MiDOG Animal Diagnostics

Time Series Report

Patient Name:	Hamadryas Baboon Troop	**Species:**	Baboon	**Ordered by:**	Dr. Example
Account:	DEMO-0001	**Breed:**	Hamadryas	**Hospital:**	Example Zoo
Owner's Name:	Example Zoo	**Gender:**	Mixed (14)	**Submissions:**	7

Submission Timeline (TS_20261022_2)

Sample ID	Type	Date	Sample ID	Type	Date	Sample ID	Type	Date
DEMO-B01	Feces (Pooled, Pre-Treatment)	10/28/2025	DEMO-B04	Feces (Pooled, Pre-Treatment)	01/06/2026	DEMO-B07	Feces (Pooled, Post-Albendazole + Cephalexin)	04/07/2026
DEMO-B02	Feces (Pooled, Pre-Treatment)	11/25/2025	DEMO-B05	Feces (Pooled, Post-Albendazole + Cephalexin)	02/03/2026			
DEMO-B03	Feces (Pooled, Pre-Treatment)	12/23/2025	DEMO-B06	Feces (Pooled, Post-Albendazole + Cephalexin)	03/03/2026			

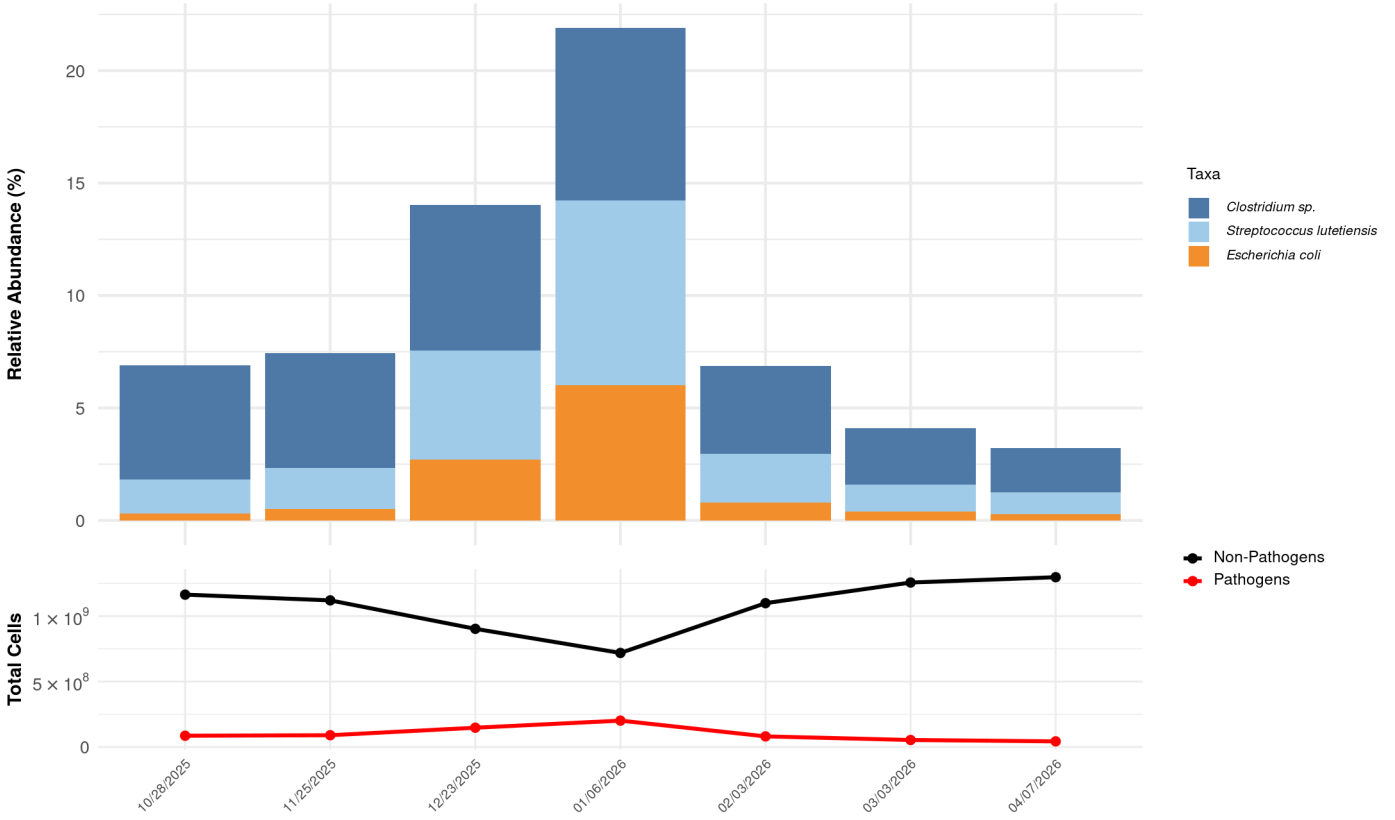
Potential Pathogenic Microbes Detected

The microbes listed here are potentially clinically relevant. These results should be interpreted alongside clinical data from the veterinarian (e.g., physical exam, history, cytology), as detected microbes may or may not be the cause of symptoms. A full list of all organisms is on page 2 and 3. Note that even commensals can become pathogenic under certain conditions, and rare or novel microbes may also appear for your clinical consideration.

