Sample_barcode67 | Horse | Sample #barcode67

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

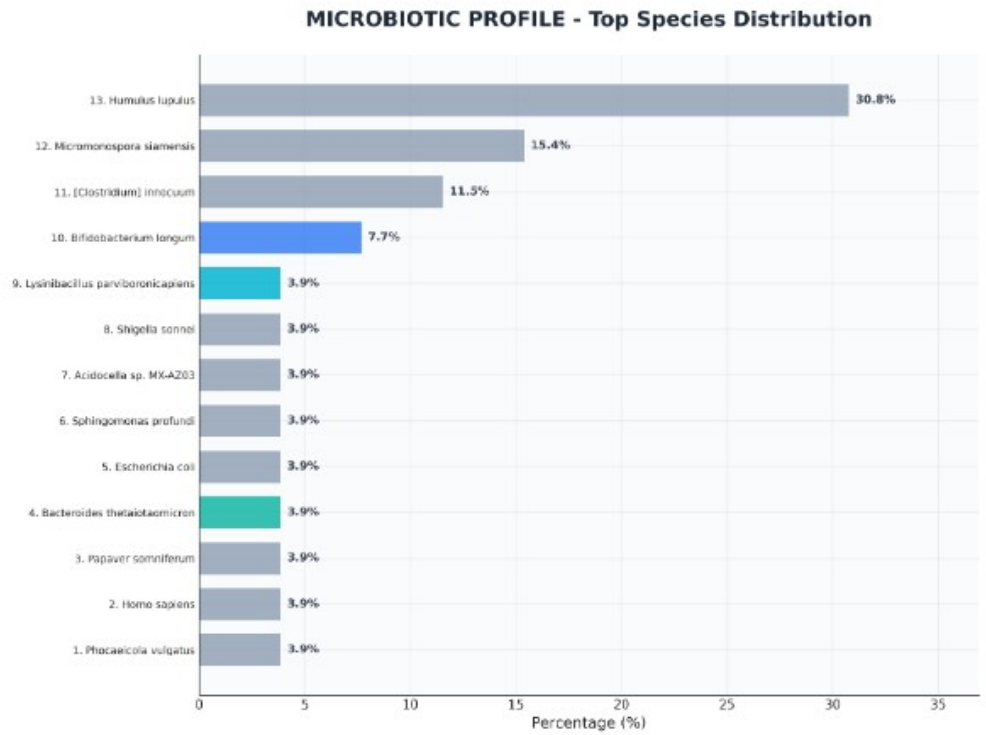
Microbiome Sequencing Results

36.0

Dysbiosis Index

Mild Dysbiosis

Bacterial Species Distribution

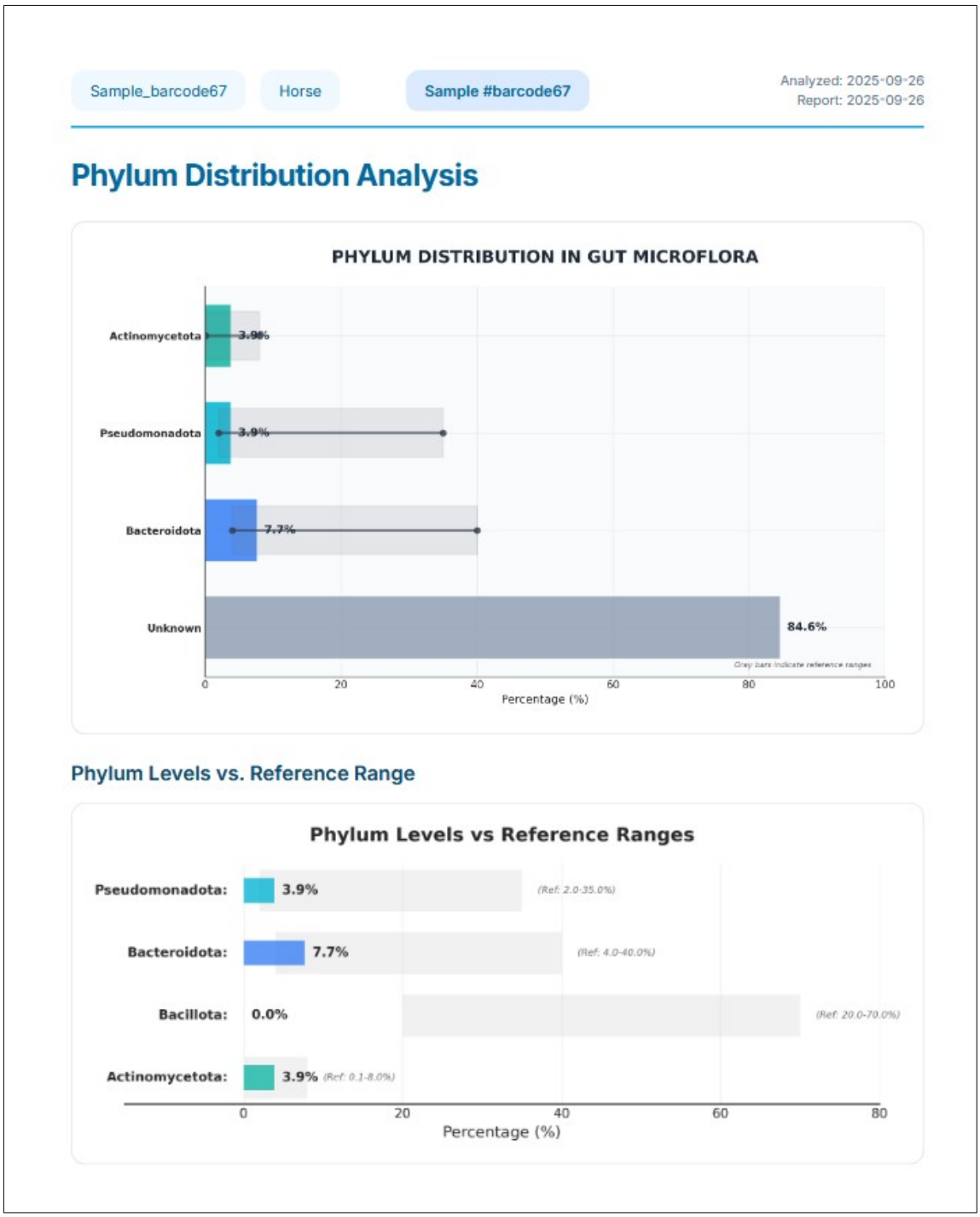


1. In the list, eukaryotes are included, but they should not be there.
2. In the table, there are numbers placed before the bacterial names - they should not appear.
3. Some bacterial names contain special characters such as square brackets, for example *[Clostridium]*. Could