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Next-level health

Intestinal Microbiota Test

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What does metagenomic analysis of the gut microbiota consist of?

A metagenomic analysis involves studying the full set of genes present in a sample, which makes it possible to analyze the microorganisms it contains and their potential functions. This approach provides a detailed characterization of the microbial communities that inhabit the gut. To do so, it examines all genetic material in the sample using third-generation (long-read) genomic sequencing platforms. This methodology enables microbial species to be identified at the highest possible resolution.

Unlike PCR-based methods or second-generation high-throughput sequencing platforms (NGS), this approach minimizes biases caused by selective amplification or by analyzing short fragments, yielding results that more closely reflect the sample's true composition. Metagenomic analysis can detect a broad spectrum of microorganisms, including bacteria, archaea, fungi, viruses, parasites, and other low-abundance groups, and characterize them based on their functional potential inferred from the genetic information obtained.

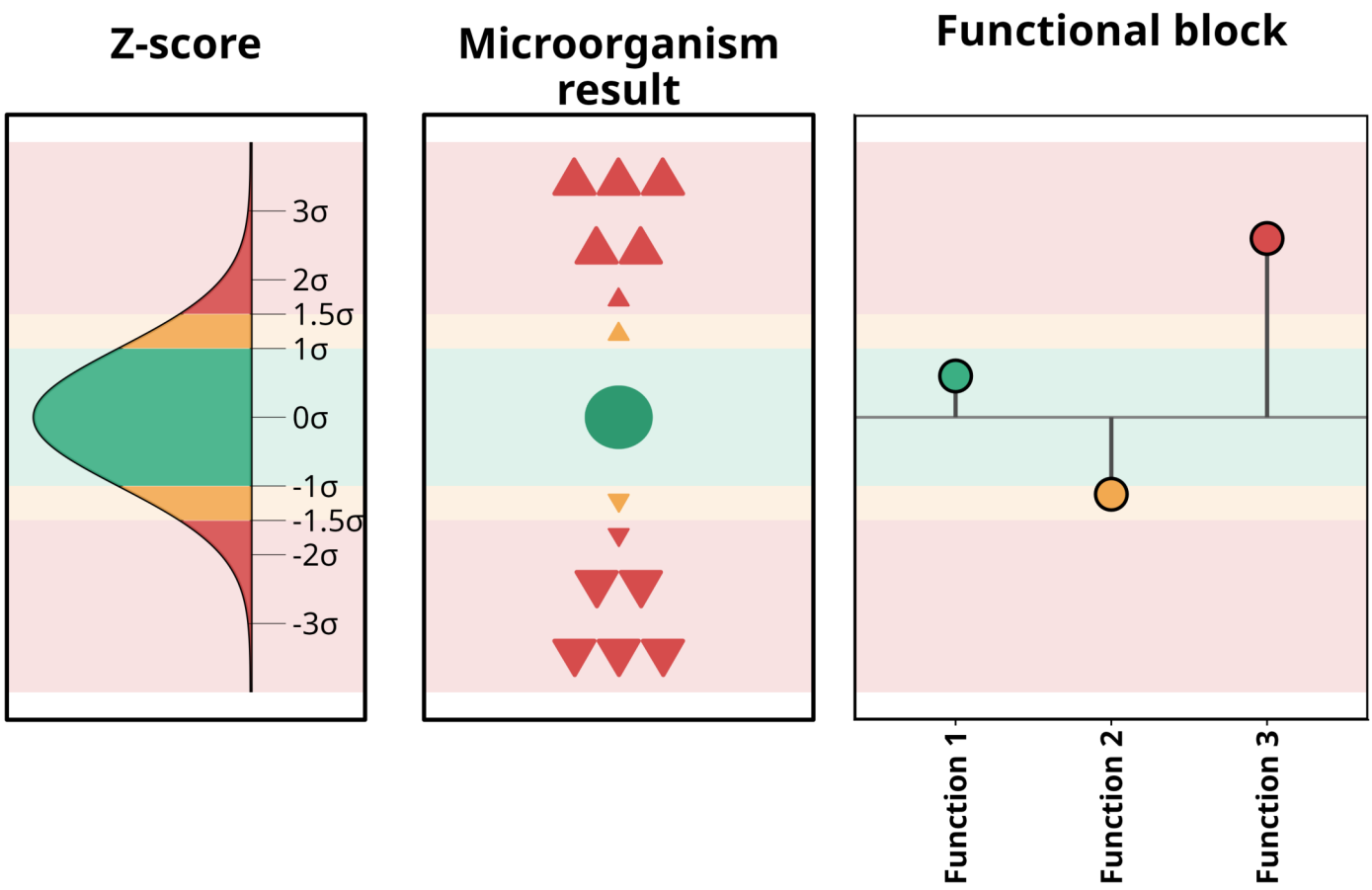
This analysis is not intended for diagnostic purposes; rather, it is designed for a clinical-preventive context. Its goal is to describe the microbial profile and estimate the functional potential associated with the detected genes, providing a global view of the gut ecosystem and how its configuration may relate to health status.

How should the results of the analysis be interpreted?

The results report the relative abundance of each microorganism detected in the sample. Rather than quantifying the absolute number of cells, abundances are expressed as percentages (%) of the total assigned sequences. This standardizes the data and enables comparison with an external reference cohort composed of healthy individuals.

To assess whether a microbial species is present at expected levels, we use a statistical parameter called the Z-score, which indicates whether the observed abundance falls within the usual range, or is above or below the average values observed in a healthy population.

The reference database used comes from large international repositories and is supported by the scientific literature. It includes data from more than 20,000 healthy individuals, compiled from over 500 clinical studies, available through open platforms such as the Human Microbiome Project (HMP), the European Nucleotide Archive (ENA), and the Sequence Read Archive (SRA), among others.



Thresholds:

- **Green**: indicates that the relative abundance of the microorganism is situated **very close to the average value** observed in the healthy population. It is the expected range for a balanced microbiota.
- **Orange**: reflects a **moderate deviation** from the mean. It does not necessarily imply a problem, but points out a variation that should be interpreted within the global context of the microbiome.
- **Red**: corresponds to a **marked and statistically significant deviation** with respect to the reference population (**95% confidence**). It may indicate a relevant imbalance that deserves attention in clinical interpretation.

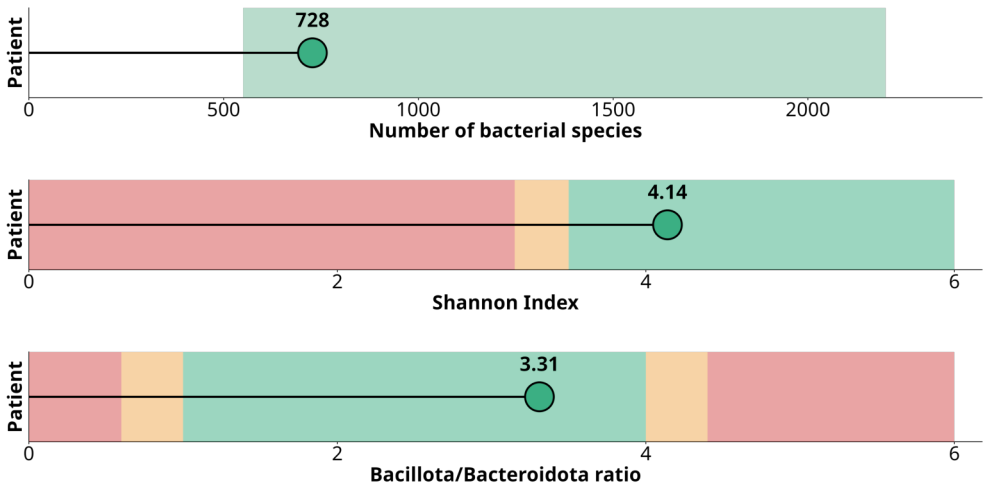
Global microbiota evaluation

Overall summary of results

Functional domain	Result	Clinical implication	Recommendation
Global diversity	Normal	Balanced gut ecosystem	Maintain current lifestyle, prioritizing a plant-rich diet and moderate physical activity.
Intestinal inflammation	Very high intestinal inflammation	Highly pro-inflammatory profile associated with barrier dysfunction and high risk of digestive symptoms.	Intensive intervention: increase polyphenols and omega-3, remove ultra-processed foods, raise prebiotic fiber and consider anti-inflammatory probiotics.
Mucosal status	Highly compromised intestinal mucosa	Excessive activity of mucus-degrading bacteria with poor regulation, carrying high risk of mucosal thinning.	Intensive intervention: increase prebiotics, soluble fiber and polyphenols, reduce ultra-processed foods; consider mucosa-supporting probiotics.
Intestinal permeability	Marked intestinal permeability with a high probability of clinical impact.	Intensive intervention, specialized medical evaluation, and a therapeutic nutritional plan. Therapeutic nutritional intervention: individualized diet, possible temporary restriction of irritating foods, easily digestible textures, and close professional follow-up.	Intensive intervention on the intestinal barrier: anti-inflammatory diet rich in vegetables, fruits and healthy fats; remove ultra-processed foods, simple sugars and alcohol; prioritize prebiotic fibers (inulin, FOS, resistant starch); consider supplementation with glutamine, zinc, omega-3 and barrier-supporting probiotics (e.g. butyrate-producing strains); review use of NSAIDs, PPIs or other drugs that may damage the mucosa.
Saccharide fermentation (SCFA)	Adequate saccharide fermentation	Balanced SCFA production adequate to maintain epithelial integrity and metabolic functions.	Maintain a plant-rich diet with varied fibers; incorporate well-tolerated fermented foods.
Butyrate balance	Adequate butyrate balance	Adequate production/consumption ratio to maintain epithelial integrity.	Maintain a balanced diet rich in plants and well-tolerated fermented foods.
Proteolysis / putrefaction	Very high intestinal proteolysis	Excessive production of proteolytic metabolites (BCFA, phenols, amines) associated with inflammation and mucosal dysfunction.	Reduce animal protein, increase fermentable fiber, polyphenols and prebiotics; consider probiotics that reduce proteolytic BCFAs.
Fat digestion	Adequate fat digestion	Bile-acid metabolism within the expected range, with no relevant findings.	Maintain current dietary pattern with healthy fats and good vegetable variety.
Gas production	Very high gas production	Simultaneous overproduction of methane and/or hydrogen sulfide associated with bloating, slowed motility or mucosal irritation.	Review fermentative diet, reduce simple sugars and sulfur-rich foods; increase soluble fiber and polyphenols and consider probiotics that regulate methane and sulfur.
Mycobiota	Mycobiota within normal range	Adequate balance between fungi and bacteria with no relevant findings.	Maintain current habits and a diet rich in varied vegetables.
Parasites	Significant absence of parasites	No relevant signs of parasitic infection observed.	Maintain good hygiene-dietary habits and a balanced, fiber-rich diet.

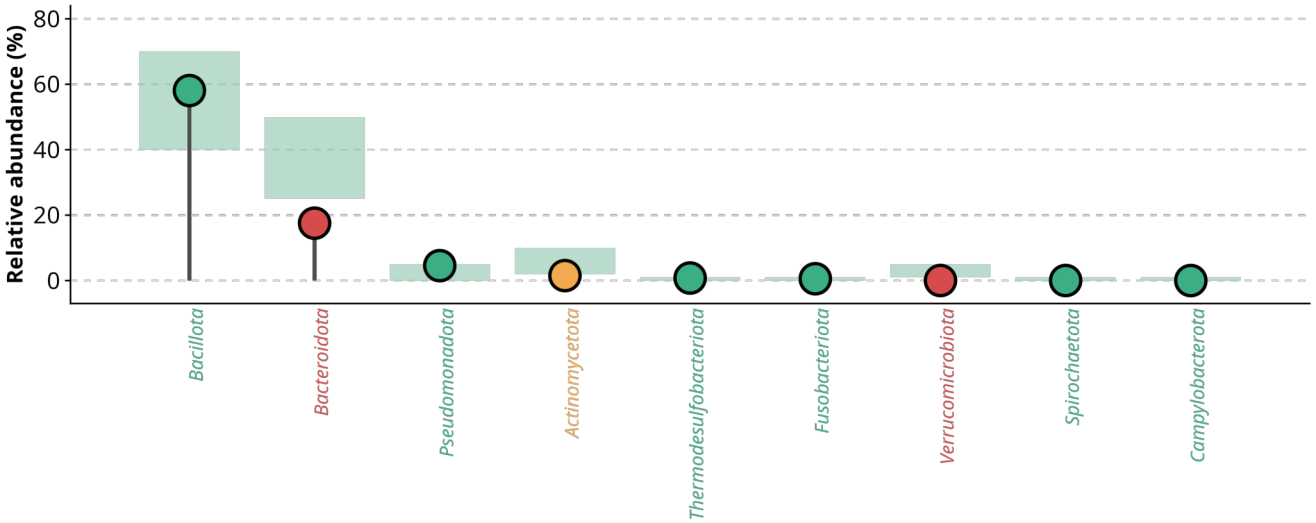
General composition of the microbiota

- **Richness:** total number of distinct bacterial species detected in a sample, regardless of their relative abundance.
- **Diversity:** measure of how varied the species are, taking into account their relative abundances within the microbial community.
- **Bacillota:Bacteroidota ratio**: the ratio between the relative abundance of *Bacillota* and *Bacteroidota*, previously known as the Firmicutes/Bacteroidetes ratio.



