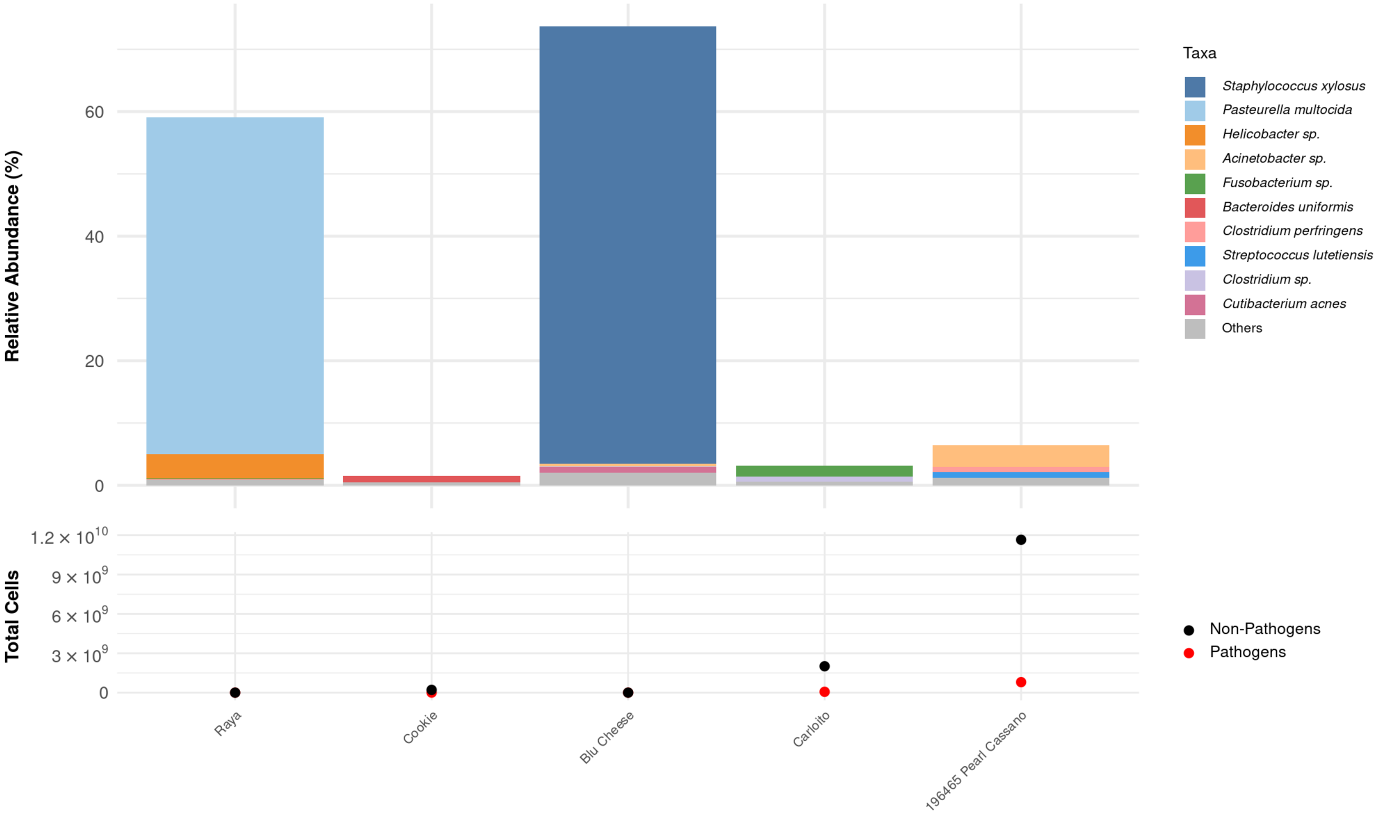
Comparison Report

Sample Collection (CR_20260401_12)

