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08-May-26

DoggyBIOME Clinical Gut Profile

Specimen type - Stool, Canine

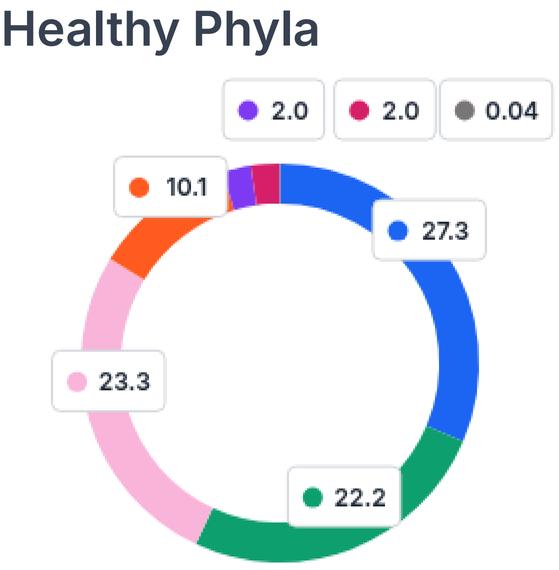
Collected
06-May-26 08:18am

KEY INSIGHTS SUMMARY

Dominant Microbiome Phyla

TEST	RESULT	H/L	REFERENCE	UNITS
● Actinobacteria Phylum	1.68		(0.01-4.00)	%
● Bacteroidetes Phylum	61.918	H	(10.000-60.000)	%
● Euryarchaeota Phylum	0.000		(<0.050)	%
● Firmicutes Phylum	31.322		(20.000-60.000)	%
● Fusobacteria Phylum	0.879	L	(1.000-30.000)	%
● Proteobacteria Phylum	4.200		(1.500-15.000)	%
● Verrucomicrobia Phylum	0.000		(<0.500)	%


Your Phyla


Healthy Phyla

KEY MICROBIAL INDICES

SERVICE	RESULT	H/L	REFERENCE	UNITS
Shannon Diversity Index	3.01	H	(2.00-3.00)	%
Firmicutes/Bacteroidetes ratio	0.51		(0.30-3.00)	ratio
Prevotella/Bacteroides ratio	0.01		(<1.00)	ratio

Parasites & Worms

No Parasites or Worms detected

Bacteria & Viruses

No Bacteria or Viruses detected

Mycology

Candida glabrata

Understanding the Canine Gut Microbiome

The canine gastrointestinal tract is home to a complex and dynamic ecosystem of microorganisms collectively referred to as the gut microbiome. This microbial community plays a critical role in digestion, nutrient absorption, immune regulation, metabolic function, and communication with the nervous system. In dogs, the health and balance of the gut microbiome are increasingly recognised as central to both gastrointestinal and systemic wellbeing.

A healthy gut microbiome is characterised by a diverse population of beneficial bacteria that support digestion, maintain the intestinal barrier, produce short-chain fatty acids, and regulate immune responses. These organisms help protect against pathogens, modulate inflammation, and contribute to overall resilience and vitality.

Conversely, an overrepresentation of potentially harmful or opportunistic bacteria, or a loss of beneficial microbial diversity, may contribute to digestive disturbances, food sensitivities, chronic inflammation, recurrent infections, and behavioural or metabolic changes. Importantly, disease does not arise from the presence of a single “bad” organism alone, but rather from imbalances within the microbial ecosystem as a whole.

Why Shotgun Metagenomic Sequencing Is Used:

This report is generated using shotgun metagenomic sequencing, an advanced genomic technology that analyses all microbial DNA present in the sample. Unlike targeted or culture-based methods, shotgun metagenomics does not rely on growing organisms in the laboratory or testing for a limited set of predefined species.