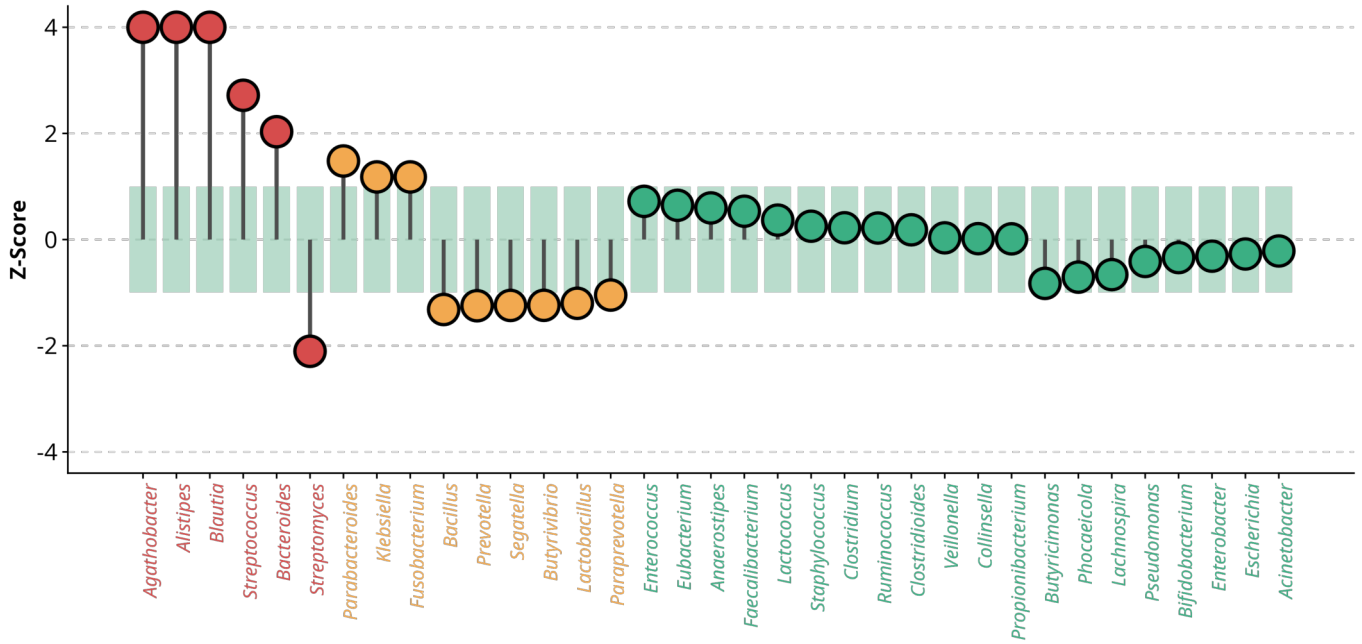
Phylum distribution

Relative proportion of the main microbial phyla present in the sample, describing the overall taxonomic structure of the gut microbiota.



Genus distribution

Relative proportion of the different microbial genera detected in the sample, allowing the taxonomic composition to be assessed at a more specific level.



Species level results

Parasites list

This section analyzes the **presence of any type of parasite** detectable in the sample through our metagenomic analysis. When **no parasite is identified**, the report shows a **list of the main parasites of clinical interest** included in the evaluation, all with a negative result. If **any other parasite** is detected, even if it is not part of the standard list, it will **appear specifically detailed** in this section, indicating its identification and level of relative abundance.

	Microorganism	Relative abundance (%)	Result
Nematodes			
	Ancylostoma duodenale	Not detected	
	Anisakis simplex	Not detected	
	Enterobius vermicularis	Not detected	
	Necator americanus	Not detected	
	Strongyloides stercoralis	Not detected	
	Ascaris lumbricoides	Not detected	
	Trichuris trichiura	Not detected	
Other parasites			
	Hymenolepis nana	Not detected	
	Taenia saginata	Not detected	
	Cryptosporidium hominis	Not detected	
	Cryptosporidium parvum	Not detected	
	Taenia solium	Not detected	
	Fasciola hepatica	Not detected	
	Schistosoma mansoni	Not detected	
	Fasciolopsis buski	Not detected	
	Entamoeba histolytica	Not detected	
	Giardia lamblia	Not detected	
	Toxoplasma gondii	Not detected	
	Blastocystis hominis	Not detected	
	Cyclospora cayetanensis	Not detected	
	Trypanosoma cruzi	Not detected	

Microorganism	Relative abundance (%)	Result
Cystoisospora belli	Not detected	
Dientamoeba fragilis	Not detected	
Balantidium coli	Not detected	

Bacterial pathogens

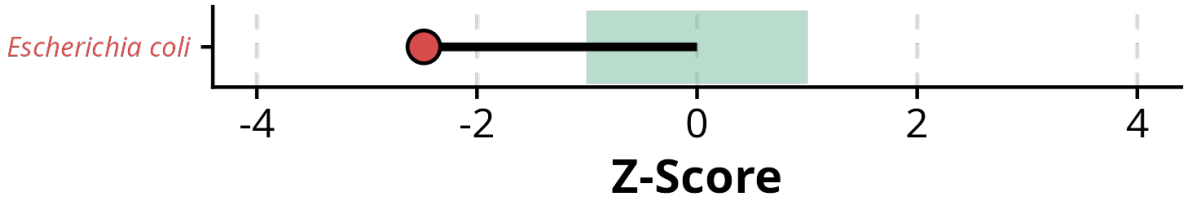
If any pathogen is detected at significant levels, it will be listed in this section, including its identification and relative abundance. The remaining bacterial species considered pathogenic are detailed in the Appendix.

If **any pathogens are detected at significant levels, they will be detailed in this section**, indicating their identification and relative abundance level.

Microorganism	Relative abundance (%)	Result
Alistipes putredinis	3.2803	▲▲
Shigella flexneri	1.4111	▲
Acinetobacter baumannii	0.0273	▲
Helicobacter pylori	0.0108	▲▲

Escherichia coli strains

Total relative abundance *Escherichia coli*: 0.11%



No subspecies of *Escherichia coli* have been detected at significant levels.

Fungi and yeasts

If any fungus or yeast is detected at significant levels, it will be listed in this section, including its identification and relative abundance. The remaining fungal and yeast species are detailed in the Appendix.

No microorganism has been detected at significant levels.

Detected DNA viruses

At present, there are no reliable population reference datasets to establish normal ranges for viruses in the human microbiome. Therefore, the analysis is limited to identifying the viruses present and reporting their relative abundance.

Microorganism	Relative abundance (%)
Caudoviricetes sp.	11.031

Microorganism	Relative abundance (%)
Bacteriophage sp.	3.215
Microviridae sp.	0.573
uncultured human fecal virus	0.367
Crassvirales sp.	0.243

Antibiotic resistance table

The detection of antibiotic resistance genes indicates the potential for the development of resistance, but it does not confirm that such resistance is active or effectively expressed. The likelihood of expression increases with the number of associated genes, although it depends on factors such as the environment, gene regulation, and microbial interactions. This analysis is preventive and informative in nature and should not be interpreted as clinical evidence of active antibiotic resistance.

Antibiotic	Resistance genes	Total genes	Total reads
Doxycycline	tet(32), tet(40), tet(M), tet(O), tet(O/32/O), tet(O/W), tet(O/W)-1, tet(Q), tet(W), tetB(P)	10	408
Tetracycline	tet(32), tet(40), tet(M), tet(O), tet(O/32/O), tet(O/W), tet(O/W)-1, tet(Q), tet(W), tetB(P)	10	408
Minocycline	tet(32), tet(M), tet(O), tet(O/32/O), tet(O/W), tet(O/W)-1, tet(Q), tet(W), tetB(P)	9	313
Lincomycin	cfr(C), erm(B), erm(F), erm(Q), lnu(C)	5	40
Clindamycin	cfr(C), erm(B), erm(F), erm(Q)	4	26
Erythromycin	erm(B), erm(F), erm(Q)	3	25
Pristinamycin_IA	erm(B), erm(F), erm(Q)	3	25
Quinupristin	erm(B), erm(F), erm(Q)	3	25
Virginiamycin_S	erm(B), erm(F), erm(Q)	3	25
Chloramphenicol	catP, catS, cfr(C)	3	12

Predominant species

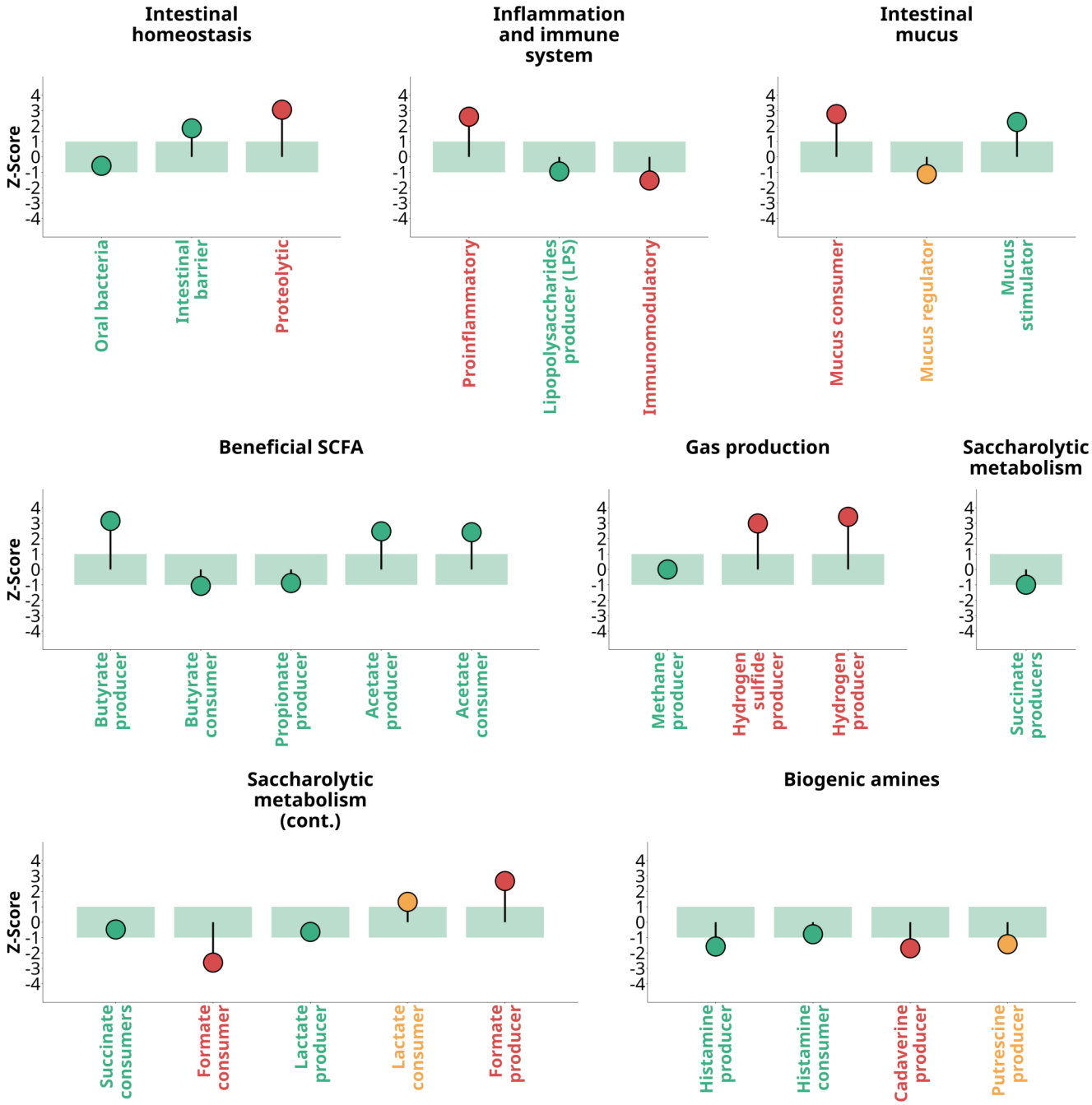
The 20 most abundant species are listed, together with their status relative to the healthy reference population and their associated functions.

Microorganism	Relative abundance (%)	Result	Functionality
Agathobacter rectalis	18.52		Butyrate producer
Caudoviricetes sp.	11.03		Viruses
Blautia wexlerae	4.38		Acetate producer, Skin protector
Oscillospiraceae bacterium	3.83		Acetate producer, Intestinal barrier
Alistipes putredinis	3.28		Proinflammatory, Proteolytic, Pathogens
Bacteriophage sp.	3.21		Viruses
[Ruminococcus] torques	3.16		Butyrate producer, Mucus consumer, Bile acid metabolizer
Phocaeicola vulgatus	2.29		Lipopolysaccharides producer (LPS), Proinflammatory, Proteolytic, Mucus consumer, Wheat sensitivity, Bile acid metabolizer, GABA producer, Glutamate producer, Ammonia producer, Succinate producers
Bacteroides eggerthii	1.75		Butyrate producer, Hydrogen producer, Indole producer, BCFA producers
Shigella flexneri	1.41		Lipopolysaccharides producer (LPS), Glutamate producer, Pathogens
Blautia obeum	1.39		Butyrate producer, Immunomodulatory, Intestinal barrier, Bile acid metabolizer
Faecalibacterium prausnitzii	1.15		Acetate consumer, Butyrate producer, Estrobolome former, Hydrogen producer, IPA producer, Skin protector, Mucus regulator, Mucus stimulator, Wheat sensitivity, Other probiotic species, Succinate producers
Dorea longicatena	1.07		Hydrogen producer, Ethanol producer, Mucus consumer
Bacteroides thetaiotaomicron	1.01		Acetate consumer, Acetate producer, Propionate producer, Histamine consumer, Spermidine producer, Hydrogen producer, Indole producer, Quinolinic acid producer, Immunomodulatory, Intestinal barrier, Mucus consumer, Mucus regulator, Bile acid metabolizer, GABA producer, Ammonia producer, BCFA producers, Lactate producer, Succinate consumers

Microorganism	Relative abundance (%)	Result	Functionality
Salmonella enterica	1.00		Hydrogen sulfide producer, Lipopolysaccharides producer (LPS), Proinflammatory, Proteolytic, Ammonia producer, Pathogens
Bacteroides uniformis	0.85		Spermidine producer, S-EQUOL consumer, Hydrogen producer, Indole producer, Lipopolysaccharides producer (LPS), Mucus consumer, Wheat sensitivity, Bile acid metabolizer, GABA producer, BCFA producers
Anaerobutyricum hallii	0.82		Acetate consumer, Butyrate producer, Mucus stimulator, Lactate consumer
Parabacteroides distasonis	0.75		Hydrogen producer, Skin protector, Immunomodulatory, GABA producer, BCFA producers, Succinate producers
Desulfovibrio piger	0.72		Hydrogen sulfide producer
Dysosmobacter welbionis	0.67		Butyrate producer, Mucus consumer

Functional microbiota evaluation

The report presents the **twenty most abundant species** detected in the sample, accompanied by their Z-score. For each one, a **brief description of its potential functionality** is also included, based on the identified genes and the role these species usually play in the balance of the intestinal ecosystem.



