



# Microbiome Report

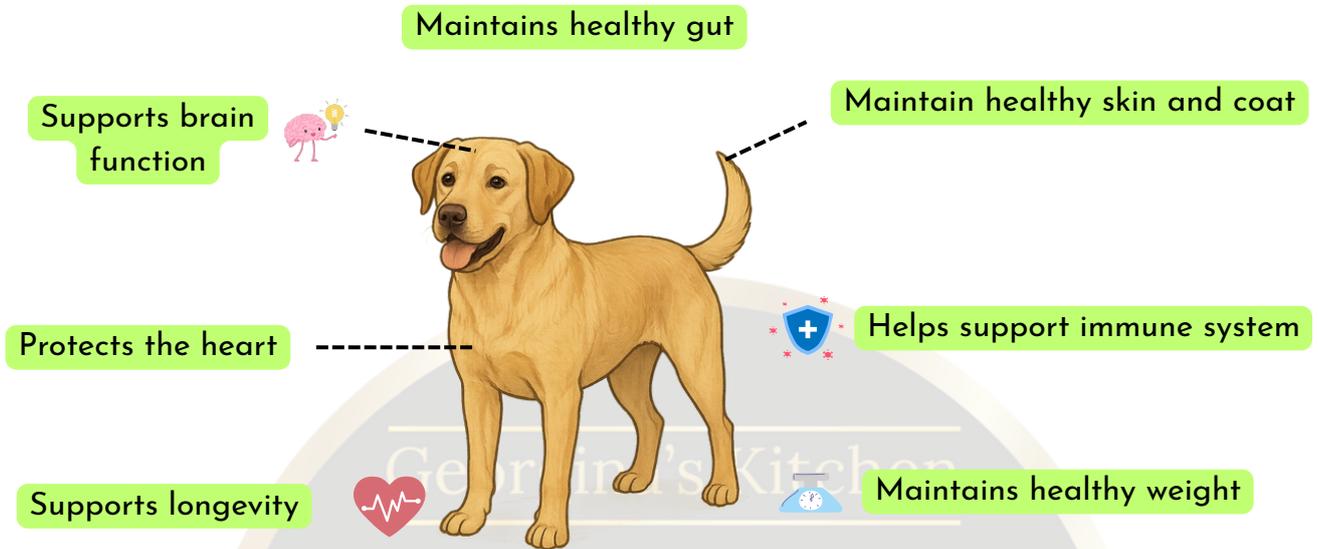


## The Best Care for Your Pet

**Sample Date:**  
**Dog's Name:** Jane  
**Breed & Age:**  
**Owner's Name:**

# Introduction

## Benefits of a Balanced Gut Microbiome



### What is the gut microbiome?

The gut microbiome is the community of bacteria, fungi, and other microbes that live in your pet's digestive tract and are essential for good health. We characterize the gut microbiome by analyzing a fecal sample because this is a non-invasive approach for gaining insights into what is going on inside of the gut.

### Where do these microbes come from and what supports them?

The gut microbiome develops at birth, specifically when the pet is passed through the vaginal canal of its mother and either inhales or ingests her natural microbes. From there, the gut microbiome develops through introduction to the environment, littermates, and the humans in the household.

A pet's diet plays a key role in maintaining the environment for the development of the gut microbiome. While diet cannot replace missing microbes within an imbalanced gut, it can provide the proper balance of protein, carbohydrates, and fiber for the native microbes of the gut to flourish and thrive.

### What are the symptoms of a gut microbiome imbalance?

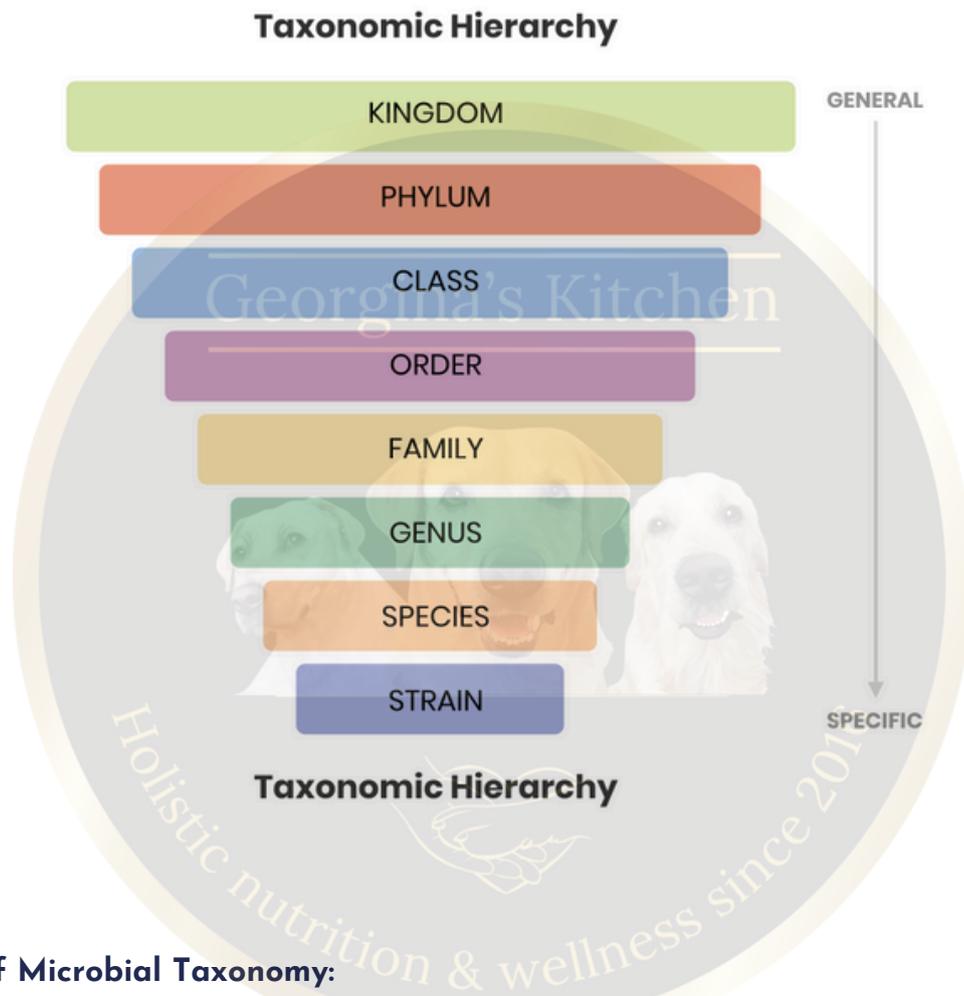
Many clients are surprised to find that the symptoms their pets are experiencing are often caused by an imbalance in the gut microbiome. Health issues like diarrhea, vomiting, constipation, itchy skin, and even bad breath can be a sign of an imbalance in your patient's gut microbiome.