		01/06/2026		02/03/2026		03/03/2026		04/07/2026	
	Species Detected	**%**	**Abundance**	**%**	**Abundance**	**%**	**Abundance**	**%**	**Abundance**
Bacteria	*Clostridium sp.*	7.67	71,000,000	3.93	46,000,000	2.49	33,000,000	1.95	26,000,000
	Streptococcus lutetiensis	8.21	76,000,000	2.16	26,000,000	1.2	16,000,000	0.97	13,000,000
	Escherichia coli	6.02	55,000,000	0.79	9,300,000	0.4	5,200,000	0.29	3,900,000
Fungi	*Candida albicans*	6.0	140	0.0	0	0	0	30.0	3
	Trichosporon sp.	13.0	310	18.0	110	0	0	0.0	0
	Aspergillus flavus	4.0	94	0.0	0	0	0	0.0	0
	Fusarium sp.	4.0	94	0.0	0	0	0	0.0	0
	Nakaseomyces glabratus	4.0	94	0.0	0	0	0	0.0	0
Other Eukaryotes	*Blastocystis sp.*	26.52	7,800	36.47	8,700	32.61	7,900	32.18	8,000
	Blastocystis hominis	20.99	6,200	29.41	7,000	28.99	7,000	28.47	7,100
	Blastocystis sp. subtype 3	19.89	5,900	28.24	6,700	26.57	6,400	25.99	6,500
	Trichuris trichiura	30.94	9,100	3.53	840	0.97	230	0.37	92
	Blastocystis sp. subtype 2	0.0	0	0.0	0	7.25	1,800	11.14	2,800
Virus									