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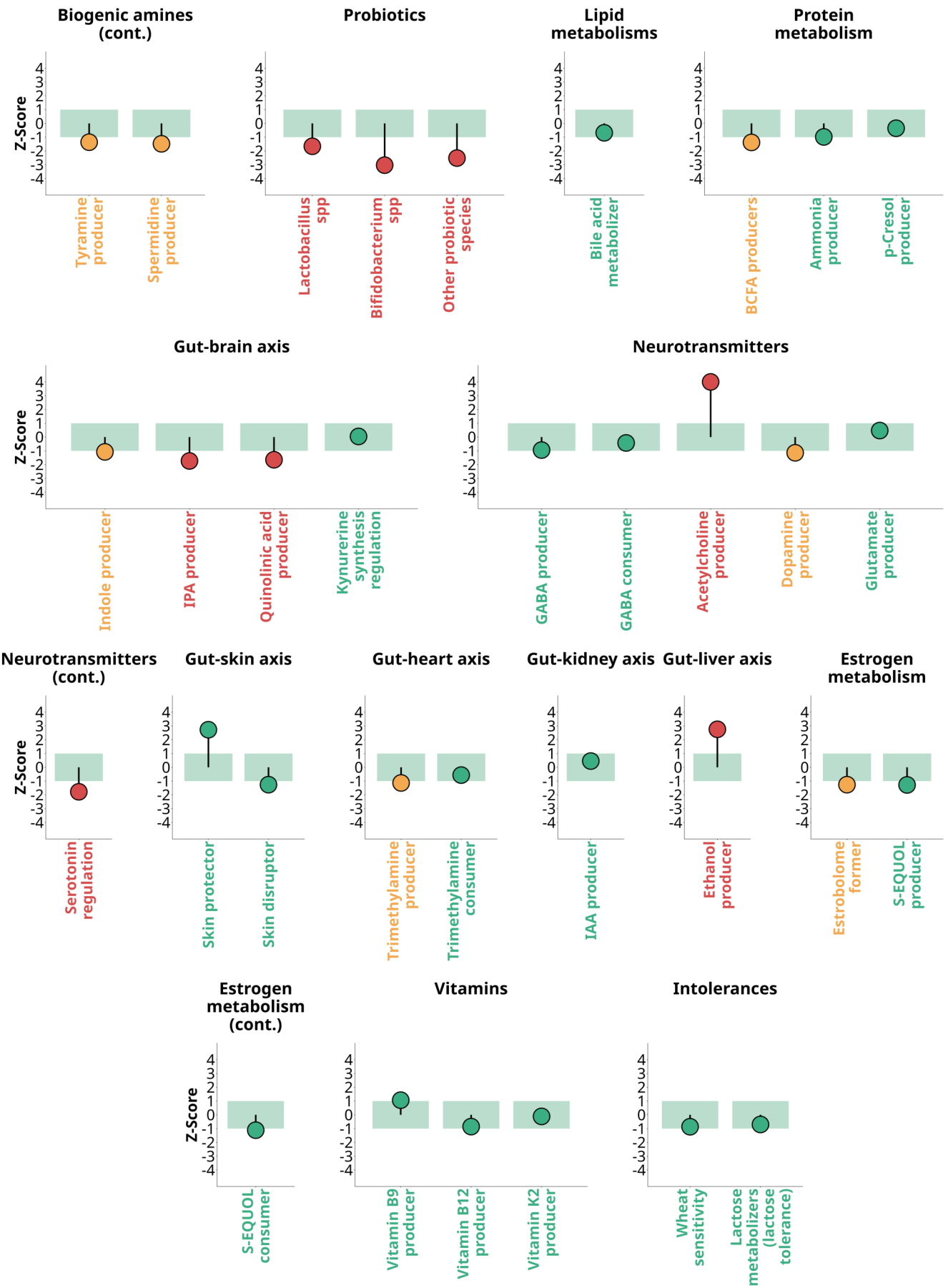

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	Functional group	Top species	State
Intestinal homeostasis			
	Oral bacteria	*Streptococcus salivarius, Segatella copri, Bacteroides heparinolyticus*	●
	Intestinal barrier	*Oscillospiraceae bacterium, Blautia obeum, Bacteroides thetaiotaomicron*	▲
	Proteolytic	*Alistipes putredinis, Phocaeicola vulgatus, Salmonella enterica*	▲▲▲
Inflammation and immune system			
	Proinflammatory	*Alistipes putredinis, Phocaeicola vulgatus, Salmonella enterica*	▲▲
	Lipopolysaccharides producer (LPS)	*Phocaeicola vulgatus, Shigella flexneri, Salmonella enterica*	●
	Immunomodulatory	*Blautia obeum, Bacteroides thetaiotaomicron, Parabacteroides distasonis*	▼
Intestinal mucus			
	Mucus consumer	*[Ruminococcus] torques, Phocaeicola vulgatus, Dorea longicatena*	▲▲
	Mucus regulator	*Faecalibacterium prausnitzii, Bacteroides thetaiotaomicron, Streptococcus thermophilus*	▼
	Mucus stimulator	*Faecalibacterium prausnitzii, Anaerobutyricum hallii, Roseburia intestinalis*	▲▲
Beneficial SCFA			
	Butyrate producer	*Agathobacter rectalis, [Ruminococcus] torques, Bacteroides eggerthii*	▲▲▲
	Butyrate consumer	*Pseudomonas aeruginosa, Pseudomonas aeruginosa, Pseudomonas fluorescens*	▼
	Propionate producer	*Bacteroides thetaiotaomicron, Parabacteroides merdae, Bacteroides finegoldii*	●
	Acetate producer	*Blautia wexlerae, Oscillospiraceae bacterium, Bacteroides thetaiotaomicron*	▲▲
	Acetate consumer	*Faecalibacterium prausnitzii, Bacteroides thetaiotaomicron, Anaerobutyricum hallii*	▲▲

	Functional group	Top species	State
Gas production			
	Methane producer		●
	Hydrogen sulfide producer	*Salmonella enterica, Desulfovibrio piger, Klebsiella pneumoniae*	▲▲
	Hydrogen producer	*Bacteroides eggerthii, Faecalibacterium prausnitzii, Dorea longicatena*	▲▲▲
Saccharolytic metabolism			
	Succinate producers	*Phocaeicola vulgatus, Faecalibacterium prausnitzii, Parabacteroides distasonis*	●
	Succinate consumers	*Bacteroides thetaiotaomicron, Phascolarctobacterium faecium, Waltera intestinalis*	●
	Formate consumer	*Escherichia coli, Clostridium perfringens, Blautia hydrogenotrophica*	▼▼
	Lactate producer	*Bacteroides thetaiotaomicron, Ruthenibacterium lactatiformans, Enterocloster asparagiformis*	●
	Lactate consumer	*Anaerobutyricum hallii, Anaerostipes hadrus, Waltera intestinalis*	▲
	Formate producer	*Lactiplantibacillus plantarum, Bifidobacterium longum, Enterobacter kobei*	▲▲
Biogenic amines			
	Histamine producer	*Klebsiella pneumoniae, Fusobacterium mortiferum, Lacticaseibacillus casei*	▼
	Histamine consumer	*Bacteroides thetaiotaomicron, Lacticaseibacillus casei, Lactiplantibacillus plantarum*	●
	Cadaverine producer	*Klebsiella pneumoniae, Escherichia coli, Escherichia fergusonii*	▼
	Putrescine producer	*Klebsiella pneumoniae, Enterococcus faecalis, Escherichia coli*	▼
	Tyramine producer	*Klebsiella pneumoniae, Enterococcus faecalis, Morganella morganii*	▼
	Spermidine producer	*Bacteroides thetaiotaomicron, Bacteroides uniformis, Escherichia coli*	▼
Probiotics			

	Functional group	Top species	State
	Lactobacillus spp	*Lacticaseibacillus paracasei, Lacticaseibacillus casei, Lactiplantibacillus plantarum*	▼
	Bifidobacterium spp	*Bifidobacterium animalis, Bifidobacterium dentium, Bifidobacterium longum*	▼▼▼
	Other probiotic species	*Faecalibacterium prausnitzii, Streptococcus thermophilus, Enterococcus faecium*	▼▼
Lipid metabolisms			
	Bile acid metabolizer	*[Ruminococcus] torques, Phocaeicola vulgatus, Blautia obeum*	●
Protein metabolism			
	BCFA producers	*Bacteroides eggerthii, Bacteroides thetaiotaomicron, Bacteroides uniformis*	▼
	Ammonia producer	*Phocaeicola vulgatus, Bacteroides thetaiotaomicron, Salmonella enterica*	●
	p-Cresol producer	*Klebsiella pneumoniae, [Eubacterium] siraeum, Clostridioides difficile*	●
Gut-brain axis			
	Indole producer	*Bacteroides eggerthii, Bacteroides thetaiotaomicron, Bacteroides uniformis*	▼
	IPA producer	*Faecalibacterium prausnitzii, Lactiplantibacillus plantarum, [Clostridium] scindens*	▼
	Quinolinic acid producer	*Bacteroides thetaiotaomicron, Lachnospiraceae bacterium, Lachnospiraceae bacterium*	▼
	Kynurerine synthesis regulation	*Lactiplantibacillus plantarum, Lactococcus lactis, Levilactobacillus brevis*	●
Neurotransmitters			
	GABA producer	*Phocaeicola vulgatus, Bacteroides thetaiotaomicron, Bacteroides uniformis*	●
	GABA consumer	*Bacillus cereus, Bacillus thuringiensis, Priestia megaterium*	●
	Acetylcholine producer	*Lactiplantibacillus plantarum*	▲▲▲

	Functional group	Top species	State
	Dopamine producer	*Lactiplantibacillus plantarum, Lactococcus lactis, Levilactobacillus brevis*	▼
	Glutamate producer	*Phocaeicola vulgatus, Shigella flexneri, Lactiplantibacillus plantarum*	●
	Serotonin regulation	*Klebsiella pneumoniae, Enterococcus faecalis, Lactiplantibacillus plantarum*	▼
Gut-skin axis			
	Skin protector	*Blautia wexlerae, Faecalibacterium prausnitzii, Parabacteroides distasonis*	▲▲
	Skin disruptor	*Enterococcus faecalis, Dorea formicigenerans, Escherichia coli*	▼
Gut-heart axis			
	Trimethylamine producer	*Klebsiella pneumoniae, Paraprevotella clara, Klebsiella michiganensis*	▼
	Trimethylamine consumer	*Citrobacter freundii*	●
Gut-kidney axis			
	IAA producer	*Klebsiella pneumoniae*	●
Gut-liver axis			
	Ethanol producer	*Dorea longicatena, Klebsiella pneumoniae, Enterocloster bolteae*	▲▲
Estrogen metabolism			
	Estrobolome former	*Faecalibacterium prausnitzii, Bacteroides ovatus, Roseburia intestinalis*	▼
	S-EQUOL producer	*Enterococcus faecalis, Bacteroides ovatus, Ruminococcus sp. SR1/5*	▼
	S-EQUOL consumer	*Bacteroides uniformis, Eggerthella lenta, Adlercreutzia equolifaciens*	▼
Vitamins			
	Vitamin B9 producer	*Lactiplantibacillus plantarum, Lactococcus lactis, Bifidobacterium animalis*	▲
	Vitamin B12 producer	*Lactiplantibacillus plantarum, Collinsella aerofaciens, Enterococcus faecium*	●
	Vitamin K2 producer	*Lactococcus lactis*	●
Intolerances			

Functional group	Top species	State
Wheat sensitivity	*Phocaeicola vulgatus, Faecalibacterium prausnitzii, Bacteroides uniformis*	
Lactose metabolizers (lactose tolerance)	*Lacticaseibacillus casei, Lactiplantibacillus plantarum, Lactococcus lactis*	

Probiotics

Lactobacillus

Microorganism	Relative abundance (%)	Result
Lacticaseibacillus casei	0.298%	▲▲▲
Lactiplantibacillus plantarum	0.251%	▲▲▲
Lacticaseibacillus paracasei	0.507%	●
Lactobacillus acidophilus	0.01%	▼▼▼
Lactobacillus reuteri	0%	▼▼▼
Lactobacillus gasseri	0%	▼▼▼
Lactobacillus fermentum	0%	▼▼▼
Lacticaseibacillus rhamnosus	0.013%	▼▼

Bifidobacterium spp

Microorganism	Relative abundance (%)	Result
Bifidobacterium longum	0.008%	●
Bifidobacterium animalis subsp. lactis	0.006%	●
Bifidobacterium longum subsp. infantis	0.001%	●
Bifidobacterium breve	0%	▼▼▼
Bifidobacterium bifidum	0%	▼▼▼
Bifidobacterium adolescentis	0%	▼▼▼

Other probiotic species

Microorganism	Relative abundance (%)	Result
Faecalibacterium prausnitzii	1.151%	●
Streptococcus thermophilus	0.026%	●
Clostridium butyricum	0.006%	▼▼▼

Microorganism	Relative abundance (%)	Result
Enterococcus durans	0%	▼▼▼
Akkermansia muciniphila	0%	▼▼▼
Saccharomyces boulardii	0%	▼▼▼
Bacillus subtilis	0%	▼▼▼
Pediococcus acidilactici	0%	▼▼▼
Leuconostoc mesenteroides	0%	▼▼▼
Christensenella minuta	0%	▼▼▼
Escherichia coli Nissle 1917	0%	▼▼▼
Enterococcus faecium	0.015%	▼▼
Heyndrickxia coagulans	0.004%	▼

Recommended prebiotic compounds

This section describes the **nutritional compounds or prebiotics** that are used by the microorganisms of each grup. This allows identifying **which substrates could improve the species in imbalance** according to the observed microbial composition.

Functionality	Nutritional component
Bifidobacterium spp	Chlorogenic acid
Dopamine producer	Levodopa
Estrobolome former	Lignans, Arabinoxylans
IPA producer	Tryptophan
Immunomodulatory	Fucose
Indole producer	Tryptophan
Lactobacillus spp	Fructooligosaccharides (FOS), Lactoferrin
Mucus regulator	Lactoferrin, Galactooligosaccharides (GOS), Fructooligosaccharides (FOS), Resistant starch
Quinolinic acid producer	Tryptophan
Serotonin regulation	Tryptophan
Trimethylamine producer	Phenylalanine, Tyrosine

Annex

Characteristics of metagenomic analysis

Long-read metagenomic analysis offers **greater precision, less bias, and better functional interpretation** than traditional methods (16S rRNA) and low-depth approaches (NGS). Below is a concise summary of the key advantages.