Clinical Interpretation:

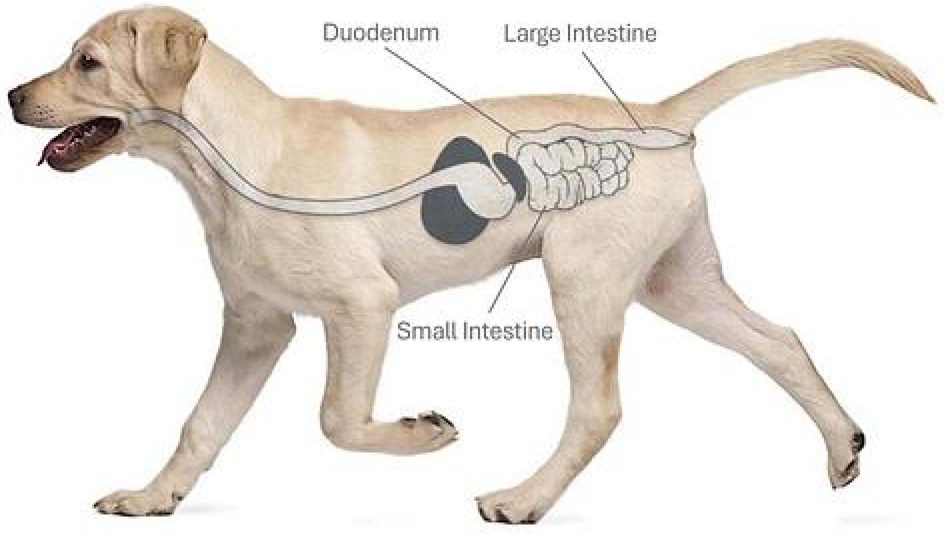
Results should be interpreted in the context of the dog’s clinical presentation, diet, environment, age, and medical history. The goal of this analysis is not simply to identify individual organisms, but to understand the overall balance, function, and resilience of the gut microbiome.

By identifying patterns of microbial health and imbalance, this report supports informed clinical decision-making and personalised strategies aimed at restoring and maintaining optimal gut function.

Duodenum
The absorption of vitamins, minerals and other nutrients starts in the duodenum, where *Firmicutes* are most abundant and play a key role in this process. Other important microorganisms found in the duodenum include *Cyanobacteria*, *Lactobacillus*, *Faecalibacterium* and *Ruminococcus*.

Large Intestine
Anaerobic bacteria dominate the large intestine, with *Firmicutes*, *Bacteroides* and *Fusobacteria* being the most prominent. The microorganisms residing in this part of the gut are highly effective at producing butyrate, a short-chain fatty acid known for it's protective role in maintaining gut health.

Small Intestine
The small intestine is predominantly inhabited by *Clostridia*, *Lactobacillales* and *Proteobacteria*. This part of the gastrointestinal tract is primarily responsible for the absorption of protein, fats, carbohydrates, trace elements, vitamins and water. When excessive bacterial growth occurs in the small intestine, it can lead to a condition known as Small Intestinal Bacterial Overgrowth (SIBO), which is characterised by symptoms such as diarrhoea, bloating and vomiting.



Microbiome Summary:

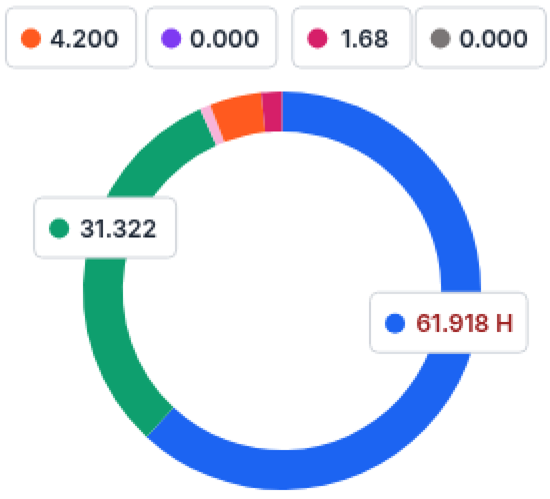
In this section, we present the microbiome phylum chart, illustrating the patient's sample in comparison with a reference healthy canine profile. This chart provides a high-level overview of the major bacterial groups present within the canine gastrointestinal tract. Bacterial phyla represent broad taxonomic categories that describe the overall structure, composition, and balance of the gut microbiome.

In healthy dogs, the gut microbiome is typically dominated by a small number of core phyla, most commonly Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, and Fusobacteria. Each of these phyla plays distinct and complementary roles in digestion, nutrient metabolism, immune modulation, and maintenance of the intestinal barrier.