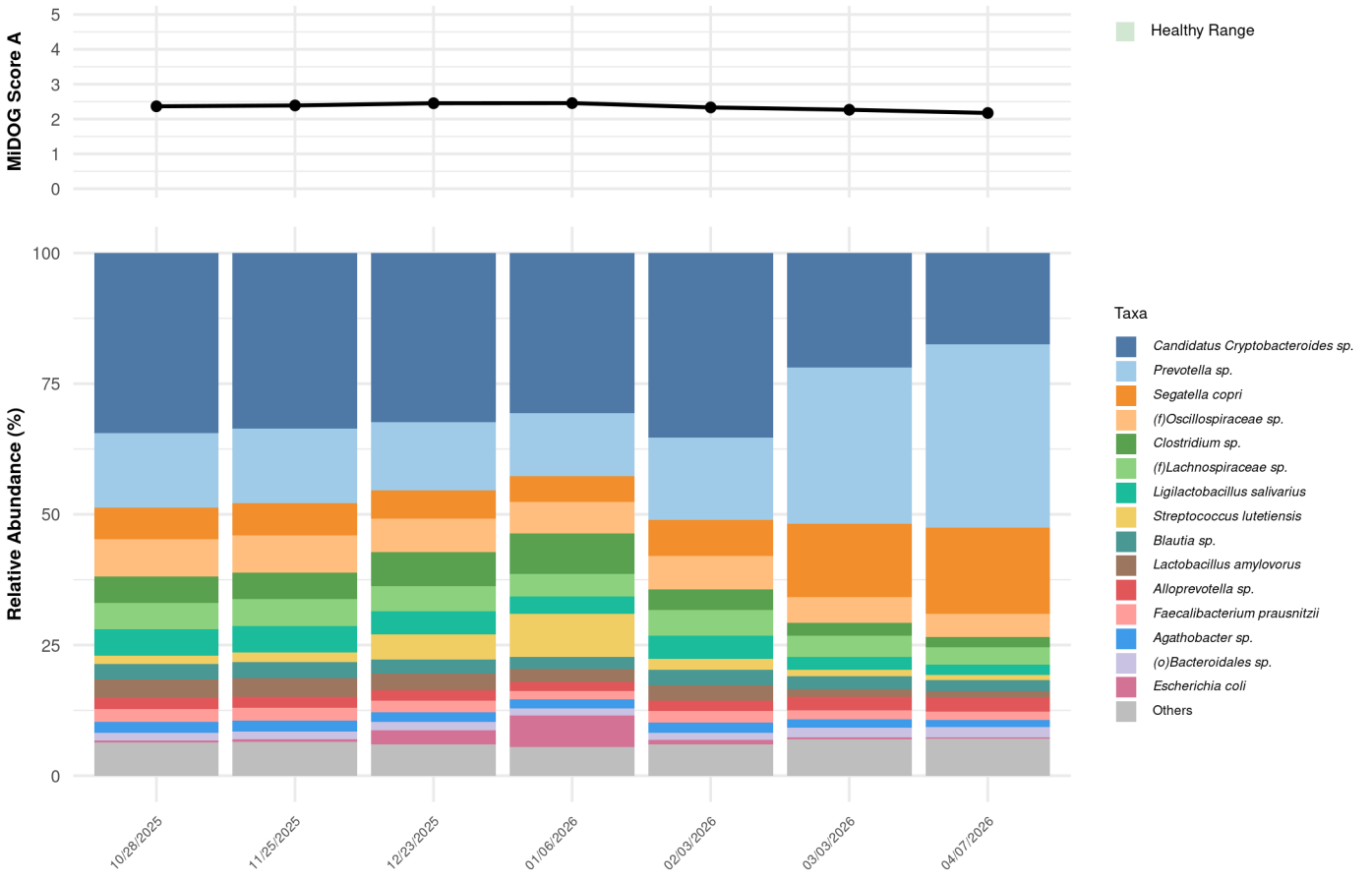
The table above summarizes the presence and abundance of key microbial species across the four most recent sample dates. Each entry includes the relative percentage of each species as well as the abundance detected per sample. The full table can be found HERE.