1. **Higher taxonomic resolution:** Identification at the species and **even strain** level. Avoids 16S biases (hypervariable regions, PCR, low discrimination). More precise than Shallow Shotgun (NGS), which is limited by its shallow depth and false positives and negatives.
2. **More reliable quantification:** Long-reads allow assigning complete reads to a single species. Reduction of artifacts and false positives. Integrated **AI** improves accuracy and consistency between samples.
3. **Detection of low-abundance species: High sensitivity** for minority microorganisms. Better ability to identify opportunists or key symbionts. 16S and Shallow Shotgun (NGS) usually lose signal at abundances <0.1%.
4. **Real functional analysis:** Direct identification of **genes and metabolic pathways** (SCFA, vitamins, bioactive metabolites, antibiotic resistance...). Provides a functional view based on real data, not inferences. 16S offers no functional information and Shallow Shotgun (NGS) only allows for partial estimates.
5. **Lower technical bias:** Does not depend on PCR, no primer or amplification biases. **Long reads** provide greater continuity and less fragmentation. Better uniformity and reproducibility.
6. **More robust results thanks to the application of AI:** Error correction and optimization of taxonomic assignment. Cross-validation and automated quality control. More coherent and clinically useful results.

Microbiota study techniques

Characteristic	Metagenomics (Long-Reads)	NGS (Shallow Shotgun)	16S rRNA
Taxonomic Resolution	Species/strain	Species (limited)	Genus
Quantification	Very precise	Moderate	Biased
Sensitivity	Very high	Medium	Low
Functional Information	Real genes	Partial	None
Technical Bias	Very low	Medium	High
Clinical Utility	Very high	Medium	Low

Taxonomic description

Lactobacillus *acidophilus* *W55*

género **especie** **cepa**

- **Genus:** *Lactobacillus* - A genus of lactic acid bacteria commonly found in the gastrointestinal and genitourinary tracts, as well as in fermented foods. Many species within this genus have probiotic properties and contribute to gut health.
- **Species:** *Lactobacillus acidophilus* - A species widely recognized for its beneficial effects on digestion, for balancing the intestinal microbiota, and for inhibiting pathogens through the production of lactic acid and bacteriocins.
- **Strain 1:** *Lactobacillus acidophilus W55* - A specific probiotic strain with immunomodulatory properties. It has been studied for its ability to strengthen the intestinal barrier, reduce inflammation, and support the treatment of allergic and inflammatory diseases.
- **Strain 2:** *Lactobacillus acidophilus ATCC 4356* - A reference strain primarily used in research.

Infection

	Microorganism	Relative abundance (%)	Result
Pathogens			
	Alistipes putredinis	3.280	▲▲
	Helicobacter pylori	0.011	▲▲
	Shigella flexneri	1.411	▲
	Acinetobacter baumannii	0.027	▲
	Salmonella enterica	0.996	●
	Klebsiella pneumoniae	0.563	●
	Fusobacterium mortiferum	0.528	●
	Enterocloster bolteae	0.239	●
	Bacteroides fragilis	0.193	●
	Enterocloster clostridioformis	0.130	●
	Staphylococcus aureus	0.108	●
	Clostridioides difficile	0.068	●
	Eggerthella lenta	0.059	●
	Clostridium perfringens	0.049	●
	[Clostridium] innocuum	0.048	●
	Stutzerimonas stutzeri	0.020	●
	Streptococcus vestibularis	0.015	●
	Borrelia miyamotoi	0.011	●
	Streptococcus agalactiae	0.010	●
	Streptococcus pneumoniae	0.010	●
	Haemophilus parainfluenzae	0.008	●
	Clostridium botulinum	0.008	●
	Enterobacter kobei	0.008	●
	Fusobacterium varium	0.005	●
Fungi			
	Fusarium oxysporum	0.011	●
	Aspergillus fumigatus	0.010	●
	Candida parapsilosis	0.009	●

	Microorganism	Relative abundance (%)	Result
	Candida albicans	0.005	●
	Rhizophagus irregularis	0.005	●
Viruses			
	Caudoviricetes sp.	11.031	▲▲▲
	Caudoviricetes sp.	11.031	▲▲▲
	uncultured human fecal virus	0.367	▲▲▲
	Bacteriophage sp.	3.215	▲
	Microviridae sp.	0.573	▲
	Crassvirales sp.	0.243	▲
	Inoviridae sp.	0.077	●
	Muvirus mu	0.037	●

Functional groups

	Microorganism	Relative abundance (%)	Result
Oral bacteria			
	Bacteroides heparinolyticus	0.008	▲▲
	Streptococcus salivarius	0.640	●
	Segatella copri	0.014	●
	Veillonella dispar	0.006	●
	Prevotella intermedia	0.005	●
	Streptococcus mitis	0.005	●
Intestinal barrier			
	Oscillospiraceae bacterium	3.826	▲▲▲
	Blautia obeum	1.394	▲
	Bacteroides thetaiotaomicron	1.014	●
	Coprococcus eutactus	0.017	●
	Klebsiella oxytoca	0.012	●
	Adlercreutzia equolifaciens	0.012	●
	Clostridium sporogenes	0.006	●
	Bifidobacterium dentium	0.022	▼▼▼
Proteolytic			
	Alistipes putredinis	3.280	▲▲
	Phocaeicola vulgatus	2.293	●
	Salmonella enterica	0.996	●
	Bacteroides caccae	0.596	●
	Alistipes shahii	0.578	●
	Klebsiella pneumoniae	0.563	●
	Enterococcus faecalis	0.426	●
	Alistipes communis	0.267	●
	Enterocloster bolteae	0.239	●
	Alistipes onderdonkii	0.166	●
	Enterocloster clostridioformis	0.130	●
	Alistipes sp. dk3624	0.127	●

	Microorganism	Relative abundance (%)	Result
	[Clostridium] scindens	0.084	●
	Clostridioides difficile	0.068	●
	Eggerthella lenta	0.059	●
	Alistipes finegoldii	0.052	●
	[Clostridium] innocuum	0.048	●
	Citrobacter freundii	0.030	●
	Lacrimispora saccharolytica	0.010	●
	Bifidobacterium longum	0.008	●
	Olsenella uli	0.008	●
	Fusobacterium varium	0.005	●
	Lacrimispora sphenoides	0.005	●
	Clostridium perfringens	0.049	▼▼▼
	Escherichia coli	0.105	▼▼
	Parabacteroides sp. CT06	0.036	▼▼
	Alistipes megaguti	0.008	▼▼
	Alistipes dispar	0.005	▼▼
Proinflammatory			
	Alistipes putredinis	3.280	▲▲
	Phocaeicola vulgatus	2.293	●
	Salmonella enterica	0.996	●
	Bacteroides caccae	0.596	●
	Klebsiella pneumoniae	0.563	●
	Alistipes communis	0.267	●
	Enterocloster bolteae	0.239	●
	Phocaeicola massiliensis	0.206	●
	Alistipes onderdonkii	0.166	●
	Enterocloster clostridioformis	0.130	●
	Alistipes sp. dk3624	0.127	●
	Staphylococcus aureus	0.108	●
	[Clostridium] scindens	0.084	●

	Microorganism	Relative abundance (%)	Result
	Clostridioides difficile	0.068	●
	Eggerthella lenta	0.059	●
	[Clostridium] innocuum	0.048	●
	Citrobacter freundii	0.030	●
	Segatella copri	0.014	●
	Lacrimispora saccharolytica	0.010	●
	Olsenella uli	0.008	●
	Enterobacter kobei	0.008	●
	Fusobacterium varium	0.005	●
	Lacrimispora sphenoides	0.005	●
	Clostridium perfringens	0.049	▼▼▼
	Streptococcus agalactiae	0.010	▼▼▼
	Escherichia coli	0.105	▼▼
	Parabacteroides sp. CT06	0.036	▼▼
	Alistipes megaguti	0.008	▼▼
	Alistipes dispar	0.005	▼▼
	Bacteroides ovatus	0.349	▼
	Bacteroides fragilis	0.193	▼
Lipopolysaccharides producer (LPS)			
	Shigella flexneri	1.411	▲
	Phocaeicola vulgatus	2.293	●
	Salmonella enterica	0.996	●
	Bacteroides caccae	0.596	●
	Klebsiella pneumoniae	0.563	●
	Alistipes communis	0.267	●
	Bacteroides xylanisolvens	0.257	●
	Alistipes onderdonkii	0.166	●
	Alistipes finegoldii	0.052	●
	Citrobacter freundii	0.030	●
	Segatella copri	0.014	●

	Microorganism	Relative abundance (%)	Result
	Escherichia coli	0.105	▼▼
	Alistipes megaguti	0.008	▼▼
	Alistipes dispar	0.005	▼▼
	Phocaeicola dorei	0.139	▼
	Bacteroides humanifaecis	0.071	▼
	Bacteroides uniformis	0.851	▼
	Bacteroides ovatus	0.349	▼
	Bacteroides cellulosilyticus	0.016	▼
Immunomodulatory			
	Blautia obeum	1.394	▲
	Bacteroides thetaiotaomicron	1.014	●
	Streptococcus salivarius	0.640	●
	Enterococcus faecalis	0.426	●
	Roseburia intestinalis	0.342	●
	Waltera intestinalis	0.100	●
	Eggerthella lenta	0.059	●
	Collinsella aerofaciens	0.043	●
	Bacteroides faecis	0.033	●
	Enterococcus cecorum	0.010	●
	Blautia producta	0.009	●
	Bifidobacterium longum	0.008	●
	Bifidobacterium dentium	0.022	▼▼▼
	Ligilactobacillus ruminis	0.007	▼▼▼
	Ruminococcus bicirculans (ex Wegman et al. 2014)	0.007	▼▼▼
	Lachnospira eligens	0.132	▼▼
	Blautia pseudococcoides	0.015	▼▼
	Enterococcus faecium	0.015	▼▼
	Parabacteroides distasonis	0.749	▼
	Blautia sp. SC05B48	0.147	▼
	Blautia argi	0.036	▼

	Microorganism	Relative abundance (%)	Result
	Roseburia hominis	0.124	▼
Mucus consumer			
	Dorea longicatena	1.069	▲▲
	[Ruminococcus] torques	3.159	▲
	Dysosmobacter welbionis	0.672	▲
	Phocaeicola vulgatus	2.293	●
	Bacteroides thetaiotaomicron	1.014	●
	Bacteroides caccae	0.596	●
	Mediterraneibacter gnavus	0.236	●
	Streptococcus thermophilus	0.026	●
	Clostridium perfringens	0.049	▼▼▼
	Bacteroides uniformis	0.851	▼
	Bacteroides fragilis	0.193	▼
	Pseudomonas aeruginosa	0.032	▼
	Bacteroides cellulosilyticus	0.016	▼
Mucus regulator			
	Faecalibacterium prausnitzii	1.151	●
	Bacteroides thetaiotaomicron	1.014	●
	Streptococcus thermophilus	0.026	●
	Bifidobacterium longum	0.008	●
	Bifidobacterium dentium	0.022	▼▼▼
Mucus stimulator			
	Anaerobutyricum hallii	0.819	▲▲▲
	Subdoligranulum variabile	0.020	▲
	Faecalibacterium prausnitzii	1.151	●
	Roseburia intestinalis	0.342	●
	Coprococcus comes	0.341	●
	Eubacterium ventriosum	0.285	●
	Butyricimonas virosa	0.205	●
	Anaerostipes hadrus	0.202	●

	Microorganism	Relative abundance (%)	Result
	Coprococcus catus	0.091	
	Roseburia inulinivorans	0.024	
	Coprococcus eutactus	0.017	
	Butyrivibrio fibrisolvens	0.016	
	Clostridium perfringens	0.049	
	Clostridium butyricum	0.006	
Butyrate producer			
	Agathobacter rectalis	18.520	
	Anaerobutyricum hallii	0.819	
	Blautia obeum	1.394	
	Subdoligranulum variabile	0.020	
	[Ruminococcus] torques	3.159	
	Dysosmobacter welbionis	0.672	
	Bacteroides eggerthii	1.748	
	Faecalibacterium prausnitzii	1.151	
	Alistipes shahii	0.578	
	Parabacteroides merdae	0.475	
	Odoribacter splanchnicus	0.345	
	Roseburia intestinalis	0.342	
	Coprococcus comes	0.341	
	Anaerotruncus colihominis	0.334	
	Eubacterium ventriosum	0.285	
	[Eubacterium] siraeum	0.221	
	Butyricimonas virosa	0.205	
	Anaerostipes hadrus	0.202	
	Coprococcus catus	0.091	
	[Ruminococcus] lactaris	0.059	
	Alistipes finegoldii	0.052	
	Lachnospiraceae bacterium Choco86	0.046	
	Collinsella aerofaciens	0.043	

Microorganism	Relative abundance (%)	Result
[Clostridium] symbiosum	0.041	
Roseburia inulinivorans	0.024	
Ruminococcus champanellensis	0.020	
Coprococcus eutactus	0.017	
Butyrivibrio fibrisolvens	0.016	
Butyrivibrio fibrisolvens	0.016	
Butyrivibrio proteoclasticus	0.009	
Butyrivibrio proteoclasticus	0.009	
Blautia producta	0.009	
Clostridium estertheticum	0.008	
Clostridium botulinum	0.008	
Anaerostipes caccae	0.006	
Fusobacterium varium	0.005	
Clostridium beijerinckii	0.005	
Clostridium perfringens	0.049	
Clostridium butyricum	0.006	
Oscillibacter sp. PEA192	0.156	
Lachnospira eligens	0.132	
Butyrivibrio hungatei	0.005	
Anaerostipes rhamnosivorans	0.005	
Coprococcus sp. ART55/1	0.028	
Lachnospiraceae bacterium GAM79	0.610	
Flavonifractor plautii	0.193	
Roseburia hominis	0.124	
Butyrivibrio crossotus	0.075	
Butyrivibrio crossotus	0.075	
butyrate-producing bacterium SS3/4	0.059	
Butyricimonas faecalis	0.020	
Intestinimonas butyriciproducens	0.017	
Butyricimonas faecihominis	0.010	