A gut microbiome is imbalanced when it is missing beneficial bacteria, has too many harmful bacteria, or does not have enough diversity in the types of bacteria. When your patient's gut is out of balance, some of the gut's important functions don't work as well. Factors like disease, age, diet, and medications – especially antibiotics – can contribute to the development of imbalances in your patient's gut.

# Microbial Taxonomy

## Taxonomy

Taxonomy is the science of classifying organisms into groups based on shared characteristics or evolutionary relatedness. All microbes, including bacteria, archaea, and fungi, are classified using taxonomic classifications.



## Ranks or Levels of Microbial Taxonomy:

Taxonomic classification is a hierarchical system where organisms are grouped into ranks of decreasing similarity. Closely related organisms are clustered at lower ranks, while broader categories group together more distantly related microbes.

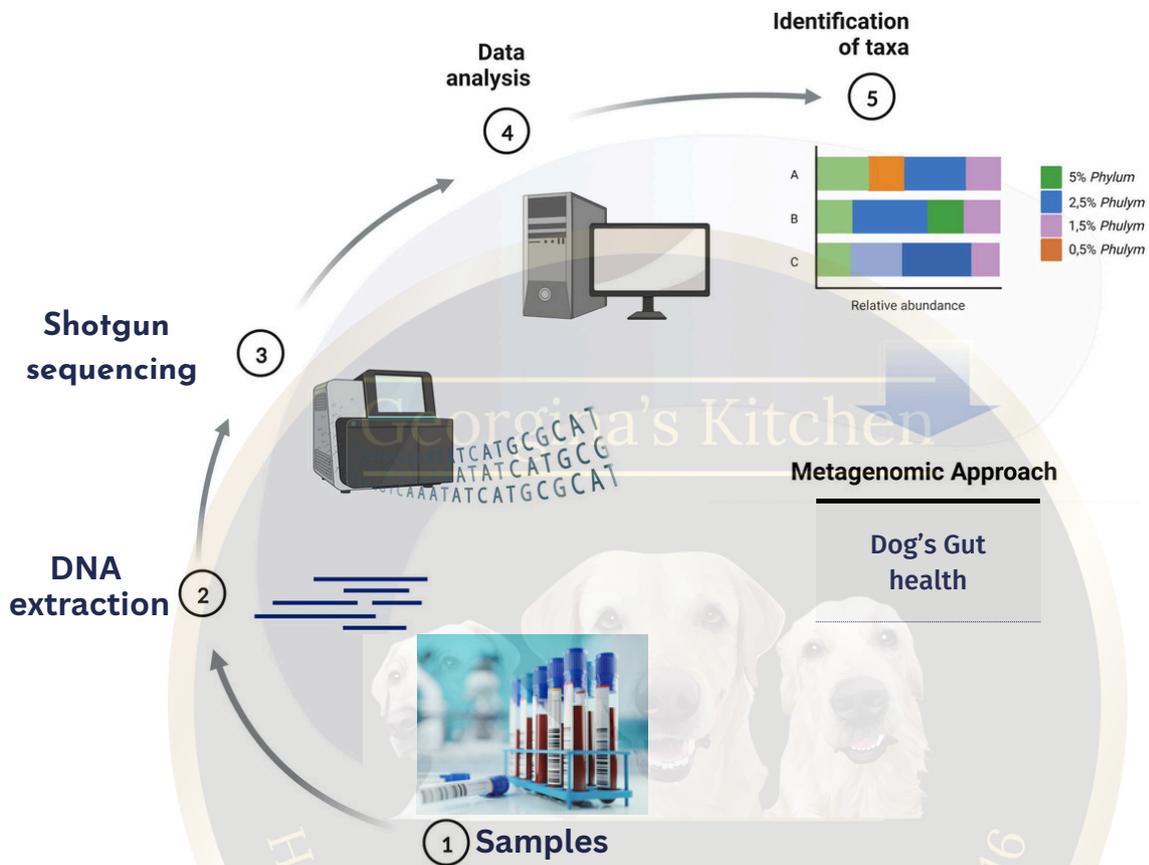
In microbial taxonomy, the most commonly used ranks in ascending order are strain, species, genus, family, order, class, phylum, and domain.