Potential Pathogenic Bacteria Detected



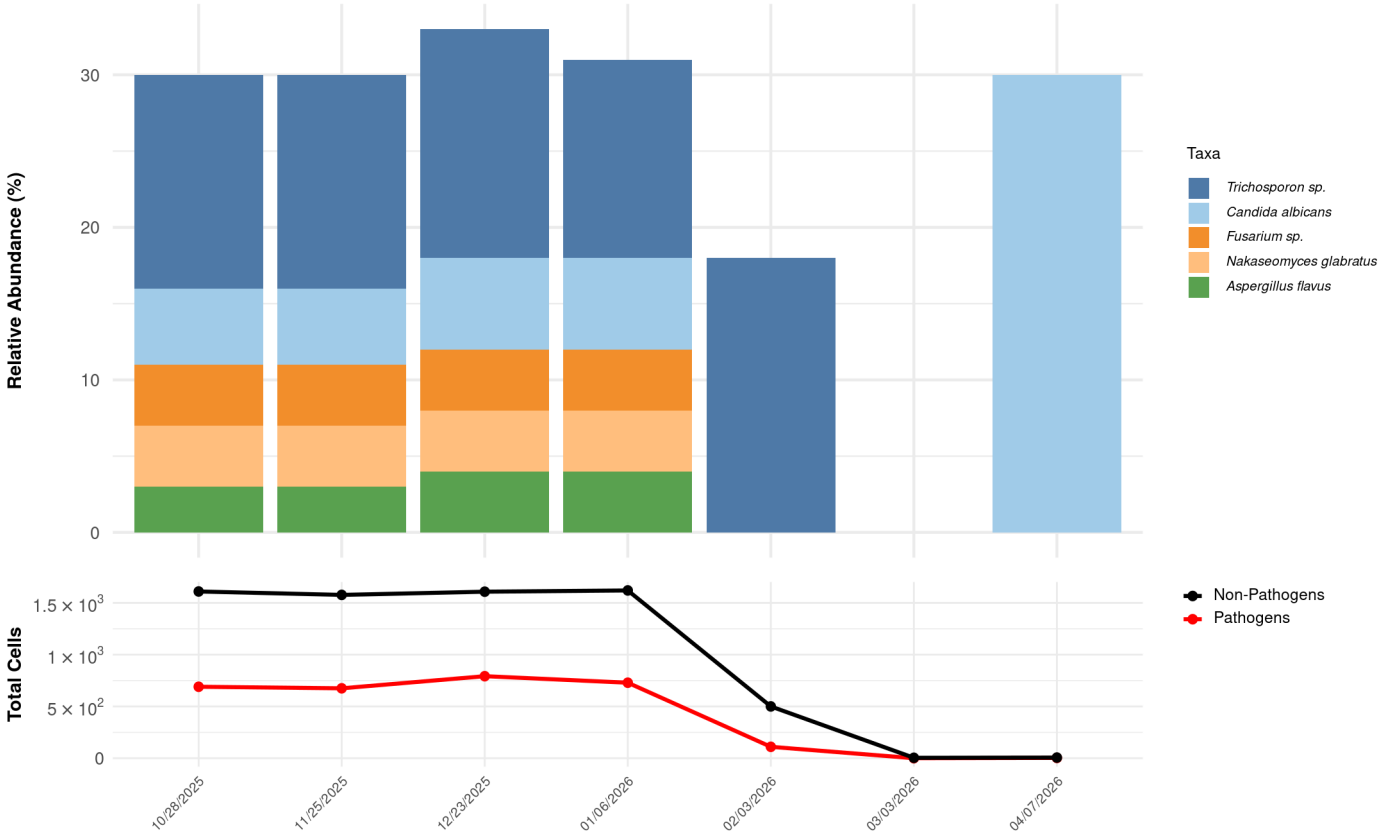
Displayed above are the cell counts and relative abundance (%) of potential pathogenic bacteria detected in above samples, with taxa distinguished by color