	Microorganism	Relative abundance (%)	Result
Butyrate consumer			
	Pseudomonas fluorescens	0.006	
	Pseudomonas aeruginosa	0.032	
	Pseudomonas aeruginosa	0.032	
Propionate producer			
	Phascolarctobacterium faecium	0.273	
	Bacteroides thetaiotaomicron	1.014	
	Parabacteroides merdae	0.475	
	Paraprevotella clara	0.180	
	Alistipes onderdonkii	0.166	
	Roseburia inulinivorans	0.024	
	Haemophilus parainfluenzae	0.008	
	Bacteroides finegoldii	0.335	
	Bacteroides cellulosilyticus	0.016	
Acetate producer			
	Blautia wexlerae	4.384	
	Oscillospiraceae bacterium	3.826	
	Enterocloster asparagiformis	0.045	
	Bacteroides thetaiotaomicron	1.014	
	Parabacteroides merdae	0.475	
	Paraprevotella clara	0.180	
	Alistipes onderdonkii	0.166	
	[Clostridium] scindens	0.084	
	Alistipes indistinctus	0.071	
	Ruminococcus champanellensis	0.020	
	Collinsella tanakaei	0.020	
	Paraprevotella xylaniphila	0.018	
	Bifidobacterium longum	0.008	
	Bifidobacterium dentium	0.022	
	Ruminococcus bicirculans (ex Wegman et al. 2014)	0.007	

	Microorganism	Relative abundance (%)	Result
	Lachnospira eligens	0.132	
	Phocaeicola dorei	0.139	
	Bacteroides cellulosilyticus	0.016	
	Blautia hydrogenotrophica	0.011	
Acetate consumer			
	Anaerobutyricum hallii	0.819	
	Faecalibacterium prausnitzii	1.151	
	Bacteroides thetaiotaomicron	1.014	
	Roseburia intestinalis	0.342	
	Ruminococcus bicirculans (ex Wegman et al. 2014)	0.007	
	Bacteroides finegoldii	0.335	
	Blautia hydrogenotrophica	0.011	
Hydrogen sulfide producer			
	Desulfovibrio piger	0.717	
	Salmonella enterica	0.996	
	Klebsiella pneumoniae	0.563	
	Staphylococcus aureus	0.108	
	Citrobacter freundii	0.030	
	Desulfovibrio desulfuricans	0.007	
	Veillonella dispar	0.006	
	Escherichia coli	0.105	
	Streptococcus anginosus	0.013	
	Pseudomonas aeruginosa	0.032	
	Nitratidesulfovibrio vulgaris	0.005	
Hydrogen producer			
	Dorea longicatena	1.069	
	Bacteroides eggerthii	1.748	
	Faecalibacterium prausnitzii	1.151	
	Bacteroides thetaiotaomicron	1.014	
	Bacteroides caccae	0.596	

	Microorganism	Relative abundance (%)	Result
	Bacteroides salyersiae	0.430	●
	Roseburia intestinalis	0.342	●
	Anaerostipes hadrus	0.202	●
	[Clostridium] scindens	0.084	●
	Collinsella aerofaciens	0.043	●
	Bacteroides nordii	0.037	●
	Bacteroides faecis	0.033	●
	Bacteroides helcogenes	0.018	●
	Bacteroides intestinalis	0.011	●
	Fusobacterium varium	0.005	●
	Clostridium perfringens	0.049	▼▼▼
	Clostridium butyricum	0.006	▼▼▼
	Escherichia coli	0.105	▼▼
	Bacteroides sp. A1C1	0.035	▼▼
	Parabacteroides distasonis	0.749	▼
	Bacteroides humanifaecis	0.071	▼
	Bacteroides caecimuris	0.008	▼
	Bacteroides uniformis	0.851	▼
	Bacteroides ovatus	0.349	▼
	Bacteroides finegoldii	0.335	▼
	Bacteroides fragilis	0.193	▼
	Bacteroides cellulosilyticus	0.016	▼
Succinate producers			
	Phocaeicola vulgatus	2.293	●
	Faecalibacterium prausnitzii	1.151	●
	Alistipes shahii	0.578	●
	Alistipes communis	0.267	●
	Paraprevotella clara	0.180	●
	Alistipes onderdonkii	0.166	●
	Alistipes sp. dk3624	0.127	●

	Microorganism	Relative abundance (%)	Result
	Alistipes sp. dk3624	0.127	
	Thomasclavelia ramosa	0.088	
	Alistipes indistinctus	0.071	
	Alistipes indistinctus	0.071	
	Alistipes finegoldii	0.052	
	Citrobacter freundii	0.030	
	Ruminococcus champanellensis	0.020	
	Paraprevotella xylaniphila	0.018	
	Alistipes megaguti	0.008	
	Alistipes dispar	0.005	
	Alistipes dispar	0.005	
	Parabacteroides distasonis	0.749	
	Parabacteroides distasonis	0.749	
	Bacteroides fragilis	0.193	
	Bacteroides cellulosilyticus	0.016	
Succinate consumers			
	Phascolarctobacterium faecium	0.273	
	Bacteroides thetaiotaomicron	1.014	
	Waltera intestinalis	0.100	
	Barnesiella viscericola	0.042	
Formate consumer			
	Clostridium estertheticum	0.008	
	Clostridium botulinum	0.008	
	Clostridium beijerinckii	0.005	
	Clostridium perfringens	0.049	
	Escherichia coli	0.105	
	Blautia hydrogenotrophica	0.011	
Lactate producer			
	Enterocloster asparagiformis	0.045	
	Bacteroides thetaiotaomicron	1.014	

	Microorganism	Relative abundance (%)	Result
	Collinsella tanakaei	0.020	
	Bifidobacterium longum	0.008	
	Ruthenibacterium lactatiformans	0.278	
Lactate consumer			
	Anaerobutyricum hallii	0.819	
	Anaerostipes hadrus	0.202	
	Waltera intestinalis	0.100	
	Veillonella dispar	0.006	
	Anaerostipes caccae	0.006	
	Anaerostipes rhamnosivorans	0.005	
Formate producer			
	Lactiplantibacillus plantarum	0.251	
	Bifidobacterium longum	0.008	
	Enterobacter kobei	0.008	
Histamine producer			
	Lacticaseibacillus casei	0.298	
	Klebsiella pneumoniae	0.563	
	Fusobacterium mortiferum	0.528	
	Lactococcus lactis	0.240	
	Enterobacter hormaechei	0.068	
	Morganella morganii	0.046	
	Fusobacterium varium	0.005	
	Clostridium perfringens	0.049	
	Escherichia coli	0.105	
Histamine consumer			
	Lacticaseibacillus casei	0.298	
	Lactiplantibacillus plantarum	0.251	
	Bifidobacterium animalis	0.239	
	Bacteroides thetaiotaomicron	1.014	
	Bifidobacterium longum	0.008	

	Microorganism	Relative abundance (%)	Result
	Lacticaseibacillus rhamnosus	0.013	▼▼
	Bacteroides fragilis	0.193	▼
Cadaverine producer			
	Klebsiella pneumoniae	0.563	●
	Escherichia fergusonii	0.004	●
	Escherichia coli	0.105	▼▼
Putrescine producer			
	Klebsiella pneumoniae	0.563	●
	Enterococcus faecalis	0.426	●
	Morganella morganii	0.046	●
	Escherichia fergusonii	0.004	●
	Escherichia coli	0.105	▼▼
Tyramine producer			
	Klebsiella pneumoniae	0.563	●
	Enterococcus faecalis	0.426	●
	Morganella morganii	0.046	●
	Enterococcus cecorum	0.010	●
	Enterococcus faecium	0.015	▼▼
Spermidine producer			
	Bacteroides thetaiotaomicron	1.014	●
	Fusobacterium varium	0.005	●
	Ruminococcus bicirculans (ex Wegman et al. 2014)	0.007	▼▼▼
	Escherichia coli	0.105	▼▼
	Bacteroides uniformis	0.851	▼
Lactobacillus spp			
	Lacticaseibacillus casei	0.298	▲▲▲
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Lacticaseibacillus paracasei	0.507	●
	Levilactobacillus brevis	0.035	▼▼▼
	Lactobacillus acidophilus	0.010	▼▼▼

	Microorganism	Relative abundance (%)	Result
	Ligilactobacillus ruminis	0.007	
	Ligilactobacillus ruminis	0.007	
	Lactobacillus reuteri	0.000	
	Lactobacillus gasseri	0.000	
	Lactobacillus fermentum	0.000	
	Lacticaseibacillus rhamnosus	0.013	
Bifidobacterium spp			
	Bifidobacterium animalis	0.239	
	Bifidobacterium longum	0.008	
	Bifidobacterium dentium	0.022	
	Bifidobacterium breve	0.000	
	Bifidobacterium bifidum	0.000	
	Bifidobacterium adolescentis	0.000	
Other probiotic species			
	Faecalibacterium prausnitzii	1.151	
	Streptococcus thermophilus	0.026	
	Clostridium butyricum	0.006	
	Enterococcus durans	0.000	
	Akkermansia muciniphila	0.000	
	Saccharomyces boulardii	0.000	
	Bacillus subtilis	0.000	
	Pediococcus acidilactici	0.000	
	Leuconostoc mesenteroides	0.000	
	Christensenella minuta	0.000	
	Escherichia coli Nissle 1917	0.000	
	Enterococcus faecium	0.015	
	Enterococcus faecium	0.015	
	Heyndrickxia coagulans	0.004	
Bile acid metabolizer			
	Lactiplantibacillus plantarum	0.251	

	Microorganism	Relative abundance (%)	Result
	Romboutsia ilealis	0.030	▲▲▲
	Blautia obeum	1.394	▲
	[Ruminococcus] torques	3.159	▲
	Phocaeicola vulgatus	2.293	●
	Bacteroides thetaiotaomicron	1.014	●
	Roseburia intestinalis	0.342	●
	Coprococcus comes	0.341	●
	Enterocloster bolteae	0.239	●
	Mediterraneibacter gnavus	0.236	●
	Enterocloster clostridioformis	0.130	●
	[Clostridium] scindens	0.084	●
	Eggerthella lenta	0.059	●
	Hungatella hathewayi	0.035	●
	Segatella copri	0.014	●
	Blautia producta	0.009	●
	Paraclostridium sordellii	0.006	●
	Blautia sp. SC05B48	0.147	▼
	Phocaeicola dorei	0.139	▼
	Blautia argi	0.036	▼
	Bacteroides uniformis	0.851	▼
	Bacteroides ovatus	0.349	▼
	Bacteroides fragilis	0.193	▼
	Roseburia hominis	0.124	▼
BCFA producers			
	Bacteroides heparinolyticus	0.008	▲▲
	Bacteroides eggerthii	1.748	●
	Bacteroides thetaiotaomicron	1.014	●
	Bacteroides caccae	0.596	●
	Bacteroides salyersiae	0.430	●
	Phocaeicola massiliensis	0.206	●

Microorganism	Relative abundance (%)	Result
[Clostridium] scindens	0.084	●
[Clostridium] scindens	0.084	●
[Clostridium] innocuum	0.048	●
[Clostridium] innocuum	0.048	●
[Clostridium] symbiosum	0.041	●
[Clostridium] symbiosum	0.041	●
Bacteroides nordii	0.037	●
Blautia coccoides	0.033	●
Bacteroides faecis	0.033	●
Bacillus cereus	0.022	●
Bacteroides helcogenes	0.018	●
Bacteroides intestinalis	0.011	●
[Clostridium] hylemonae	0.011	●
[Clostridium] hylemonae	0.011	●
Bacillus thuringiensis	0.010	●
Priestia megaterium	0.008	●
Clostridium estertheticum	0.008	●
Clostridium botulinum	0.008	●
Clostridium sporogenes	0.006	●
Clostridium beijerinckii	0.005	●
Clostridium beijerinckii	0.005	●
Clostridium perfringens	0.049	▼▼▼
Clostridium butyricum	0.006	▼▼▼
Bacteroides stercoris	0.393	▼▼
Escherichia coli	0.105	▼▼
Bacteroides sp. A1C1	0.035	▼▼
Parabacteroides distasonis	0.749	▼
Bacteroides humanifaecis	0.071	▼
Bacteroides caecimuris	0.008	▼
Heyndrickxia coagulans	0.004	▼

	Microorganism	Relative abundance (%)	Result
	Bacteroides uniformis	0.851	
	Bacteroides ovatus	0.349	
	Bacteroides finegoldii	0.335	
	Bacteroides fragilis	0.193	
	Bacteroides cellulosilyticus	0.016	
Ammonia producer			
	Helicobacter pylori	0.011	
	Acinetobacter baumannii	0.027	
	Phocaeicola vulgatus	2.293	
	Bacteroides thetaiotaomicron	1.014	
	Salmonella enterica	0.996	
	Klebsiella pneumoniae	0.563	
	Klebsiella pneumoniae	0.563	
	Phocaeicola massiliensis	0.206	
	Staphylococcus aureus	0.108	
	Thomasclavelia ramosa	0.088	
	Clostridioides difficile	0.068	
	Alistipes finegoldii	0.052	
	Morganella morganii	0.046	
	Citrobacter freundii	0.030	
	Bacillus cereus	0.022	
	Stutzerimonas stutzeri	0.020	
	Pseudomonas putida	0.017	
	Klebsiella oxytoca	0.012	
	Clostridium sporogenes	0.006	
	Pseudomonas fluorescens	0.006	
	Clostridium perfringens	0.049	
	Escherichia coli	0.105	
	Klebsiella michiganensis	0.027	
	Bacteroides fragilis	0.193	

	Microorganism	Relative abundance (%)	Result
	Pseudomonas aeruginosa	0.032	▼
p-Cresol producer			
	Klebsiella pneumoniae	0.563	●
	[Eubacterium] siraeum	0.221	●
	Clostridioides difficile	0.068	●
	Olsenella uli	0.008	●
	Blautia hydrogenotrophica	0.011	▼
Indole producer			
	Clostridiales bacterium	0.167	▲▲▲
	Oxalobacter formigenes	0.106	▲
	Bacteroides eggerthii	1.748	●
	Bacteroides thetaiotaomicron	1.014	●
	Alistipes shahii	0.578	●
	Bacteroides salyersiae	0.430	●
	Lachnospiraceae bacterium	0.303	●
	Alistipes communis	0.267	●
	Bacteroides xylanisolvens	0.257	●
	Alistipes onderdonkii	0.166	●
	Alistipes sp. dk3624	0.127	●
	Alistipes indistinctus	0.071	●
	Alistipes finegoldii	0.052	●
	Bacteroides intestinalis	0.011	●
	Clostridium sporogenes	0.006	●
	Prevotella intermedia	0.005	●
	Bacteroides stercoris	0.393	▼▼
	Escherichia coli	0.105	▼▼
	Alistipes megaguti	0.008	▼▼
	Alistipes dispar	0.005	▼▼
	Bacteroides uniformis	0.851	▼
	Bacteroides ovatus	0.349	▼

