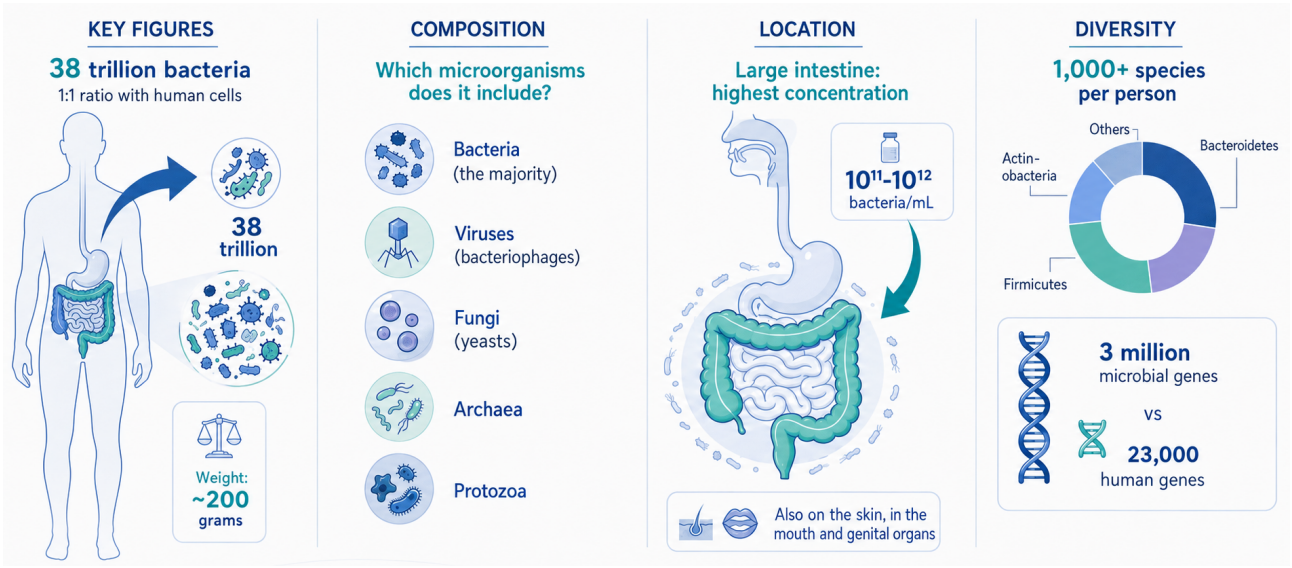
Gut Microbiota Test

METAGENOMICS

My Biota

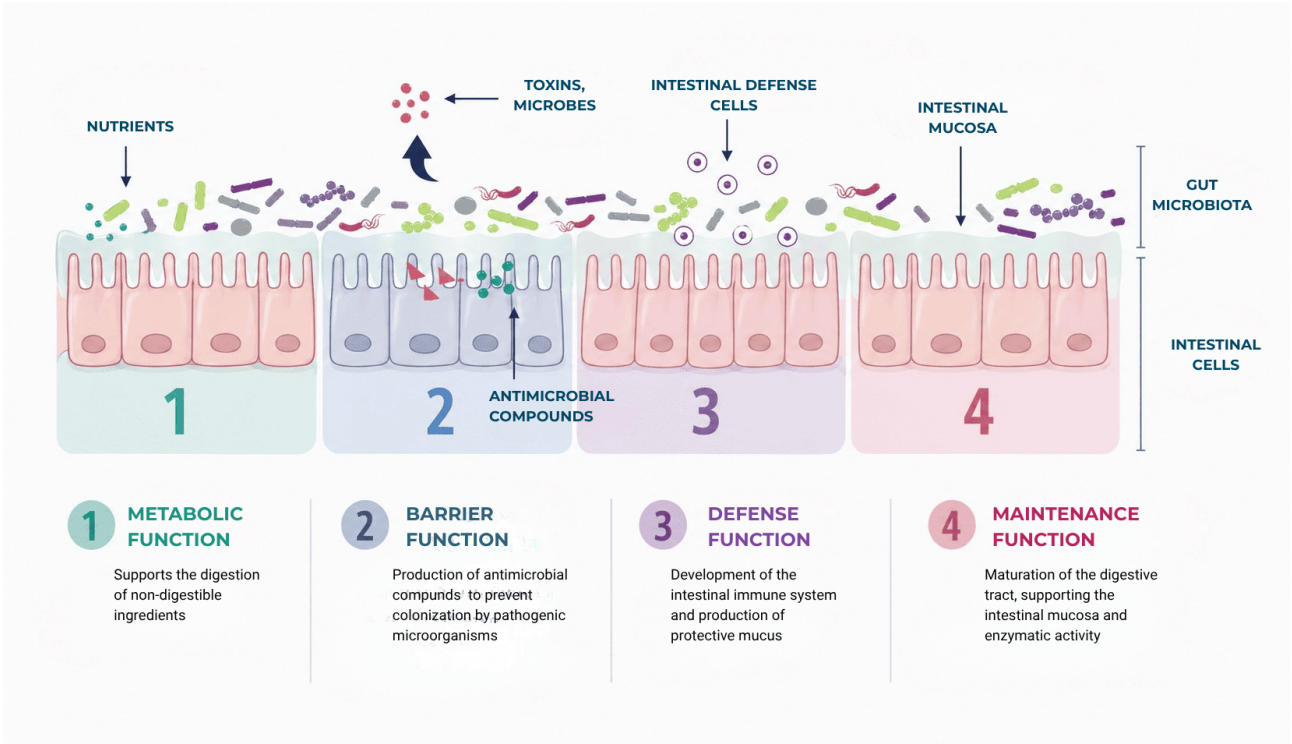
Gut microbiome

The gut microbiome refers to the community of microorganisms that live in the human intestine, including bacteria, archaea, fungi and viruses.



Functions

These microorganisms play a fundamental role in health, participating in functions such as digestion, metabolite production, regulation of the immune system, and protection against pathogens. The balance between these microbial communities is key to overall wellbeing.



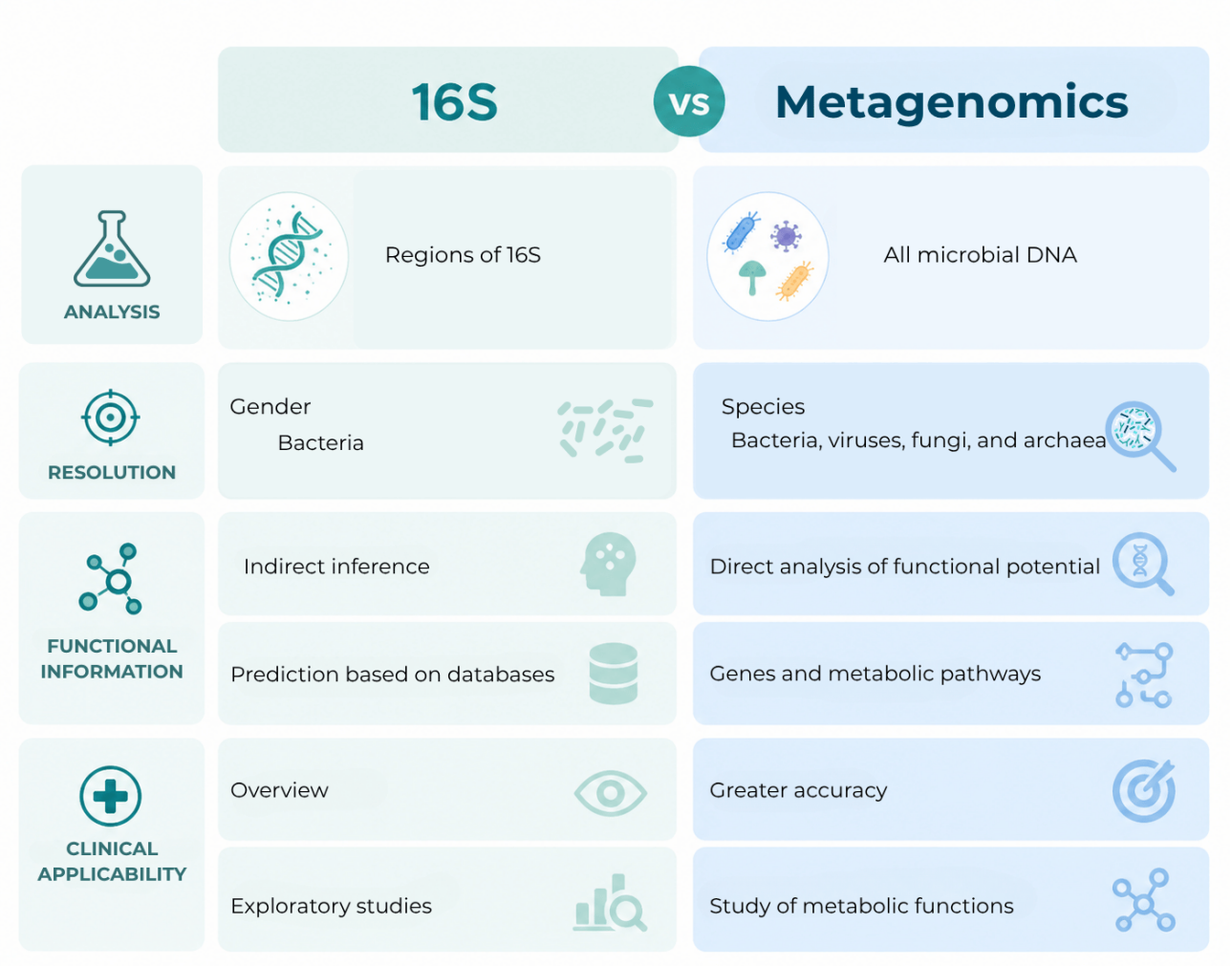
Metagenomics:

What it is and its benefits

Human metagenomics is the study of the collective genetic material of all the microorganisms (bacteria, fungi, viruses and archaea) that naturally inhabit the human body. This study uses long-read DNA sequencing technology, which, unlike more limited methods such as 16S rRNA gene sequencing via NGS or traditional microbiological cultures, makes it possible to characterize the complete microbial DNA. This allows:

- Identifying a greater number of microorganisms, including those present in low proportions
- Analyzing not only which microorganisms are present, but also their functions
- Detecting possible pathogens or microbial imbalances
- Assessing intestinal diversity, considered an important health marker

Thanks to this technology, a more complete and precise view of the intestinal ecosystem is obtained.



1. GLOBAL SUMMARY

The following summarizes the status of the different functional domains analyzed, indicating the result obtained and its possible clinical implication.

Functional domain	Result	Clinical implication
OVERALL DIVERSITY	Overloaded	High diversity is not always protective if it coexists with excess fermentation, oral microorganisms or opportunistic organisms.
INTESTINAL HOMEOSTASIS	Unfavorable	Combined imbalance of barrier function, immunity, fermentation and colonization resistance, with low ecosystem resilience.
INTESTINAL MUCUS*	Unfavorable	Predominance of mucin consumption over its production and regulation, with reduced epithelial protection.
INTESTINAL PERMEABILITY	Unfavorable	The functional balance of mucus, epithelium and butyrate metabolism suggests reduced containment capacity against antigens and LPS, and does not constitute a direct diagnosis of hyperpermeability.
GUT INFLAMMATION AND IMMUNE SYSTEM AXIS	Unfavorable	Relative excess of LPS-producing/pro-inflammatory functions and a deficit of anti-inflammatory functions, with possible impact on the mucosa and immune activation.
INFECTION	Unfavorable	The detection of pathogens or opportunistic organisms may be clinically relevant depending on species, abundance, virulence factors and symptoms.
BIOGENIC AMINES	Unfavorable	Greater potential production of histamine, cadaverine or tyramine and/or reduced histamine degradation, usually associated with proteolysis, and requires correlation with symptoms.
BENEFICIAL SCFAS	Unfavorable	Low potential capacity to generate butyrate, acetate and propionate, with reduced energy support for colonocytes and the barrier.
BUTYRATE BALANCE	Unfavorable	Significant mismatch between butyrate production and consumption, with reduced potential availability for the colonic epithelium.
GAS PRODUCTION	Unfavorable	Imbalance of hydrogen, methane and/or hydrogen sulfide, which may be associated with bloating, slow transit or irritation depending on the predominant gas.
SACCHAROLYTIC METABOLISM	Balanced	Lactate and succinate production and consumption maintain a balanced metabolic flow.
FAT METABOLISM	Balanced	Microbial bile acid transformation within a physiological balance.

PROTEIN METABOLISM	Unfavorable	Potential excess of ammonium, p-cresol, cadaverine and other proteolytic metabolites, with possible mucosal irritation.
PROBIOTIC SPECIES	Balanced	Balanced presence of species with probiotic functions.
MYCOBIOTA	Absence	No significant fungal signal is detected, and its absence in the sample does not completely exclude colonization.
PARASITES	Absence	No relevant parasites are detected in this sample, and this does not exclude infection if shedding is intermittent.
ESTROGEN METABOLISM	Unfavorable	Imbalance between deconjugation, elimination and transformation of estrogens, with possible modification of their enterohepatic recirculation.
VITAMINS	Unfavorable	Low potential capacity to produce folates, menaquinones and/or B12-related compounds, and does not allow inferring systemic status.
NEUROTRANSMITTERS	Balanced	Microbial neuroactive pathways within a physiological balance.
GUT-BRAIN AXIS	Balanced	Adequate balance of barrier function, inflammation and tryptophan-derived metabolites.
GUT-SKIN AXIS	Balanced	Adequate balance between barrier function, immunity and protective skin functions.
GUT-HEART AXIS	Balanced	Adequate balance between microbial production and consumption of TMA.
GUT-LIVER AXIS	Balanced	Adequate balance of barrier function, endotoxins and bile metabolism.
FOOD INTOLERANCES	Balanced	Functional capacity compatible with tolerance, without excluding host disorders.

* The functional balance between the bacteria that maintain the mucus and those that degrade it, together with the balance between butyrate producers and consumers, is one of the main microbiological determinants of intestinal barrier maintenance and of the risk of increased intestinal permeability.

INTERPRETATION OF THE RESULT

UNFAVORABLE	Altered microbial profile, associated with a possible unfavorable functional and clinical repercussion.
SLIGHTLY UNFAVORABLE	Mild alterations relative to the reference range, with a possible functional repercussion.
BALANCED	Microbial profile within the reference range, with no relevant functional alterations.
FAVORABLE	Microbial profile compatible with a beneficial functional contribution.

HOW IS THIS CLASSIFICATION OBTAINED?

The classification is obtained by comparing the microbial profile of each functional domain with a reference cohort of healthy individuals. The result reflects the overall status of the domain evaluated.

MICROBIAL METABOLITES

Microbial metabolites are compounds produced by the gut microbiota during its metabolic activity. These metabolites play a fundamental role in communication between the gut and other organs, participating in processes such as immune regulation, intestinal barrier integrity, metabolism and the gut-brain axis. Their analysis provides a better understanding of the microbiome's functional impact on health.

