

Sample\_barcode67

Horse

Sample #barcode67

Analyzed: 2025-09-26  
Report: 2025-09-26

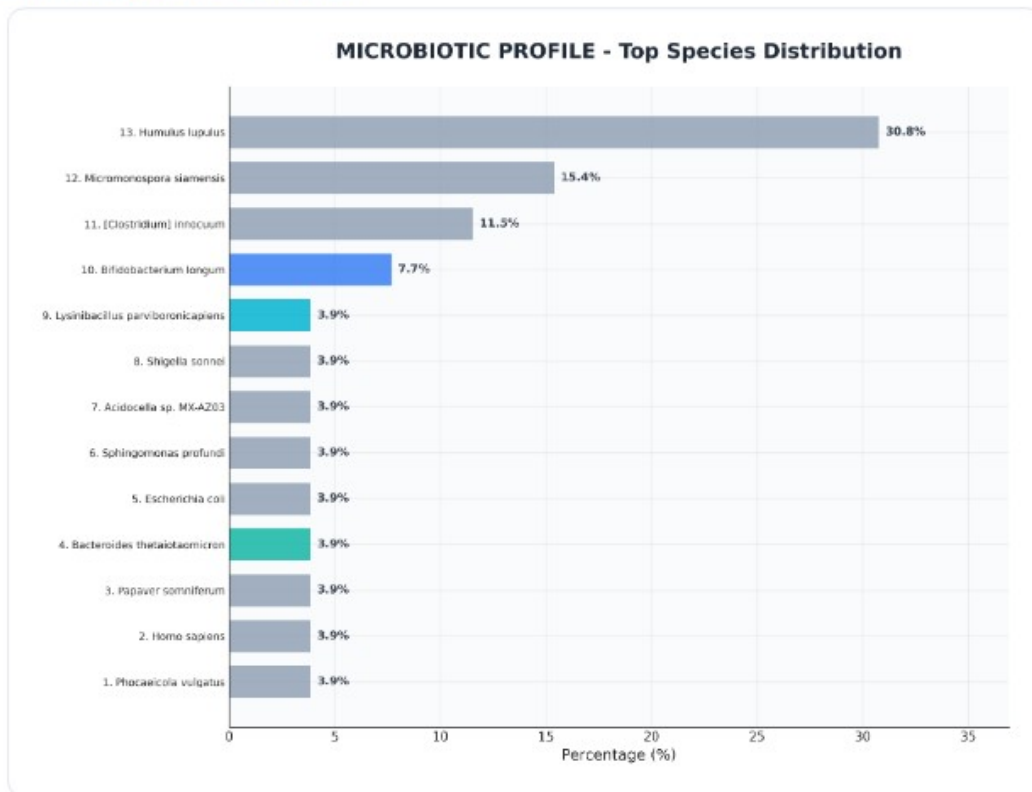
## Microbiome Sequencing Results

36.0

Dysbiosis Index

Mild Dysbiosis

### Bacterial Species Distribution



1. In the list, eukaryotes are included, but they should not be there.
2. In the table, there are numbers placed before the bacterial names - they should not appear.
3. Some bacterial names contain special characters such as square brackets, for example *[Clostridium]*. Could the algorithm detect these cases and output the names without such special characters?

### Dominant Species

Species	Abundance (%)	Phylum
Phocaeicola vulgatus	30.77%	Unknown
Homo sapiens	15.38%	Unknown
Papaver somniferum	11.54%	Unknown
Bacteroides thetaiotaomicron	7.69%	Bacteroidota
Escherichia coli	3.85%	Pseudomonadota
Sphingomonas profundus	3.85%	Unknown
Acidocella sp. MX-AZ03	3.85%	Unknown
Shigella sonnei	3.85%	Unknown
Lysinibacillus parviboronicapiens	3.85%	Unknown
Bifidobacterium longum	3.85%	Actinomycetota

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1. What is the difference between the first two figures in the report? Why are the represented data different?
2. We can keep the bar chart showing the top 15/20 most abundant taxa, but we still need, for example, a complete list of all other detected bacterial species along with their relative abundance in the microbiome.
3. It should be “MIMT Genetics Laboratory” and not “MEMT.”
4. The page numbering in the report is incorrect.