	Microorganism	Relative abundance (%)	Result
	Bacteroides cellulosilyticus	0.016	▼
IPA producer			
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Faecalibacterium prausnitzii	1.151	●
	[Clostridium] scindens	0.084	●
	[Clostridium] innocuum	0.048	●
	[Clostridium] innocuum	0.048	●
	[Clostridium] symbiosum	0.041	●
	[Clostridium] symbiosum	0.041	●
	Blautia coccoides	0.033	●
	[Clostridium] hylemonae	0.011	●
	[Clostridium] hylemonae	0.011	●
	Clostridium estertheticum	0.008	●
	Clostridium botulinum	0.008	●
	Clostridium sporogenes	0.006	●
	Clostridium beijerinckii	0.005	●
	Clostridium beijerinckii	0.005	●
	Clostridium perfringens	0.049	▼▼▼
	Clostridium butyricum	0.006	▼▼▼
Quinolinic acid producer			
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Bacteroides thetaiotaomicron	1.014	●
	Lachnospiraceae bacterium	0.303	●
	Lachnospiraceae bacterium	0.303	●
	Mediterraneibacter gnavus	0.236	●
	Staphylococcus aureus	0.108	●
	[Clostridium] scindens	0.084	●
	[Clostridium] innocuum	0.048	●
	[Clostridium] innocuum	0.048	●
	[Clostridium] symbiosum	0.041	●

	Microorganism	Relative abundance (%)	Result
	[Clostridium] symbiosum	0.041	
	Blautia coccoides	0.033	
	Bacillus cereus	0.022	
	Ruminococcus champanellensis	0.020	
	[Clostridium] hylemonae	0.011	
	[Clostridium] hylemonae	0.011	
	Streptococcus pneumoniae	0.010	
	Clostridium estertheticum	0.008	
	Clostridium botulinum	0.008	
	Clostridium sporogenes	0.006	
	Clostridium sporogenes	0.006	
	Clostridium sporogenes	0.006	
	Clostridium beijerinckii	0.005	
	Clostridium beijerinckii	0.005	
	Clostridium perfringens	0.049	
	Lactobacillus acidophilus	0.010	
	Clostridium butyricum	0.006	
	Escherichia coli	0.105	
Kynurerine synthesis regulation			
	Lactiplantibacillus plantarum	0.251	
	Lactococcus lactis	0.240	
	Pseudomonas fluorescens	0.006	
	Levilactobacillus brevis	0.035	
	Pseudomonas aeruginosa	0.032	
GABA producer			
	Lactiplantibacillus plantarum	0.251	
	Phocaeicola vulgatus	2.293	
	Bacteroides thetaiotaomicron	1.014	
	Bacteroides caccae	0.596	
	Lacticaseibacillus paracasei	0.507	

	Microorganism	Relative abundance (%)	Result
	Parabacteroides merdae	0.475	●
	Lactococcus lactis	0.240	●
	Alistipes indistinctus	0.071	●
	Alistipes finegoldii	0.052	●
	Streptococcus thermophilus	0.026	●
	Bifidobacterium longum	0.008	●
	Levilactobacillus brevis	0.035	▼▼▼
	Bifidobacterium dentium	0.022	▼▼▼
	Parabacteroides distasonis	0.749	▼
	Phocaeicola dorei	0.139	▼
	Bacteroides uniformis	0.851	▼
	Bacteroides ovatus	0.349	▼
	Bacteroides fragilis	0.193	▼
GABA consumer			
	Bacillus cereus	0.022	●
	Bacillus thuringiensis	0.010	●
	Priestia megaterium	0.008	●
	Heyndrickxia coagulans	0.004	▼
Acetylcholine producer			
	Lactiplantibacillus plantarum	0.251	▲▲▲
Dopamine producer			
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Lactococcus lactis	0.240	●
	Streptococcus thermophilus	0.026	●
	Levilactobacillus brevis	0.035	▼▼▼
	Enterococcus faecium	0.015	▼▼
	Serratia marcescens	0.006	▼▼
	Heyndrickxia coagulans	0.004	▼
Glutamate producer			
	Lactiplantibacillus plantarum	0.251	▲▲▲

	Microorganism	Relative abundance (%)	Result
	Shigella flexneri	1.411	▲
	Phocaeicola vulgatus	2.293	●
Serotonin regulation			
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Bifidobacterium animalis	0.239	▲
	Klebsiella pneumoniae	0.563	●
	Enterococcus faecalis	0.426	●
	Lactococcus lactis	0.240	●
	Streptococcus parasanguinis	0.143	●
	Streptococcus thermophilus	0.026	●
	Enterococcus cecorum	0.010	●
	Bifidobacterium longum	0.008	●
	Bifidobacterium longum	0.008	●
	Streptococcus suis	0.007	●
	Streptococcus mitis	0.005	●
	Streptococcus dysgalactiae	0.005	●
	Bifidobacterium dentium	0.022	▼▼▼
	Streptococcus agalactiae	0.010	▼▼▼
	Enterococcus faecium	0.015	▼▼
Skin protector			
	Blautia wexlerae	4.384	▲▲▲
	Faecalibacterium prausnitzii	1.151	●
	Roseburia intestinalis	0.342	●
	Paraprevotella clara	0.180	●
	Streptococcus thermophilus	0.026	●
	Bifidobacterium longum	0.008	●
	Lacticaseibacillus rhamnosus	0.013	▼▼
	Parabacteroides distasonis	0.749	▼
Skin disruptor			
	Helicobacter pylori	0.011	▲▲

	Microorganism	Relative abundance (%)	Result
	Enterococcus faecalis	0.426	●
	Dorea formicigenerans	0.133	●
	Clostridioides difficile	0.068	●
	Collinsella aerofaciens	0.043	●
	Escherichia coli	0.105	▼▼
Trimethylamine producer			
	Klebsiella pneumoniae	0.563	●
	Paraprevotella clara	0.180	●
	Paraprevotella xylaniphila	0.018	●
	Pseudomonas putida	0.017	●
	Streptococcus sanguinis	0.015	●
	Klebsiella oxytoca	0.012	●
	Clostridium botulinum	0.008	●
	Desulfovibrio desulfuricans	0.007	●
	Clostridium sporogenes	0.006	●
	Prevotella intermedia	0.005	●
	Lacrimispora sphenoides	0.005	●
	Serratia marcescens	0.006	▼▼
	Klebsiella michiganensis	0.027	▼
Trimethylamine consumer			
	Citrobacter freundii	0.030	●
IAA producer			
	Klebsiella pneumoniae	0.563	●
Ethanol producer			
	Dorea longicatena	1.069	▲▲
	Candida parapsilosis	0.009	▲▲
	Candida albicans	0.005	▲
	Klebsiella pneumoniae	0.563	●
	Enterocloster bolteae	0.239	●
	Mediterraneibacter gnavus	0.236	●

	Microorganism	Relative abundance (%)	Result
	[Clostridium] scindens	0.084	
	Collinsella aerofaciens	0.043	
	Lachnospira eligens	0.132	
	Escherichia coli	0.105	
Estrobolome former			
	Faecalibacterium prausnitzii	1.151	
	Roseburia intestinalis	0.342	
	Bacteroides xylanisolvens	0.257	
	Mediterraneibacter gnavus	0.236	
	Staphylococcus aureus	0.108	
	Lachnospira eligens	0.132	
	Bacteroides ovatus	0.349	
	Roseburia hominis	0.124	
S-EQUOL producer			
	Bifidobacterium animalis	0.239	
	Enterococcus faecalis	0.426	
	Ruminococcus sp. SR1/5	0.241	
	Eggerthella lenta	0.059	
	Lactococcus garvieae	0.016	
	Adlercreutzia equolifaciens	0.012	
	Blautia producta	0.009	
	Bifidobacterium longum	0.008	
	Enterococcus faecium	0.015	
	Enterococcus faecium	0.015	
	Bacteroides ovatus	0.349	
S-EQUOL consumer			
	Eggerthella lenta	0.059	
	Adlercreutzia equolifaciens	0.012	
	Bacteroides uniformis	0.851	
Vitamin B9 producer			

	Microorganism	Relative abundance (%)	Result
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Bifidobacterium animalis	0.239	▲
	Lactococcus lactis	0.240	●
	Streptococcus thermophilus	0.026	●
	Bifidobacterium longum	0.008	●
Vitamin B12 producer			
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Collinsella aerofaciens	0.043	●
	Priestia megaterium	0.008	●
	Enterococcus faecium	0.015	▼▼
Vitamin K2 producer			
	Lactococcus lactis	0.240	●
Wheat sensitivity			
	Phocaeicola vulgatus	2.293	●
	Faecalibacterium prausnitzii	1.151	●
	Staphylococcus aureus	0.108	●
	Streptococcus thermophilus	0.026	●
	Rothia mucilaginosa	0.018	●
	Bifidobacterium longum	0.008	●
	Bacteroides uniformis	0.851	▼
	Bacteroides fragilis	0.193	▼
	Pseudomonas aeruginosa	0.032	▼
Lactose metabolizers (lactose tolerance)			
	Lacticaseibacillus casei	0.298	▲▲▲
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Bifidobacterium animalis	0.239	▲
	Lactococcus lactis	0.240	●
	Streptococcus thermophilus	0.026	●
	Bifidobacterium longum	0.008	●
	Lactobacillus acidophilus	0.010	▼▼▼

Microorganism	Relative abundance (%)	Result
Lacticaseibacillus rhamnosus	0.013	

Full list of detected species

	Microorganism	Relative abundance (%)	Result
Bacteria			
	Agathobacter rectalis	18.520	▲▲▲
	Blautia wexlerae	4.384	▲▲▲
	Oscillospiraceae bacterium	3.826	▲▲▲
	Anaerobutyricum hallii	0.819	▲▲▲
	Desulfovibrio piger	0.717	▲▲▲
	Megamonas funiformis	0.367	▲▲▲
	Lacticaseibacillus casei	0.298	▲▲▲
	Collinsella stercoris	0.293	▲▲▲
	Phascolarctobacterium faecium	0.273	▲▲▲
	Lactiplantibacillus plantarum	0.251	▲▲▲
	Clostridiales bacterium	0.167	▲▲▲
	Enterocloster asparagiformis	0.045	▲▲▲
	Romboutsia ilealis	0.030	▲▲▲
	Alistipes putredinis	3.280	▲▲
	Dorea longicatena	1.069	▲▲
	Helicobacter pylori	0.011	▲▲
	Bacteroides heparinolyticus	0.008	▲▲
	Shigella flexneri	1.411	▲
	Blautia obeum	1.394	▲
	Bifidobacterium animalis	0.239	▲
	Acinetobacter baumannii	0.027	▲
	Subdoligranulum variabile	0.020	▲
	[Ruminococcus] torques	3.159	△
	Dysosmobacter welbionis	0.672	△
	Oxalobacter formigenes	0.106	△
	Phocaeicola vulgatus	2.293	●
	Bacteroides eggerthii	1.748	●
	Faecalibacterium prausnitzii	1.151	●

Microorganism	Relative abundance (%)	Result
Bacteroides thetaiotaomicron	1.014	
Salmonella enterica	0.996	
Streptococcus salivarius	0.640	
Bacteroides caccae	0.596	
Alistipes shahii	0.578	
Klebsiella pneumoniae	0.563	
Fusobacterium mortiferum	0.528	
Lacticaseibacillus paracasei	0.507	
Parabacteroides merdae	0.475	
Catenibacterium mitsuokai	0.446	
Bacteroides salyersiae	0.430	
Enterococcus faecalis	0.426	
Odoribacter splanchnicus	0.345	
Roseburia intestinalis	0.342	
Coprococcus comes	0.341	
Anaerotruncus colihominis	0.334	
Lachnospiraceae bacterium	0.303	
Eubacterium ventriosum	0.285	
Alistipes communis	0.267	
Bacteroides xylanisolvens	0.257	
Ruminococcus sp. SR1/5	0.241	
Lactococcus lactis	0.240	
Enterocloster bolteae	0.239	
Mediterraneibacter gnavus	0.236	
[Eubacterium] siraeum	0.221	
Phocaeicola massiliensis	0.206	
Butyricimonas virosa	0.205	
Anaerostipes hadrus	0.202	
Bacteroides fragilis	0.193	
Paraprevotella clara	0.180	

Microorganism	Relative abundance (%)	Result
Parabacteroides goldsteinii	0.171	
Schaalia odontolytica	0.170	
Alistipes onderdonkii	0.166	
Streptococcus parasanguinis	0.143	
Dorea formicigenerans	0.133	
Enterocloster clostridioformis	0.130	
Alistipes sp. dk3624	0.127	
Alistipes senegalensis	0.115	
Staphylococcus aureus	0.108	
Waltera intestinalis	0.100	
Coprococcus catus	0.091	
Thomasclavelia ramosa	0.088	
[Clostridium] scindens	0.084	
Faecalitalea cylindroides	0.079	
Alistipes indistinctus	0.071	
Megamonas hypermegale	0.069	
Enterobacter hormaechei	0.068	
Clostridioides difficile	0.068	
[Ruminococcus] lactaris	0.059	
Parabacteroides johnsonii	0.059	
Eggerthella lenta	0.059	
Alistipes finegoldii	0.052	
Gordonibacter pamelaeae	0.049	
Clostridium perfringens	0.049	
[Clostridium] innocuum	0.048	
Lawsonibacter asaccharolyticus	0.047	
Morganella morganii	0.046	
Lachnospiraceae bacterium Choco86	0.046	
Collinsella aerofaciens	0.043	
Barnesiella viscericola	0.042	