This table shows only the metabolites with unfavorable or slightly unfavorable results. Metabolites within the functional balance are not included

Metabolite	Status	Bacteria*	Affected function	Interpretation
Ammonium / Ammonia	High	*Clostridium perfringens, Phocaeicola vulgatus*	Ammonium-producing	Higher local toxic load, mucosal irritation, and possible detox overload.
Beta-glucuronidase / Estrobolome	High	*Bacteroides ovatus, Ruminococcus sp. SR1/5, Blautia producta*	S-equol-producing	Greater estrogen deconjugation and recirculation; relevant for hormonal symptoms.
Butyrate	Low	*Bilophila wadsworthia, Desulfovibrio fairfieldensis*	Butyrate-consuming	Less barrier support, lower anti-inflammatory tone, and greater mucosal vulnerability.
GABA	High	*Alistipes indistinctus, Bacteroides ovatus, Phocaeicola vulgatus*	GABA-producing	Excess is not always clinically useful; interpret together with microbiota and symptoms.
H2S / Hydrogen sulfide	High	*Bilophila wadsworthia, Desulfovibrio fairfieldensis*	Hydrogen sulfide-producing	May be associated with sulfurous gases, mucosal irritation, diarrhea, or contextual inflammation.
Histamine	High	*Enterococcus faecium, Clostridium perfringens*	Histamine-producing	May contribute to headache, hives, rhinitis, diarrhea, anxiety, or food reactivity.
Hydrogen	High	*Bacteroides salyersiae, Bacteroides nordii, Bacteroides ovatus*	Hydrogen-producing	May be associated with bloating, gas, and excessive fermentation.
LPS / Endotoxin	High	*Alistipes onderdonkii, Bilophila wadsworthia, Bacteroides ovatus*	Lipopolysaccharide (LPS)-producing	Higher risk of low-grade inflammation, permeability, and immune activation.
Mucin / mucosal degradation	Low	*Clostridium perfringens, Phocaeicola vulgatus*	Mucus-consuming	May reflect low mucolytic activity; assess Akkermansia in context.
Succinate	High	*Alistipes onderdonkii, Paraprevotella xylaniphila, Alistipes shahii*	Succinate-producing	Associated with incomplete fermentation, possible inflammation, and contextual gram-negative dysbiosis.

* The table lists the bacteria related to each function whose abundance falls outside the reference ranges.

INTERPRETATION OF THE RESULT

● **UNFAVORABLE**	Relevant alteration of the metabolite relative to the reference profile, with potential impact on the associated microbial functions
● **SLIGHTLY UNFAVORABLE**	Moderate alteration of the metabolite relative to the reference profile, indicative of a lower-intensity functional imbalance

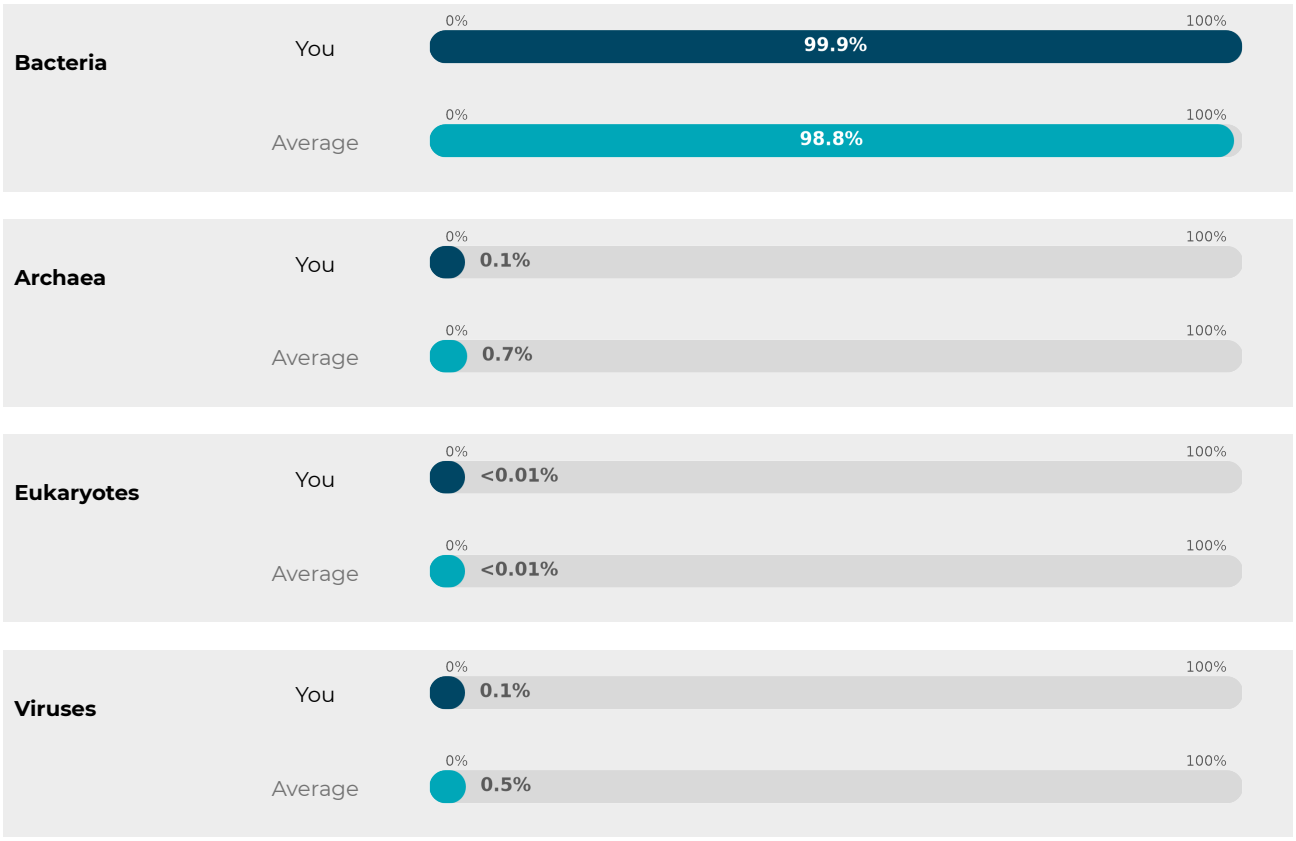
2. SAMPLE COMPOSITION

This section summarizes the main quality and balance indicators of your gut microbiota. Through these parameters we assess richness, the balance between key bacterial groups, and overall microorganism diversity, providing an overview of the status of your intestinal ecosystem.

Parameter	Reference ranges	Result
Diversity (Shannon index)	2.15-3.42	3.69
Firmicutes / *Bacteroidetes* ratio	1-10	0.27
Richness	200-800	432

Most of the DNA present in the sample corresponds to microorganisms, especially bacteria. In addition to other groups such as archaea, eukaryotes and viruses.

Below is the **proportion of taxonomic groups** present in your sample compared to the average values from the reference database.



3. MICROBIOLOGICAL SECTION

Top 20 species by abundance

Below are the **20 species with the highest relative abundance detected** in the sample, together with their taxonomic classification, their abundance, and the corresponding reference range.

Microorganism	Domain	Reference (%)	Abundance (%)
Phocaeicola vulgatus	Bacteria	0.000 – 15.430	20.952
Bacteroides salyersiae	Bacteria	0.000 – 0.315	6.047
Alistipes putredinis	Bacteria	0.000 – 8.339	5.059
Bacteroides ovatus	Bacteria	0.000 – 2.012	4.097
Bacteroides stercoris	Bacteria	0.000 – 4.875	4.086
Odoribacter splanchnicus	Bacteria	0.000 – 1.132	3.458
Akkermansia muciniphila	Bacteria	0.000 – 4.192	3.070
Bacteroides uniformis	Bacteria	0.011 – 14.355	3.042
Phascolarctobacterium faecium	Bacteria	0.000 – 0.613	2.829
Alistipes shahii	Bacteria	0.000 – 0.643	2.728
Faecalibacterium prausnitzii	Bacteria	0.959 – 12.099	2.575
Bilophila wadsworthia	Bacteria	0.000 – 0.139	2.070
Bacteroides caccae	Bacteria	0.000 – 2.288	1.940
Segatella copri	Bacteria	0.000 – 35.000	1.913
Bacteroides xylanisolvens	Bacteria	0.000 – 1.014	1.761
[Ruminococcus] lactaris	Bacteria	0.000 – 1.243	1.731
Parabacteroides distasonis	Bacteria	0.000 – 2.902	1.688
Phocaeicola dorei	Bacteria	0.000 – 7.980	1.670
Bacteroides thetaiotaomicron	Bacteria	0.000 – 1.933	1.646
Alistipes finegoldii	Bacteria	0.000 – 1.732	1.530

BACTERIA

This section presents an **overview of the bacterial composition of the gut microbiome.** It includes bacteria whose abundance falls outside the reference range (elevated or decreased), indicating for each one its relative abundance, the reference range, and its possible functional relevance.

Elevated bacteria

The **species whose abundance is above the reference range** are shown. Depending on the clinical context, these alterations may be associated with relevant functional changes in the intestinal ecosystem.

Microorganism	Reference (%)	Abundance (%)	Functional impact
Bacteroides salyersiae	0.0 – 0.315	6.047	Hydrogen-producing, BCFA-producing, Indole-producing
Alistipes onderdonkii	0.0 – 0.01	0.755	Lipopolysaccharide (LPS)-producing, Propionate-producing, Succinate-producing
Bilophila wadsworthia	0.0 – 0.139	2.07	Hydrogen sulfide-producing, Pro-inflammatory, Lipopolysaccharide (LPS)-producing
Phascolarctobacterium faecium	0.0 – 0.613	2.829	Propionate-producing, Succinate-consuming
Parabacteroides johnsonii	0.0 – 0.043	0.621	Immunomodulatory
Desulfovibrio fairfieldensis	0.0 – 0.0	0.203	Hydrogen sulfide-producing, Butyrate-consuming
Paraprevotella xylaniphila	0.0 – 0.472	1.161	Acetate-producing, Succinate-producing, Trimethylamine-producing
Parabacteroides goldsteinii	0.0 – 0.085	0.293	BCFA-producing
Alistipes shahii	0.0 – 0.643	2.728	Butyrate-producing, Succinate-producing, Indole-producing
Bacteroides nordii	0.0 – 0.005	0.182	Hydrogen-producing, BCFA-producing

Decreased bacteria

The **species whose abundance is below the reference range** are shown. Their reduction may indicate a lower representation of microorganisms.

Microorganism	Reference (%)	Abundance (%)	Functional impact
Bacteroides sp. ZJ-18	8.0 – 45.0	0.002	No functional category described
Bacteroides sedimenti	8.0 – 45.0	0.004	No functional category described
Bacteroides graminisolvens	8.0 – 45.0	0.005	Hydrogen-producing, BCFA-producing
Bacteroides maternus	8.0 – 45.0	0.006	No functional category described
Bacteroides zoogleoformans	8.0 – 45.0	0.008	BCFA-producing
Bacteroides helcogenes	8.0 – 45.0	0.01	Hydrogen-producing, BCFA-producing
Bacteroides pyogenes	8.0 – 45.0	0.016	No functional category described
Bacteroides mucinivorans	8.0 – 45.0	0.017	No functional category described
Bacteroides sp. HF-162	8.0 – 45.0	0.036	No functional category described
Bacteroides caecimuris	8.0 – 45.0	0.04	Hydrogen-producing, BCFA-producing

FUNGI AND YEASTS

This section evaluates the **presence of potentially relevant fungi and yeasts** within the gut microbiome. Although they are part of the microbial ecosystem in low abundance, excessive growth of certain species may be associated with dysbiosis and alterations in gut health.

No fungi or yeasts were detected at significant levels in the analyzed sample

Panel analyzed	Result
48 species	Not detected

Genera analyzed:

Aspergillus spp., Blastomyces spp., Candida spp., Clavispora spp., Coccidioides spp., Cryptococcus spp., Debaryomyces spp., Fusarium spp., Galactomyces spp., Geotrichum spp., Histoplasma spp., Kluyveromyces spp., Malassezia spp., Meyerozyma spp., Mucor spp., Paracoccidioides spp., Penicillium spp., Pichia spp., Rhizopus spp., Rhodotorula spp., Saccharomyces spp., Trichosporon spp., Yarrowia spp.

See ANNEX II for the full list of species analyzed.

PARASITES

This section analyzes the **presence of intestinal parasites of clinical interest** using metagenomic sequencing techniques. The detection of these microorganisms can be useful in the study of gastrointestinal processes and other associated disorders.

No parasites were detected at significant levels in the analyzed sample

Panel analyzed	Result
33 species	Not detected

Genera analyzed:

Ancylostoma spp., Anisakis spp., Ascaris spp., Blastocystis spp., Chilomastix spp., Cryptosporidium spp., Cyclospora spp., Cystoisospora spp., Dientamoeba spp., Diphyllobothrium spp., Endolimax spp., Entamoeba spp., Enterobius spp., Fasciola spp., Giardia spp., Hymenolepis spp., Iodamoeba spp., Isospora spp., Microsporidia, Necator spp., Pentatrichomonas spp., Schistosoma spp., Strongyloides spp., Taenia spp., Toxoplasma spp., Trichuris spp., Trypanosoma spp.

See ANNEX II for the full list of species analyzed.

VIRUSES

This section presents the **viruses identified in the intestinal sample**. Most of the detected viruses belong to the intestinal virome, composed mainly of bacteriophages, microorganisms that infect bacteria and play an important role in the balance and regulation of the microbiota.

Virus	Abundance (%)
uncultured phage cr23_1	0.0204
Faecalibacterium phage FP_Brigit	0.0061
Wujia chipingensis	0.0031
uncultured phage cr13_1	0.002
Klebsiella phage KP8	0.0015
Carjivirus communis	0.0015
Jahgtovirus gastrointestinalis	0.0014

RESISTANCE GENES

These genes make up what is known as the intestinal resistome, a set of genetic determinants that can confer resistance to different families of antibiotics, and whose presence reflects the resistance potential of the microbial ecosystem.
The detection of these genes does not necessarily mean that an infection is present or that the microorganisms present are clinically resistant; rather, it provides information about the genetic resistance profile of the microbiota and should always be interpreted within the patient's clinical and microbiological context.

Gene	Antibiotic family	Main carrier	Reads
tet_Q	TETRACYCLINE	Bacteroidota	261
mef_En2	MACROLIDE	Unclassified (no Kraken2)	157
aadE	AMINOGLYCOSIDE	Unclassified (no Kraken2)	82
lnu_AN2	LINCOSAMIDE	Bacteroidota	74
tet_32	TETRACYCLINE	Bacillota	70
catA13	PHENICOL	Unclassified (no Kraken2)	57

4. FUNCTIONALITY

This section presents the main functions evaluated for the gut microbiome. For each function, the imbalanced microorganisms are shown, along with the direction of the alteration relative to the reference range and its possible functional repercussion.