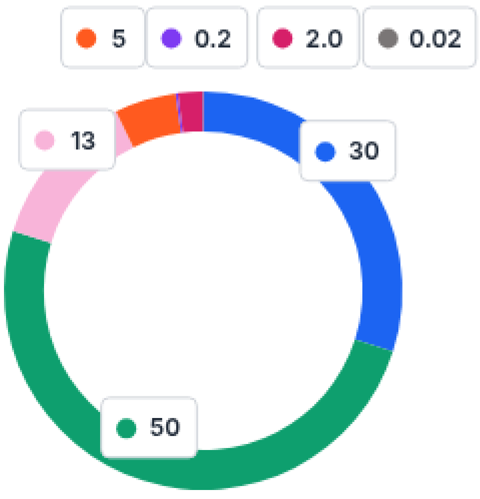
MICROBIOTA PHYLA

TEST	RESULT	H/L	REFERENCE	UNITS
● **Actinobacteria Phylum**	**1.68**		(0.01-4.00)	%
● **Bacteroidetes Phylum**	**61.918**	**H**	(10.000-60.000)	%
● **Euryarchaeota Phylum**	**0.000**		(<0.050)	%
● **Firmicutes Phylum**	**31.322**		(20.000-60.000)	%
● **Fusobacteria Phylum**	**0.879**	**L**	(1.000-30.000)	%
● **Proteobacteria Phylum**	**4.200**		(1.500-15.000)	%
● **Verrucomicrobia Phylum**	**0.000**		(<0.500)	%

Your Phyla



Healthy Phyla



The Shannon Diversity Index and Why It Matters

The Shannon diversity index is a quantitative measure of microbial diversity, capturing both:

Richness (how many different microbial species are present), and
Evenness (how evenly those species are distributed).

In canine gut health, microbial diversity is widely recognised as a marker of ecosystem resilience and stability. A higher Shannon index generally indicates a more diverse and balanced microbiome, which is associated with improved digestive function, immune regulation, and resistance to pathogenic overgrowth.

Conversely, a reduced Shannon diversity index suggests a loss of microbial diversity, which may occur following antibiotic exposure, dietary restriction, gastrointestinal inflammation, or chronic disease. Lower diversity does not diagnose disease on its own but may indicate reduced adaptive capacity of the gut microbiome.

GUT MICROBIAL DIVERSITY

TEST	RESULT	H/L	REFERENCE	UNITS
Shannon Diversity Index	3.01	H	(2.00-3.00)	%

Dysbiosis Index Ratio:

A healthy Firmicute/Bacteroidetes (F/B) ratio ranges between 0.2 and 0.5. A ratio below this range may indicate inflammation or inflammatory bowel disease (IBD), while a higher ratio suggests a possible infection.

DYSBIOSIS INDEX RATIO

TEST	RESULT	H/L	REFERENCE	UNITS
Firmicutes/Bacteroidetes ratio	0.51		(0.30-3.00)	ratio

ENTERIC & ZOONOTIC PATHOGENS

SERVICE	RESULT	H/L	REFERENCE	UNITS
🟠 **Campylobacter jejuni**	**<DL**		(<0.010)	%
🟠 **Campylobacter coli**	**<DL**		(<0.010)	%
🟠 **Campylobacter upsaliensis**	**0.014**		(<0.220)	%
🟢 **Clostridioides difficile**	**<DL**		(<0.100)	%
🟢 **Clostridium perfringens**	**0.205**		(<10.000)	%
🟠 **Salmonella enterica**	**<DL**		(<0.010)	%
🟠 **Yersinia enterocolitica**	**<DL**		(<0.010)	%

OPPORTUNISTIC/DYSBIOSIS-ASSOCIATED BACTERIA

SERVICE	RESULT	H/L	REFERENCE	UNITS
🟢 **Enterococcus faecalis**	**<DL**		(<0.490)	%
🟢 **Enterococcus faecium**	**<DL**		(<0.510)	%
🟢 **Enterococcus cecorum**	**<DL**		(<0.050)	%
🟠 **Escherichia coli**	**0.014**		(<7.500)	%
🟠 **Klebsiella pneumoniae**	**<DL**		(<0.010)	%
🟢 **Staphylococcus aureus**	**<DL**		(<0.010)	%
🟢 **Streptococcus species**	**<DL**		(<15.000)	%
🟢 **Peptoclostridium species**	**<DL**		(<20.000)	%
🟠 **Helicobacter species**	**0.092**		(<0.500)	%