Microorganism	Relative abundance (%)	Result
[Clostridium] symbiosum	0.041	
Bacteroides nordii	0.037	
Hungatella hathewayi	0.035	
Blautia coccoides	0.033	
Bacteroides faecis	0.033	
Citrobacter freundii	0.030	
Streptococcus thermophilus	0.026	
Roseburia inulinivorans	0.024	
Bacillus cereus	0.022	
Ruminococcus champanellensis	0.020	
Collinsella tanakaei	0.020	
Marvinbryantia formatexigens	0.020	
Stutzerimonas stutzeri	0.020	
Bacteroides helcogenes	0.018	
Rothia mucilaginosa	0.018	
Paraprevotella xylaniphila	0.018	
Streptococcus oralis	0.017	
Coprococcus eutactus	0.017	
Pseudomonas putida	0.017	
Butyrivibrio fibrisolvens	0.016	
Lactococcus garvieae	0.016	
Streptococcus sanguinis	0.015	
Streptococcus vestibularis	0.015	
Segatella copri	0.014	
Intestinibacter bartlettii	0.014	
Gordonibacter urolithinfaciens	0.013	
Klebsiella oxytoca	0.012	
Adlercreutzia equolifaciens	0.012	
Streptococcus pasteurianus	0.011	
Bacteroides intestinalis	0.011	

Microorganism	Relative abundance (%)	Result
[Clostridium] hylemonae	0.011	
Borrelia miyamotoi	0.011	
Oscillibacter valericigenes	0.010	
Enterococcus cecorum	0.010	
Lacrimispora saccharolytica	0.010	
Bacillus thuringiensis	0.010	
Streptococcus agalactiae	0.010	
Streptococcus pneumoniae	0.010	
Butyrivibrio proteoclasticus	0.009	
Blautia producta	0.009	
Priestia megaterium	0.008	
Bifidobacterium longum	0.008	
Actinomyces graevenitzii	0.008	
Clostridium estertheticum	0.008	
Olsenella uli	0.008	
Staphylococcus pseudintermedius	0.008	
Haemophilus parainfluenzae	0.008	
Clostridium botulinum	0.008	
Enterobacter kobei	0.008	
Streptococcus suis	0.007	
Bradyrhizobium diazoefficiens	0.007	
Thomasclavelia spiroformis	0.007	
Desulfovibrio desulfuricans	0.007	
Clostridium sporogenes	0.006	
Mogibacterium diversum	0.006	
Paenibacillus polymyxa	0.006	
Paraclostridium sordellii	0.006	
Veillonella dispar	0.006	
Pseudomonas fluorescens	0.006	
Plesiomonas shigelloides	0.006	

Microorganism	Relative abundance (%)	Result
Kluyvera ascorbata	0.006	●
Actinomyces israelii	0.006	●
Phocaeicola salanitronis	0.006	●
Anaerostipes caccae	0.006	●
Slackia heliotrinireducens	0.006	●
Mammaliicoccus sciuri	0.005	●
Ralstonia pickettii	0.005	●
Prevotella intermedia	0.005	●
Erysipelothrix rhusiopathiae	0.005	●
Streptococcus mitis	0.005	●
Lacrimispora sphenoides	0.005	●
Clostridium beijerinckii	0.005	●
Granulicatella adiacens	0.005	●
Streptococcus dysgalactiae	0.005	●
Ethanoligenens harbinense	0.005	●
Fusobacterium varium	0.005	●
Escherichia fergusonii	0.004	●
Levilactobacillus brevis	0.035	▼▼▼
Bifidobacterium dentium	0.022	▼▼▼
Lactobacillus acidophilus	0.010	▼▼▼
Ligilactobacillus ruminis	0.007	▼▼▼
Ruminococcus bicirculans (ex Wegman et al. 2014)	0.007	▼▼▼
Clostridium butyricum	0.006	▼▼▼
Citrobacter braakii	0.005	▼▼▼
Bacteroides stercoris	0.393	▼▼
Oscillibacter sp. PEA192	0.156	▼▼
Lachnospira eligens	0.132	▼▼
Escherichia coli	0.105	▼▼
Parabacteroides sp. CT06	0.036	▼▼
Bacteroides sp. A1C1	0.035	▼▼

Microorganism	Relative abundance (%)	Result
Blautia pseudococcoides	0.015	▼▼
Enterococcus faecium	0.015	▼▼
Lacticaseibacillus rhamnosus	0.013	▼▼
Streptococcus anginosus	0.013	▼▼
Alistipes megaguti	0.008	▼▼
Serratia marcescens	0.006	▼▼
Actinomyces oris	0.006	▼▼
Butyrivibrio hungatei	0.005	▼▼
Anaerostipes rhamnosivorans	0.005	▼▼
Alistipes dispar	0.005	▼▼
Parabacteroides distasonis	0.749	▼
Blautia sp. SC05B48	0.147	▼
Phocaeicola dorei	0.139	▼
Simiaoa sunii	0.099	▼
Bacteroides humanifaecis	0.071	▼
Blautia argi	0.036	▼
Coprococcus sp. ART55/1	0.028	▼
Klebsiella michiganensis	0.027	▼
Bacteroides caecimuris	0.008	▼
Heyndrickxia coagulans	0.004	▼
Bacteroides uniformis	0.851	▼
Lachnospiraceae bacterium GAM79	0.610	▼
Bacteroides ovatus	0.349	▼
Bacteroides finegoldii	0.335	▼
Ruthenibacterium lactatiformans	0.278	▼
Flavonifractor plautii	0.193	▼
Roseburia hominis	0.124	▼
Butyrivibrio crossotus	0.075	▼
butyrate-producing bacterium SS3/4	0.059	▼
Pseudomonas aeruginosa	0.032	▼

Microorganism	Relative abundance (%)	Result
Butyricimonas faecalis	0.020	▼
Intestinimonas butyriciproducens	0.017	▼
Bacteroides cellulosilyticus	0.016	▼
Blautia hydrogenotrophica	0.011	▼
Butyricimonas faecihominis	0.010	▼
Variovorax paradoxus	0.006	▼
Nitratidesulfovibrio vulgaris	0.005	▼
Clostridiaceae bacterium Marseille-Q4149	2.650	●
Eisenbergiella porci	1.726	●
uncultured bacterium	0.995	●
Faecalibacterium taiwanense	0.915	●
Blautia sp. KLE_1732_HM_1032	0.627	●
Vescimonas coprocola	0.284	●
Cloacibacillus porcorum	0.268	●
Blautia luti	0.262	●
Vescimonas fastidiosa	0.229	●
Faecalimonas umbilicata	0.219	●
Streptomyces sp. NBC_01463	0.172	●
Clostridium sp. M62/1	0.135	●
Roseburia rectibacter	0.124	●
Escherichia sp. KS167_9B	0.121	●
Salmonella sp.	0.120	●
Alistipes ihumii	0.119	●
Faecalibacterium duncaniae	0.115	●
Bacteroides sp. PHL 2737	0.099	●
Catenibacterium sp. co_0103	0.093	●
Faecalibacterium sp. HTF-F	0.092	●
[Bacteroides] pectinophilus	0.086	●
Mycoplasmopsis bovis	0.083	●
Victivallales bacterium CCUG 44730	0.082	●

Microorganism	Relative abundance (%)	Result
Roseburia sp. 831b	0.080	
Oscillospiraceae bacterium NTUH-002-81	0.079	
Shigella boydii	0.060	
Erysipelotrichaceae bacterium GAM147	0.060	
Holdemania massiliensis	0.059	
Bacteroides sp. CACC 737	0.059	
bacterium	0.057	
uncultured Alphaproteobacteria bacterium	0.054	
Clostridia bacterium i40-0019-1A8	0.054	
Clostridiales bacterium CCNA10	0.054	
Faecalibacillus intestinalis	0.050	
Ruminococcus sp. FMBCY1	0.048	
Wujia chipingensis	0.047	
Streptococcus sp. FDAARGOS_192	0.047	
Faecalibacterium sp. I2-3-92	0.046	
Christensenellaceae bacterium	0.046	
Streptococcus sp. LPB0220	0.046	
Bacteroidales bacterium	0.045	
Streptococcus sp. S5	0.043	
uncultured Eubacteriales bacterium	0.043	
Blautia massiliensis (ex Durand et al. 2017)	0.041	
Escherichia albertii	0.039	
Roseburia sp. 499	0.035	
Bacteroides sp. DH3716P	0.034	
Coprococcus phoceensis	0.034	
Pusillibacter faecalis	0.034	
Flintibacter sp. KGMB00164	0.033	
Ruegeria sp. B32	0.032	
Lactococcus sp.	0.032	

Microorganism	Relative abundance (%)	Result
Streptomyces albidoflavus	0.032	
Lactococcus cremoris	0.032	
Lentisphaeria bacterium	0.030	
Enorma phocaeensis	0.030	
uncultured Coriobacteriaceae bacterium	0.030	
Ensifer adhaerens	0.030	
Faecalicatena sp. Marseille-Q4148	0.029	
Lachnospiraceae bacterium JLR.KK009	0.029	
Candidatus Brevundimonas colombiensis	0.029	
Raoultella ornithinolytica	0.029	
Pseudoflavonifractor gallinarum	0.028	
Dysosmobacter sp. Marseille-Q4140	0.028	
Collinsella ihumii	0.027	
Lachnospiraceae bacterium JLR.KK008	0.027	
Mediterraneibacter glycyrrhizinilyticus	0.027	
Candidatus Gemmiger excrementipullorum	0.027	
Bacteroides sp. HF-162	0.026	
Streptomyces sp. NBC_01136	0.024	
Candidatus Faecalibacterium intestinigallinarum	0.024	
Lachnospiraceae bacterium KM106-2	0.023	
Actinomadura sp. WMMA1423	0.022	
Amedibacterium intestinale	0.022	
Schaalia sp. HMT-172	0.021	
uncultured Bacteroidales bacterium	0.021	
Ruminococcus bovis	0.021	
Bacteroides sp. D2	0.020	
Escherichia marmotae	0.020	
Streptococcus sp. S1	0.020	
Streptococcus sp. ZB199	0.020	

Microorganism	Relative abundance (%)	Result
Opitutia bacterium KCR 482	0.019	
Ruegeria pomeroyi	0.019	
Buchnera aphidicola	0.019	
Citrobacter portucalensis	0.019	
Oscillibacter hominis	0.018	
Lachnoclostridium phocaeense	0.018	
Streptococcus sp. CP1998	0.018	
Intestinibacillus sp. NTUH-41-i26	0.017	
Alistipes sp. i18-0019-D1	0.017	
Methyloversatilis sp. RAC08	0.017	
Dehalococcoidia bacterium	0.016	
Claveliimonas bilis	0.016	
Butyricimonas paravirosa	0.016	
Microlunatus elymi	0.016	
Eubacterium sp. MSJ-33	0.016	
Streptococcus sp. FSL W7-1342	0.016	
Candidatus Limiplasma sp.	0.015	
Erysipelotrichaceae bacterium 66202529	0.015	
Pseudomonadales bacterium	0.015	
Bacillus velezensis	0.015	
Prolixibacteraceae bacterium	0.015	
[Eubacterium] hominis	0.015	
Streptococcus sp. FSL R7-0248	0.015	
Sellimonas intestinalis	0.015	
Clostridium sp. SY8519	0.014	
Bacteroides zhangwenhongii	0.014	
Duodenibacillus massiliensis	0.014	
Wolbachia pipientis	0.014	
Streptomyces sp. NBC_01310	0.013	
Ruminococcus sp.	0.013	

Microorganism	Relative abundance (%)	Result
Streptococcus australis	0.013	
Streptococcus lactarius	0.013	
Anaerotruncus sp.	0.013	
uncultured Oscillospiraceae bacterium	0.013	
Candidatus Scatomonas sp.	0.012	
Terriglobia bacterium	0.012	
Odoribacteraceae bacterium	0.012	
Barnesiella sp. An22	0.012	
butyrate-producing bacterium SM4/1	0.012	
Wansuia hejianensis	0.011	
Eubacterium callanderi	0.011	
Streptomyces sp. NBC_01283	0.011	
Collinsella sp. i05-0019-G5	0.011	
Klebsiella quasipneumoniae	0.011	
Coriobacteriaceae bacterium	0.011	
Oscillospiraceae bacterium D1	0.011	
Streptococcus ilei	0.011	
Novisyntrophococcus fermenticellae	0.010	
Bacteroides faecium	0.010	
Massilistercora timonensis	0.010	
Bacteroidaceae bacterium	0.010	
Longicatena caecimuris	0.010	
Qiania dongpingensis	0.009	
Lacrimispora xylanisolvens	0.009	
Alphaproteobacteria bacterium	0.009	
Vallitalea guaymasensis	0.009	
Citrobacter sp. RHBSTW-00667	0.009	
Agathobaculum sp. NTUH-O15-33	0.009	
Blautia parvula	0.009	
uncultured Clostridia bacterium	0.009	

Microorganism	Relative abundance (%)	Result
Lachnospiraceae bacterium KGMB03038	0.009	
Sorangium cellulosum	0.009	
Enterobacter asburiae	0.009	
Bacteroides luhongzhouii	0.009	
Vallitaleaceae bacterium	0.009	
Emergencia sp. JLR.KK010	0.009	
Lactonifactor longoviformis	0.008	
Verrucomicrobia bacterium S94	0.008	
Shewanella dokdonensis	0.008	
Lacrimispora xylanolytica	0.008	
Ruminococcus gauvreauii	0.008	
Bacteroides sp. M10	0.008	
Firmicutes bacterium ASF500	0.008	
Chordicoccus furentiruminis	0.008	
Candidatus Poribacteria bacterium	0.008	
Pseudomonas sp. GXZC	0.008	
Klebsiella variicola	0.008	
Alkaliphilus sp. B6464	0.008	
Blautia liquoris	0.008	
Sphingomonas sp. NIBR02145	0.008	
Anaerostipes sp. PC18	0.008	
Enterobacter roggenkampii	0.008	
Candidatus Cloacimonadales bacterium	0.007	
Peribacillus simplex	0.007	
Streptococcus sp. A12	0.007	
Parabacteroides sp. AD58	0.007	
Kineothrix sp. MB12-C1	0.007	
Blattabacterium cuenoti	0.007	
Desulfobacterales bacterium	0.007	
Solobacterium moorei	0.007	