Species is the basic taxonomic unit in microbial classification. Groups of species are collected into genera (singular: genus), genera into families, families into orders, orders into classes, classes into phyla (singular: phylum), and phyla into domains—the highest taxonomic rank.

Different microbial groups (bacteria, archaea, and fungi) may have unique naming conventions at each rank, often reflected in their suffixes.

# What we do once we get your sample?

## Shotgun Metagenomics Sequencing



### Taxonomic Resolution

Shotgun metagenomics sequencing allows for the identification of bacterial taxonomy at the highest resolution possible – at the strain level. In contrast, 16S rRNA sequencing generally provides a much lower resolution, typically only reaching the genus level.

This distinction is important because species, and even strains within the same genus, can vary greatly in their metabolic capabilities and pathogenicity (the ability to cause disease).

Unlike shotgun metagenomics, which enables the detection of all DNA in a sample (including bacteria, viruses, fungi, and other microorganisms), 16S rRNA sequencing is limited to bacteria and archaea only, as the 16S gene is absent in viruses and fungi.

### Functional Profiling

Whole genome shotgun sequencing enables accurate characterization of the metabolic capabilities of a microbial community, as it captures the complete gene content present in the sample.

In contrast, 16S rRNA sequencing cannot provide this information, as it sequences only a small region of a single gene (16S rRNA). When functional profiles are generated from 16S data, they rely on predictive models based on publicly available genomes, not on the actual genes found in the sample.

Therefore, functional profiling based on 16S data can be highly inaccurate and should be interpreted cautiously.

# Summary Report

Jane - Raw dysbiosis score



Georgina's Kitchen

## Probiotics - The Good Microbes

- *Faecalibacterium prausnitzii* (0.0097%)
- *Enterococcus faecium* (0.0060%)
- *Lactobacillus johnsonii* (0.0015%)
- *Bifidobacterium breve* (0.0007%)
- *Bifidobacterium longum* (0.0005%)
- *Akkermansia muciniphila* (0.0003%)
- *Lactobacillus acidophilus* (0.00009%)
- *Bifidobacterium animalis* (0.00007%)

## Pathogen - The Bad Microbes

- |  |  |
|--|--|
| • <i>Clostridium perfringens</i> (0.5192%)         | • <i>Klebsiella pneumoniae</i> (0.0008%)   |
| • <i>Escherichia coli</i> (0.0227%)                | • <i>Bacillus cereus</i> (0.0007%)         |
| • <i>Clostridium botulinum</i> (0.0059%)           | • <i>Salmonella enterica</i> (0.0004%)     |
| • <i>Campylobacter jejuni</i> (0.0045%)            | • <i>Pseudomonas aeruginosa</i> (0.0003%)  |
| • <i>Staphylococcus aureus</i> (0.0028%)           | • <i>Yersinia enterocolitica</i> (0.0003%) |
| • <i>Staphylococcus pseudintermedius</i> (0.0010%) | • <i>Proteus mirabilis</i> (0.0002%)       |
| • <i>Helicobacter pylori</i> (0.0009%)             |  |

"Several potential gut pathogens have been detected, including *Clostridium perfringens*, *E. coli*, *Campylobacter jejuni*, and *Helicobacter* spp. While some are normal gut inhabitants, elevated levels or specific pathogenic strains could be associated with gastrointestinal symptoms. Please correlate clinically, and consult a veterinarian if any signs of illness are present."

# Detailed Report

## Kingdom Distribution

Microbial Group	Range	Your Sample Value
Bacteria	90-99%	98.82
Eukaryota	0.1-3%	0.068 
Archaea	0.1-2%	0.003 
Viruses	0.1-5%	0.2



# Detailed Microbial Composition

## 1. Bacteria (98.82%)

Bacteria constitute the majority of the microbial population, accounting for 98.82% of the total microbiome. These microorganisms play crucial roles in maintaining gut health, aiding in digestion, synthesizing essential vitamins, and regulating immune functions. The bacterial community consists of various phyla, including:

- Firmicutes: Beneficial for gut health and metabolism.
- Bacteroidetes: Essential for breaking down complex carbohydrates.
- Proteobacteria: Some members are opportunistic pathogens.
- Actinobacteria: Includes probiotics like Bifidobacterium that support gut balance.

Bacteria contribute to both probiotic and pathogenic effects. While beneficial bacteria like Lactobacillus and Bifidobacterium help maintain a healthy gut, harmful species such as Escherichia coli and Clostridium difficile can cause infections if they proliferate excessively.