GAS-ASSOCIATED BACTERIA

SERVICE	RESULT	H/L	REFERENCE	UNITS
⚪ **Methanobrevibacter smithii**	**<DL**		(<0.200)	%

INFLAMMATORY-ASSOCIATED BACTERIA

SERVICE	RESULT	H/L	REFERENCE	UNITS
🟠 **Sutterella species**	**0.910**		(<4.100)	%
🔵 **Absiella dolichum**	**0.009**		(<0.920)	%
🟠 **Desulfovibrio piger**	**0.071**		(<0.500)	%

● Actinobacteria Phylum 🔵 Bacteroidetes Phylum ⚫ Euryarchaeota Phylum ● Fusobacteria Phylum 🟢 Firmicutes Phylum 🟠 Proteobacteria Phylum 🟣 Verrucomicrobia Phylum

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CORE COMMENSAL & METABOLIC BACTERIA

SERVICE	RESULT	H/L	REFERENCE	UNITS
🔵 **Bacteroides fragilis**	**<DL**		(<15.000)	%
🔵 **Bacteroides thetaiotaomicron**	**<DL**		(<18.000)	%
🔵 **Bacteroides uniformis**	**0.110**		(<22.000)	%
🔵 **Phocaeicola vulgatus**	**17.100**		(<22.000)	%
🟢 **Blautia hansenii**	**2.390**		(0.050-3.000)	%
🟢 **Blautia obeum**	**<DL**		(<4.000)	%
🟢 **Blautia producta**	**<DL**		(<1.500)	%
🟢 **Blautia wexlerae**	**2.500**		(<4.500)	%
🟢 **Faecalibacterium prausnitzii**	**<DL**		(<5.000)	%
🩷 **Fusobacterium mortiferum**	**0.010**		(<22.000)	%
🩷 **Fusobacterium nucleatum**	**<DL**		(<20.000)	%
🩷 **Fusobacterium perfoetens**	**0.837**		(<22.000)	%
🩷 **Fusobacterium varium**	**<DL**		(<18.000)	%
🔵 **Prevotella copri**	**0.367**		(<5.000)	%
🟢 **Ruminococcus species**	**<DL**		(<4.000)	%
🔴 **Collinsella species**	**1.600**		(<5.000)	%
🟢 **Megamonas funiformis**	**3.320**		(<20.000)	%
🟢 **Romboutsia sedimentorum**	**0.002**		(<5.500)	%
🟢 **Allobaculum stercoricanis**	**0.053**		(<2.000)	%

BENEFICIAL & PROTECTIVE BACTERIA

SERVICE	RESULT	H/L	REFERENCE	UNITS
🟣 **Akkermansia muciniphila**	**<DL**	**L**	(0.250-3.000)	%
🔴 **Bifidobacterium adolescentis**	**<DL**		(<0.300)	%
🔴 **Bifidobacterium animalis**	**<DL**		(<1.000)	%
🔴 **Bifidobacterium longum**	**<DL**		(<1.000)	%
🔴 **Bifidobacterium pseudolongum**	**<DL**		(<2.000)	%
🟢 **Lactobacillus acidophilus**	**<DL**		(<1.000)	%
🟢 **Lactobacillus johnsonii**	**<DL**		(<1.500)	%
🟢 **Lactobacillus plantarum**	**<DL**		(<1.000)	%
🟢 **Lactobacillus reuteri**	**<DL**		(<1.000)	%
🟢 **Weissella cibaria**	**<DL**		(<0.010)	%

🔴 Actinobacteria Phylum 🔵 Bacteroidetes Phylum ⚫ Euryarchaeota Phylum 🩷 Fusobacteria Phylum 🟢 Firmicutes Phylum 🟠 Proteobacteria Phylum 🟣 Verrucomicrobia Phylum