Microorganism	Relative abundance (%)	Result
Nitrospirales bacterium	0.007	
Acinetobacter seifertii	0.007	
Bacteroidales bacterium SW299	0.007	
Caproiciproducens sp. CPB-2	0.007	
Candidatus Avichristensenella intestinipullorum	0.007	
Desulfovibrionaceae bacterium	0.007	
Tepidiformaceae bacterium	0.007	
Candidatus Gallibacteroides avistercoris	0.007	
Mordavella massiliensis	0.007	
Candidatus Aveggerthella excrementigallinarum	0.007	
Bartonella sp. WD16.2	0.007	
Pelagovum pacificum	0.007	
Bacteroides zoogleoformans	0.006	
Agathobaculum massiliense	0.006	
Victivallales bacterium	0.006	
Bacillus shivajii	0.006	
Ruminococcaceae bacterium BL-6	0.006	
Chloroflexota bacterium	0.006	
Allocoprobacillus halotolerans	0.006	
Christensenella massiliensis	0.006	
Kineothrix sp. IPX-CK	0.006	
Sphaerochaetaceae bacterium	0.006	
uncultured Atopobiaceae bacterium	0.006	
Tenericutes bacterium MO-XQ	0.006	
Lachnoclostridium phytofermentans	0.006	
Filimonas lacunae	0.006	
Candidatus Limicola stercorigallinarum	0.006	
Lachnospiraceae bacterium oral taxon 096	0.006	

Microorganism	Relative abundance (%)	Result
Anaerocolumna sp. AGMB13025	0.006	
Anaerocolumna sp. MB42-C2	0.006	
Planctomycetota bacterium	0.006	
Raoultibacter timonensis	0.006	
Parabacteroides faecis	0.006	
Hafnia paralvei	0.006	
Solibaculum mannosilyticum	0.006	
Pseudobutyrivibrio xylanivorans	0.006	
Spirochaetia bacterium	0.006	
Coprobacillaceae bacterium	0.006	
Anaerolineales bacterium	0.005	
Massilimicrobiota timonensis	0.005	
Kluyvera cryocrescens	0.005	
Neptunomonas concharum	0.005	
Bacteroides sp. MSB163	0.005	
Lacrimispora sp. BS-2	0.005	
Terrisporobacter petrolearius	0.005	
Romboutsia sp. CE17	0.005	
Janthinobacterium rivuli	0.005	
Olsenella sp. An293	0.005	
Vicinamibacterales bacterium	0.005	
Bradyrhizobium barranii	0.005	
Oceanotoga sp. DSM 15011	0.005	
Gammaproteobacteria bacterium	0.005	
Rhizobium leguminosarum	0.005	
Propionibacterium acidifaciens	0.005	
Staphylococcus gallinarum	0.005	
Deltaproteobacteria bacterium	0.005	
Sarcina sp. JB2	0.005	
Hafnia alvei	0.005	

	Microorganism	Relative abundance (%)	Result
	Gordonibacter massiliensis (ex Traore et al. 2017)	0.005	
	Anaeromicropila herbilytica	0.005	
	Lachnoanaerobaculum gingivalis	0.005	
	Streptococcus rubneri	0.005	
	Kluyvera sichuanensis	0.005	
	Emergencia timonensis	0.005	
	Lactobacillus jensenii	0.005	
	Anaerocolumna sp. AGMB13020	0.005	
	Coprobacillaceae bacterium CR2/5/TPMF4	0.005	
	Rhodothermales bacterium	0.005	
	Desulfurobacterium thermolithotrophum	0.005	
	Aeromonas sp. ASNIH3	0.005	
	Phycisphaerales bacterium	0.005	
	Thermodesulfobacteriota bacterium	0.005	
	Parolsenella massiliensis	0.005	
	Allobaculum sp. Allo2	0.005	
	Phocaeicola coprophilus	0.004	
	uncultured Dehalococcoidia bacterium	0.004	
	Anaerovoracaceae bacterium	0.004	
	Paludicola sp. MB14-C6	0.004	
	Leclercia adecarboxylata	0.004	
	Actinomyces pacaensis	0.004	
	Paenibacillus sp. FSL E2-0151	0.004	
Fungi			
	Fusarium oxysporum	0.011	
	Aspergillus fumigatus	0.010	
	Candida parapsilosis	0.009	
	Candida albicans	0.005	
	Rhizophagus irregularis	0.005	

	Microorganism	Relative abundance (%)	Result
	uncultured fungus	0.034	
	Gaeumannomyces tritici	0.010	
	Penicillium expansum	0.007	
	fungal sp.	0.007	
	Paecilomyces variotii	0.007	
	Fibroporia radiculosa	0.006	
	Drepanopeziza brunnea	0.005	
	Colletotrichum tamarilloi	0.005	
	Fusarium verticillioides	0.005	
	Penicillium citrinum	0.005	
	Penicillium soppii	0.004	
	Penicillium maclennaniae	0.004	
	Penicillium solitum	0.004	
Archaea			
	uncultured archaeon	0.006	
Viruses			
	Caudoviricetes sp.	11.031	
	uncultured human fecal virus	0.367	
	Bacteriophage sp.	3.215	
	Microviridae sp.	0.573	
	Crassvirales sp.	0.243	
	Inoviridae sp.	0.077	
	Muvirus mu	0.037	
	uncultured phage	0.072	
	Moumouvirus australiense	0.032	
	Siphoviridae sp. ct89Z21	0.023	
	Microvirus sp.	0.018	
	Myoviridae sp. ctm8X17	0.017	
	Siphoviridae sp. ctDmQ3	0.010	
	Oengusvirus oengus	0.007	

	Microorganism	Relative abundance (%)	Result
	Siphoviridae sp. ctoWO12	0.006	
	Siphoviridae sp. ctLKT1	0.006	
	Herelleviridae sp.	0.005	
Metazoa			
	Spirometra erinaceieuropaei	0.044	
	Dicrocoelium dendriticum	0.022	
	Caenorhabditis elegans	0.011	
	Strongyloides papillosus	0.008	
	Strongyloides ratti	0.007	
	Schistosoma haematobium	0.005	

Glossary

Pro-inflammatory: Main microorganisms associated with activation of the immune system and chronic intestinal inflammation. Their high abundance may contribute to the development of inflammatory and metabolic diseases.

Lipopolysaccharides producers (LPS): Main gram-negative bacteria that produce lipopolysaccharides, a molecule capable of inducing systemic inflammation and increasing intestinal permeability.

BCFA producers: Bacteria that generate branched-chain fatty acids (BCFAs) as a metabolic byproduct. BCFAs derive from protein metabolism and are linked to inflammatory processes when in excess.

Hydrogen sulfide producers: Microorganisms able to generate H₂S, a compound toxic at high concentrations that can damage the intestinal epithelium. In excess, they may promote dysbiosis and symptoms such as bloating, producing excessive foul-smelling gas (similar to “rotten egg”).

Hydrogen producers: Main microorganisms that produce hydrogen gas as a fermentative byproduct. In excess, they may promote dysbiosis and symptoms like bloating.

Indole producers: Bacteria that metabolize tryptophan into indoles, compounds that can have beneficial or harmful effects depending on context and concentration.

Quinolinic acid producers: Microorganisms that synthesize quinolinic acid, a neuroactive tryptophan-derived metabolite associated with neuroinflammation if it accumulates.

Tryptamine producers: Microorganisms that convert tryptophan into tryptamine, an intestinal neuromodulator that can influence motility, intestinal secretion, and immunomodulatory function.

Skin disruptors: Bacteria related to alterations in the skin barrier through metabolites they release and that are absorbed into the bloodstream.

Ethanol producers: Microorganisms capable of fermenting substrates to generate ethanol. Their overproduction has been linked to auto-brewery syndrome and liver damage.

Histamine producers: Microorganisms that generate histamine from amino acids, which can contribute to inflammation, allergies, and gastrointestinal dysfunctions.

Proteolytic bacteria: Bacteria that degrade proteins, producing metabolites such as ammonia, indoles, or phenols. Their elevated activity can be harmful to the intestinal mucosa, promoting inflammation and bacterial translocation.

Ammonia producers: Microorganisms that release ammonia as a byproduct of nitrogen metabolism. Its accumulation is toxic and can affect intestinal, mental, and physical function.

Oral bacteria: Microorganisms typically found in the oral cavity detected in the intestine. These bacteria usually do not survive passage through the stomach nor colonize the intestine, so their presence may indicate an imbalance in the gut microbial ecosystem.

Bile acid metabolizers: Bacteria that modify primary bile acids, affecting fat digestion and metabolic signaling.

Butyrate producers: Beneficial microorganisms that generate butyrate, a key short-chain fatty acid for intestinal health, anti-inflammatory and a nutrient for colonocytes. They are associated with most microbiota benefits in both the gut and the brain.

Mucus consumers: Bacteria that degrade intestinal mucus. While some are commensal, in excess they can compromise intestinal barrier integrity and promote permeability.

GABA producers: Microorganisms that produce gamma-aminobutyric acid, a neurotransmitter that can modulate the gut-brain axis and gastrointestinal motility. An imbalance may cause diarrhea or constipation.

Glutamate producers: Bacteria that synthesize glutamate, an excitatory neurotransmitter involved in neuronal and metabolic functions. An imbalance may cause diarrhea or constipation.

Succinate producers: Microorganisms that generate succinate, an intermediate metabolite that in excess can promote inflammation. It is a precursor to propionate (SCFA). Its impact depends on microbiota balance; if overproduced, it can become harmful.

Wheat sensitivity: Bacteria associated with wheat degradation that can exacerbate the immune response in gluten-sensitive individuals, inducing intestinal symptoms.

Mucus regulators: Microorganisms capable of both stimulating production and degrading mucin (the main component of intestinal mucus). In balance, they help maintain a healthy, functional mucus layer; in excess or deficiency, they can compromise the barrier.

Mucus stimulators: Bacteria that induce mucus production by goblet cells, contributing to pathogen defense, epithelial maintenance, and prevention of bacterial translocation.

Acetate consumers: Microorganisms that use acetate as a substrate, modulating the production of other beneficial fatty acids, as it is a precursor to butyrate.

IPA producers: Bacteria that synthesize indole-3-propionic acid, an anti-inflammatory and antioxidant metabolite with neuroprotective effects that promotes intestinal homeostasis.

Skin protectors: Bacteria that may have beneficial effects on the skin barrier via metabolites that enter the circulation.

Estrobolome formers: The estrobolome is the functional part of the gut microbiota capable of transforming conjugated (inactive) estrogens into free (active) forms that can recirculate. Its imbalance influences hormonal health.

Immunomodulators: Bacteria that interact with the immune system to promote tolerance and prevent excessive inflammatory reactions.

Acetate producers: Microorganisms that generate acetate, a short-chain fatty acid that nourishes intestinal cells, maintains barrier integrity, and modulates the immune system. It also participates in energy metabolism and appetite regulation.

S-Equol producers: Bacteria capable of converting isoflavones into S-equol, a compound with weak estrogenic activity that contributes to hormonal balance and may alleviate menopausal symptoms.

IAA producers: Microorganisms that produce indole-3-acetic acid, a signaling molecule in the gut-brain axis that can be transformed into indoxyl sulfate, which has toxic effects on the kidney.

p-Cresol producers: Bacteria that produce p-cresol, a toxic metabolite derived from bacterial protein metabolism that damages the intestinal mucosa and, if it accumulates, acts as a uremic toxin.

Trimethylamine producers: Microorganisms that metabolize choline and carnitine into trimethylamine, a precursor to TMAO, a compound linked to cardiovascular risk.

Propionate producers: Bacteria that synthesize propionate, a short-chain fatty acid with beneficial functions that contributes to appetite control, metabolic health, and immune function.

Succinate consumers: Microorganisms that metabolize succinate, helping to control its accumulation and inflammatory effects.

Histamine consumers: Bacteria that degrade histamine, contributing to the reduction of inflammatory processes and allergic reactions.

Lactate producers: Microorganisms that generate lactate, a short-chain fatty acid that can be beneficial if converted into butyrate or propionate by other bacteria. However, its excessive accumulation can lead to intestinal acidification, dysbiosis, and muscle fatigue.

Serotonin regulation: Bacteria involved in serotonin synthesis or modulation, affecting mood, intestinal motility, and appetite regulation.

Lactate consumers: Bacteria that use lactate produced by other species to generate beneficial metabolites such as butyrate or propionate, and to regulate its accumulation.

Lactose metabolizers (lactose tolerance): Bacteria capable of digesting lactose, facilitating its metabolism in intolerant individuals.

Vitamin B9 producers: Microorganisms capable of synthesizing folic acid, essential for DNA synthesis and cellular health.

Vitamin K2 producers: Bacteria that generate menaquinone (vitamin K2), important for blood coagulation and bone health.

Vitamin B12 producers: Bacteria that produce cobalamin, a key vitamin for the nervous system and red blood cell formation.

Methane producers: Archaeal microorganisms that generate methane during gut fermentation, associated with slow intestinal transit and accumulation of odorless gas.

Dopamine producers: Microorganisms that synthesize dopamine, a neurotransmitter involved in motivation, pleasure, and gut regulation.

Other probiotic species: Microorganisms with beneficial properties for gut health, either through metabolite production or competition with pathogens.

S-Equol consumers: Bacteria that degrade S-equol, modulating its concentration and hormonal effects.

Butyrate consumers: Bacteria that use butyrate as an energy source, which can reduce its local availability and prevent beneficial functions.

Kynurenine synthesis regulators: Microorganisms that modulate the tryptophan-to-kynurenine pathway, involved in neuroinflammation and mental health.

Acetylcholine producers: Bacteria that produce acetylcholine, a neurotransmitter involved in intestinal motility and neural communication.

GABA consumers: Microorganisms that degrade GABA, affecting its local availability and role in the gut-brain axis.

Bifidobacterium spp: A genus of beneficial bacteria widely studied for its probiotic capacity and anti-inflammatory effect.

Lactobacillus spp: A group of lactic acid bacteria known for their role in digestive and immune health and their use as probiotics.

Intestinal barrier: Microorganisms involved in maintaining epithelial integrity and protection against pathogens.

Trimethylamine consumers: Bacteria that degrade trimethylamine, helping to reduce TMAO formation and cardiovascular risk.

Formate producers: Group of microorganisms capable of producing formate (formic acid) as a metabolic end product, mainly through anaerobic fermentation of carbohydrates and amino acids, contributing to microbial energy metabolism and cross-feeding interactions.

Tyramine producers: Group of microorganisms able to produce tyramine, a biogenic amine derived from decarboxylation of tyrosine, with potential neuromodulatory, vascular and immunological effects at intestinal and systemic levels.

Cadaverine producers: Cadaverine, a biogenic amine generated by microbial decarboxylation of lysine, involved in the modulation of intestinal barrier function, inflammatory responses and host–microbe interactions.

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