INTERPRETATION OF THE RESULT

UNFAVORABLE		
↑	**Elevated**	Alteration above the reference range with a possible unfavorable functional repercussion.
↓	**Decreased**	Alteration below the reference range with a possible unfavorable functional repercussion.
SLIGHTLY UNFAVORABLE		
↑	**Elevated**	Mild alteration above the reference range with a possible unfavorable functional repercussion.
↓	**Decreased**	Mild alteration below the reference range with a possible unfavorable functional repercussion.
FAVORABLE		
↑	**Elevated**	Alteration above the reference range associated with a favorable functional repercussion.
↓	**Decreased**	Alteration below the reference range associated with a favorable functional repercussion.
BALANCED		
↔	**Within range**	No alterations outside the reference range.

NOTE: The presence of imbalanced bacteria does not necessarily imply an alteration in the overall status of the function.

INTESTINAL HOMEOSTASIS

It assesses the ability of the microbiota to maintain intestinal balance and protect the integrity of the epithelial barrier

INTESTINAL BARRIER

Top imbalanced bacteria	Status	Functional impact
Bacteroides thetaiotaomicron, *Blautia obeum*, *Adlercreutzia equolifaciens*	↔	Reinforce the tight junctions of the intestinal epithelium; they protect against antigens entering the bloodstream.

ORAL BACTERIA

Top imbalanced bacteria	Status	Functional impact
Streptococcus pasteurianus	↑	Their prominent presence suggests translocation from the mouth; it signals alterations in transit or oral health.

INTESTINAL MUCUS

Evaluates the activity of microorganisms involved in the preservation, stimulation and degradation of the intestinal mucus layer

MUCUS-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Clostridium perfringens, *Phocaeicola vulgatus*	↑	Degrade the protective mucus layer; their excess thins the barrier and favors intestinal hyperpermeability.

MUCUS-REGULATING

Top imbalanced bacteria	Status	Functional impact
Akkermansia muciniphila, *Faecalibacterium prausnitzii*, *Bacteroides thetaiotaomicron*	↔	Maintain the balance between mucus production and renewal; key for a healthy intestinal mucosa.

MUCUS-STIMULATING

Top imbalanced bacteria	Status	Functional impact
Butyricimonas virosa, *Subdoligranulum variabile*, *Clostridium perfringens*	↔	Actively reinforce the protective mucus layer; their presence is associated with a more resilient intestinal mucosa.

GUT INFLAMMATION AND IMMUNE SYSTEM AXIS

It assesses the microbiome's ability to maintain an appropriate balance between immune tolerance and inflammatory response

IMMUNOMODULATORY

Top imbalanced bacteria	Status	Functional impact
Parabacteroides johnsonii, *Blautia pseudococcoides*, *Blautia sp. SC05B48*	↔	Educate the immune system, favoring tolerance (Tregs, IL-10); their deficiency is associated with dysregulated immune responses.

LIPOPOLYSACCHARIDE (LPS)-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes onderdonkii, *Bilophila wadsworthia*, *Bacteroides ovatus*	↑	Release LPS endotoxin; their excess can cross the intestinal barrier and trigger systemic inflammation.

PRO-INFLAMMATORY

Top imbalanced bacteria	Status	Functional impact
Alistipes onderdonkii, *Bilophila wadsworthia*, *Bacteroides ovatus*	↑	Activate inflammatory pathways (TNF-□, IL-6); their overrepresentation is associated with low-grade intestinal inflammation.

ANTI-INFLAMMATORY

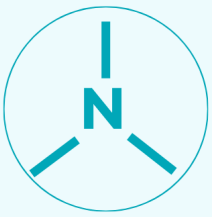
Top imbalanced bacteria	Status	Functional impact
Faecalibacterium taiwanense, *Faecalibacterium duncaniae*	↔	Curb local inflammatory activation; a deficiency leaves the ecosystem without a counterweight to the pro-inflammatory profile.

INFECTION

Evaluate the presence of microorganisms with pathogenic or opportunistic potential that can alter the balance of the intestinal ecosystem

PATHOGENS

Top imbalanced bacteria	Status	Functional impact
Enterococcus faecium, *Clostridium perfringens*, *Enterocloster clostridioformis*	↑	Potential pathogens; at relevant levels they can cause symptomatic infection or act as cofactors of chronic inflammation.



BIOGENIC AMINES

Evaluate the microbial potential to produce or degrade biogenic amines, such as histamine, derived from amino acid metabolism

SPERMIDINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bacteroides ovatus	↔	Produce spermidine, a polyamine with an autophagic, anti-aging effect that improves the intestinal barrier.

HISTAMINE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Bacteroides thetaiotaomicron, *Bacteroides fragilis*, *Bifidobacterium longum*	↔	Break down histamine released in the gut; they protect against symptoms of intolerance or sensitivity.

HISTAMINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Enterococcus faecium, *Clostridium perfringens*	↑	Release histamine; in people with low tolerance it can induce itching, headache, or digestive symptoms.

CADAVERINE-PRODUCING

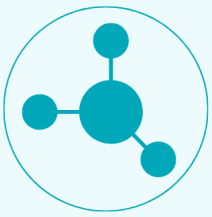
Top imbalanced bacteria	Status	Functional impact
Escherichia coli, *Klebsiella pneumoniae*	↑	Produce cadaverine, a biogenic amine marking intestinal protein putrefaction.

PUTRESCINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Escherichia coli	↑	Generate putrescine; in excess it indicates overwhelmed protein fermentation and stress on the mucosa.

TYRAMINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Enterococcus faecium, *Enterococcus faecalis*	↔	Produce tyramine; in excess it can cause hypertensive crises (MAOI interaction) and migraine in sensitive individuals.



BENEFICIAL SCFAs

It assesses the potential of the microbiota to produce beneficial short-chain fatty acids, primarily acetate, propionate, and butyrate

FORMATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bacteroides ovatus, *Blautia luti*, *Phocaeicola vulgatus*	↑	Produce formate as a fermentation byproduct; a substrate for methanogens and acetogens via the Wood-Ljungdahl pathway.

BUTYRATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes shahii, *Butyricimonas virosa*, *[Clostridium] symbiosum*	↔	Produce butyrate, the colonocyte's main energy source; it reinforces the intestinal barrier and modulates local inflammation.

ACETATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes onderdonkii, *Paraprevotella xylaniphila*, *Alistipes indistinctus*	↔	Provide acetate, a cross-feeding substrate for butyrate producers and a modulator of lipid metabolism.

PROPIONATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes onderdonkii, *Phascolarctobacterium faecium*, *Paraprevotella clara*	↔	Generate propionate, a short-chain fatty acid with a satiating effect, a glucose regulator, and a systemic anti-inflammatory.

ACETATE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Anaerostipes caccae, *Blautia hydrogenotrophica*	↔	Recycle acetate into butyrate, optimizing the energy utilization of the intestinal ecosystem.

BUTYRATE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Bilophila wadsworthia, *Desulfovibrio fairfieldensis*	↑	Reduce butyrate availability; an excess compromises colonic energy supply and barrier maintenance.

FORMATE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Anaerobutyricum hallii, *Methanobrevibacter smithii*, *Anaerostipes hadrus*	↔	Recycle formate, preventing its accumulation; they participate in regulating intestinal H2 and associated gases.

BUTYRATE BALANCE

It assesses the microbiome's ability to produce butyrate, a short-chain fatty acid essential for maintaining the integrity of the intestinal barrier, modulating inflammation, and providing energy to colonocytes

BUTYRATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes shahii, *Butyricimonas virosa*, *[Clostridium] symbiosum*	↔	Produce butyrate, the colonocyte's main energy source; it reinforces the intestinal barrier and modulates local inflammation.

BUTYRATE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Bilophila wadsworthia, *Desulfovibrio fairfieldensis*	↑	Reduce butyrate availability; an excess compromises colonic energy supply and barrier maintenance.

GAS PRODUCTION

Evaluate the microbial pathways related to gas production and consumption during intestinal fermentation

HYDROGEN-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bacteroides salyersiae, *Bacteroides nordii*, *Bacteroides ovatus*	↑	Release H2 during fermentation; this is normal in moderate amounts, but an excess causes bloating and flatulence.

HYDROGEN SULFIDE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bilophila wadsworthia, *Desulfovibrio fairfieldensis*	↑	Produce H2S, a genotoxic gas that damages colonocyte DNA and favors inflammation when elevated.

METHANE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Methanobrevibacter smithii	↔	Produce methane by consuming H2; the excess is associated with slow bowel transit and constipation.

SACCHAROLYTIC METABOLISM

It assesses the ability of the microbiota to ferment carbohydrates and fibers, generating metabolites that influence the intestinal environment

SUCCINATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes onderdonkii, *Paraprevotella xylaniphila*, *Alistipes shahii*	↔	Generate succinate, a metabolic intermediate; an excess can irritate the mucosa if not consumed in time.

SUCCINATE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Phascolarctobacterium faecium	↔	Recycle succinate into propionate, preventing accumulations that could favor intestinal discomfort.

LACTATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Enterocloster asparagiformis	↔	Produce lactate as a substrate for other beneficial bacteria; in balance it favors saccharide fermentation.

LACTATE-CONSUMING

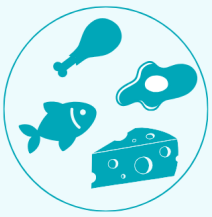
Top imbalanced bacteria	Status	Functional impact
Anaerostipes caccae	↔	Prevent lactate accumulation and redirect it toward beneficial SCFAs; key for efficient cross-feeding metabolism.

FAT METABOLISM

It evaluates the participation of the microbiota in the transformation of fats and bile acids within the intestinal environment

BILE ACID-METABOLIZING

Top imbalanced bacteria	Status	Functional impact
Bilophila wadsworthia, *Bacteroides ovatus*, *[Clostridium] scindens*	↔	Modify bile acids; an imbalance can affect fat absorption and produce pro-inflammatory secondary bile acids.



PROTEIN METABOLISM

It evaluates the microbial capacity to metabolize proteins and amino acids and generate different fermentation products

PROTEOLYTIC

Top imbalanced bacteria	Status	Functional impact
Alistipes onderdonkii, *Alistipes shahii*, *Enterococcus faecium*	↑	Ferment undigested proteins, generating toxic metabolites (ammonia, phenols); an excess irritates the mucosa.

AMMONIUM-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Clostridium perfringens, *Phocaeicola vulgatus*	↑	Release ammonia that irritates the mucosa and overloads the liver's detoxification process; their excess is pro-inflammatory.

BCFA-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bacteroides salyersiae, *Parabacteroides goldsteinii*, *Bacteroides nordii*	↑	Generate branched-chain fatty acids, markers of intestinal putrefaction and excessive protein fermentation.

P-CRESOL PRODUCTION

Top imbalanced bacteria	Status	Functional impact
Blautia hydrogenotrophica	↔	Produce p-cresol, a uremic toxin associated with oxidative stress and impaired kidney function.

PROBIOTICS

It assesses the presence of microorganisms associated with the balance of the microbiota, the barrier function and the modulation of the intestinal environment

OTHER PROBIOTIC SPECIES

Top imbalanced bacteria	Status	Functional impact
Faecalibacterium duncaniae	↔	Endogenous probiotics (Akkermansia, F. prausnitzii); markers of a healthy, resilient intestinal ecosystem.

BIFIDOBACTERIUM SPP

Top imbalanced bacteria	Status	Functional impact
Bifidobacterium longum, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*	↔	Key probiotics: they produce lactate and acetate, modulate immunity, and promote the maturation of the intestinal mucosa.

LACTOBACILLUS SPP

Top imbalanced bacteria	Status	Functional impact
No associated bacteria detected	↔	Classic lactic acid probiotics; they reinforce the barrier, inhibit pathogens, and modulate the immune response.

ESTROGEN METABOLISM

It assesses the potential of the microbiota to transform estrogens and participate in their circulation and availability in the body

ESTROBOLOME-FORMING

Top imbalanced bacteria	Status	Functional impact
Bacteroides ovatus, *Bacteroides xylanisolvens*	↔	Recycle estrogens via β-glucuronidase; their balance influences hormonal, breast, and endometrial health.

S-EQUOL-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bacteroides ovatus, *Ruminococcus sp. SR1/5*, *Blautia producta*	↑	Convert isoflavones (soy) into S-equol, a phytoestrogen with a protective effect on cardiovascular and bone health.

S-EQUOL-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Bacteroides uniformis, *Adlercreutzia equolifaciens*	↑	Break down S-equol; an excess reduces the availability of this beneficial metabolite.

VITAMINS

It assesses the potential of the microbiota to participate in the synthesis, transformation, and utilization of certain vitamins

VITAMIN K2-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Clostridium perfringens, *Enterococcus faecalis*, *Blautia hydrogenotrophica*	↑	Synthesize menaquinones (K2), involved in coagulation, bone health, and proper calcium deposition.

VITAMIN B12-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Collinsella aerofaciens	↔	Produce vitamin B12, key for nerve function and hematopoiesis; the intestinal contribution complements dietary intake.

VITAMIN B9-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bifidobacterium longum, *Bifidobacterium adolescentis*, *Streptococcus thermophilus*	↔	Synthesize folate (B9), essential for methylation, DNA synthesis, and red blood cell maturation.

NEUROTRANSMITTERS

It assesses the functional capacity of the microbiota to produce, consume, and modulate neurotransmitters and other neuroactive compounds involved in communication between the gut and the nervous system

GABA-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Alistipes indistinctus, *Bacteroides ovatus*, *Phocaeicola vulgatus*	↔	Synthesize GABA, an inhibitory neurotransmitter that modulates the gut-brain axis and supports stress regulation.

GLUTAMATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Phocaeicola vulgatus	↔	Release free glutamate, an excitatory neurotransmitter and GABA precursor; its balance is key in the gut-brain axis.

SEROTONIN REGULATION

Top imbalanced bacteria	Status	Functional impact
Enterococcus faecalis	↔	Modulate intestinal serotonin production (90 % of the body's total); they influence mood and motility.

DOPAMINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Hafnia paralvei	↔	Produce peripheral dopamine that participates in the gut-brain axis and mood regulation.

ACETYLCHOLINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Streptococcus thermophilus, *Streptococcus salivarius*	↔	Synthesize acetylcholine, a neurotransmitter involved in intestinal motility and inflammatory modulation via the vagus nerve.

GABA-CONSUMING

Top imbalanced bacteria	Status	Functional impact
No associated bacteria detected	↔	Break down local GABA; their overrepresentation reduces the availability of this calming neurotransmitter.

GUT-BRAIN AXIS

It analyzes the microbial functions related to bidirectional communication between the gut and the brain, involved in regulating mood, stress response, and cognitive function

INDOLE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Bacteroides salyersiae, *Alistipes onderdonkii*, *Alistipes shahii*	↔	Produce indole and AhR receptor ligand derivatives; they reinforce the intestinal barrier and mucosal immunity.

QUINOLINATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
[Clostridium] symbiosum, *[Clostridium] scindens*, *Ruminococcus albus*	↔	Produce quinolinate via the kynurenine pathway; in excess it can have an excitotoxic effect on the nervous system.

IPA-PRODUCING

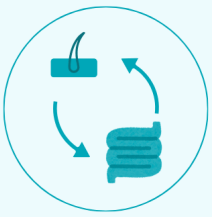
Top imbalanced bacteria	Status	Functional impact
[Clostridium] symbiosum, *[Clostridium] scindens*, *Clostridium perfringens*	↔	Synthesize indole-3-propionic acid, an antioxidant and neuroprotectant that crosses the blood-brain barrier.

IMIDAZOLE PROPIONATE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Adlercreutzia equolifaciens, *Eggerthella lenta*	↔	Produce imidazole propionate (ImP) from histidine; elevated ImP is associated with insulin resistance and type 2 diabetes.

KYNURENINE SYNTHESIS-REGULATING

Top imbalanced bacteria	Status	Functional impact
No associated bacteria detected	↔	Regulate the kynurenine/tryptophan balance, key for the balance between serotonin and inflammatory pathways.



GUT-SKIN AXIS

It analyzes the microbial functions that can influence the gut-skin axis, participating in processes related to systemic inflammation, the immune response, and the maintenance of skin health

SKIN PROTECTOR

Top imbalanced bacteria	Status	Functional impact
Paraprevotella clara	↔	Their presence strengthens the gut-skin axis; it is associated with better skin hydration and less dermatological inflammation.

SKIN DISRUPTOR

Top imbalanced bacteria	Status	Functional impact
Clostridium perfringens, *Enterococcus faecalis*	↔	Their overabundance has been associated with acne flare-ups, atopic dermatitis, and other inflammatory skin conditions.

INTESTINE-HEART AXIS

It analyzes microbial functions related to the production of metabolites that can influence cardiovascular health, lipid metabolism, and vascular function

TRIMETHYLAMINE-PRODUCING

Top imbalanced bacteria	Status	Functional impact
Paraprevotella xylaniphila, *Paraprevotella clara*	↔	Produce TMA from choline/carnitine; the liver converts it into TMAO, a cardiovascular risk marker.

TRIMETHYLAMINE-CONSUMING

Top imbalanced bacteria	Status	Functional impact
Methanobrevibacter smithii	↔	Reduce the TMA load before it reaches the liver; they protect the cardiovascular profile.

GUT-LIVER AXIS

It evaluates the functions of the microbiome involved in bile acid metabolism, detoxification, and functional communication between the gut and liver

ETHANOL-PRODUCING

Top imbalanced bacteria	Status	Functional impact
[Clostridium] scindens	↔	Generate endo-ethanol that overloads the liver; their excess is associated with non-alcoholic fatty liver disease (NAFLD).

INTOLERANCES

It analyzes the microbial functions related to the degradation and metabolism of different food compounds, whose alteration can favor intolerance processes or a lower digestive tolerance

LACTOSE-METABOLIZING

Top imbalanced bacteria	Status	Functional impact
Bacteroides thetaiotaomicron, *Bifidobacterium longum*, *Bifidobacterium adolescentis*	↔	Hydrolyze intestinal lactose; a good representation indicates good digestive tolerance to dairy products.

WHEAT SENSITIVITY

Top imbalanced bacteria	Status	Functional impact
Eubacterium ramulus, *Bifidobacterium longum*, *Rothia mucilaginosa*	↔	Their presence is associated with better gluten digestion and fewer symptoms in non-celiac gluten-sensitive individuals (NCGS).

5. GENERAL RECOMMENDATIONS

The following **recommendations have been drawn up based on the functional domains showing alterations** in the sample analyzed. Their purpose is to help restore the balance of the gut microbiome through nutritional interventions, lifestyle habits and support strategies.

NOTE: The recommendations proposed constitute suggestions based on the microbiological profile observed and should be individualized according to the clinical situation, the patient's progress, and the healthcare professional's judgment.

OVERALL DIVERSITY

Before increasing fiber intake, it is advisable to assess the microbiota composition, the presence of gas, the bowel transit pattern, and digestive symptoms. It is also advisable to avoid excessive consumption of polyols or concentrated prebiotics, and to consider evaluating possible bacterial overgrowth only when the clinical picture justifies it, avoiding any treatment based solely on high diversity.

INTESTINAL HOMEOSTASIS

Oral bacteria

Foods	Actively prioritize: Polyphenol-rich fruits and vegetables, red berries, pomegranate, green tea, pure cocoa, extra virgin olive oil, oily fish and foods rich in vitamin C and zinc, and encourage proper chewing.
Prebiotics	Priority, progressive intervention: Pectin, PHGG, beta-glucans and polyphenols, adjusting fiber to bowel transit and tolerance.
Probiotics	Consider *Streptococcus salivarius* or *Lactobacillus reuteri*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Consider oral probiotics with *Streptococcus salivarius* or *Lactobacillus reuteri*, and intestinal probiotics according to the profile, plus zinc and vitamin D only if there is a deficiency.

INTESTINAL MUCUS

Mucus-consuming

Foods	Actively prioritize: Cooked vegetables, mucilages: soaked chia/flaxseed, okra, oats, pumpkin, carrot, oily fish, olive oil and red berries
Prebiotics	Priority, progressive intervention: PHGG, pectin, acacia fiber, beta-glucans and mucilages
Probiotics	Consider *Lacticaseibacillus rhamnosus*, *Lactiplantibacillus plantarum*, *Bifidobacterium longum* or *Akkermansia muciniphila*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Zinc-carnosine, L-glutamine, vitamin A/D if deficient, and omega-3

INTESTINAL PERMEABILITY

It is advisable to reinforce intestinal barrier function through a progressive increase in soluble fiber and resistant starch, accompanied by vegetables, fruits, well-tolerated legumes, olive oil, and dietary sources of omega-3. It is also recommended to eliminate alcohol and ultra-processed food consumption, review with a doctor the use of NSAIDs, proton pump inhibitors, and the presence of constipation, and consider supplements such as zinc, vitamin D, or L-glutamine only when there is a clinical indication, avoiding systematic butyrate supplementation.

GUT INFLAMMATION AND IMMUNE SYSTEM AXIS

Lipopolysaccharide (LPS)-producing

Foods	Actively prioritize: Increase vegetables, oats, tolerated legumes, apple, pear, red berries, pomegranate, pure cocoa, extra virgin olive oil and oily fish, and reduce ultra-processed foods, alcohol, free sugars and excess saturated fat.
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans and acacia fiber, plus polyphenols and resistant starch introduced gradually.
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactiplantibacillus plantarum*., selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Consider omega-3, vitamin D if deficient, zinc-carnosine, L-glutamine, and probiotics with *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactobacillus plantarum*.

Pro-inflammatory

Foods	Actively prioritize: An anti-inflammatory Mediterranean diet: cooked and raw vegetables according to tolerance, red berries, pomegranate, extra virgin olive oil, oily fish, walnuts, flaxseed and chia, and reduce ultra-processed foods, alcohol, free sugars and trans fats.
Prebiotics	Priority, progressive intervention: PHGG, pectin and beta-glucans, prebiotic polyphenols, and gOS or inulin/FOS only if they do not increase gas or pain.
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactiplantibacillus plantarum*., selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Consider omega-3, vitamin D if deficient, curcumin, zinc-carnosine, and probiotics with *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactobacillus plantarum*.

INFECTION

Pathogens

Foods	Actively prioritize: A simple, well-tolerated Mediterranean diet, cooked vegetables, rice, potato or sweet potato, whole fruit, extra virgin olive oil, fish and lean protein, and reduce free sugars, alcohol, ultra-processed foods and foods with hygiene risk.
Prebiotics	Priority, progressive intervention: PHGG or pectin as a first option if tolerated, beta-glucans and acacia fiber. Avoid starting inulin/FOS if there is severe diarrhea, marked bloating or suspected overgrowth.
Probiotics	Consider *Saccharomyces boulardii*, *Lacticaseibacillus rhamnosus*, *Lactiplantibacillus plantarum* or *Bifidobacterium lactis*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Consider *Saccharomyces boulardii*, *Lactobacillus rhamnosus*, *Lactobacillus plantarum* or *Bifidobacterium lactis* depending on the microorganism, symptoms and clinical situation, plus zinc-carnosine, vitamin D if deficient, and omega-3. This does not replace medical treatment when indicated.

BIOGENIC AMINES

Histamine-producing

Foods	Actively prioritize: Fresh foods: rice, potato, fresh chicken/turkey, very fresh/frozen fish, courgette, carrot, cucumber, apple, pear, blueberries, olive oil
Prebiotics	Priority, progressive intervention: PHGG, pectin, acacia fiber, and avoid aggressive fermented foods/prebiotics at the start
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactiplantibacillus plantarum*., selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: DAO if appropriate, vitamin C, quercetin, B6, non-histamine-producing probiotics and omega-3

Cadaverine-producing

Foods	Actively prioritize: An anti-inflammatory Mediterranean diet, cooked vegetables, low-fermentation fruits according to tolerance, extra virgin olive oil, oily fish, eggs if tolerated, moderate lean protein, tubers, rice, quinoa, polyphenols: red berries, pomegranate, pure cocoa, green tea, aromatic herbs, mild broths and ground seeds if tolerated
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans, acacia fiber, resistant starch with caution, gOS/inulin only if there is no gas/SIBO, polyphenols, mucilages, always introducing the prebiotic gradually
Probiotics	Consider *Saccharomyces boulardii*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Omega-3, polyphenols, curcumin, zinc-carnosine, L-glutamine, Saccharomyces boulardii if appropriate, non-histamine-producing modulating probiotics, individualized digestive support, and avoiding megadoses

Putrescine-producing

Foods	Actively prioritize: An anti-inflammatory Mediterranean diet, cooked vegetables, low-fermentation fruits according to tolerance, extra virgin olive oil, oily fish, eggs if tolerated, moderate lean protein, tubers, rice, quinoa, polyphenols: red berries, pomegranate, pure cocoa, green tea, aromatic herbs, mild broths and ground seeds if tolerated
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans, acacia fiber, resistant starch with caution, gOS/inulin only if there is no gas/SIBO, polyphenols, mucilages, always introducing the prebiotic gradually
Probiotics	Consider *Saccharomyces boulardii*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Omega-3, polyphenols, curcumin, zinc-carnosine, L-glutamine, Saccharomyces boulardii if appropriate, non-histamine-producing modulating probiotics, individualized digestive support, and avoiding megadoses

BENEFICIAL SCFAS

Formate-producing

Foods	Actively prioritize: A personalized Mediterranean diet, cooked vegetables, soluble fiber, polyphenols, moderate protein, tolerated complex carbohydrates and olive oil
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans, acacia fiber, chosen according to tolerance
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Probiotics/supplements only according to the axis, omega-3 and polyphenols

Butyrate-consuming

Foods	Actively prioritize: Prioritize foods that support sustained, balanced butyrate production: oats, tolerated legumes, tubers or cooled rice, a variety of vegetables, red berries, extra virgin olive oil and nuts.
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans and resistant starch introduced gradually, adjusting according to gas and bowel transit.
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactobacillus plantarum* to improve the fermentative balance, plus omega-3, vitamin D if deficient, and mucosal support when clinically indicated.

BUTYRATE BALANCE

Butyrate-consuming

Foods	Actively prioritize: Prioritize foods that support sustained, balanced butyrate production: oats, tolerated legumes, tubers or cooled rice, a variety of vegetables, red berries, extra virgin olive oil and nuts.
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans and resistant starch introduced gradually, adjusting according to gas and bowel transit.
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Consider *Bifidobacterium longum*, *Bifidobacterium breve* or *Lactobacillus plantarum* to improve the fermentative balance, plus omega-3, vitamin D if deficient, and mucosal support when clinically indicated.

GAS PRODUCTION

Hydrogen-producing

Foods	Actively prioritize: A personalized Mediterranean diet, cooked vegetables, soluble fiber, polyphenols, moderate protein, tolerated complex carbohydrates and olive oil
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans, acacia fiber, chosen according to tolerance
Probiotics	Consider *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Probiotics/supplements only according to the axis, omega-3 and polyphenols

Hydrogen sulfide-producing

Foods	Actively prioritize: Rice, potato, pumpkin, carrot, cucumber, courgette, olive oil, red berries, pomegranate and moderate, spread-out protein intake
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans and mild fiber
Probiotics	Consider *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Molybdenum under clinical judgment, zinc-carnosine, omega-3, and activated charcoal/adsorbents only under supervision

PROTEIN METABOLISM

Proteolytic

Foods	Actively prioritize: Cooked vegetables, tolerated complex carbohydrates, rice/potato, oats, cooked fruit, olive oil, small amounts of legumes if tolerated and moderate portions of fish
Prebiotics	Priority, progressive intervention: PHGG, pectin, mild resistant starch and beta-glucans
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: polyphenols, omega-3 and digestive enzymes if protein digestion is poor

Ammonium-producing

Foods	Actively prioritize: Tolerated complex carbohydrates, cooked vegetables, fruit, soluble fiber, olive oil and moderate protein
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans and mild resistant starch
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Ornithine/aspartate only under medical judgment, zinc and polyphenols

BCFA-producing

Foods	Actively prioritize: Cooked vegetables, tubers, rice, oats, cooked fruit, olive oil and more plant-based protein or moderate fish
Prebiotics	Priority, progressive intervention: PHGG, pectin and mild resistant starch
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: polyphenols, omega-3 and digestive support

ESTROGEN METABOLISM

S-equol-producing

Foods	Actively prioritize: Fermented/non-fermented soy according to tolerance: tempeh, tofu, edamame, legumes, flaxseed, sesame, fiber, vegetables and polyphenol-rich fruits
Prebiotics	Priority, progressive intervention: GOS, inulin if tolerated, pHGG, pectin and polyphenols
Probiotics	Consider *Bifidobacterium longum*, *Bifidobacterium animalis subsp. lactis* or *Lactiplantibacillus plantarum*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Isoflavones only under clinical judgment, and omega-3

S-equol-consuming

Foods	Actively prioritize: An anti-inflammatory Mediterranean diet, cooked vegetables, low-fermentation fruits according to tolerance, extra virgin olive oil, oily fish, eggs if tolerated, moderate lean protein, tubers, rice, quinoa, polyphenols: red berries, pomegranate, pure cocoa, green tea, aromatic herbs, mild broths and ground seeds if tolerated
Prebiotics	Priority, progressive intervention: PHGG, pectin, beta-glucans, acacia fiber, resistant starch with caution, gOS/inulin only if there is no gas/SIBO, polyphenols, mucilages, always introducing the prebiotic gradually
Probiotics	Consider *Saccharomyces boulardii*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Omega-3, polyphenols, curcumin, zinc-carnosine, L-glutamine, Saccharomyces boulardii if appropriate, non-histamine-producing modulating probiotics, individualized digestive support, and avoiding megadoses

VITAMINS

Vitamin K2-producing

Foods	Actively prioritize: Oats, barley, cooled rice/potato, green banana, legumes according to tolerance, artichoke, asparagus, leek, onion, mild garlic, cooked carrot, pumpkin, cooked apple/pear, red berries, pomegranate, citrus, pure cocoa, extra virgin olive oil, walnuts, almonds, flax/chia seeds, yogurt/kefir if tolerated and a variety of seasonal vegetables
Prebiotics	Priority, progressive intervention: Inulin/FOS if tolerated, gOS, resistant starch, pHGG, pectin, beta-glucans, arabinoxylans, acacia fiber, prebiotic polyphenols, lactoferrin for the *Lactobacillus* axis, and chlorogenic acid when applicable
Probiotics	Consider *Bifidobacterium longum* or *Bifidobacterium animalis subsp. lactis*, selecting the species according to symptoms, the altered axis and the clinical goal.
Supplements	Consider individually: Probiotics targeted to the axis: *Bifidobacterium*/*Lactobacillus*, omega-3, vitamin D if deficient, zinc-carnosine, L-glutamine, magnesium, polyphenols, mucilages, and a multi-strain formula only if tolerated

ANNEX I: MICROORGANISMS DETECTED

This annex presents the list of **bacteria, archaea and eukaryotes** detected and included in the general analysis of the gut microbiome. This list does not include microorganisms evaluated using specific panels for viruses, fungi, yeasts and parasites, whose results are presented separately.