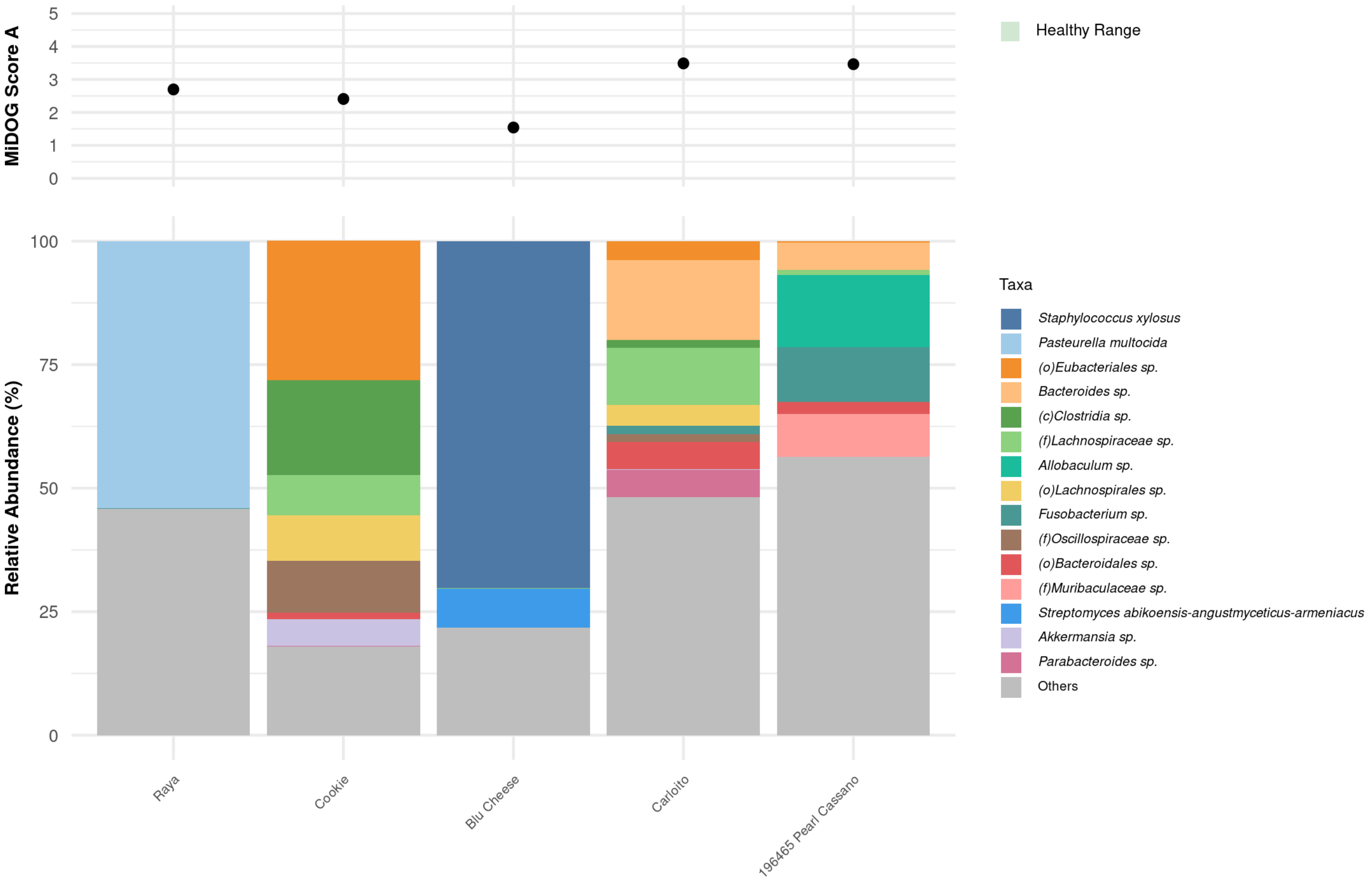
Sample ID	Type	Patient	Sample ID	Type	Patient	Sample ID	Type	Patient
Mi260941004835	Nose	Raya (Other)	Mi265274000747	Skin, back and under arm (Scales)	Blu Cheese (Other)	MiV269139000480	Feces	196465 Pearl Cassano (Other)
MiU267335000481	Free Catch	Cookie (Other)	Mi254012002451	Feces	Carloito (Healthy)			

Potential Pathogenic Bacteria Detected



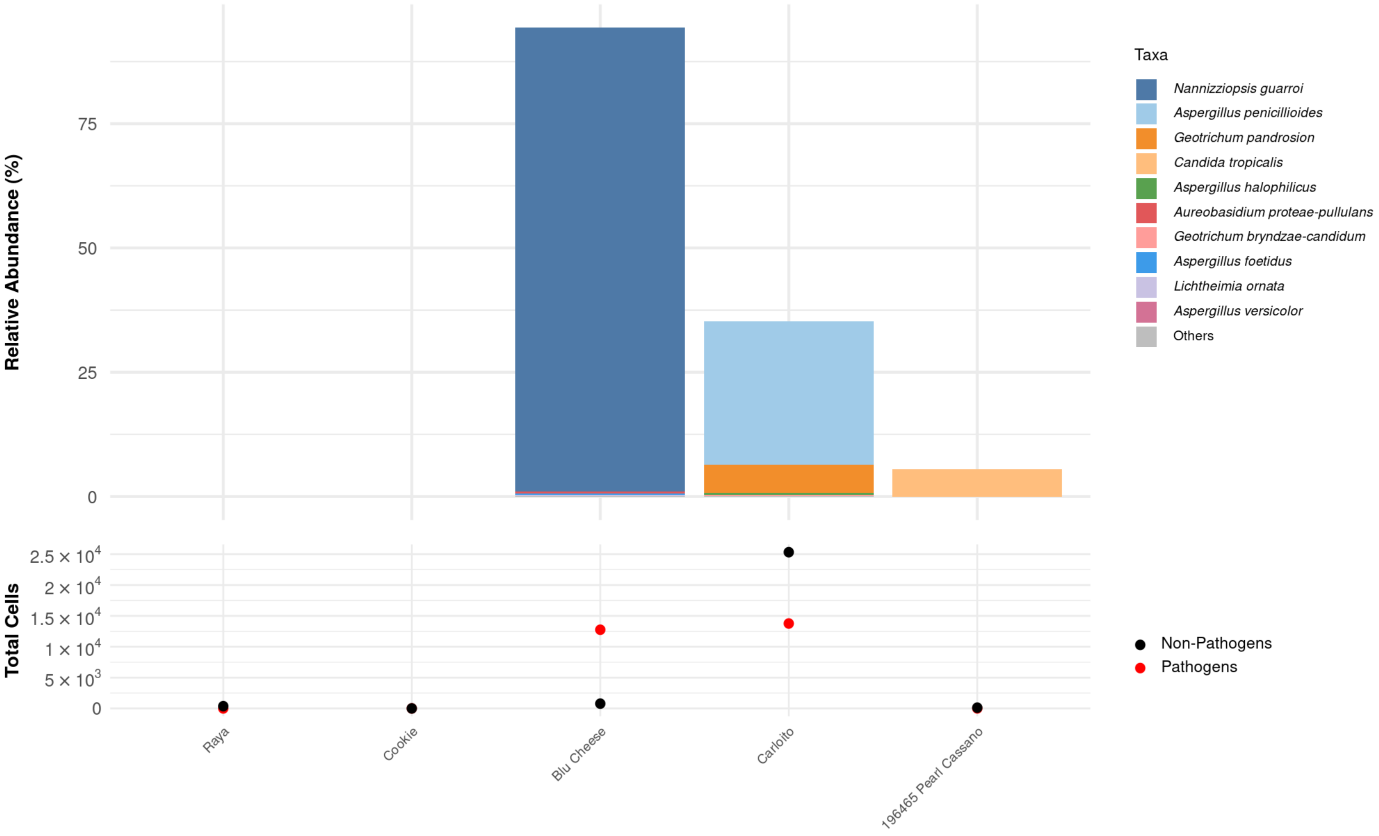
Displayed above are the cell counts and relative abundance (%) of potential pathogenic bacteria detected in above samples, with taxa distinguished by color