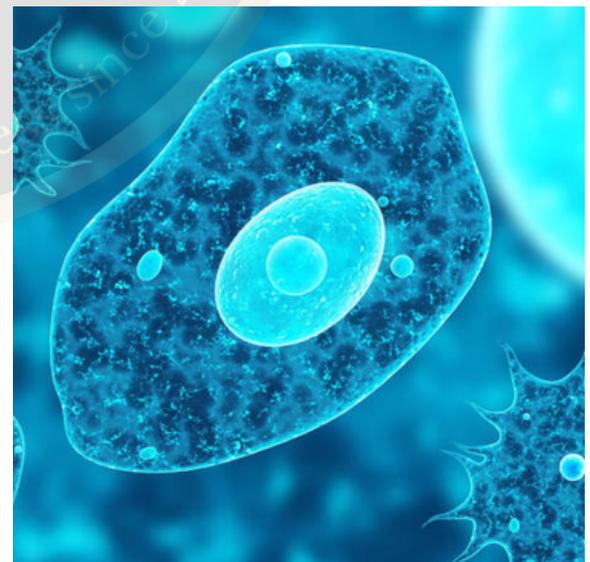


## 2. Eukaryota (0.068%)

Eukaryotic microorganisms represent 0.068% of the total microbiome. This group includes fungi, protozoa, and other complex microorganisms. Some key eukaryotic members include:

- Fungi: Such as Candida species, which can be part of the normal flora but may overgrow in cases of imbalance, leading to infections.
- Protozoa: Includes single-celled eukaryotic organisms, some of which can be pathogenic (Giardia, Cryptosporidium).
- Yeasts: While some are beneficial, certain species may contribute to dysbiosis if not regulated properly.

Eukaryotic microbes often interact with bacterial communities and can influence gut health, immune response, and disease susceptibility.



### 3. Archaea (0.003%)

Archaea are a lesser-known group of microorganisms, making up 0.003% of the microbiome. Unlike bacteria, archaea have distinct biochemical properties and often thrive in extreme environments. Within the microbiome, methanogenic archaea, such as *Methanobrevibacter smithii*, play a role in:

- Methane production during digestion.
- Regulation of gut fermentation processes.
- Interaction with bacteria to maintain microbial homeostasis.

Although archaea are generally considered non-pathogenic, their overabundance has been linked to conditions such as constipation and irritable bowel syndrome (IBS).

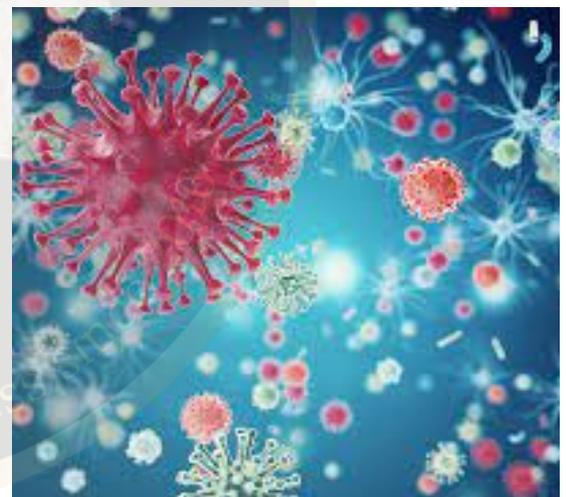


### 4. Viruses (0.2%)

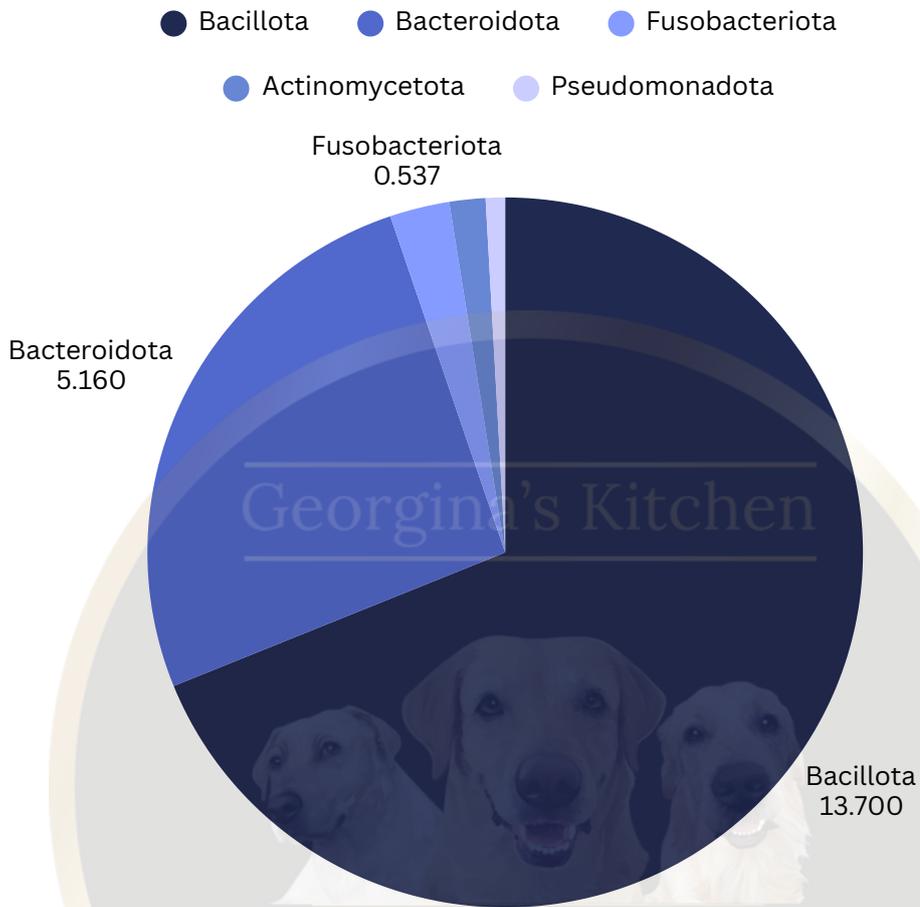
Viruses account for 0.2% of the microbiome and primarily include bacteriophages—viruses that infect bacteria. Their role in microbial ecosystems includes:

- Regulation of bacterial populations by infecting and lysing specific bacterial strains.
- Influencing gut microbiome dynamics by transferring genetic material between bacterial species (horizontal gene transfer).
- Potential therapeutic applications, as some bacteriophages can be used to target antibiotic-resistant bacteria.