the algorithm detect these 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 profundi	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

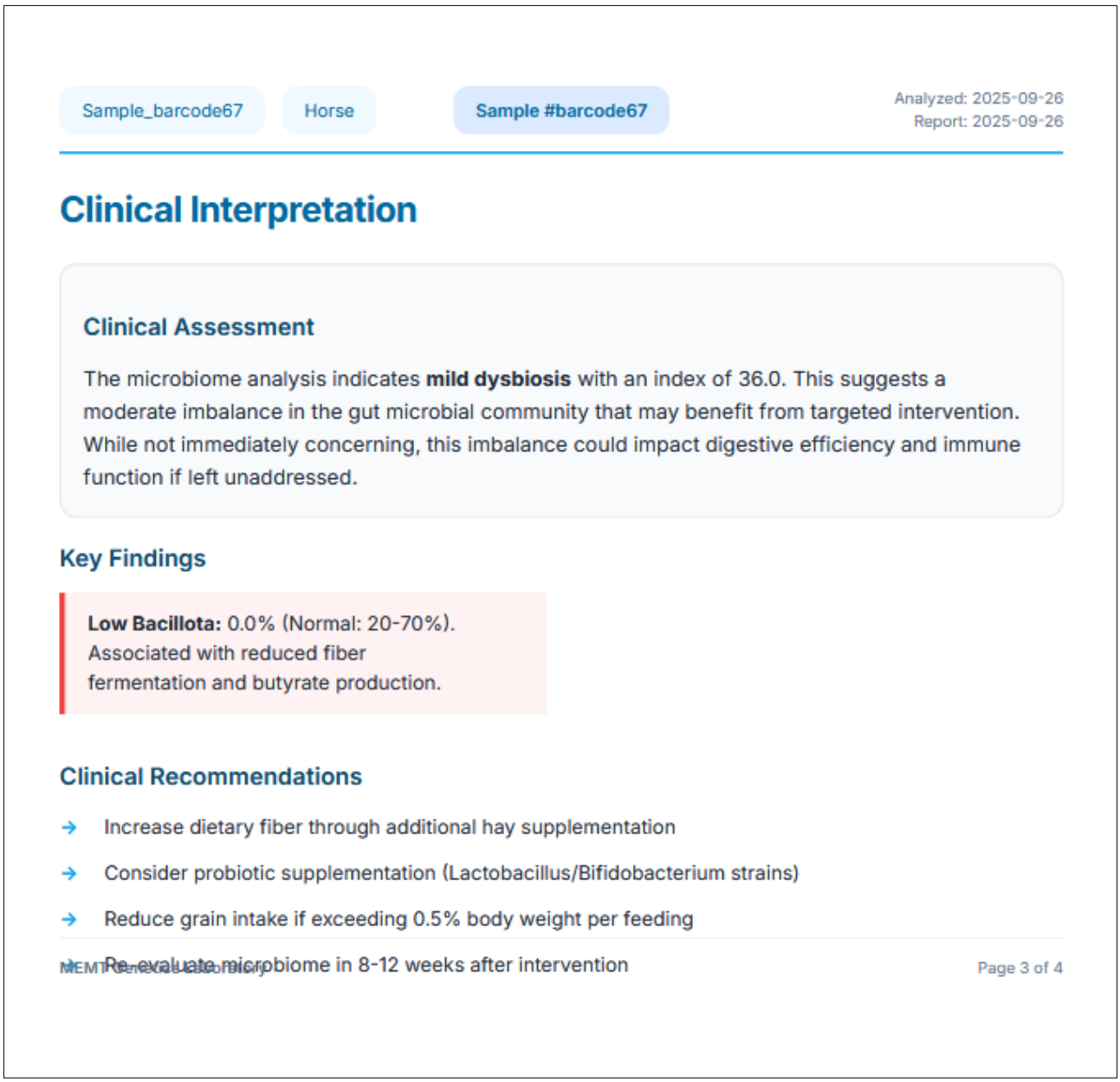
1. What is the difference between the first two figures in the report? Why are the represented data different?
2. We can keep the bar chart showing the top 15/20 most abundant taxa, but we still need, for example, a complete list of all other detected bacterial species along with their relative abundance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