Total Bacterial Composition



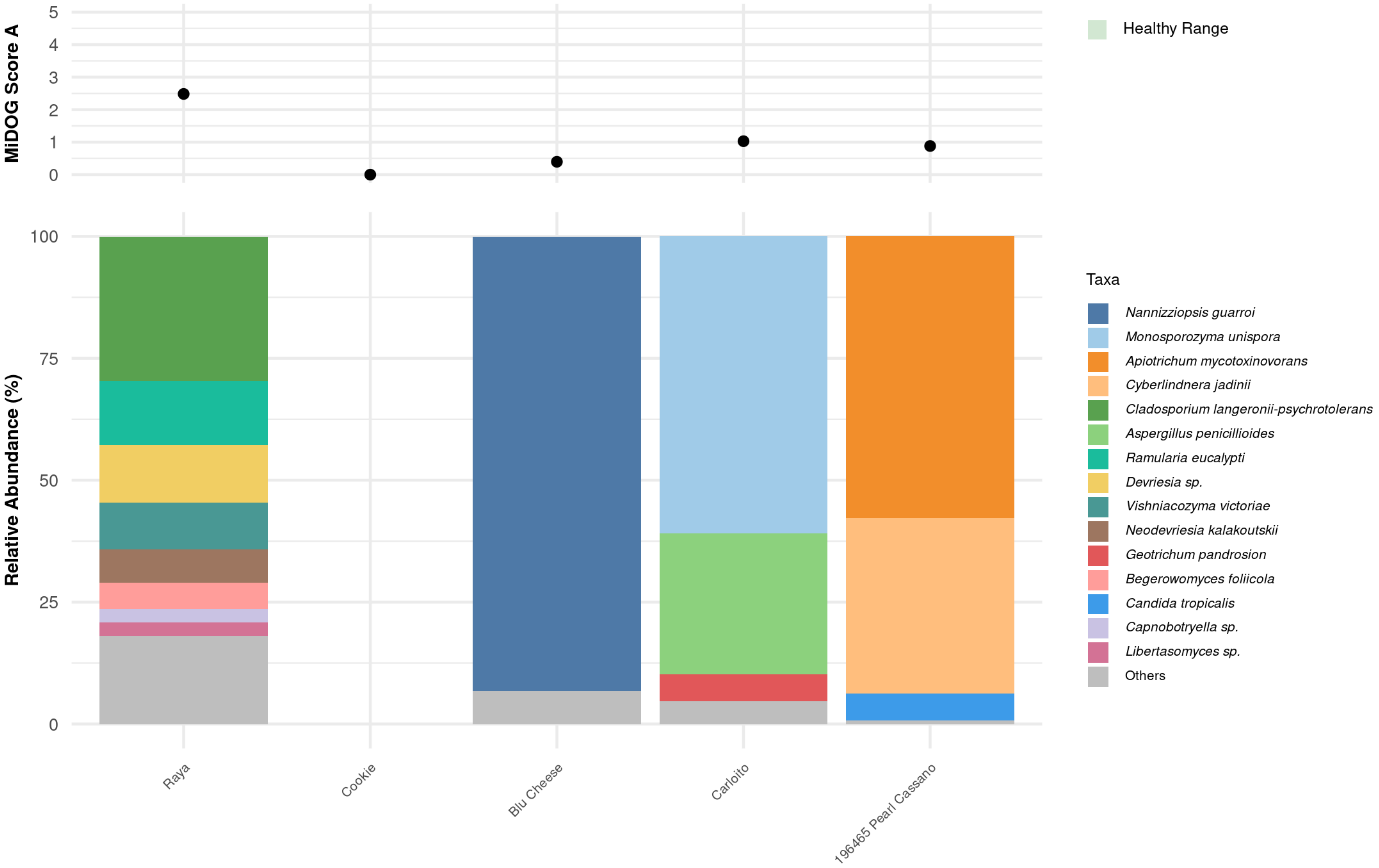
Total bacterial composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full bacterial composition spreadsheet can be found HERE.