Certain human-associated viruses, such as adenoviruses and enteroviruses, may also be present in low abundances. While many viruses in the microbiome are harmless or beneficial, the presence of pathogenic viruses can have clinical significance, particularly in immunocompromised individuals.

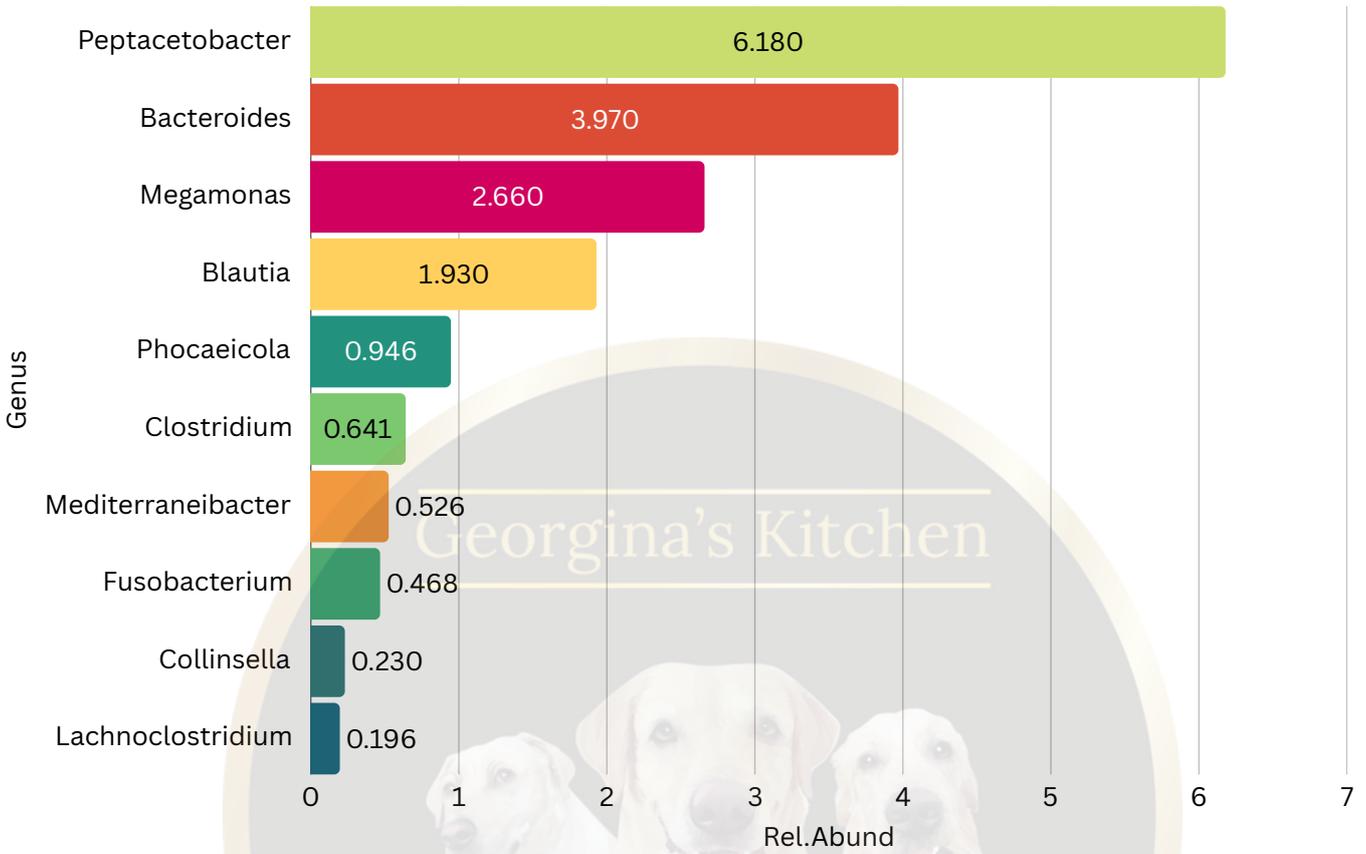


# Phylum Composition



Phylum	Relative Abundance
<i>Bacillota</i>	13.7
<i>Bacteroidota</i>	5.16
<i>Fusobacteriota</i>	0.537
<i>Actinomycetota</i>	0.324
<i>Pseudomonadota</i>	0.174

# Genus Composition



Genus	Relative Abundance
<i>Peptacetobacter</i>	6.18
<i>Bacteroides</i>	3.97
<i>Megamonas</i>	2.66
<i>Blautia</i>	1.93
<i>Phocaeicola</i>	0.946



# Top Abundant Species

## Top abundant species of Bacteria in your sample

<i>Peptacetobacter hiranonis</i>	6.18	<i>Clostridium perfringens</i>	0.519
<i>Bacteroides stercoris</i>	3.55	<i>Mediterraneibacter gnavus</i>	0.393
<i>Megamonas funiformis</i>	2.66	<i>Blautia obeum</i>	0.233
<i>Blautia hansenii</i>	1.07	<i>Blautia argi</i>	0.216
<i>Phocaeicola vulgatus</i>	0.806	<i>Collinsella stercoris</i>	0.178