FUNGAL SPECIES

SERVICE	RESULT	H/L	REFERENCE	UNITS
Candida albicans	**0.00**		(<1.00)	x10^5 CFU/g
Candida dubliniensis	**<DL**		(<1.00)	x10^5 CFU/g
Candida famata	**<DL**		(<1.00)	x10^5 CFU/g
Candida glabrata	**1.20**	**H**	(<1.00)	x10^5 CFU/g
Candida guilliermondii	**<DL**		(<1.00)	x10^5 CFU/g
Candida intermedia	**<DL**		(<1.00)	x10^5 CFU/g
Candida kefyr	**<DL**		(<1.00)	x10^5 CFU/g
Candida krusei	**<DL**		(<1.00)	x10^5 CFU/g
Candida lambica	**<DL**		(<1.00)	x10^5 CFU/g
Candida lipolytica	**<DL**		(<1.00)	x10^5 CFU/g
Candida lusitaniae	**<DL**		(<1.00)	x10^5 CFU/g
Candida parapsilosis	**<DL**		(<1.00)	x10^5 CFU/g
Candida tropicalis	**<DL**		(<1.00)	x10^5 CFU/g
Geotrichum species	**<DL**		(<1.00)	x10^5 CFU/g
Rhodotorula species	**<DL**		(<1.00)	x10^5 CFU/g
Saccharomyces cerevisiae	**<DL**		(<1.00)	x10^5 CFU/g

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PARASITES

TEST	RESULT	H/L		REFERENCE	UNITS
Blastocystis hominis	<DL			(<1.00)	x10^5 org/g
Cryptosporidium species	<DL			(<1.00)	x10^5 org/g
Cyclospora cayetanensis	<DL			(<1.00)	x10^5 org/g
Dientamoeba fragilis	<DL			(<1.00)	x10^5 org/g
Entamoeba histolytica	<DL			(<1.00)	x10^5 org/g
Enterocytozoon species	<DL			(<1.00)	x10^5 org/g
Giardia intestinalis	<DL			(<1.00)	x10^5 org/g

HELMINTHS/WORMS

TEST	RESULT
Ancylostoma species Hookworm	Not Detected
Ascaris species, Roundworm	Not Detected
Enterobius vermicularis, Pinworm	Not Detected
Hymenolepis spp, Tapeworm	Not Detected
Necator americanus, Hookworm	Not Detected
Strongyloides spp, Roundworm	Not Detected
Taenia species, Tapeworm	Not Detected
Trichuris trichiura, Whipworm	Not Detected

VIRUSES

TEST	RESULT
Adenovirus 40/41	Not Detected
Astrovirus (hAstro)	Not Detected
Norovirus GI/II	Not Detected
Rotavirus A	Not Detected
Sapovirus (I,II,IV,V)	Not Detected

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HEALTH RISKS

SERVICE	RESULT
Dermatological Immune Reactivity	Normal
Gastrointestinal Gas and Fermentation	Normal
Intestinal Inflammatory Activity	Normal
Metabolic Regulation	LOW

HEALTH RISKS

SERVICE	RESULT
Neurobehavioural Regulation	Normal
Oral Health	#N/A
SCFA Production	LOW

ANIMAL SYMPTOMS

Behavioural Changes

SERVICE	RESULT
Aggression	None
Depression	Playful
Restlessness/Anxiety	Normal

ANIMAL SYMPTOMS

Digestive Symptoms

SERVICE	RESULT
Constipation	No Response
Diarrhea	Occasional
Gas/Flatulence	Mild
Vomiting	None

GENERAL HEALTH SYMPTOMS

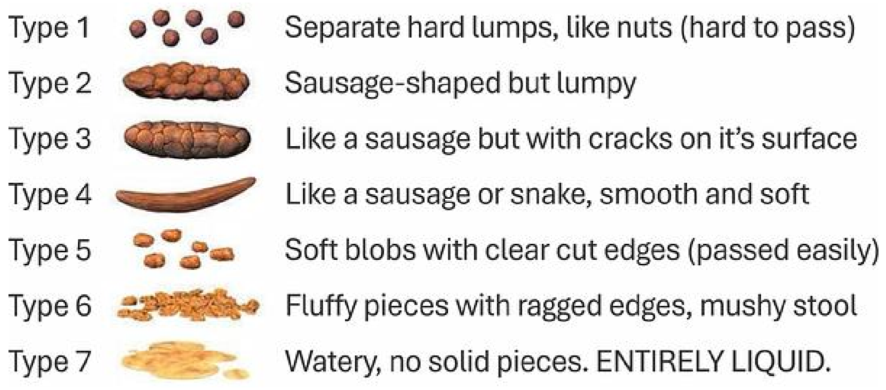
SERVICE	RESULT
Appetite	Normal
Bad Breath	NO
Dandruff	Absent
Energy Levels	Normal
Hair Loss/Shedding	Bald Patches