Potential Pathogenic Fungi Detected



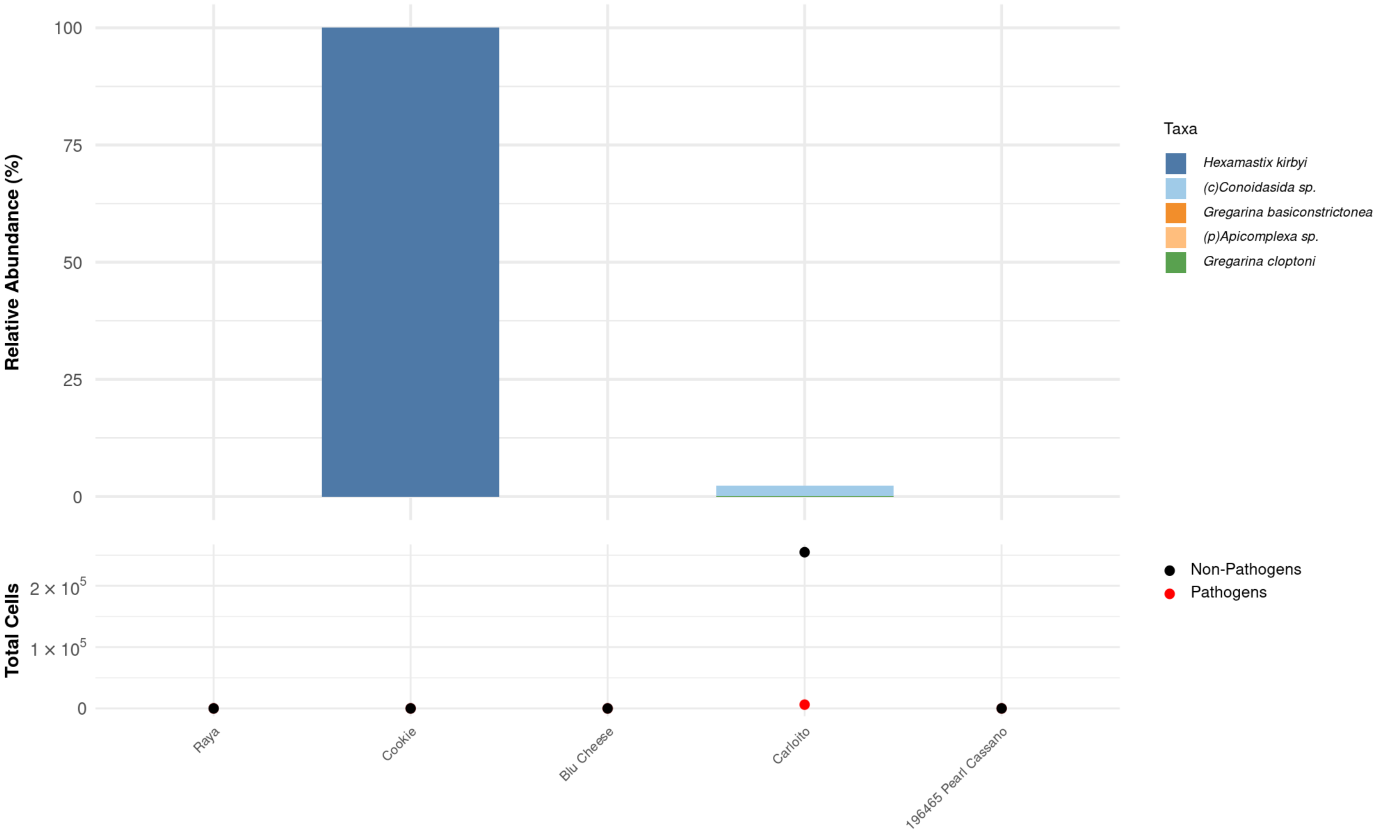
Displayed above are the cell counts and relative abundance (%) of potential pathogenic fungi detected in above samples, with taxa distinguished by color