Microorganism	Domain	Ref. min. (%)	Ref. max. (%)	Abundance (%)
Phocaeicola vulgatus	Bacteria	0.000	15.430	20.952
Bacteroides salyersiae	Bacteria	0.000	0.315	6.047
Alistipes putredinis	Bacteria	0.000	8.339	5.059
Bacteroides ovatus	Bacteria	0.000	2.012	4.097
Bacteroides stercoris	Bacteria	0.000	4.875	4.086
Odoribacter splanchnicus	Bacteria	0.000	1.132	3.458
Akkermansia muciniphila	Bacteria	0.000	4.192	3.070
Bacteroides uniformis	Bacteria	0.011	14.355	3.042
Phascolarctobacterium faecium	Bacteria	0.000	0.613	2.829
Alistipes shahii	Bacteria	0.000	0.643	2.728
Faecalibacterium prausnitzii	Bacteria	0.959	12.099	2.575
Bilophila wadsworthia	Bacteria	0.000	0.139	2.070
Bacteroides caccae	Bacteria	0.000	2.288	1.940
Segatella copri	Bacteria	0.000	35.000	1.913
Bacteroides xylanisolvens	Bacteria	0.000	1.014	1.761
[Ruminococcus] lactaris	Bacteria	0.000	1.243	1.731
Parabacteroides distasonis	Bacteria	0.000	2.902	1.688
Phocaeicola dorei	Bacteria	0.000	7.980	1.670
Bacteroides thetaiotaomicron	Bacteria	0.000	1.933	1.646
Alistipes finegoldii	Bacteria	0.000	1.732	1.530
Parabacteroides merdae	Bacteria	0.000	2.217	1.224
Paraprevotella xylaniphila	Bacteria	0.000	0.472	1.161
Simiaoa sunii	Bacteria	-	-	1.023
uncultured Alistipes sp.	Bacteria	-	-	0.994
Ruminococcus bicirculans (ex Wegman et al. 2014)	Bacteria	0.100	8.000	0.945
Alistipes communis	Bacteria	0.500	12.000	0.903
Escherichia coli	Bacteria	0.000	1.743	0.826
Alistipes onderdonkii	Bacteria	0.000	0.010	0.755
[Ruminococcus] torques	Bacteria	0.000	2.632	0.712
Mediterraneibacter gnavus	Bacteria	0.050	3.500	0.691
Butyricimonas virosa	Bacteria	0.000	0.210	0.690
Parabacteroides johnsonii	Bacteria	0.000	0.043	0.621
Blautia obeum	Bacteria	0.000	1.685	0.620
Bacteroides fragilis	Bacteria	0.000	1.152	0.554
Alistipes dispar	Bacteria	0.500	12.000	0.521
Vescimonas coprocola	Bacteria	-	-	0.440
Alistipes indistinctus	Bacteria	0.000	0.201	0.434
Dorea longicatena	Bacteria	0.000	3.152	0.424
Dysosmobacter welbionis	Bacteria	-	-	0.370
Blautia wexlerae	Bacteria	0.001	1.180	0.370

Lachnospira eligens	Bacteria	0.000	3.814	0.327
Collinsella aerofaciens	Bacteria	0.000	6.241	0.325
Parabacteroides goldsteinii	Bacteria	0.000	0.085	0.293
Eubacterium ramulus	Bacteria	0.000	0.360	0.277
Barnesiella intestinihominis	Bacteria	0.000	2.650	0.255
Sutterella wadsworthensis	Bacteria	-	-	0.250
Eubacterium ventriosum	Bacteria	0.000	0.410	0.246
Allocoprococcus comes	Bacteria	-	-	0.245
Vescimonas fastidiosa	Bacteria	-	-	0.244
Flavonifractor plautii	Bacteria	0.000	0.504	0.204
Desulfovibrio fairfieldensis	Bacteria	0.000	0.000	0.203
Faecalibacterium duncaniae	Bacteria	1.000	18.000	0.186
Alistipes senegalensis	Bacteria	0.500	12.000	0.186
Faecalibacterium sp. I4-1-79	Bacteria	1.000	18.000	0.182
Bacteroides nordii	Bacteria	0.000	0.005	0.182
Intestinimonas butyriciproducens	Bacteria	0.000	0.067	0.177
Faecalibacillus intestinalis	Bacteria	-	-	0.177
Butyricimonas faecihominis	Bacteria	-	-	0.176
Bacteroides zhangwenhongii	Bacteria	8.000	45.000	0.175
Bacteroides sp. M10	Bacteria	8.000	45.000	0.173
Ruthenibacterium lactatiformans	Bacteria	0.000	0.439	0.172
Mediterraneibacter faecis	Bacteria	0.050	3.500	0.169
Alistipes sp. dk3624	Bacteria	0.500	12.000	0.164
Clostridioides difficile	Bacteria	0.000	0.500	0.156
Dorea formicigenerans	Bacteria	0.000	1.006	0.151
Hominenteromicrobium mulieris	Bacteria	-	-	0.127
[Clostridium] symbiosum	Bacteria	0.000	0.022	0.125
Faecalibacterium sp. PGM34	Bacteria	1.000	18.000	0.125
Pusillibacter faecalis	Bacteria	-	-	0.123
Faecalibacterium sp. I3-3-33	Bacteria	1.000	18.000	0.122
Lawsonibacter asaccharolyticus	Bacteria	0.000	0.155	0.118
Bacteroides finegoldii	Bacteria	0.000	0.353	0.117
Bacteroides difficilis	Bacteria	8.000	45.000	0.115
Barnesiella sp. An22	Bacteria	-	-	0.114
Adlercreutzia equolifaciens	Bacteria	0.000	0.460	0.105
Phocaeicola salanitronis	Bacteria	1.000	25.000	0.105
Agathobacter rectalis	Bacteria	0.500	10.000	0.103
Thomasclavelia spiroformis	Bacteria	-	-	0.099
Roseburia intestinalis	Bacteria	0.000	2.023	0.095
Alistipes ihumii	Bacteria	0.500	12.000	0.094
Bacteroides eggerthii	Bacteria	0.000	1.356	0.093
Bacteroides sp. D2	Bacteria	0.000	0.000	0.088
Anaerobutyricum hallii	Bacteria	0.000	2.631	0.088
Bacteroides cellulosilyticus	Bacteria	0.000	1.205	0.085
Alistipes sp. i18-0019-D1	Bacteria	0.500	12.000	0.085
Anaerotruncus colihominis	Bacteria	0.000	0.019	0.079
[Clostridium] innocuum	Bacteria	0.000	0.034	0.076
Owariibacterium komagatae	Bacteria	-	-	0.073

Bacteroides hominis	Bacteria	8.000	45.000	0.073
Enterococcus faecium	Bacteria	0.000	0.000	0.072
Butyricimonas paravirosa	Bacteria	-	-	0.072
Paraprevotella clara	Bacteria	0.000	0.012	0.071
Eggerthella lenta	Bacteria	0.000	0.169	0.070
Faecalibacterium sp. IP-3-29	Bacteria	1.000	18.000	0.070
Pseudoprevotella muciniphila	Bacteria	-	-	0.068
Roseburia hominis	Bacteria	0.000	0.994	0.068
Bacteroides celer	Bacteria	8.000	45.000	0.068
Faecalibacterium sp. IP-1-18	Bacteria	1.000	18.000	0.067
Blautia massiliensis (ex Durand et al. 2017)	Bacteria	1.000	12.000	0.066
Faecalibacterium sp. I2-3-92	Bacteria	1.000	18.000	0.065
Bacteroides sp. CACC 737	Bacteria	8.000	45.000	0.065
Coprobacter secundus	Bacteria	0.000	0.036	0.063
Bacteroides faecis	Bacteria	0.000	0.393	0.061
Faecalibacterium sp. I3-3-89	Bacteria	1.000	18.000	0.060
Jutongia sp. SJQ-6	Bacteria	-	-	0.059
Bacteroides sp. A1C1	Bacteria	8.000	45.000	0.059
Dysosmobacter sp. Phy	Bacteria	-	-	0.057
Parabacteroides sp. CT06	Bacteria	0.500	8.000	0.057
Bacteroides luhongzhouii	Bacteria	8.000	45.000	0.055
Ruminococcus sp. SR1/5	Bacteria	0.100	8.000	0.054
Dorea amylophila	Bacteria	0.100	4.000	0.053
Faecalibacterium sp. i21-0019-B1	Bacteria	1.000	18.000	0.049
Bacteroides sp. DH3716P	Bacteria	8.000	45.000	0.047
Blautia sp. SC05B48	Bacteria	1.000	12.000	0.047
Bacteroides parvus	Bacteria	8.000	45.000	0.046
Roseburia faecis	Bacteria	0.000	6.476	0.044
Bacteroides faecium	Bacteria	8.000	45.000	0.044
Faecalibacterium hominis (ex Afrizal et al. 2022)	Bacteria	1.000	18.000	0.043
[Clostridium] scindens	Bacteria	0.000	0.000	0.043
Enterocloster lavalensis	Bacteria	0.000	0.008	0.042
Faecalibacterium sp. I4-3-84	Bacteria	1.000	18.000	0.042
Blautia luti	Bacteria	1.000	12.000	0.042
Oxalobacter aliiformigenes	Bacteria	-	-	0.041
Clostridium sp. M62/1	Bacteria	0.000	1.000	0.041
Bacteroides caecimuris	Bacteria	8.000	45.000	0.040
Coprobacter fastidiosus	Bacteria	0.000	0.215	0.040
Oscillibacter hominis	Bacteria	-	-	0.040
Bacteroides intestinalis	Bacteria	0.000	0.338	0.038
Pseudoflavonifractor gallinarum	Bacteria	-	-	0.037
Barnesiella viscericola	Bacteria	-	-	0.036
Bacteroides sp. HF-162	Bacteria	8.000	45.000	0.036
Enterocloster bolteae	Bacteria	0.000	0.043	0.034
Subdoligranulum variabile	Bacteria	0.050	3.000	0.034
Emergencia timonensis	Bacteria	-	-	0.033
Muribaculum intestinale	Bacteria	-	-	0.033
Faecalibacterium taiwanense	Bacteria	1.000	18.000	0.032

Butyricimonas faecalis	Bacteria	-	-	0.029
Eisenbergiella porci	Bacteria	-	-	0.029
Faecalibacterium sp. 7	Bacteria	1.000	18.000	0.027
Enterocloster clostridioformis	Bacteria	0.000	0.005	0.027
Sellimonas catena	Bacteria	-	-	0.026
Adlercreutzia hattorii	Bacteria	0.000	1.500	0.024
Holdemania massiliensis	Bacteria	-	-	0.024
Gordonibacter urolithinfaciens	Bacteria	-	-	0.024
Faecalibacterium sp. i25-0019-C1	Bacteria	1.000	18.000	0.023
Collinsella sp. i05-0019-G5	Bacteria	0.000	5.000	0.023
Anaerostipes hadrus	Bacteria	0.002	3.908	0.022
Blautia producta	Bacteria	0.000	0.000	0.021
Faecalibacterium wellingii	Bacteria	1.000	18.000	0.020
Hungatella hathewayi	Bacteria	0.000	0.012	0.020
uncultured Subdoligranulum sp.	Bacteria	-	-	0.020
Parabacteroides absconsus	Bacteria	0.500	8.000	0.020
Ruminococcus callidus	Bacteria	0.000	0.034	0.019
Flintibacter sp. KGMB00164	Bacteria	-	-	0.019
Bacteroides mucinivorans	Bacteria	8.000	45.000	0.017
Parabacteroides sp. ASD2025	Bacteria	0.500	8.000	0.017
Oscillibacter sp. PEA192	Bacteria	-	-	0.017
Eshraghiella crossota	Bacteria	-	-	0.017
Christensenella massiliensis	Bacteria	-	-	0.017
Bacteroides pyogenes	Bacteria	8.000	45.000	0.016
Hungatella sp. SB206	Bacteria	-	-	0.016
Enterocloster asparagiformis	Bacteria	0.000	0.004	0.016
Muribaculum gordoncarteri	Bacteria	-	-	0.015
Blautia hansenii	Bacteria	0.000	0.000	0.015
Phocaeicola coprophilus	Bacteria	0.000	0.000	0.015
Paramuribaculum intestinale	Bacteria	-	-	0.015
Blautia hydrogenotrophica	Bacteria	0.000	0.004	0.015
Ruminococcus champanellensis	Bacteria	0.100	8.000	0.014
Segatella hominis	Bacteria	0.000	35.000	0.013
Desulfovibrio piger	Bacteria	0.000	0.327	0.013
Hoskinsella hominis	Bacteria	-	-	0.012
Wansuia hejianensis	Bacteria	-	-	0.011
Solibaculum mannosilyticum	Bacteria	-	-	0.011
Coprococcus sp. ART55/1	Bacteria	0.100	5.000	0.011
Roseburia rectibacter	Bacteria	0.500	10.000	0.010
Marvinbryantia formatexigens	Bacteria	-	-	0.010
Bacteroides helcogenes	Bacteria	8.000	45.000	0.010
Blautia argi	Bacteria	0.000	0.000	0.010
Sellimonas intestinalis	Bacteria	0.000	0.011	0.009
Acutalibacter muris	Bacteria	-	-	0.009
Catenibacterium sp. co_0103	Bacteria	-	-	0.009
Eubacterium callanderi	Bacteria	0.000	0.000	0.009
Streptococcus pneumoniae	Bacteria	0.050	3.000	0.008
Bacteroides zoogleoformans	Bacteria	8.000	45.000	0.008