Total Bacterial Composition



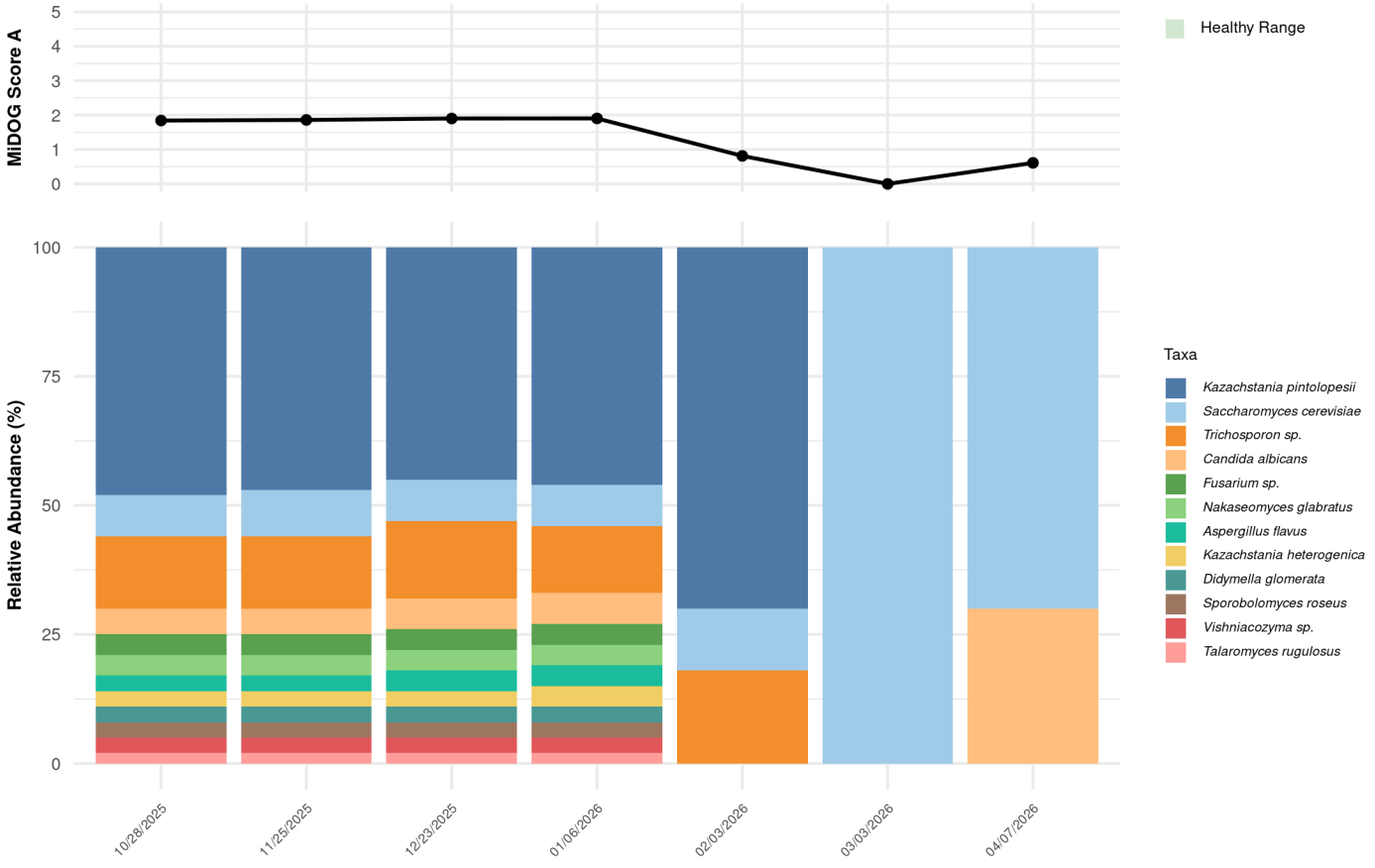
Total bacterial composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full bacterial composition spreadsheet can be found HERE.