Total Fungi Composition



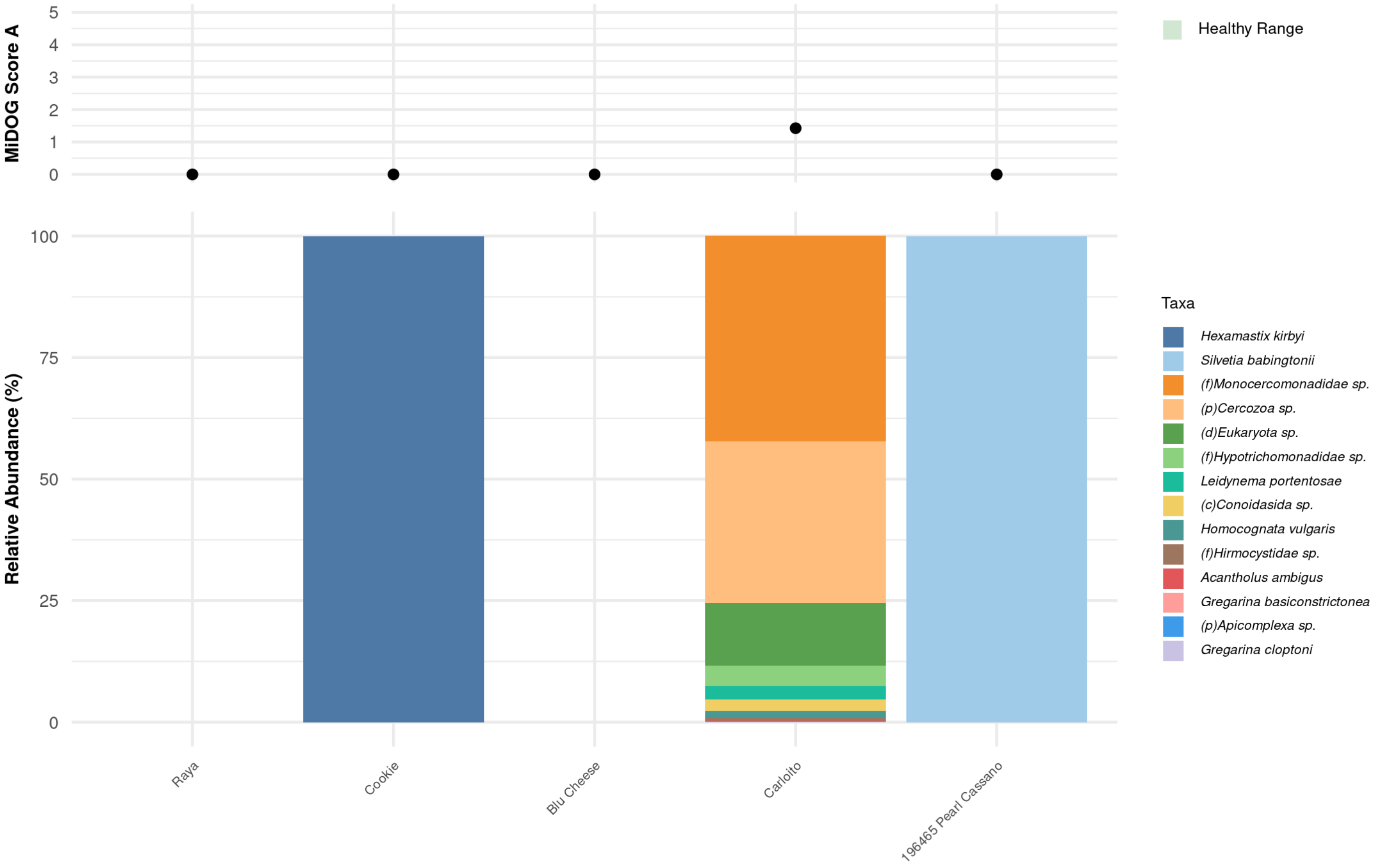
Total fungal composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full fungal composition spreadsheet can be found HERE.

Potential Eukaryotic Pathogen Detected



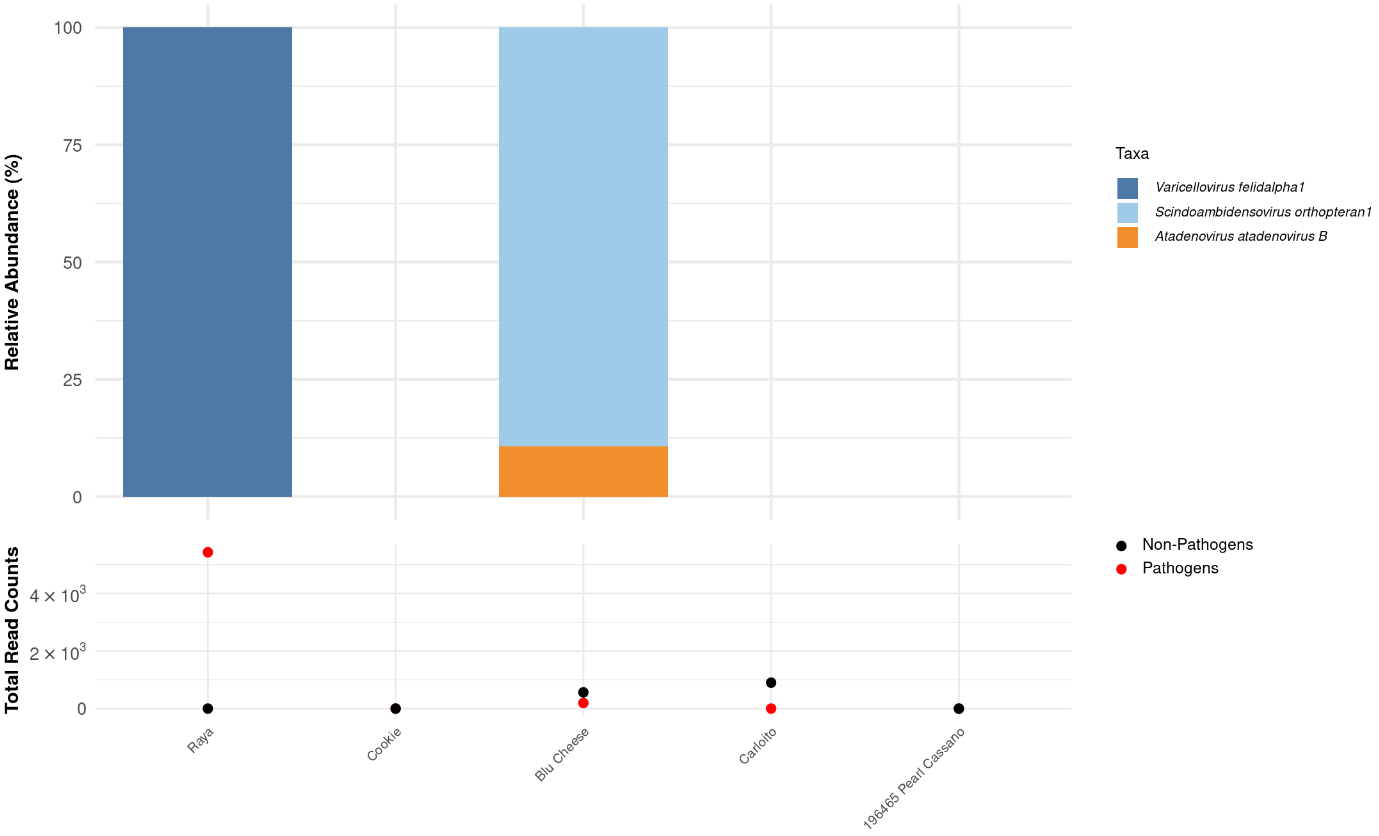
Displayed above are the cell counts and relative abundance (%) of potential parasites detected in above samples, with taxa distinguished by color