Clostridium cadaveris	Bacteria	0.000	1.000	0.008
Eubacterium maltosivorans	Bacteria	0.100	5.000	0.008
Sodaliphilus pleomorphus	Bacteria	-	-	0.008
Parabacteroides chongii	Bacteria	0.500	8.000	0.007
Duncaniella dubosii	Bacteria	-	-	0.007
Butyricicoccus porcorum	Bacteria	-	-	0.007
Clostridium sp. BJN0013	Bacteria	0.000	1.000	0.007
Qiania dongpingensis	Bacteria	-	-	0.007
Roseburia sp. 831b	Bacteria	0.500	10.000	0.007
Parabacteroides faecis	Bacteria	0.500	8.000	0.006
Clostridium perfringens	Bacteria	0.000	0.000	0.006
Agathobaculum massiliense	Bacteria	-	-	0.006
[Clostridium] hylemonae	Bacteria	0.000	1.000	0.006
Coprococcus eutactus	Bacteria	0.000	3.036	0.006
Bacteroides maternus	Bacteria	8.000	45.000	0.006
Kineothrix sedimenti	Bacteria	-	-	0.006
Romboutsia ilealis	Bacteria	0.000	0.011	0.006
Schaalia odontolytica	Bacteria	0.000	0.008	0.006
Thomasclavelia ramosa	Bacteria	-	-	0.006
Actinomyces sp. oral taxon 414	Bacteria	-	-	0.005
Sporosarcina sp. P37	Bacteria	-	-	0.005
Claveliimonas bilis	Bacteria	-	-	0.005
Gordonibacter pamelaeae	Bacteria	0.000	0.161	0.005
Amedibacterium intestinale	Bacteria	-	-	0.005
Acidaminobacterium chupaoyuni	Bacteria	-	-	0.005
Lactonifactor longoviformis	Bacteria	0.000	0.000	0.005
Spiroplasma endosymbiont of Crioceris asparagi	Bacteria	-	-	0.005
Christensenella minuta	Bacteria	0.000	0.000	0.005
Faecalibaculum rodentium	Bacteria	-	-	0.005
Caproiciproducens sp. LBM24188	Bacteria	-	-	0.005
Bacteroides graminisolvens	Bacteria	8.000	45.000	0.005
Clostridium sp. OS1-26	Bacteria	0.000	1.000	0.005
Eubacterium sp. MSJ-33	Bacteria	0.100	5.000	0.005
Mesoplasma florum	Bacteria	-	-	0.004
Massilimicrobiota timonensis	Bacteria	0.000	0.000	0.004
Clostridium sp. MB40-C1	Bacteria	0.000	1.000	0.004
Christensenella sp. MSJ-20	Bacteria	-	-	0.004
Pediococcus claussenii	Bacteria	-	-	0.004
Streptococcus sanguinis	Bacteria	0.000	0.001	0.004
Bacteroides sedimenti	Bacteria	8.000	45.000	0.004
Sporanaerobacter sp.	Bacteria	-	-	0.004
Neoehrlichia mikurensis	Bacteria	-	-	0.004
Mitsuokella multacida	Bacteria	0.000	0.000	0.004
Companilactobacillus sp. DQM5	Bacteria	-	-	0.004
Chordicoccus furentiruminis	Bacteria	-	-	0.004
Faecalimonas umbilicata	Bacteria	-	-	0.004
Blautia pseudococcoides	Bacteria	1.000	12.000	0.004
Brevibacterium luteolum	Bacteria	-	-	0.004

Floricoccus penangensis	Bacteria	-	-	0.004
Agathobaculum sp. NTUH-O15-33	Bacteria	-	-	0.004
Sporosarcina sp. FSL K6-1522	Bacteria	-	-	0.004
Roseburia sp. 499	Bacteria	0.500	10.000	0.004
Spiroplasma endosymbiont of Virgichneumon dumeticola	Bacteria	-	-	0.004
Gemella sp. zg-570	Bacteria	-	-	0.004
Streptococcus pyogenes	Bacteria	0.050	3.000	0.004
Vagococcus jeotgali	Bacteria	-	-	0.004
Parabacteroides sp. APC149_11_2_Y6	Bacteria	0.500	8.000	0.004
Clostridium sp. SY8519	Bacteria	0.000	1.000	0.004
Rummeliibacillus stabekisii	Bacteria	-	-	0.004
Paraglaciecola psychrophila	Bacteria	-	-	0.003
Shewanella benthica	Bacteria	-	-	0.003
Romboutsia hominis	Bacteria	-	-	0.003
Geosporobacter ferrireducens	Bacteria	-	-	0.003
Caproiciproducens puteiluti	Bacteria	-	-	0.003
Intestinibacter bartlettii	Bacteria	0.000	0.255	0.003
Mediterraneibacter glycyrrhizinilyticus	Bacteria	0.050	3.500	0.003
Streptococcus canis	Bacteria	0.050	3.000	0.003
Desulfosporosinus youngiae	Bacteria	-	-	0.003
Bifidobacterium longum	Bacteria	0.000	4.324	0.003
Erysipelatoclostridium sp. An173	Bacteria	-	-	0.003
Flavobacterium sp. N3904	Bacteria	-	-	0.003
uncultured Bacteroides sp.	Bacteria	-	-	0.003
Paenibacillus sp. FSL R10-2734	Bacteria	-	-	0.003
Streptobacillus moniliformis	Bacteria	-	-	0.003
Clostridium sp. HCS.1	Bacteria	0.000	1.000	0.003
Eubacterium limosum	Bacteria	0.000	0.000	0.003
Sellimonas caecigallum	Bacteria	-	-	0.003
Hominifimenecus sp. rT4P-3	Bacteria	-	-	0.003
Bacillus sp. AK128	Bacteria	-	-	0.003
Tannerella serpentiformis	Bacteria	-	-	0.003
Bengtsoniella intestinalis	Bacteria	-	-	0.003
Ruminococcus albus	Bacteria	0.100	8.000	0.003
Blautia parvula	Bacteria	1.000	12.000	0.003
Streptococcus urinalis	Bacteria	0.050	3.000	0.003
Prevotella communis	Bacteria	0.000	35.000	0.003
Fusobacterium necrophorum	Bacteria	-	-	0.003
Ruminococcus bovis	Bacteria	0.100	8.000	0.003
Porphyromonas gingivalis	Bacteria	-	-	0.003
Prevotella melaninogenica	Bacteria	0.000	35.000	0.003
Candidatus Pelagibacter sp. RS40	Bacteria	-	-	0.003
Enterococcus casseliflavus	Bacteria	-	-	0.003
*Clostridium sp. 10cd**	Bacteria	0.000	1.000	0.003
Lactobacillus jensenii	Bacteria	0.000	2.000	0.003
Haemophilus pittmaniae	Bacteria	0.000	0.000	0.003
Prevotella intermedia	Bacteria	0.000	35.000	0.003
Collinsella stercoris	Bacteria	0.000	5.000	0.003

Seonamhaeicola sp. ML3	Bacteria	-	-	0.003
Streptococcus suis	Bacteria	0.050	3.000	0.003
Ehrlichia chaffeensis	Bacteria	-	-	0.002
Lacrimispora sp. BS-2	Bacteria	-	-	0.002
Ruminococcus gauvreauii	Bacteria	0.100	8.000	0.002
Porphyromonas levii	Bacteria	-	-	0.002
Vibrio sp. DW001	Bacteria	-	-	0.002
Vibrio parahaemolyticus	Bacteria	-	-	0.002
Pontibacter akesuensis	Bacteria	-	-	0.002
Vibrio artabrorum	Bacteria	-	-	0.002
Streptococcus pasteurianus	Bacteria	0.000	0.000	0.002
Streptococcus australis	Bacteria	0.000	0.001	0.002
Finegoldia magna	Bacteria	0.000	0.000	0.002
Parolsenella catena	Bacteria	-	-	0.002
Salinimonas lutimaris	Bacteria	-	-	0.002
Campylobacter sp. RM16192	Bacteria	-	-	0.002
Clostridium sp. C1	Bacteria	0.000	1.000	0.002
Clostridium pasteurianum	Bacteria	0.000	1.000	0.002
Trichlorobacter lovleyi	Bacteria	-	-	0.002
Trueperella pyogenes	Bacteria	-	-	0.002
Slackia heliotrinireducens	Bacteria	-	-	0.002
Rhodococcus erythropolis	Bacteria	-	-	0.002
Olsenella sp. oral taxon 807	Bacteria	-	-	0.002
Hujiaoplasma nucleasis	Bacteria	-	-	0.002
Hafnia paralvei	Bacteria	0.000	0.000	0.002
Chromobacterium sp. IIBBL 290-4	Bacteria	-	-	0.002
Neokomagataea tanensis	Bacteria	-	-	0.002
Paenibacillus konkukensis	Bacteria	-	-	0.002
Haemophilus parainfluenzae	Bacteria	0.000	0.078	0.002
Caproicibacterium amylolyticum	Bacteria	-	-	0.002
Oceanidesulfovibrio marinus	Bacteria	-	-	0.002
Spiroplasma mirum	Bacteria	-	-	0.002
Rothia mucilaginosa	Bacteria	0.000	0.006	0.002
Lacrimispora sp. HJ-01	Bacteria	-	-	0.002
Gemella sanguinis	Bacteria	0.000	0.004	0.002
Proteiniphilum saccharofermentans	Bacteria	-	-	0.002
Streptococcus mitis	Bacteria	0.000	0.005	0.002
Parvimonas micra	Bacteria	0.000	0.000	0.002
Polaribacter gangjinensis	Bacteria	-	-	0.002
Intestinibacillus sp. NTUH-41-i26	Bacteria	-	-	0.002
Klebsiella pneumoniae	Bacteria	0.000	0.056	0.002
Novisyntrophococcus fermenticellae	Bacteria	-	-	0.002
Salinibacter ruber	Bacteria	-	-	0.002
Mycoplasma phocoenae	Bacteria	-	-	0.002
Lacrimispora saccharolytica	Bacteria	0.000	0.007	0.002
Butyrivibrio fibrisolvens	Bacteria	-	-	0.002
Bifidobacterium adolescentis	Bacteria	0.000	8.382	0.002
Bacteroides sp. ZJ-18	Bacteria	8.000	45.000	0.002

Anaerostipes caccae	Bacteria	0.000	0.000	0.002
Ethanoligenens harbinense	Bacteria	-	-	0.002
Longicatena caecimuris	Bacteria	-	-	0.002
Streptococcus thermophilus	Bacteria	0.000	0.493	0.002
Bacillus gobiensis	Bacteria	-	-	0.002
Enterococcus faecalis	Bacteria	0.000	0.000	0.002
Thermodesulfobacterium sp. TA1	Bacteria	-	-	0.002
Caproicibacterium sp. BJN0003	Bacteria	-	-	0.002
Aristaeella lactis	Bacteria	-	-	0.002
Pediococcus argentinicus	Bacteria	-	-	0.002
Xylanibacter ruminicola	Bacteria	-	-	0.002
Clostridium sp. MB05	Bacteria	0.000	1.000	0.002
Anaerostipes sp. PC18	Bacteria	0.050	3.000	0.002
Pseudomonas putida	Bacteria	-	-	0.002
Eggerthella guodeyinii	Bacteria	-	-	0.002
Bifidobacterium pseudocatenulatum	Bacteria	0.000	0.613	0.002
Slackia exigua	Bacteria	-	-	0.002
Schaalia sp. HMT-172	Bacteria	-	-	0.002
Guyparkeria halophila	Bacteria	-	-	0.002
Leptodesmis sichuanensis	Bacteria	-	-	0.002
Leucobacter triazinivorans	Bacteria	-	-	0.002
Neorhizobium sp. CSC1952	Bacteria	-	-	0.002
Hymenobacter weizhouensis	Bacteria	-	-	0.002
Mixta gaviniae	Bacteria	-	-	0.002
Porphyromonas sp. oral taxon 275	Bacteria	-	-	0.002
Prevotella sp. E13-17	Bacteria	0.000	35.000	0.002
Prevotella heparinolytica	Bacteria	0.000	35.000	0.002
Prevotella sp. Rep29	Bacteria	0.000	35.000	0.002
Achromobacter deleyi	Bacteria	-	-	0.002
Arabiibacter massiliensis	Bacteria	-	-	0.002
Francisella adeliensis	Bacteria	-	-	0.002
Paenibacillus sp. FSL H8-0537	Bacteria	-	-	0.002
Bosea sp. PAMC 26642	Bacteria	-	-	0.002
Emergencia sp. JLR.KK010	Bacteria	-	-	0.002
Methylomarinum roseum	Bacteria	-	-	0.002
Calditerrivibrio nitroreducens	Bacteria	-	-	0.002
Mycoplasmopsis gallinarum	Bacteria	-	-	0.002
Bifidobacterium sp. ESL0769	Bacteria	0.500	12.000	0.002
Porphyromonas asaccharolytica	Bacteria	0.000	0.000	0.002
Shewanella basaltis	Bacteria	-	-	0.002
Segatella oris	Bacteria	0.000	35.000	0.002
Amycolatopsis bartoniae	Bacteria	-	-	0.002
Fusobacterium hominis	Bacteria	-	-	0.002
Phascolarctobacterium succinatutens	Bacteria	0.000	1.752	0.002
Lachnoclostridium phytofermentans	Bacteria	-	-	0.002
Mycoplasma sp. 1018B	Bacteria	-	-	0.002
Clostridium botulinum	Bacteria	0.000	1.000	0.002
Maricaulis sp. MIT060901	Bacteria	-	-	0.002

Microtetraspora malaysiensis	Bacteria	-	-	0.002
Akkermansia sp. EB-AMDK43	Bacteria	0.050	4.000	0.001
Breznakiella homolactica	Bacteria	-	-	0.001
Haliangium ochraceum	Bacteria	-	-	0.001
Frigoribacterium sp. NBH87	Bacteria	-	-	0.001
Fusarium oxysporum	Bacteria	-	-	0.001
Aristaeella hokkaidonensis	Bacteria	-	-	0.001
Eggerthella sp. YY7918	Bacteria	-	-	0.001
Deinococcus soli (ex Cha et al. 2016)	Bacteria	-	-	0.001
Ruminiclostridium herbifermentans	Bacteria	-	-	0.001
Raoultibacter timonensis	Bacteria	-	-	0.001
Pseudomonas sp. LB3P93	Bacteria	-	-	0.001
Proteiniclasticum sp. QWL-01	Bacteria	-	-	0.001
Campylobacter vicugnae	Bacteria	-	-	0.001
Corynebacterium durum	Bacteria	0.000	0.000	0.001
Lachnoanaerobaculum gingivalis	Bacteria	-	-	0.001
Paludibacter propionicigenes	Bacteria	-	-	0.001
Cereibacter azotoformans	Bacteria	-	-	0.001
Lacrimispora xylanolytica	Bacteria	-	-	0.001
Labilithrix luteola	Bacteria	-	-	0.001
Nocardioides sp. HDW12B	Bacteria	-	-	0.001
Verrucomicrobium sp. GAS474	Bacteria	-	-	0.001
Ornithobacterium rhinotracheale	Bacteria	-	-	0.001
Murdochiella vaginalis	Bacteria	-	-	0.001
Clostridium cellulovorans	Bacteria	0.000	1.000	0.001
Anaerofustis stercorihominis	Bacteria	0.000	0.000	0.001
Arachidicoccus terrestris	Bacteria	-	-	0.001
Sporomusa rhizae	Bacteria	-	-	0.001
Streptococcus oralis	Bacteria	0.000	0.002	0.001
Acidovorax sp.	Bacteria	-	-	0.001
Caproicibacterium lactatifermentans	Bacteria	-	-	0.001
Cellulophaga lytica	Bacteria	-	-	0.001
Pseudomonas sp. R1-1	Bacteria	-	-	0.001
Prevotella sp. oral taxon 475	Bacteria	0.000	35.000	0.001
Phenylobacterium zucineum	Bacteria	-	-	0.001
Porphyromonas somerae	Bacteria	-	-	0.001
Monoglobus pectinilyticus	Bacteria	0.000	0.149	0.001
Paraburkholderia atlantica	Bacteria	-	-	0.001
Luteibacter flocculans	Bacteria	-	-	0.001
Paenibacillus sp. P36	Bacteria	-	-	0.001
Xiamenia xianingshaonis	Bacteria	-	-	0.001
Streptococcus salivarius	Bacteria	0.000	0.584	0.001
Streptomyces canus	Bacteria	-	-	0.001
Selenomonas sp. oral taxon 478	Bacteria	-	-	0.001
Sphingomonas aerolata	Bacteria	-	-	0.001
Allobaculum sp. Allo2	Bacteria	-	-	0.001

Microorganism	Domain	Ref. min. (%)	Ref. max. (%)	Abundance (%)
Methanobrevibacter smithii	Archaea	-	-	0.077
Methanobrevibacter sp. TLL-48-HuF1	Archaea	-	-	0.002
Methanobrevibacter intestini	Archaea	-	-	0.001

ANNEX II: SPECIFIC PANELS FOR FUNGI, YEASTS AND PARASITES

This annex details the species included in the fungi, yeast and parasite panels analyzed.