Potential Pathogenic Fungi Detected



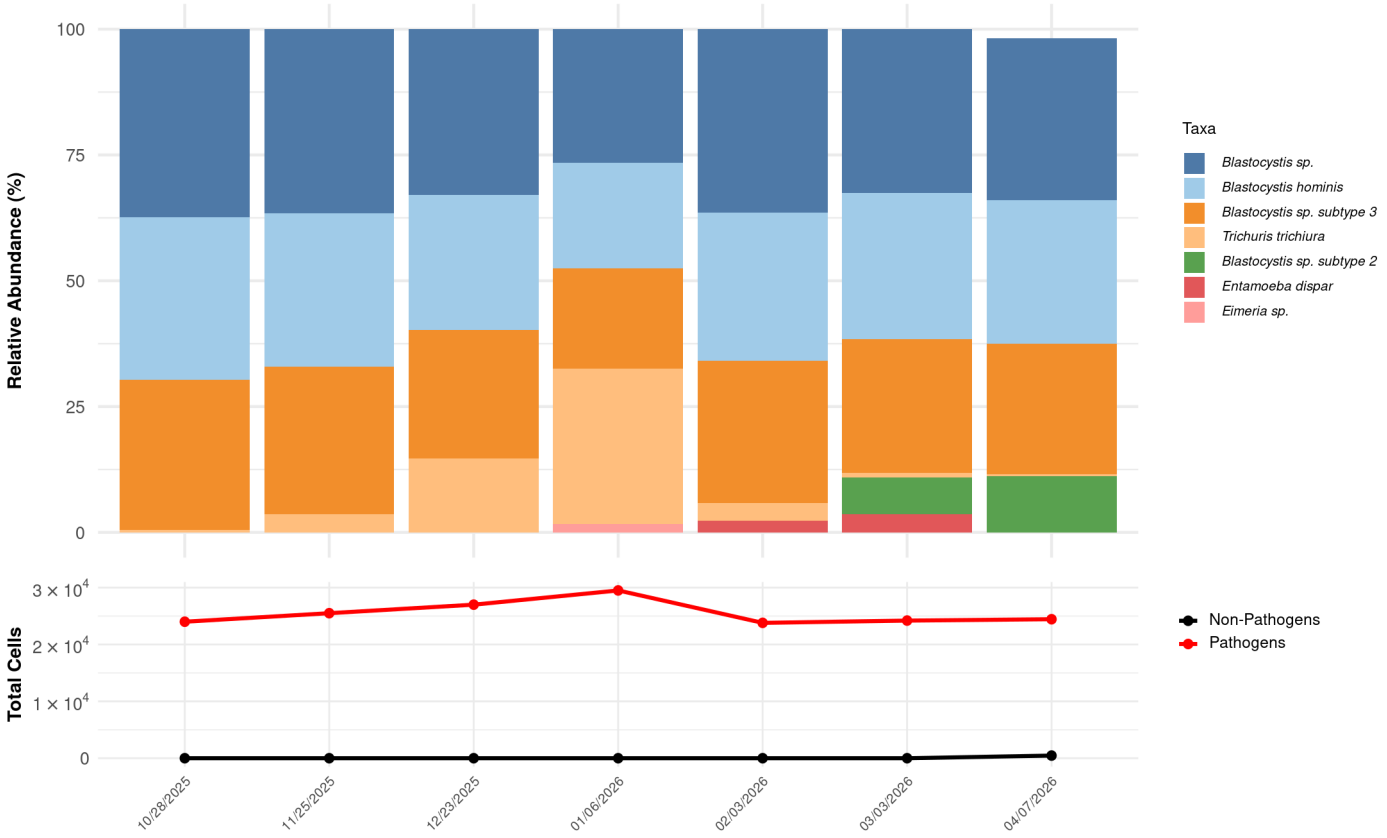
Displayed above are the cell counts and relative abundance (%) of potential pathogenic fungi detected in above samples, with taxa distinguished by color