## Top abundant species of Archaea in your sample

<i>Methanosarcina barkeri</i>	0.000627	<i>Methanococcus maripaludis</i>	0.000327
<i>Methanobacterium congolense</i>	0.000474	<i>Uncultured Methanobacterium sp.</i>	0.000287
<i>Methanomicrobium antiquum</i>	0.000374	<i>Methanosarcina mazei</i>	0.000280
<i>Methanobrevibacter olleyae</i>	0.000347	<i>Methanoplanus limicola</i>	0.000233
<i>Methanotherix soehngeni</i>	0.000334	<i>Methanothermococcus okinawensis</i>	0.000233

## Top abundant species of Eukaryota in your sample

<i>Saccharomyces</i>	0.00158	<i>Candidatus Erwinia haradaeae</i>	0.000420
<i>Candidatus Syntrophocurv alkaliphilum</i>	0.000954	<i>Candidatus Arthromitus sp. SFB-Rat-YIT</i>	0.000414
<i>Aspergillus</i>	0.000894	<i>Candida</i>	0.000407
<i>Candidatus Paraluminiphilus aquimaris</i>	0.000567	<i>Candidatus Symbiobacter mobilis</i>	0.000394
<i>Candidatus Pelagibacter sp. RS39</i>	0.000494	<i>Candidatus Nitrosacidococcus tergens</i>	0.000334

**Top abundant species of Virus in your sample**

<i>Delmidovirus</i>	0.0391	<i>Tupanvirus</i>	0.000167
<i>Aurodevirus</i>	0.000480	<i>Lymphocystivirus</i>	0.000160
<i>Afonbuvirus</i>	0.000287	<i>Wilsonroadvirus SD1</i>	0.000153
<i>Webervirus IMGroot</i>	0.000267	<i>Treponema phagedenis</i>	0.000147
<i>Moumouvirus</i>	0.000193	<i>Orpheovirus ihumi-lcc2</i>	0.000133

**Top abundant species of bacteriophages Virus in your sample**

<i>Streptococcus phage p7574</i>	0.0000667
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**The Role of Beneficial Bacteriophages in Gut Health**

While bacteria often get the most attention in microbiome studies, viruses—specifically bacteriophages—play a crucial role in maintaining gut health. One such virus detected in this sample is Streptococcus phage P7574.

**What Are Bacteriophages?**

Bacteriophages (or "phages") are viruses that infect and destroy bacteria. Unlike harmful viruses that attack human or animal cells, phages specifically target bacterial populations and help maintain a balanced microbiome.

**Why Is Streptococcus phage P7574 Important?**

- It naturally controls pathogenic bacteria like certain Streptococcus species, which can cause infections.
- It contributes to gut microbiome stability by preventing harmful bacteria from overgrowing.
- Phages are being explored as natural alternatives to antibiotics, especially against antibiotic-resistant bacteria.

**Conclusion**

Rather than being a sign of disease, the presence of Streptococcus phage P7574 is likely a **positive** indicator of a healthy bacterial balance in the gut. Including phages in microbiome analysis can provide deeper insights into how microbial communities regulate themselves naturally.

# Pathogen Characterization

identifies and characterizes many pathogens commonly known to cause gut infections and other health issues. These pathogens are reported with "indicative tags", which can be interpreted as described below. This is not a diagnostic and are not correlated clinically with cfu/ug.

## Bacterial Pathogens / Primary Pathogens

<i>Mycobacterium</i>	0.00249
<i>Neisseria</i>	0.000407
<i>Salmonella</i>	0.000420
<i>Shigella</i>	0.000367
<i>Vibrio</i>	0.00611
<i>Yersinia</i>	0.000901

## Opportunistic Bacteria

<i>Acinetobacter</i>	0.00312
<i>Enterobacter</i>	0.00436
<i>Klebsiella</i>	0.00352
<i>Pseudomonas</i>	0.00628
<i>Serratia</i>	0.00139
<i>Stenotrophomonas</i>	0.000747

## Dysbiotic / Overgrowth Bacteria

<i>Bacteroides</i>	3.97
<i>Clostridium</i>	0.641
<i>Escherichia</i>	0.0231
<i>Fusobacterium</i>	0.468
<i>Prevotella</i>	0.0199

## Potential Autoimmune Triggers

<i>Borrelia</i>	0.00201
<i>Campylobacter</i>	0.0153
<i>Helicobacter</i>	0.00531
<i>Mycoplasma</i>	0.00213
<i>Streptococcus</i>	0.0384



# Antibiotic Resistance

Some bacteria are known to possess genes that can lead to resistance to antibiotics. Our algorithm based output provides information on possible antibiotic resistance based on the genomic analysis of the sample. This is not a microbiological assay based output and hence clinical validation is necessary.