FUNGI AND YEASTS

Species included in the panel		
Aspergillus flavus	*Candida tropicalis*	*Meyerozyma guilliermondii*
Aspergillus fumigatus	*Clavispora lusitaniae*	*Mucor circinelloides*
Aspergillus nidulans	*Coccidioides immitis*	*Paracoccidioides brasiliensis*
Aspergillus niger	*Cryptococcus gattii*	*Penicillium camemberti*
Aspergillus oryzae	*Cryptococcus neoformans*	*Penicillium chrysogenum*
Aspergillus terreus	*Debaryomyces hansenii*	*Penicillium expansum*
Blastomyces dermatitidis	*Fusarium oxysporum*	*Penicillium roqueforti*
Candida albicans	*Galactomyces candidum*	*Pichia kudriavzevii*
Candida auris	*Geotrichum candidum*	*Rhizopus microsporus*
Candida dubliniensis	*Histoplasma capsulatum*	*Rhizopus oryzae*
Candida glabrata	*Kluyveromyces lactis*	*Rhodotorula mucilaginosa*
Candida krusei	*Kluyveromyces marxianus*	*Saccharomyces boulardii*
Candida lusitaniae	*Malassezia furfur*	*Saccharomyces cerevisiae*
Candida metapsilosis	*Malassezia globosa*	*Saccharomyces paradoxus*
Candida orthopsilosis	*Malassezia restricta*	*Trichosporon asahii*
Candida parapsilosis	*Malassezia sympodialis*	*Yarrowia lipolytica*

PARASITES

Species included in the panel		
Ancylostoma duodenale	*Diphyllobothrium latum*	*Isospora belli*
Anisakis simplex	*Endolimax nana*	*Microsporidia*
Ascaris lumbricoides	*Entamoeba dispar*	*Necator americanus*
Blastocystis hominis	*Entamoeba histolytica*	*Pentatrichomonas hominis*
Blastocystis sp.	*Enterobius vermicularis*	*Schistosoma mansoni*
Chilomastix mesnili	*Fasciola hepatica*	*Strongyloides stercoralis*
Cryptosporidium hominis	*Giardia duodenalis*	*Taenia saginata*
Cryptosporidium parvum	*Giardia intestinalis*	*Taenia solium*
Cyclospora cayetanensis	*Giardia lamblia*	*Toxoplasma gondii*
Cystoisospora belli	*Hymenolepis nana*	*Trichuris trichiura*
Dientamoeba fragilis	*Iodamoeba butschlii*	*Trypanosoma cruzi*

ANNEX III: DEFINITION OF THE FUNCTIONS ANALYZED

Term	Definition
Oral bacteria	Microorganisms characteristic of the oral cavity that are detected in the gut. Since they do not normally colonize the intestinal ecosystem in a stable way, their elevated presence can reflect a microbiota imbalance, alterations in the digestive barriers, or changes in gastrointestinal transit.
Intestinal barrier	Microorganisms involved in maintaining the integrity of the intestinal epithelium. They help reinforce the junctions between cells, protect against pathogens, modulate intestinal permeability, and preserve an adequate mucosal defense function.
Bifidobacterium spp.	Bacterial genus widely studied for its probiotic potential. It is associated with beneficial effects on digestion, the production of healthy metabolites, immune modulation, and the reduction of intestinal inflammatory processes.
Acetate-consuming	Microorganisms that use acetate as a metabolic substrate. Their activity helps modulate the availability of this short-chain fatty acid and may favor the production of other beneficial metabolites, such as butyrate.
Butyrate-consuming	Bacteria capable of using butyrate as an energy source. When present in excess, they can reduce the local availability of this metabolite, limiting its beneficial effects on the intestinal mucosa and its anti-inflammatory function.
GABA-consuming	Microorganisms that break down or use gamma-aminobutyric acid (GABA), reducing its local availability. This activity can influence gut-brain axis communication, intestinal motility, and neuroimmune regulation.
Histamine-consuming	Bacteria capable of breaking down histamine. Their presence can help regulate the accumulation of this biogenic amine and reduce responses associated with inflammation, hypersensitivity, allergies, or gastrointestinal discomfort.
Lactate-consuming	Bacteria that use lactate as a substrate to generate beneficial metabolites, mainly butyrate and propionate. They help prevent excessive lactate accumulation and contribute to the metabolic balance of the intestinal ecosystem.
Mucus-consuming	Bacteria capable of degrading intestinal mucus. Although some are part of a balanced commensal microbiota, their excess can compromise the mucus layer, increase intestinal permeability, and favor direct interaction between bacteria and the epithelium.
S-equol-consuming	Bacteria that break down or consume S-equol, modulating its intestinal and systemic availability. Their activity can influence the hormonal effects associated with this isoflavone-derived metabolite.
Succinate-consuming	Microorganisms that metabolize succinate and help control its accumulation. This function contributes to the metabolic balance of the microbiota and can limit pro-inflammatory effects associated with elevated succinate concentrations.
Trimethylamine-consuming	Bacteria capable of breaking down trimethylamine (TMA), helping to reduce its availability as a precursor of TMAO. This function may be relevant in modulating cardiometabolic risk.
Mucus-stimulating	Bacteria that promote mucus production by intestinal goblet cells. They help reinforce the mucus barrier, protect against pathogens, maintain the epithelium, and reduce bacterial translocation.
Estrobolome-forming	Microorganisms that are part of the estrobolome, the functional set of the microbiota capable of transforming inactive conjugated estrogens into active free forms that can recirculate. Its imbalance can influence hormonal homeostasis.
Immunomodulatory	Bacteria that interact with the immune system and help regulate tolerance, the response to pathogens, and control of inflammation. A balanced profile helps prevent excessive inflammatory responses.
Lactobacillus spp.	Group of lactic acid bacteria widely used in the probiotic field. It is related to digestive health, the production of organic acids, competition against pathogens, and modulation of the immune response.
Bile acid-metabolizing	Bacteria capable of transforming primary bile acids into secondary bile acids through processes such as deconjugation. This activity can influence fat digestion, metabolic signaling, and intestinal balance.
Lactose-metabolizing (lactose tolerance)	Bacteria capable of metabolizing lactose and facilitating its use in the gut. Their presence can help improve digestive tolerance in people with a reduced capacity to digest this sugar.
Other probiotic species	Microorganisms with potential benefit to the host due to their ability to produce healthy metabolites, compete with pathogens, modulate the immune system, or contribute to the functional balance of the gut microbiota.

Skin disruptor	Bacteria associated with alterations of the skin barrier through metabolites that can be absorbed and circulate systemically. Their imbalance can contribute to inflammatory processes or skin-related dysfunctions.
Skin protector	Bacteria that can promote skin barrier health through the production of metabolites with beneficial systemic effects. Their activity can contribute to inflammatory modulation and the maintenance of skin integrity.
IAA-producing	Microorganisms that generate indole-3-acetic acid (IAA), a tryptophan-derived metabolite with signaling functions in the gut-brain axis. In certain contexts it can be transformed into compounds such as indoxyl sulfate, with potential renal impact if it accumulates.
Lipopolysaccharide (LPS)-producing	Gram-negative bacteria that produce lipopolysaccharides, structural molecules of the bacterial outer membrane. High release of LPS can activate immune responses, favor systemic inflammation, and increase intestinal permeability.
S-equol-producing	Bacteria capable of converting isoflavones into S-equol, a metabolite with weak estrogenic activity. Its production can contribute to hormonal balance and has been linked to the relief of certain menopause-related symptoms.
Acetate-producing	Microorganisms that produce acetate, a short-chain fatty acid relevant to energy metabolism, appetite regulation, maintenance of the intestinal barrier, and modulation of the immune system.
Acetylcholine-producing	Bacteria capable of producing acetylcholine, a neurotransmitter involved in intestinal motility, neuronal communication, and the regulation of physiological functions of the gut-brain axis.
Ammonium-producing	Microorganisms that release ammonium as a byproduct of nitrogen metabolism. Its accumulation can be toxic and negatively affect intestinal function, metabolic balance, and overall wellbeing.
BCFA-producing	Bacteria that generate branched-chain fatty acids (BCFAs) as a result of protein metabolism. Although part of normal microbial metabolism, elevated production can be related to excess protein fermentation and intestinal inflammation.
Butyrate-producing	Beneficial microorganisms that produce butyrate, a short-chain fatty acid essential for intestinal health. Butyrate acts as an energy source for colonocytes, reinforces the intestinal barrier, and exerts anti-inflammatory effects.
Cadaverine-producing	Microorganisms capable of producing cadaverine, a biogenic amine derived from the decarboxylation of lysine. Its accumulation can play a role in modulating intestinal permeability, the inflammatory response, and microbe-host interactions.
Dopamine-producing	Microorganisms capable of synthesizing dopamine, a neurotransmitter related to motivation, reward, intestinal regulation, and gut-brain axis communication.
Ethanol-producing	Microorganisms that ferment substrates and generate ethanol. Intestinal overproduction can be associated with dysbiosis, liver damage, or auto-fermentation phenomena in specific contexts.
Formate-producing	Microorganisms capable of generating formate or formic acid as a metabolic product, mainly through anaerobic fermentation of carbohydrates and amino acids. They participate in microbial energy metabolism and in trophic interactions between species.
GABA-producing	Microorganisms that produce gamma-aminobutyric acid (GABA), an inhibitory neurotransmitter capable of modulating gastrointestinal motility, visceral sensitivity, and gut-brain axis communication.
Glutamate-producing	Bacteria that synthesize glutamate, an excitatory neurotransmitter involved in neuronal, metabolic, and intestinal functions. Its imbalance can influence motility and contribute to symptoms such as diarrhea or constipation.
Hydrogen-producing	Microorganisms that produce hydrogen as a byproduct of intestinal fermentation. High production can contribute to gas accumulation, bloating, abdominal distension, and fermentative imbalances.
Histamine-producing	Microorganisms capable of producing histamine from amino acids. An excess can contribute to inflammation, allergic symptoms, food hypersensitivity, and gastrointestinal alterations.
Indole-producing	Bacteria that metabolize tryptophan and generate indoles. These compounds can have beneficial or harmful effects depending on the context, concentration, and functional balance of the microbiota.
IPA-producing	Bacteria that synthesize indole-3-propionic acid (IPA), a tryptophan-derived metabolite with antioxidant, anti-inflammatory, and potentially neuroprotective properties, associated with the maintenance of intestinal homeostasis.
Lactate-producing	Microorganisms that generate lactate as a fermentation product. Lactate can be beneficial when other bacteria convert it into butyrate or propionate, but its excessive accumulation can favor acidification, dysbiosis, and digestive discomfort.

Methane-producing	Intestinal archaea that produce methane during fermentation. Their elevated presence has been associated with slower intestinal transit, gas accumulation, and symptoms compatible with constipation or abdominal distension.
p-Cresol-producing	Bacteria that produce p-cresol, a metabolite derived from protein metabolism. In excess it can damage the intestinal mucosa and, if it accumulates systemically, act as a uremic toxin.
Propionate-producing	Bacteria that synthesize propionate, a short-chain fatty acid with beneficial functions on energy metabolism, appetite control, metabolic health, and immune regulation.
Quinolinate-producing	Microorganisms capable of synthesizing quinolinate, a neuroactive metabolite derived from the tryptophan-kynurenine pathway. Its accumulation has been associated with neuroinflammatory processes and alterations in neuroimmune balance.
Hydrogen sulfide-producing	Microorganisms capable of generating hydrogen sulfide (H_2S). At physiological concentrations it can participate in signaling, but in excess it can damage the intestinal epithelium, favor dysbiosis, and generate gases with a characteristic strong odor.
Tyramine-producing	Microorganisms capable of producing tyramine, a biogenic amine derived from the decarboxylation of tyrosine. Its accumulation can have neuromodulatory, vascular, and immunological effects at the intestinal and systemic level.
Trimethylamine-producing	Microorganisms that metabolize choline, carnitine, and other dietary compounds to generate trimethylamine (TMA), a precursor of TMAO. This metabolite has been linked to cardiometabolic processes and cardiovascular risk.
Tryptamine-producing	Microorganisms that convert tryptophan into tryptamine, an intestinal neuromodulator capable of influencing motility, intestinal secretion, and local immune regulation.
Vitamin B12-producing	Bacteria capable of producing cobalamin or vitamin B12, an essential micronutrient for the nervous system, DNA synthesis, and red blood cell formation.
Vitamin B9-producing	Microorganisms capable of synthesizing folic acid or vitamin B9, an essential nutrient for DNA synthesis, cell division, and the maintenance of key metabolic functions.
Vitamin K2-producing	Bacteria that generate menaquinones or vitamin K2, compounds important for coagulation, bone metabolism, and the regulation of processes related to cardiovascular health.
Pro-inflammatory	Microorganisms associated with the activation of the immune system and chronic intestinal inflammatory processes. An elevated presence can contribute to dysbiosis and be related to inflammatory or metabolic diseases, or alterations in intestinal permeability.
Proteolytic	Bacteria that break down proteins and produce metabolites such as ammonium, indoles, phenols, or biogenic amines. High proteolytic activity can be harmful to the intestinal mucosa and favor inflammation or bacterial translocation.
Serotonin regulation	Bacteria involved in the synthesis, availability, or modulation of serotonin. This function can influence mood, intestinal motility, visceral sensitivity, and appetite regulation.
Kynurenine synthesis-regulating	Microorganisms that modulate the tryptophan-kynurenine pathway, involved in communication between metabolism, the immune system, and the nervous system. Its imbalance can be related to neuroinflammation and mental health.
Mucus-regulating	Microorganisms capable of stimulating the production or degradation of mucin, the main component of intestinal mucus. In balance they help maintain a functional mucosa; in excess or deficiency they can compromise the intestinal barrier.
Wheat sensitivity	Bacteria associated with the breakdown of wheat components and with the modulation of immune responses in people sensitive to gluten or other cereal compounds. Their imbalance can contribute to intestinal symptoms.

