.510	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_gnavus_group___		(0.28-0.83)	0.281	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_torques_group___		(0.52-0.8)	0.267	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus_Ruminococcus_bicirculans	*	(0.29-0.52)	4.187	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus___	*	(0.1-0.49)	1.489	⇑
Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella___		(0-0.62)	0.042	⇔

Reference values. Reference values have been established based on all samples from healthy individuals stored in the CLOM database.

Test identification data

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DATE	:	**24 September 2024**
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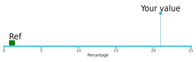
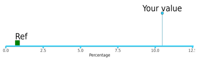
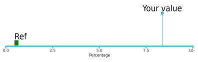
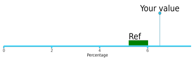
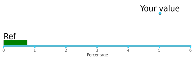
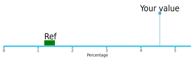
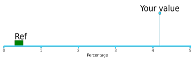
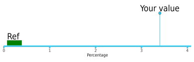
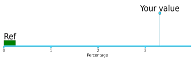
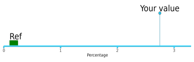
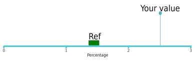
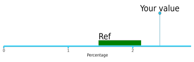
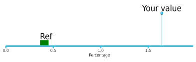
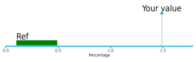
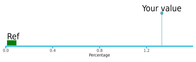
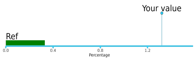
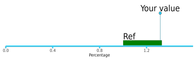
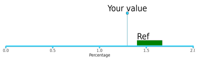
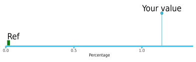
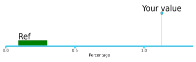
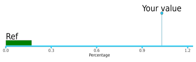
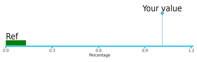
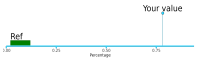
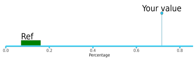
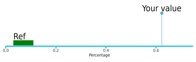
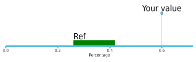
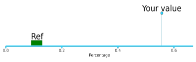
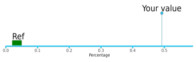
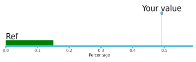
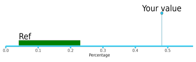
Sex (M/F)	:	**Male**
Height (cm)	:	**154**
Weitght(Kg)	:	**78**
BMI	:	**32.9** (obesity)

TOP30. Here are the 30 most abundant species in your microbiota.

Domain Phylum Class Order Family Genus Species	Referenece	YOUR VALUES %		top30
Clostridia_Oscillospirales_Ruminococcaceae_CAG-352_uncultured_bacterium	(0.69-1.47)	20.973	⇧	
Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes___	(0.62-0.93)	10.473	⇧	
Clostridia_Oscillospirales_Eubacterium_coprostanoligenes_group_Eubacterium_coprostanoligenes_group_gut_metagenome	(0.46-0.67)	8.365	⇧	
Clostridia_Lachnospirales_Lachnospiraceae_Blautia___	(5.21-6.02)	6.510	⇧	
Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia___	(0-0.76)	5.021	⇧	
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes___	(1.18-1.49)	4.552	⇧	
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus_Ruminococcus_bicirculans	(0.29-0.52)	4.187	⇧	
Clostridia_Christensenellales_Christensenellaceae_Christensenellaceae_R-7_group_human_gut	(0.07-0.39)	3.400	⇧	
Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Intestinibacter___	(0-0.25)	3.311	⇧	
Clostridia_Oscillospirales_Oscillospiraceae_UCG-002___	(0.1-0.25)	2.749	⇧	
Clostridia_Lachnospirales_Lachnospiraceae______	(1.36-1.53)	2.510	⇧	
Clostridia_Lachnospirales_Lachnospiraceae_Agathobacter___	(1.47-2.13)	2.421	⇧	
Clostridia_Monoglobales_Monoglobaceae_Monoglobus___	(0.36-0.45)	1.644	⇧	
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus___	(0.1-0.49)	1.489	⇧	
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia_gut_metagenome	(0.01-0.09)	1.330	⇧	
Clostridia_Clostridiales_Clostridiaceae_Clostridium_sensu_stricto_1___	(0-0.33)	1.321	⇧	
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia___	(1-1.33)	1.316	⇔	