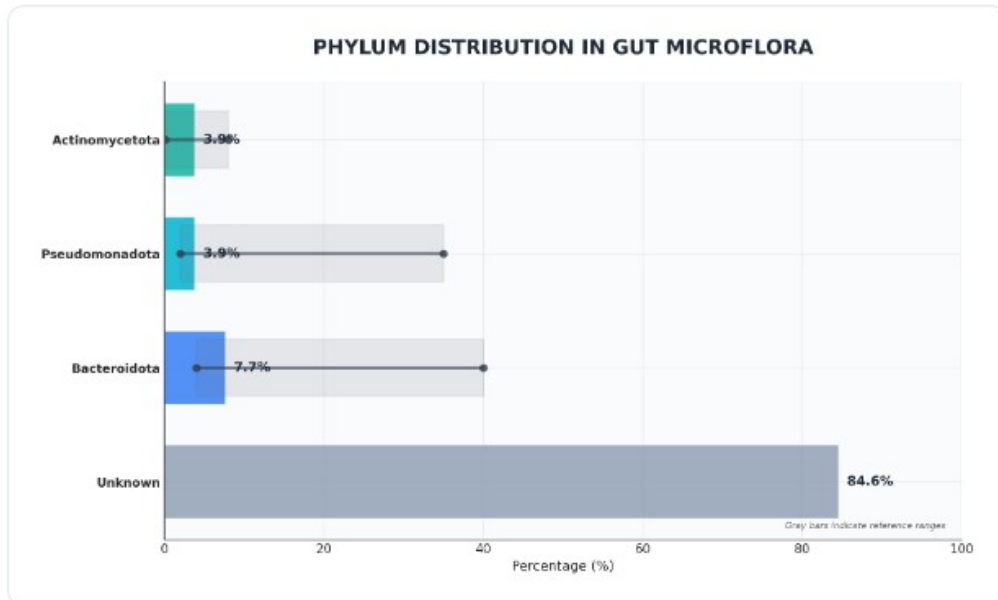
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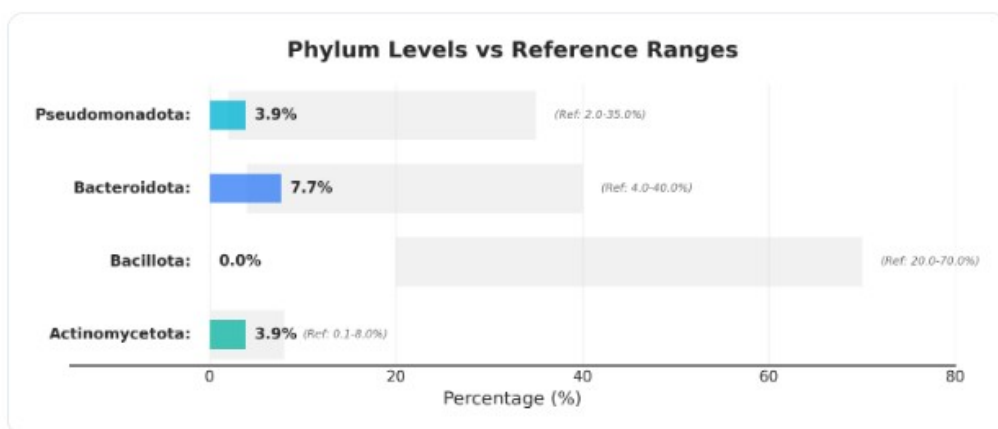
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## Phylum Distribution Analysis



### Phylum Levels vs. Reference Range



1. How are the percentage values in these charts calculated? We need them to be calculated as follows: **bacterial phylum counts / sum of only bacterial phylum detected counts × 100%**. Otherwise, the percentage results are distorted.

Phylum	Patient (%)	Normal Range (%)	Status
Unknown	84.64	0.0 - 100.0	Normal
Bacteroidota	7.69	4.0 - 40.0	Normal
Pseudomonadota	3.85	2.0 - 35.0	Normal
Actinomycetota	3.85	0.1 - 8.0	Normal

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1. If we already have the above chart, then this table is not needed.

## Clinical Interpretation

### Clinical Assessment

The microbiome analysis indicates **mild dysbiosis** with an index of 36.0. This suggests a moderate imbalance in the gut microbial community that may benefit from targeted intervention. While not immediately concerning, this imbalance could impact digestive efficiency and immune function if left unaddressed.

### Key Findings

**Low Bacillota:** 0.0% (Normal: 20-70%).  
Associated with reduced fiber  
fermentation and butyrate production.

### Clinical Recommendations

- Increase dietary fiber through additional hay supplementation
- Consider probiotic supplementation (Lactobacillus/Bifidobacterium strains)
- Reduce grain intake if exceeding 0.5% body weight per feeding
- Re-evaluate microbiome in 8-12 weeks after intervention

1. I have not yet reviewed the clinical interpretation — I will return to this later.

## Summary & Management Guidelines

### Report Summary

**Dysbiosis Index:** 36.0**Category:** Mild**Dominant Phylum:** Unknown**Total Species Identified:** 13**Sample Quality:** Adequate**Analysis Method:** 16S rRNA NGS

### Understanding the Dysbiosis Index

The Dysbiosis Index (DI) quantifies the degree of microbial imbalance in the gut:

- **0-20:** Normal, healthy microbiome
- **21-50:** Mild dysbiosis requiring dietary adjustment
- **>50:** Severe dysbiosis requiring intervention

### Management Guidelines

#### Correcting Mild Dysbiosis

- Increase forage intake to at least 1.5-2% body weight
- Reduce grain meals to <0.5% body weight per feeding
- Add probiotic supplement ( $10^9$  CFU daily)
- Consider prebiotic fiber sources (beet pulp, psyllium)
- Ensure adequate water intake (30-50L daily)

### Follow-up Testing

Dysbiosis Category	Re-test Timeline	Monitoring Focus
Normal	12 months	Annual health screening
Mild	2-3 months	Response to dietary changes
Severe	4-6 weeks	Treatment efficacy

#### For questions regarding this report, please contact:

MEMT Genetics Laboratory

Email: [lab@memtgenetics.com](mailto:lab@memtgenetics.com) | Phone: +48 XXX XXX XXXReport generated using Next-Gen Gut Profiling (nGG-<sup>GP</sup>) technology  
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### 1. Analysis method is Shotgun metagenomic NGS

#### General comment:

We need to be able to enter our case number, the patient's name, and the results of other analyses (e.g., microscopic or biochemical). Ideally, these should be presented as separate sections of the report that can be added or removed as needed, along with the NGS section.