Bacterial Species	Common Antibiotic Resistance	Detected in Sample?
<i>Clostridium perfringens</i>	Metronidazole, Clindamycin	✓ Yes (0.5192%)
<i>Escherichia coli</i>	β-lactams (Penicillins, Cephalosporins), Fluoroquinolones, Aminoglycosides	✓ Yes (0.0227%)
<i>Klebsiella pneumoniae</i>	Carbapenems, Cephalosporins	✓ Yes (0.0008%)
<i>Staphylococcus pseudintermedius</i>	Methicillin (MRSP), Clindamycin	✓ Yes (0.0010%)
<i>Staphylococcus aureus</i>	Methicillin (MRSA), Vancomycin	✓ Yes (0.0028%)
<i>Salmonella enterica</i>	Ampicillin, Fluoroquinolones	✓ Yes (0.0004%)
<i>Pseudomonas aeruginosa</i>	Carbapenems, Fluoroquinolones, Aminoglycosides	✓ Yes (0.0003%)
<i>Proteus mirabilis</i>	β-lactams, Tetracyclines	✓ Yes (0.0002%)
<i>Yersinia enterocolitica</i>	β-lactams, Aminoglycosides	✓ Yes (0.0003%)
<i>Helicobacter pylori</i>	Clarithromycin, Metronidazole	✓ Yes (0.0009%)
<i>Bacillus cereus</i>	Penicillins, Cephalosporins	✓ Yes (0.0007%)
<i>Clostridium botulinum</i>	Rarely resistant	✓ Yes (0.0059%)
<i>Campylobacter jejuni</i>	Macrolides (Erythromycin), Fluoroquinolones	✓ Yes (0.0045%)





# Brief Summary

## Microbiome Analysis Summary

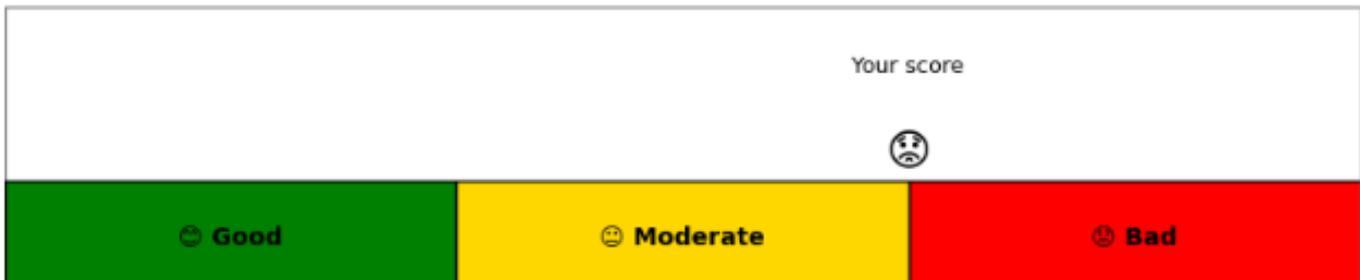
### Overview

This microbiome analysis provides a comprehensive snapshot of the microbial community in the gastrointestinal tract. A balanced and diverse gut microbiome is essential for digestion, immune function, and overall health.

### Most Prevalent Bacteria

- *Peptacetobacter hiranonis*
- *Bacteroides stercoris*
- *Megamonas funiformis*
- *Blautia hansenii*
- *Phocaeicola vulgatus*

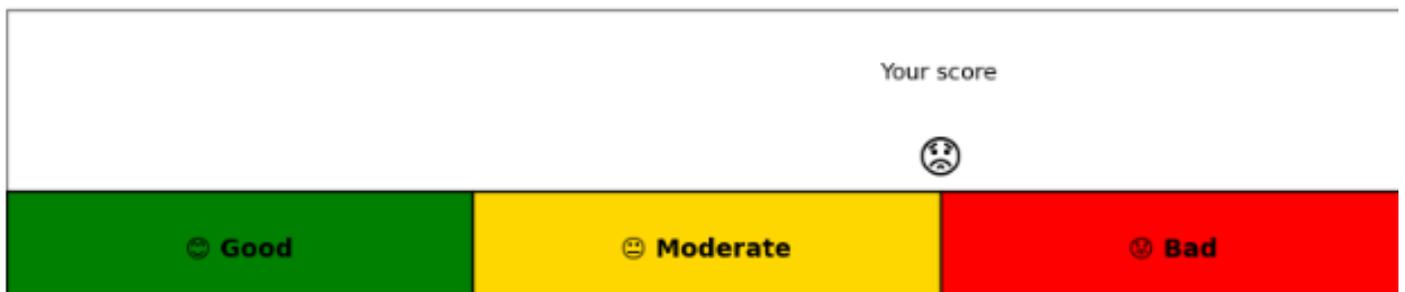
### Bacterial Diversity



### Beneficial Bacteria (Low Abundance)

- *Faecalibacterium prausnitzii*
- *Enterococcus faecium*
- *Lactobacillus johnsonii*
- *Bifidobacterium breve*
- *Bifidobacterium longum*

### Beneficial Bacteria

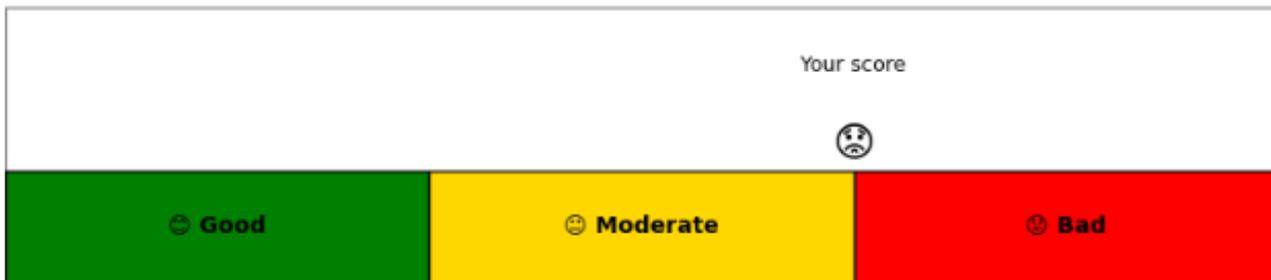


### Potential Pathogens Detected

- Clostridium perfringens
- Escherichia coli
- Clostridium botulinum
- Campylobacter jejuni
- Staphylococcus aureus