ANNEX IV: GENERAL FOOD RECOMMENDATIONS BY FUNCTIONAL DOMAIN

INFLAMMATION / LPS

The foods in this section promote the production of Short-Chain Fatty Acids (SCFAs), help modulate intestinal inflammation, and contribute to microbial balance.

Food	Component
Canola oil	Olive oil polyphenols
Cod liver oil	Olive oil polyphenols
Flaxseed oil	Fiber and polyphenols
Extra virgin olive oil	Olive oil polyphenols
Fish oil	Omega-3 (EPA/DHA)
Salmon oil	Omega-3 (EPA/DHA)
Black olives	Fermentable fiber
Swiss chard	Fermentable fiber
Chicory	Fermentable fiber
Avocado	Fermentable fiber
Apricot	Fermentable fiber
Caper	Fermentable fiber
Clams	Fermentable fiber
Almonds	Fiber and polyphenols
Beans	Galactooligosaccharides (GOS)
Kidney beans	Galactooligosaccharides (GOS)
Cashews	Fermentable fiber
Anchovies	Fermentable fiber
Eel	Fermentable fiber
Blueberries	Fermentable fiber
Herring	Fermentable fiber
Mugwort	Fermentable fiber
Tuna	Omega-3 (EPA/DHA)
Hazelnuts	Fiber and polyphenols
Saffron	Fermentable fiber
Cod	Fermentable fiber
Burdock	Fermentable fiber
Elderberries	Fermentable fiber
Eggplant	Fermentable fiber
Anchovies (fresh)	Fermentable fiber
Broccoli	Fermentable fiber
Mackerel	Omega-3 (EPA/DHA)
Peanuts	Fermentable fiber
Cocoa	Fermentable fiber
Coffee	Fermentable fiber
Pork	Fermentable fiber
Veal	Fermentable fiber
Grass-fed beef	Fermentable fiber

Food	Component
Dandelion leaves	Fermentable fiber
Eggs	Fermentable fiber
Jicama	Fermentable fiber
Beans	Galactooligosaccharides (GOS)
Kale	Fermentable fiber
Kamut	Fermentable fiber
Kiwi	Fermentable fiber
Milk	Fermentable fiber
Soy milk	Fermentable fiber
Whole milk	Fermentable fiber
Lettuce	Fermentable fiber
Lentils	Galactooligosaccharides (GOS)
Lime	Fermentable fiber
Lemon	Pectins
Sea bass	Fermentable fiber
Corn	Fermentable fiber
Mandarin	Fermentable fiber
Mango	Fermentable fiber
Butter	Fermentable fiber
Passion fruit	Fermentable fiber
Melon	Fermentable fiber
Quince	Fermentable fiber
Honey	Fermentable fiber
Millet	Fermentable fiber
Miso	Fermentable fiber
Blackberries	Fermentable fiber
Orange	Pectins
Nectarines	Fermentable fiber
Walnuts	Fermentable fiber
Rye bread	Fermentable fiber
Whole grain bread	Fermentable fiber
Papaya	Fermentable fiber
Turkey	Fermentable fiber
Chicken breast	Fermentable fiber
Parsley	Fermentable fiber
Bell pepper	Fermentable fiber
Red bell pepper	Fermentable fiber
Green bell pepper	Fermentable fiber
Pineapple	Fermentable fiber
Sunflower seeds	Fermentable fiber
Banana	Resistant starch

Food	Component
Beef	Fermentable fiber
Barley	Fermentable fiber
Rye	Fermentable fiber
Cherries	Fermentable fiber
Chia	Fermentable fiber
Dark chocolate	Fermentable fiber
Plums	Fermentable fiber
Coconut	Fermentable fiber
Cabbage	Fermentable fiber
Chinese cabbage	Fermentable fiber
Brussels sprouts	Fermentable fiber
Red cabbage	Fermentable fiber
Kale	Fermentable fiber
Brussels sprouts	Fermentable fiber
Cauliflower	Fermentable fiber
Lamb	Fermentable fiber
Bindweed	Fermentable fiber
Curry	Fermentable fiber
Edamame	Fermentable fiber
Asparagus	Fructooligosaccharides (FOS) and Inulin
Spinach	Fermentable fiber
Blackcurrant extract	Fermentable fiber
Raspberries	Fermentable fiber
Strawberries	Fermentable fiber
Beans	Fermentable fiber
Berries	Fermentable fiber
Shrimp	Fermentable fiber
Chickpeas	Galactooligosaccharides (GOS)
Turnip greens	Fermentable fiber
Blackcurrants	Fermentable fiber
Guava	Fermentable fiber
Peas	Fermentable fiber
Fava beans	Fermentable fiber
Whole wheat flour	Fermentable fiber
Liver	Fermentable fiber
Chicken liver	Fermentable fiber
Veal liver	Fermentable fiber
Beef liver	Fermentable fiber
Figs	Fermentable fiber
Fennel	Fermentable fiber
Fenugreek leaves	Fermentable fiber
Mugwort leaves	Fermentable fiber

Food	Component
Plantain	Resistant starch
Green banana	Resistant starch
Chicken	Fermentable fiber
Grapefruit	Fermentable fiber
Purslane	Fermentable fiber
Cheese	Fermentable fiber
Cheddar cheese	Fermentable fiber
Soft cheeses	Fermentable fiber
Hard cheeses	Fermentable fiber
Quinoa	Fermentable fiber
Radish	Fermentable fiber
Chicory root	Fermentable fiber
Dandelion root	Fermentable fiber
Beetroot	Fermentable fiber
Cabbage	Fermentable fiber
Salmon	Omega-3 (EPA/DHA)
Wheat bran	Fermentable fiber
Sardines	Omega-3 (EPA/DHA)
Fenugreek seeds	Fiber and polyphenols
Sunflower seeds	Fiber and polyphenols
Flaxseeds	Fiber and polyphenols
Evening primrose seeds	Fiber and polyphenols
Sesame seeds	Fiber and polyphenols
Sesame	Fermentable fiber
Soy	Fermentable fiber
Black tea	Fermentable fiber
Green tea	Fermentable fiber
Tempeh	Fermentable fiber
Veal	Fermentable fiber
Bacon	Fermentable fiber
Tofu	Fermentable fiber
Tomato	Fermentable fiber
Whole grain wheat	Fermentable fiber
Whole wheat	Fermentable fiber
Buckwheat	Fermentable fiber
Trout	Fermentable fiber
Grapes	Fermentable fiber
Purple grapes	Fermentable fiber
Red grapes	Fermentable fiber
Egg yolk	Fermentable fiber
Cassava	Fermentable fiber
Cooked and cooled cassava	Fermentable fiber

INTESTINAL BARRIER

The foods in this section promote butyrate production, improve intestinal barrier function, and help maintain intercellular junctions *(tight junctions)*.

Food	Component
Garlic	Fructooligosaccharides (FOS) and Inulin
Spring garlic	Fructooligosaccharides (FOS) and Inulin
Artichoke	Fructooligosaccharides (FOS) and Inulin
Rice	Resistant starch
Cooked and cooled rice	Resistant starch
Brown rice	Resistant starch
Oats	Resistant starch
Sweet potato	Resistant starch
Cooked and cooled sweet potato	Resistant starch
Pumpkin	Pectins
Onion	Fructooligosaccharides (FOS) and Inulin
Red onion	Fructooligosaccharides (FOS) and Inulin
Kefir	Lactic fermentation (lactate and acetate)
Apples	Pectins
Apples (with skin)	Pectins
Baked potato with skin	Resistant starch
Cooked and cooled potato	Resistant starch
Pear	Pectins
Leek	Fructooligosaccharides (FOS) and Inulin
Rice bran	Resistant starch
Pumpkin seeds	Pectins
Fermented soy	Lactic fermentation (lactate and acetate)
Whole yogurt	Lactic fermentation (lactate and acetate)
Carrot	Pectins

ANNEX V: PREBIOTICS GUIDE

The gut microbiome contains microbial species that digest both fiber and protein. **Prebiotics are food components that certain gut microorganisms** use selectively, producing potentially beneficial effects for health.

TYPES OF PREBIOTICS

Not all prebiotics act in the same way. Each type can favor different bacterial groups and functions, such as short-chain fatty acid production, maintenance of the intestinal barrier, or immune regulation. The abundance indicated reflects its estimated presence in the selection of recommended foods, not the amount that should be consumed.

Abbreviation	Prebiotic	Abundance	Function
PAC	Proanthocyanidins	5 %	Polyphenols with an antioxidant and anti-inflammatory effect. They modulate the microbiome and help inhibit pathogenic bacteria.
RS	Resistant starch	27 %	Ferments in the colon and increases butyrate production, improving intestinal and metabolic health.
PEC	Pectin	27 %	Fermentable soluble fiber that favors beneficial bacteria and improves intestinal barrier function.
AX	Arabinoxylan	32 %	Stimulates short-chain fatty acid-producing bacteria, especially butyrate producers.
GOS	Galactooligosaccharides	45 %	Favor bifidobacteria and lactobacilli. Support immune function.
INU	Inulin	59 %	Fermentable fiber that stimulates beneficial bacteria and improves intestinal transit.
FOS	Fructooligosaccharides	86 %	Main source of prebiotic energy for beneficial bacteria. Promotes microbial diversity.

BENEFICIAL BACTERIA AND ASSOCIATED PREBIOTICS

This table relates certain beneficial bacteria to the prebiotics that can favor their growth or activity. These associations serve as guidance for personalizing diet, but the response depends on the microbiome as a whole, digestive tolerance, and each person's clinical situation.

Species name	Prebiotics to increase growth
Agathobacter faecis	FOS, AX, RS
Agathobacter rectalis	FOS, INU, AX, RS
Akkermansia muciniphila	FOS, PAC
Anaerostipes hadrus	FOS, INU
Bifidobacterium adolescentis	FOS, INU, GOS, PEC, AX
Bifidobacterium angulatum	FOS, GOS
Bifidobacterium animalis	FOS, INU
Bifidobacterium bifidum	FOS, INU, GOS
Bifidobacterium breve	FOS, INU, GOS, PEC, AX, RS
Bifidobacterium catenulatum	FOS, GOS
Bifidobacterium infantis	FOS, INU, GOS, AX
Bifidobacterium longum	FOS, INU, GOS, PEC
Bifidobacterium pseudocatenulatum	GOS
Coprococcus comes	FOS, INU
Coprococcus eutactus	FOS, INU
Faecalibacterium prausnitzii (A)	FOS, INU, PEC
Faecalibacterium prausnitzii (C)	FOS, INU, PEC
Lactobacillus gasseri	GOS, PEC
Roseburia hominis	FOS, AX
Roseburia intestinalis	FOS, AX, RS
Roseburia inulinivorans	FOS, INU, RS
Ruminococcus bromii	GOS, RS

POTENTIALLY HARMFUL MICROORGANISMS

The presence of these microorganisms does not necessarily imply disease. Their relevance depends on their abundance, their balance with the rest of the microbiota, and the clinical context. Dietary recommendations are aimed at limiting the conditions that favor their expansion and promoting a more balanced intestinal ecosystem.

Species	Dietary recommendation
Bilophila wadsworthia	Increase inulin and reduce saturated fats.
Fusobacterium nucleatum	Increase flavonoids.

FOODS AND ASSOCIATED PREBIOTICS

The green dots indicate which types of prebiotics each food mainly provides. This table makes it possible to combine different plant sources to increase the diversity of substrates available to the microbiota. Incorporation should be gradual and adapted to digestive tolerance, especially if there is bloating, gas, or intestinal sensitivity.

Food	FOS	INU	GOS	PEC	AX	RS	PAC
Garlic	●	●					
Apricot				●			
Jerusalem artichoke		●					
Almonds							●
Cashews	●						●
Rice (cooked and cooled)						●	
Blueberries	●			●			●
Cranberries							●
Hazelnuts							●
Oats						●	
Sweet potato				●			
Eggplant				●			
Peanuts							●
Pumpkin				●			
Cinnamon							●
Barley		●			●	●	
Onion	●	●					
Scallions	●	●					
Rye					●	●	
Cereals (bran)	●				●		
Dark chocolate							●
Plum				●			
Brussels sprouts	●						
Raspberries	●			●			●
Strawberries				●			
Chickpeas			●			●	
Peas				●			
Fennel		●					
White beans	●		●			●	
Kidney beans	●		●			●	
Kiwi				●			
Red lentils	●		●			●	
Lemon				●			

Apple				●			
Blackberries				●			●
Orange				●			
Rye bread	●				●	●	
Whole grain bread	●				●		
Cooled pasta						●	
Cooled potato						●	
Pear				●			
Pistachios	●						●
Green banana						●	
Leek	●	●					
Chicory root		●					
Beetroot	●	●					
Wheat bran	●				●		
Tomato				●			
Whole wheat					●		
Carrot				●			

ANNEX VI: TECHNOLOGY

Metagenomic analysis is performed using massive DNA sequencing with **Oxford Nanopore** technology, based on the direct reading of individual molecules through nanopores. This approach makes it possible to obtain long reads (*long-reads*), enabling a more complete characterization of the microbiome and greater taxonomic resolution compared with short-read technologies.

The reads obtained undergo quality control, filtering, and bioinformatic analysis processes to produce technically valid data. Taxonomic classification is performed using a specific *pipeline* for Nanopore metagenomics, making it possible to identify the microorganisms present and estimate their relative abundance from domain level down to species level.

In addition, the analysis incorporates functional information associated with the microbial community, providing a complementary view of its potential metabolic capabilities. The results are generated in structured tabular files that include abundances by species, taxonomic classification, and functional annotation, forming the basis for the clinical interpretation of the intestinal metagenomic profile.

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Contact:

Scientific Park
Valencia University

St, Agustín Escardino Benlloch, 9
Paterna, Valencia

(+34) 617 28 05 82

info@overgenes.com
www.overgenes.com