Total Fungi Composition



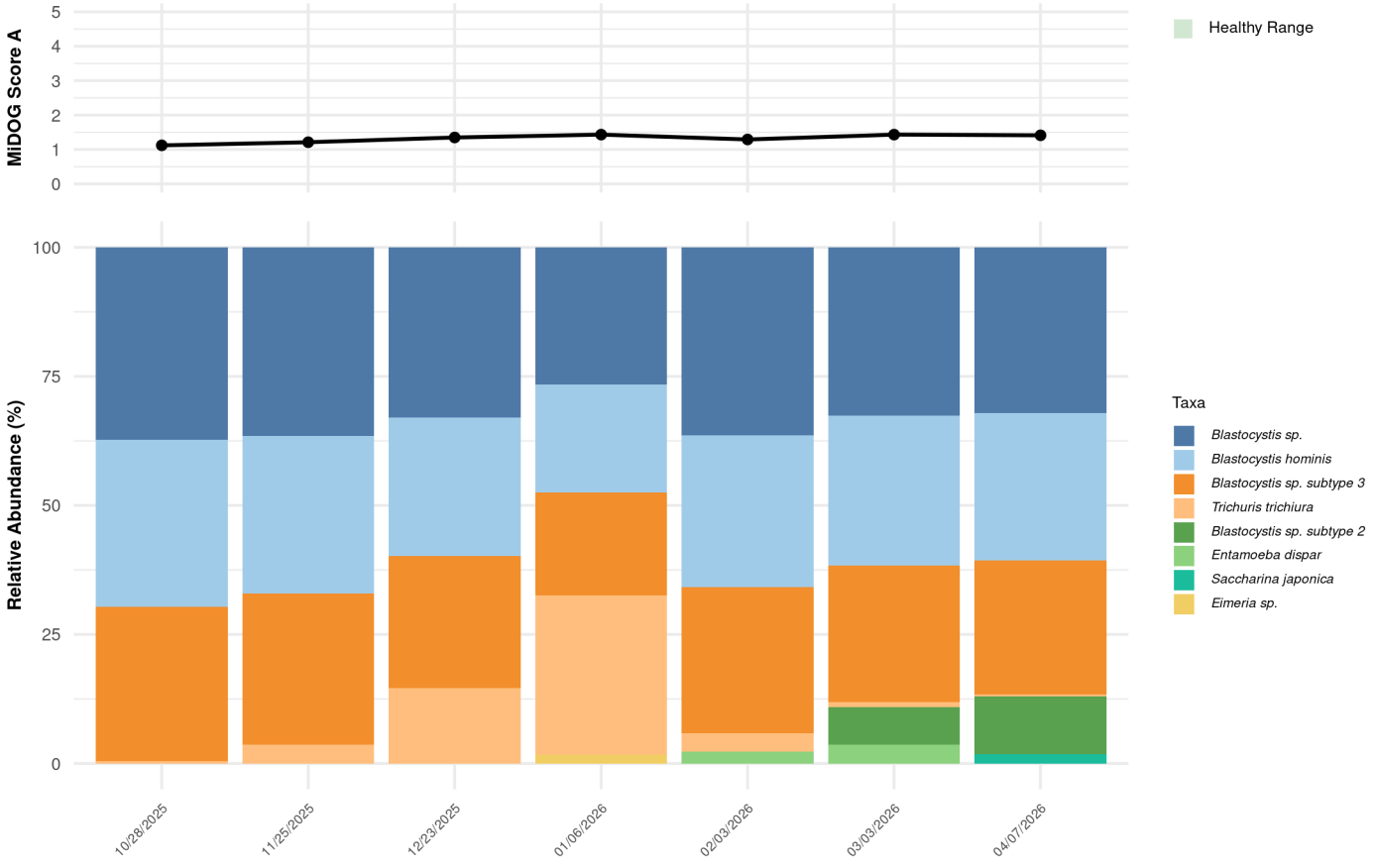
Total fungal composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full fungal composition spreadsheet can be found HERE.