(continued)

Domain Phylum Class Order Family Genus Species	Referenece	YOUR VALUES %		top30
Clostridia_Oscillospirales_Ruminococcaceae_Subdoligranulum___	(1.4-1.67)	1.297	⇓	
Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_Family_XIII_AD3011_group_uncultured_organism	(0.01-0.03)	1.147	⇑	
Clostridia_Oscillospirales_Butyricicoccaceae______	(0.09-0.3)	1.129	⇑	
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea___	(0-0.17)	1.030	⇑	
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium___	(0-0.13)	1.012	⇑	
Clostridia_Lachnospirales_Lachnospiraceae_Sellimonas___	(0.02-0.12)	0.782	⇑	
Clostridia_Lachnospirales_Lachnospiraceae_Sellimonas_uncultured_bacterium	(0.07-0.16)	0.717	⇑	
Clostridia_Lachnospirales_Lachnospiraceae_Frisingicoccus___	(0.03-0.11)	0.623	⇑	
Clostridia_Lachnospirales_Lachnospiraceae_Lachnospira___	(0.26-0.42)	0.600	⇑	
Clostridia_Oscillospirales_Oscillospiraceae_uncultured___	(0.09-0.13)	0.557	⇑	
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium_Clostridium_spiroforme	(0.02-0.05)	0.492	⇑	
Clostridia_Lachnospirales_Lachnospiraceae_Eubacterium_hallii_group_uncultured_bacterium	(0-0.15)	0.492	⇑	
Bacilli_Izemoplasmatales_Izemoplasmatales_Izemoplasmatales_uncultured_organism	(0.04-0.23)	0.482	⇑	

Reference values. Reference values have been established based on all samples from healthy individuals stored in the CLOM database.

2 Technical annex

2.1 Analysis methods

This report is generated from massive second-generation sequencing of PCR amplification of the V3-V4 region of 16S ribosomal gene. This method is currently the most used in microbiomics, characterized by its great robustness and reproducibility.

Sequence data are obtained in the standard FASTQ format and processed using the following workflow.

- Removal of universal bacterial primers amplifying the 16S ribosomal gene (V3-V4 region) using the *cutadapt* program (Martin, 2011).
- The sequences, with primers removed, undergo extensive quality control and error correction, end joining and removal of chimeric sequences using the `DADA2` (Callahan et al., 2016) workflow. This workflow is executed using the *R* platform (R Core Team, 2012). The `DADA2` workflow generates, from the initial data set, a set of non-redundant sequences called ASV (Amplicon Sequence Variant). Each one is derived from a specific kind of bacteria and its relative abundance reflects the prevalence of each bacterial type in the entire microbiota. These sequences are used for the next step of taxonomic annotation.
- Each sequence is compared with a database to find out the type of bacteria from which it comes. This taxonomic annotation step is carried out in the `qiime2` environment (Bolyen et al., 2019) by comparing each sequence with those stored in the Silva database (version 138) . The taxonomic annotation, together with the counts of each sequence per sample, define the user microbiome profile. The taxonomic annotation is carried out by applying sufficiently strict filters to guarantee confidence and reliability in the result obtained.
- All the data obtained has been obtaiend in the *R* programming environment using several open source libraries: *vegan*, *dplyr*, *reshape2*, *phyloseq*, *tidyverse*, *rmarkdown*, *knitcitations*, *knitr*, *kableExtra*.

2.2 Sequencing results.

The number of sequences obtained through the amplification process (PCR), of the 16S ribosomal gene (V3-V4 region) are reported below.

	Number of sequences
Obtaiend sequences	25409
Filtered sequences	22123
Corrected sequences (forward)	21913
Corrected sequences (reverse)	21969
Joined sequences	21392
No chimeric sequences	21351

2.3 Complete taxonomy

This section reports the complete taxonomy of all the organisms found in the analyzed sample.