Total Other Eukaryotes Composition



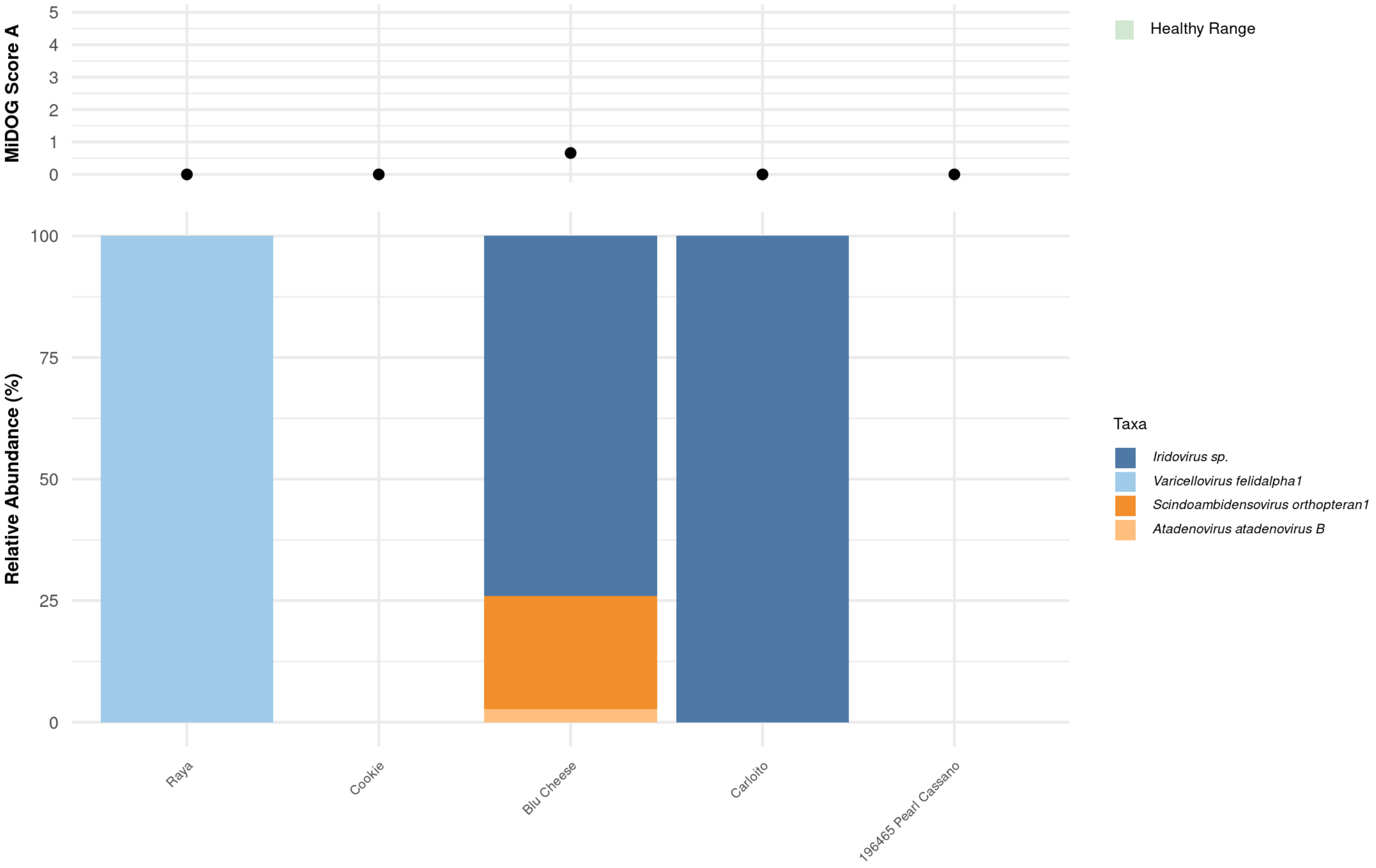
Total other eukaryota composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full eukaryota composition spreadsheet can be found HERE.