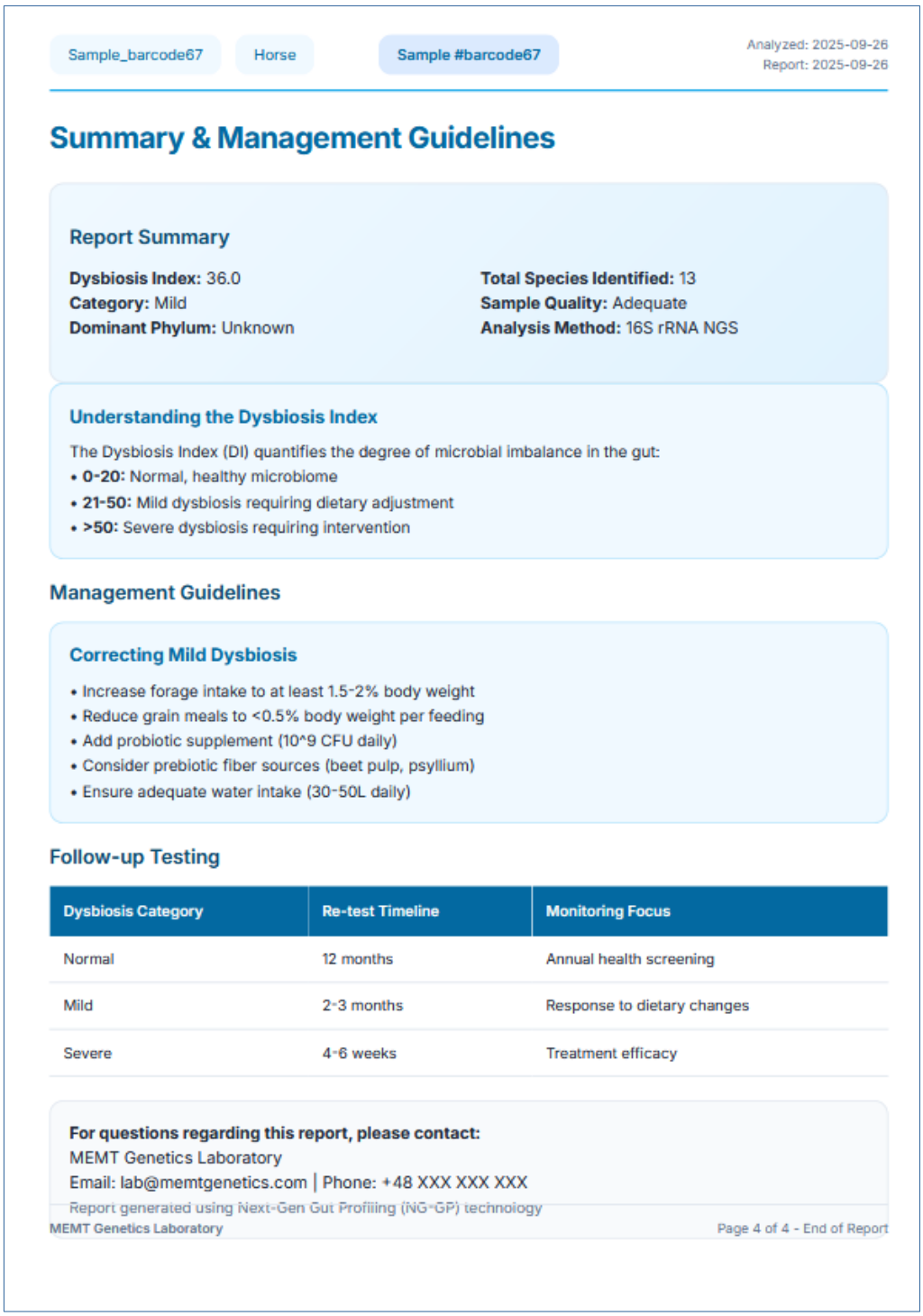
1. How are the percentage values in these charts calculated? We need them to be calculated as follows: **bacterial phylum counts / sum of only bacterial phylum detected counts × 100%**. Otherwise, the percentage results are distorted.

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

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



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



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.