Organisms are reported following taxonomic ranks in alphabetical order.

Reference values have been established based on all samples from healthy individuals stored in the CLOM database.

Domain Phylum Class Order Family Genus Species	Referenece CLOM's healthy samples	YOUR VALUES %	
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium_Clostridium_spiroforme	(0.02-0.05)	0.492	⇑
Bacilli_Erysipelotrichales_Erysipelatoclostridiaceae_Erysipelatoclostridium___	(0-0.13)	1.012	⇑
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Clostridium_innocuum_group___	(0-0.11)	0.126	⇑
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea_Absiella_argi	(0-0.29)	0.211	⇔
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea___	(0-0.17)	1.030	⇑
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Holdemania_uncultured_bacterium	(0.01-0.03)	0.220	⇑
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Turicibacter___	(0-0.44)	0.201	⇔
Bacilli_Erysipelotrichales_Erysipelotrichaceae_Turicibacter_uncultured_bacterium	(0-0.16)	0.173	⇑
Bacilli_Izemoplasmatales_Izemoplasmatales_Izemoplasmatales_uncultured_organism	(0.04-0.23)	0.482	⇑
Bacilli_Lactobacillales_Streptococcaceae_Streptococcus_Streptococcus_salivarius	(0.04-0.37)	0.066	⇔
Bacilli_RF39_RF39_RF39_uncultured_bacterium	(0-0.14)	0.056	⇔
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides_Bacteroides_stercoris	(1.33-2.11)	0.028	⇓
Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides___	(5.79-6.85)	0.056	⇓
Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes___	(0.62-0.93)	10.473	⇑
Clostridia_Christensenellales_Christensenellaceae_Christensenellaceae_R-7_group_human_gut	(0.07-0.39)	3.400	⇑
Clostridia_Christensenellales_Christensenellaceae_Christensenellaceae_R-7_group_uncultured_bacterium	(NA-NaN)	0.215	⇔
Clostridia_Christensenellales_Christensenellaceae_Christensenellaceae_R-7_group_uncultured_marine	(0.01-0.02)	0.019	⇔
Clostridia_Clostridia_Hungateiclostridiaceae______	(0-0.07)	0.066	⇔
Clostridia_Clostridia_vadinBB60_group_Clostridia_vadinBB60_group_Clostridia_vadinBB60_group_gut_metagenome	(0-0.08)	0.033	⇔
Clostridia_Clostridiales_Clostridiaceae_Clostridium_sensu_stricto_1___	(0-0.33)	1.321	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Agathobacter___	(1.47-2.13)	2.421	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes_Anaerostipes_caccae	(0.03-0.12)	0.112	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Anaerostipes___	(1.18-1.49)	4.552	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Blautia___	(5.21-6.02)	6.510	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Eisenbergiella___	(0-0.09)	0.356	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Epulopiscium_uncultured_organism	(0.08-0.72)	0.056	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Eubacterium_hallii_group_uncultured_bacterium	(0-0.15)	0.492	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Eubacterium_ventriosum_group_uncultured_Clostridiales	(0.04-0.1)	0.023	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Eubacterium_xylanophilum_group___	(0.22-0.32)	0.136	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Frisingicoccus___	(0.03-0.11)	0.623	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Fusicatenibacter___	(1.17-1.62)	0.066	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Clostridium_scindens	(0.03-0.1)	0.084	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium_Eubacterium_sp.	(0.01-0.12)	0.276	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnoclostridium___	(0.37-0.5)	0.070	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Lachnospira___	(0.26-0.42)	0.600	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Lachnospiraceae_ND3007_group___	(0.1-0.18)	0.136	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Lachnospiraceae_NK4A136_group___	(0.27-0.39)	0.337	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Lactonifactor___	(0.01-0.02)	0.052	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Marvinbryantia___	(0.04-0.06)	0.141	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia___	(1-1.33)	1.316	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Roseburia_gut_metagenome	(0.01-0.09)	1.330	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_gnavus_group___	(0.28-0.83)	0.281	⇔
Clostridia_Lachnospirales_Lachnospiraceae_Ruminococcus_torques_group___	(0.52-0.8)	0.267	⇓
Clostridia_Lachnospirales_Lachnospiraceae_Sellimonas___	(0.02-0.12)	0.782	⇑
Clostridia_Lachnospirales_Lachnospiraceae_Sellimonas_uncultured_bacterium	(0.07-0.16)	0.717	⇑
Clostridia_Lachnospirales_Lachnospiraceae______	(1.36-1.53)	2.510	⇑
Clostridia_Lachnospirales_Lachnospiraceae_uncultured_butyrate-producing_bacterium	(0-1.34)	0.150	⇔
Clostridia_Lachnospirales_Lachnospiraceae_uncultured_uncultured_Eubacterium	(0.06-0.08)	0.117	⇑
Clostridia_Monoglobales_Monoglobaceae_Monoglobus___	(0.36-0.45)	1.644	⇑
Clostridia_Oscillospirales_Butyricicoccaceae_Butyricicoccus___	(0.5-0.57)	0.112	⇓
Clostridia_Oscillospirales_Butyricicoccaceae______	(0.09-0.3)	1.129	⇑
Clostridia_Oscillospirales_Eubacterium_coprostanoligenes_group_Eubacterium_coprostanoligenes_group___	(0.27-0.36)	0.150	⇓
Clostridia_Oscillospirales_Eubacterium_coprostanoligenes_group_Eubacterium_coprostanoligenes_group_gut_metagenome	(0.46-0.67)	8.365	⇑
Clostridia_Oscillospirales_Oscillospiraceae_Colidextribacter___	(0.08-0.1)	0.098	⇔
Clostridia_Oscillospirales_Oscillospiraceae_Flavonifractor___	(0.09-0.13)	0.061	⇓
Clostridia_Oscillospirales_Oscillospiraceae_NK4A214_group___	(0.1-0.16)	0.037	⇓