GENERAL HEALTH SYMPTOMS

SERVICE	RESULT
Mucous	PRESENT
Occult Blood	Absent
Skin Redness/Irritation	YES
Thirst Level	Normal
Weight Change	No Change

SPECIMEN APPEARANCE

TEST	BRISTOL TYPE
Stool Appearance	4



Type 1	Separate hard lumps, like nuts (hard to pass)
Type 2	Sausage-shaped but lumpy
Type 3	Like a sausage but with cracks on it's surface
Type 4	Like a sausage or snake, smooth and soft
Type 5	Soft blobs with clear cut edges (passed easily)
Type 6	Fluffy pieces with ragged edges, mushy stool
Type 7	Watery, no solid pieces. ENTIRELY LIQUID.

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Dominant Phyla Comment

Bacteroidetes–Elevated:

Elevated Bacteroidetes are commonly observed in dogs and often reflect dietary composition, particularly fibre and carbohydrate intake. This finding is generally not concerning unless accompanied by reduced diversity or clinical signs.

Microbiota Ratios Comment

Shannon Diversity–Elevated:

Higher Shannon Diversity is generally considered favourable and reflects a more stable and resilient gut microbiome.

Beneficial Bacteria Comment

Akkermansia muciniphila-Low:

Phylum: Verrucomicrobiota

Low levels of Akkermansia muciniphila suggest reduced support for the protective mucus layer that lines the gut. In dogs, this mucus layer is essential for maintaining a strong intestinal barrier and preventing irritation from food particles, bacteria, and toxins. Reduced levels may be seen in dogs with chronic digestive upset, loose stools, inflammatory bowel conditions, or following antibiotic use. This finding can indicate a gut environment that is more vulnerable to inflammation and increased intestinal permeability (“leaky gut”).

Mycology Comment

Candida glabrata–Elevated:

Kingdom: Fungi (Ascomycota)

Candida glabrata is a yeast that may be detected at low levels in the canine gut. Elevated abundance may be associated with reduced bacterial competition, particularly following antibiotic exposure or during periods of intestinal stress.

Diet considerations:

Dietary strategies may focus on supporting bacterial diversity and limiting excessive simple carbohydrate intake to reduce competitive advantage for yeast organisms.

DISCLAIMER:

The following health risk insights are derived from shotgun metagenomic sequencing, which evaluates the relative abundance and functional potential of microbial genes present in the canine gut microbiome. These findings reflect microbial patterns and metabolic capacity, not direct measurement of host physiology, immune activity, or clinical disease. Results should be interpreted alongside clinical history, physical examination findings, and other diagnostic tests. This test is not intended to diagnose disease but to provide supportive insight into gut-related functional tendencies.

Health Risks Comment

Mucous – Detected:

The presence of mucous in canine stool suggests increased mucus secretion by the intestinal lining, which may occur in response to irritation, inflammation, or altered gut motility. Mucous is produced as a protective mechanism to lubricate and protect the intestinal mucosa; however, increased or visible mucous may be associated with colonic irritation, dietary sensitivity, stress-related gastrointestinal changes, or microbial imbalance.

This finding is non-specific and does not, on its own, diagnose intestinal disease. Interpretation should be made in conjunction with stool consistency, frequency, clinical signs (such as straining, urgency, or discomfort), and veterinary assessment.

Short-Chain Fatty Acid (SCFA) Production – Low

(Butyrate-focused interpretation)

Low SCFA production potential, particularly involving butyrate-producing pathways, suggests reduced microbial capacity to generate butyrate, a key short-chain fatty acid that serves as a primary energy source for colonic epithelial cells in dogs. Adequate butyrate production is essential for maintaining intestinal barrier integrity, supporting mucosal healing, and regulating local immune activity within the gut. Reduced butyrate-related activity may be associated with a gut environment that is less supportive of anti-inflammatory balance and mucosal resilience, potentially increasing susceptibility to gastrointestinal sensitivity or inflammation.

Methodology

Microscopy, Metagenomic Next Generation Sequencing (mNGS), Quantitative PCR (qPCR), Polymerase Chain Reaction (PCR)