**These species are present at levels that require monitoring, though they do not indicate an active infection.**

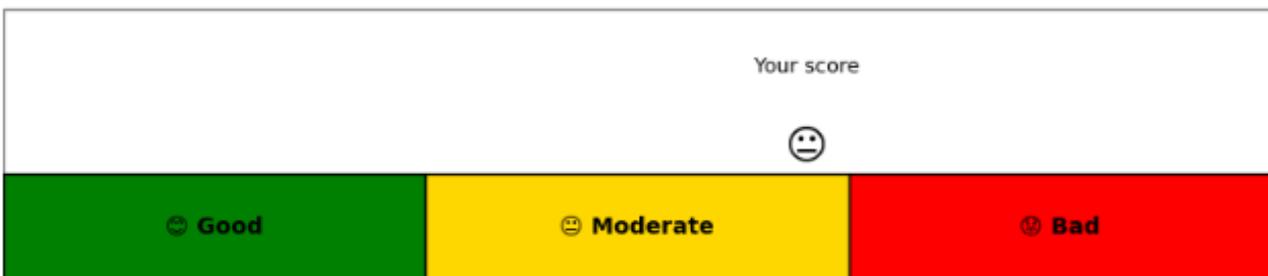
#### Potential Pathogens



### Dysbiosis Score: 4.89 (Moderate)

This score indicates a mild but noticeable imbalance in the gut microbiota. Implications If unaddressed, it could impact digestion, immunity, and inflammation

#### Dysbiosis Score



### Recommendations

- Begin probiotic supplementation
- Adjust diet to support microbial diversity and beneficial bacteria growth

### Conclusion

The microbiome profile reflects a moderately imbalanced gut ecosystem. While no acute infections or severe imbalances are observed, the low levels of beneficial microbes and presence of resistant strains warrant attention.

# Microbiome Handbook

## Disease Description

### Inflammatory Bowel Disease (IBD)

Inflammatory Bowel Disease (IBD) in dogs is a chronic condition caused by an abnormal immune response to gut bacteria. Dysbiosis leads to a loss of beneficial bacteria like *Faecalibacterium prausnitzii* and an overgrowth of *Escherichia coli* and *Clostridium perfringens*, which trigger inflammation. The degradation of the mucus layer by *Roseburia* and *Actinobacteria* allows opportunistic pathogens to thrive, causing severe irritation and damage to the gastrointestinal lining.

### Small Intestinal Bacterial Overgrowth (SIBO)

SIBO occurs when there is an excessive bacterial population in the small intestine, often due to an imbalance in gut microbiota. Increased levels of Proteobacteria like *Escherichia coli* and *Klebsiella pneumoniae* contribute to malabsorption, leading to chronic diarrhea, flatulence, and nutrient deficiencies. A decline in beneficial microbes like *Lactobacillus* and *Bifidobacterium* results in reduced short-chain fatty acid production, which is essential for gut health.

### Clostridial Enterotoxigenesis

Overgrowth of *Clostridium perfringens* in the gut leads to the production of enterotoxins that damage intestinal epithelial cells, resulting in acute or chronic diarrhea. Dysbiosis plays a key role in this condition, with low levels of beneficial *Bacteroides* and *Firmicutes* failing to suppress pathogenic bacteria, allowing toxin-producing strains to proliferate.

### Obesity & Metabolic Syndrome

Microbiome dysbiosis in obese dogs is often characterized by an increased *Firmicutes*-to-*Bacteroidetes* ratio. *Akkermansia muciniphila*, a keystone species in gut health, is reduced in overweight dogs, affecting gut barrier integrity. The gut microbiota also regulates metabolism by influencing fat storage through microbial fermentation of fibers, leading to increased energy extraction from food and contributing to excessive weight gain.

### Allergies & Atopic Dermatitis

A disrupted gut microbiome affects immune function, leading to hypersensitivity reactions and chronic skin inflammation. Beneficial bacteria like *Lactobacillus* and *Bifidobacterium* regulate immune responses, but their depletion allows *Staphylococcus* and Proteobacteria to dominate, triggering inflammatory pathways that contribute to skin allergies, itching, and rashes.

### Anxiety & Stress-Related Disorders

The gut-brain axis links microbiota composition to canine behavior. Dysbiosis, characterized by a decrease in *Lactobacillus* and *Bifidobacterium*, reduces the production of neurotransmitters like GABA and serotonin, which regulate stress responses. This imbalance can manifest as anxiety, excessive barking, or aggressive behavior.

### Helicobacter Gastritis

Overgrowth of *Helicobacter canis* and other *Helicobacter* species in the stomach causes chronic gastritis in dogs. These bacteria disrupt the stomach's mucosal lining, leading to vomiting, reduced appetite, and stomach discomfort. Dysbiosis contributes to this condition by reducing protective microbes that normally inhibit *Helicobacter* proliferation.

### Parasitic Infections (Giardia & Blastocystis)

Dogs with gut microbiome imbalances are more prone to infections by protozoan parasites like *Giardia* and *Blastocystis*. A reduction in protective bacteria such as *Lactobacillus* and *Faecalibacterium* allows these opportunistic pathogens to colonize the gut, leading to chronic diarrhea and malabsorption.

# Evidences

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This report has been researched & developed by:



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