Potential Viral Pathogen Detected



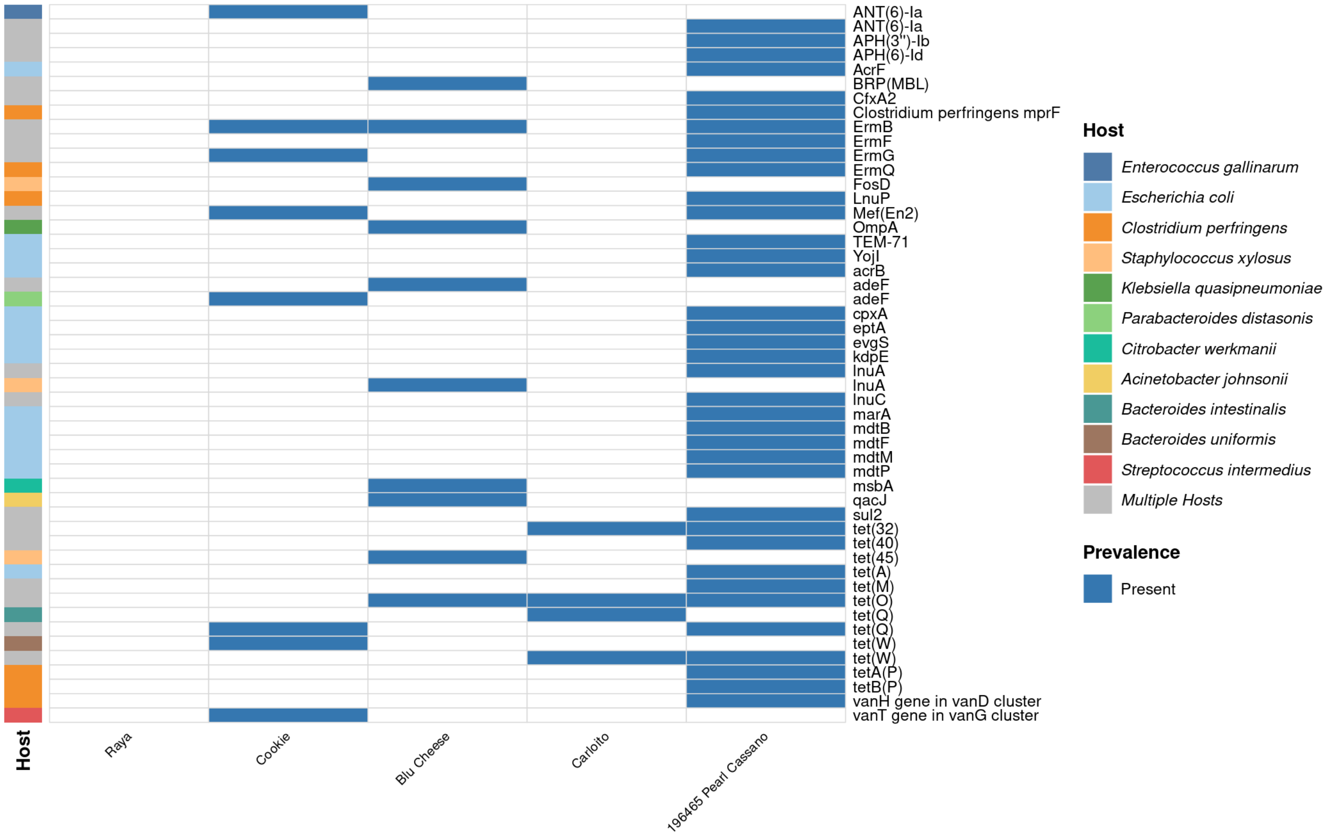
Displayed above are the cell counts and relative abundance (%) of potential pathogenic virus detected in above samples, with taxa distinguished by color