(continued)

Domain Phylum Class Order Family Genus Species	Referenece CLOM's healthy samples	YOUR VALUES %	
Clostridia_Oscillospirales_Oscillospiraceae_Oscillibacter___	(0.09-0.13)	0.206	⇑
Clostridia_Oscillospirales_Oscillospiraceae_Papillibacter_uncultured_bacterium	(0-0.01)	0.014	⇑
Clostridia_Oscillospirales_Oscillospiraceae_UCG-002___	(0.1-0.25)	2.749	⇑
Clostridia_Oscillospirales_Oscillospiraceae______	(0.05-0.08)	0.103	⇑
Clostridia_Oscillospirales_Oscillospiraceae_uncultured_Clostridium_sp.	(0.06-0.08)	0.042	⇓
Clostridia_Oscillospirales_Oscillospiraceae_uncultured___	(0.09-0.13)	0.557	⇑
Clostridia_Oscillospirales_Oscillospirales_Hydrogenoanaerobacterium_Selenomonadales_bacterium	(0.02-0.08)	0.103	⇑
Clostridia_Oscillospirales_Ruminococcaceae_CAG-352_uncultured_bacterium	(0.69-1.47)	20.973	⇑
Clostridia_Oscillospirales_Ruminococcaceae_DTU089___	(0.02-0.04)	0.066	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Eubacterium_siraeum_group___	(0.05-0.27)	0.009	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Faecalibacterium___	(6.44-7.23)	0.173	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Incertae_Sedis___	(0.1-0.26)	0.080	⇓
Clostridia_Oscillospirales_Ruminococcaceae_Incertae_Sedis_uncultured_bacterium	(0-0.07)	0.290	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Incertae_Sedis_uncultured_organism	(0.05-0.06)	0.103	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Negativibacillus_uncultured_bacterium	(0.05-0.08)	0.089	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus_Ruminococcus_bicirculans	(0.29-0.52)	4.187	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Ruminococcus___	(0.1-0.49)	1.489	⇑
Clostridia_Oscillospirales_Ruminococcaceae_Subdoligranulum___	(1.4-1.67)	1.297	⇓
Clostridia_Oscillospirales_Ruminococcaceae_UBA1819_uncultured_organism	(0.02-0.06)	0.084	⇑
Clostridia_Oscillospirales_Ruminococcaceae______	(0.42-0.66)	0.155	⇓
Clostridia_Oscillospirales_Ruminococcaceae_uncultured___	(0.04-0.06)	0.042	⇔
Clostridia_Oscillospirales_Ruminococcaceae_uncultured_uncultured_bacterium	(0-0.05)	0.047	⇔
Clostridia_Oscillospirales_________	(NA-NA)	0.066	⇔
Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_Eubacterium_brachy_group_uncultured_bacterium	(0.01-0.03)	0.066	⇑
Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_Eubacterium_nodatum_group_Ihubacter_massiliensis	(0.01-0.03)	0.070	⇑
Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_Family_XIII_AD3011_group_uncultured_bacterium	(0.01-0.03)	0.061	⇑
Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_Family_XIII_AD3011_group_uncultured_organism	(0.01-0.03)	1.147	⇑
Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Intestinibacter___	(0-0.25)	3.311	⇑
Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Romboutsia___	(0-0.28)	0.300	⇑
Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Terrisporobacter_uncultured_bacterium	(0-0.3)	0.290	⇔
Clostridia____________	(NA-NA)	0.141	⇔
Coriobacteriia_Coriobacteriales_Eggerthellaceae_Adlercreutzia___	(0.04-0.08)	0.375	⇑
Coriobacteriia_Coriobacteriales_Eggerthellaceae_CHKCI002_Coriobacteriaceae_bacterium	(0-0.22)	0.023	⇔
Coriobacteriia_Coriobacteriales_Eggerthellaceae_Eggerthella_uncultured_bacterium	(0.03-0.08)	0.234	⇑
Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella___	(0-0.62)	0.042	⇔
Negativicutes_Veillonellales-Selenomonadales_Veillonellaceae_Dialister___	(0.43-0.62)	0.201	⇓
Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia___	(0-0.76)	5.021	⇑