Total Virus Composition



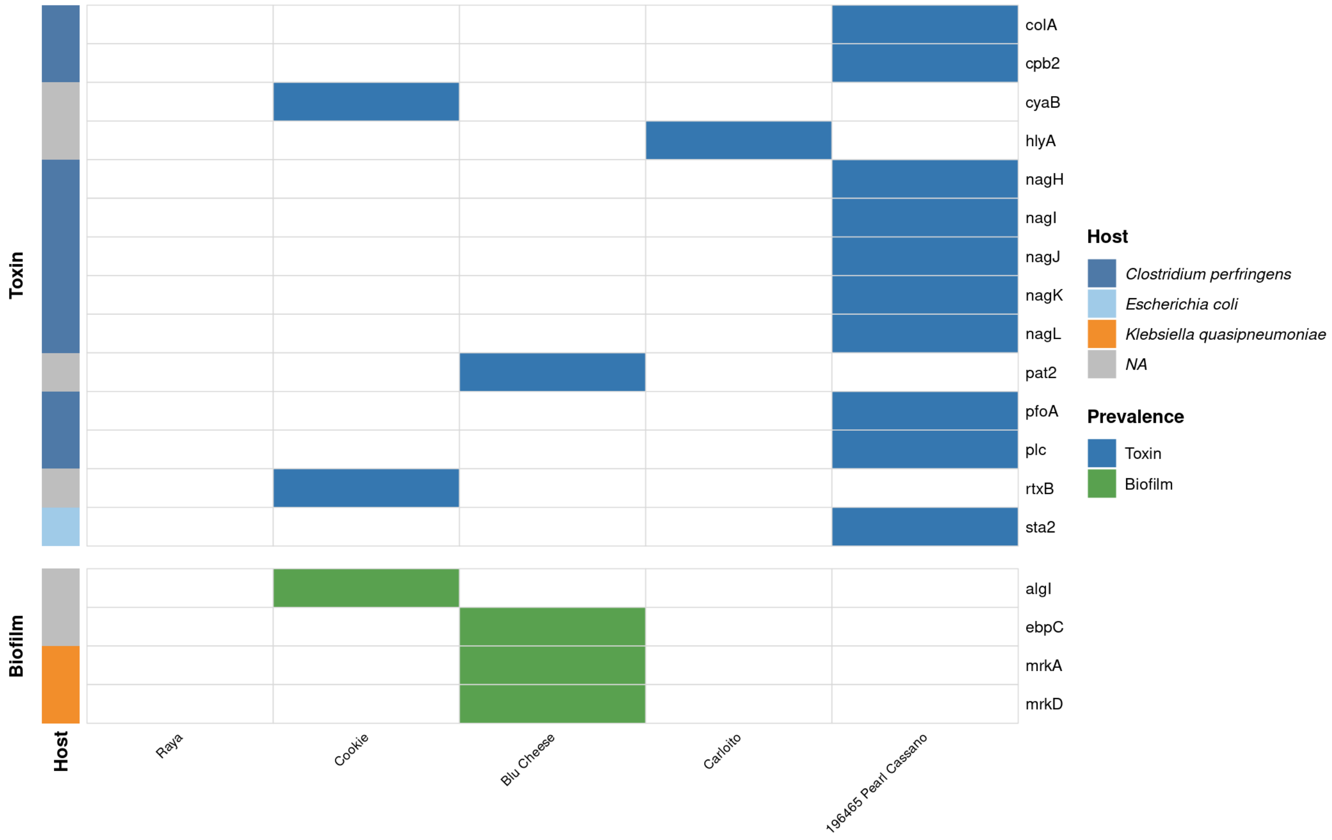
Total viral composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full viral composition spreadsheet can be found HERE.

Antimicrobial Resistance Heatmap (Up To Top 50 AMR Genes)



The above heatmap shows up to top 50 most prevalent antimicrobial resistance genes over time based on read counts. Dark blue cells indicate that the resistance genes are present, while white cells show no resistance gene present. The rows list the exact antimicrobial resistance genes detected along with the host species, and the columns represent the sample names. Full AMR genes information can be found HERE.

Toxins/Biofilms Heatmap (Up To Top 50 Virulence Genes)



The above heatmap shows up to top 50 most prevalent toxins/biofilms genes over time based on read counts. Dark blue cells indicate that the virulence genes are present, while white cells show no virulence gene present. The rows list the exact virulence genes detected along with the host species, and the columns represent the sample names. Full virulence genes information can be found HERE.

References

References are located in each individual MiDOG® report.

Methods

The MiDOG® All-in-One Microbial Test is a targeted, Next-generation DNA sequencing testing service able to identify molecular signatures unique to the identity and character of a specific microorganism. This test relies on safeguarded preservation and transport of collected samples, thorough extraction of DNA from all microbes present in the specimen, select amplification of microbial DNA followed by Next-generation DNA sequencing using the latest technologies from Illumina (Illumina, Inc., San Diego, CA). Data handling is done via curated microbial databases to accurately align DNA sequences to ensure precise and accurate (species-level) identification of all microbes present in the specimen.

When no Microbial Species are Detected

When no Microbial species are detected in this test, this result may be due to a very low microbial load and/or low concentration of microbial DNA in the sample provided. In this case, we recommend re-sampling the area of interest and re-submitting specimen for analysis.

Phylogenetic Rank Abbreviations

If the detected bacterial or fungal taxon could not be identified down to the genus level, the closest phylogenetic rank identified is provided. An abbreviation indicating the level of the rank is displayed aside. The meaning of the abbreviations is shown as: (p) Phylum level, (c) Class level, (o) Order level, and (f) Family level.

Disclaimer

The information contained in this MiDOG® report is intended only to be factor for use in a diagnosis and treatment regime for the animal patient. As with any diagnosis or treatment regime, you should use clinical discretion with each animal patient based on a complete evaluation of the animal patient, including history, physical presentation and complete laboratory data, including confirmatory tests. All test results should be evaluated in the context of the patient’s individual clinical presentation. The information in the MiDOG® report has not been evaluated by the FDA.

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