2.4 Community profiles

The community profiles stored in the CLOM database have been grouped into categories using mathematical models known as *Dirichlet Multinomial Mixture models* (Holmes et al., 2012).

To define each of the 14 communities, an exhaustive biostatistical analysis has been carried out to identify risk or protection profiles associated with certain diseases. These profiles have been generated within the framework of a meta-analysis carrying out stratifying taxonomic and clinical data from scientific articles indexed in the common databases for biomedical bibliographic data. Therefore, the characteristics that describe each community and disease come from a meta-analysis of correlation between thousands of microbial community profiles and the associated clinical data, using binary logistic regression analysis.

It is important to highlight that, in the phase of predicting the association of a new sample with a certain type of community, it does not belong to the CLOM database, and its eventual association with a community and its risk profile does not imply direct evidence about the clinical status of the individual under study. Therefore, the prediction of belonging to a type of community and the association with a certain risk profile represents a guide and should NOT be considered a clinical diagnosis.

3 Bibliographic references.

(1) E. Bolyen et al. “Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2”. In: *Nat Biotechnol* 37.8 (ago. 2019). (PubMed Central:PMC7015180) (DOI:10.1038/s41587-019-0209-9) (PubMed:31341288) , pp. 852-857.

(2) B. J. Callahan et al. “DADA2: High-resolution sample inference from Illumina amplicon data”. In: *Nat. Methods* 13.7 (jul. 2016). (PubMed Central:PMC4927377) (DOI:10.1038/nmeth.3869) (PubMed:27214047) , pp. 581-583.

(3) I. Holmes et al. “Dirichlet multinomial mixtures: generative models for microbial metagenomics”. In: *PLoS One* 7.2 (2012), p. e30126.

(4) M. Martin. “Cutadapt removes adapter sequences from high-throughput sequencing reads”. In: *EMBnet* 17.1 (may. 2011), pp. 10-12.

(5) R Core Team. *R: A Language and Environment for Statistical Computing*. ISBN 3-900051-07-0. R Foundation for Statistical Computing. Vienna, Austria, 2012. http://www.R-project.org/.

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