Potential Eukaryotic Pathogen Detected



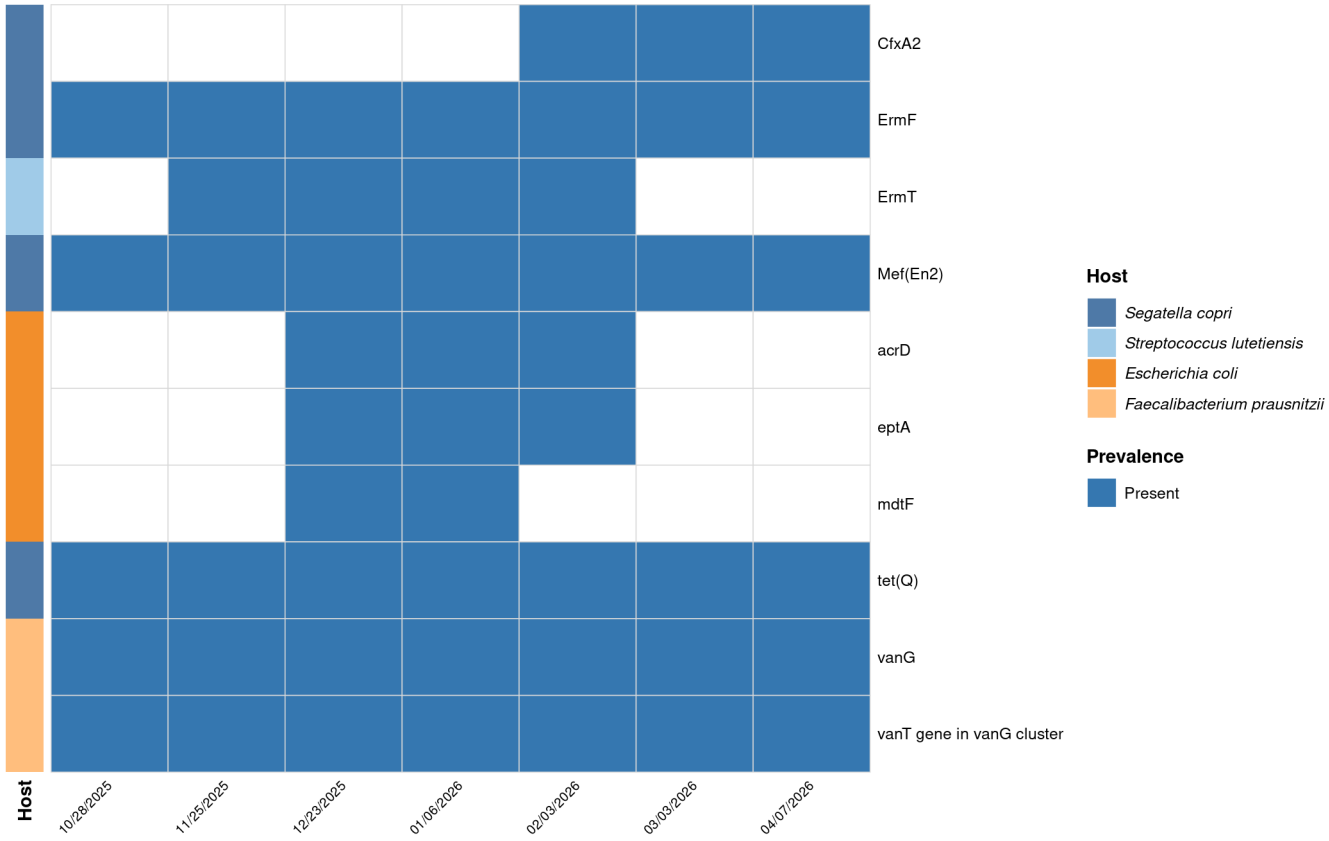
Displayed above are the cell counts and relative abundance (%) of potential parasites detected in above samples, with taxa distinguished by color

Total Other Eukaryotes Composition



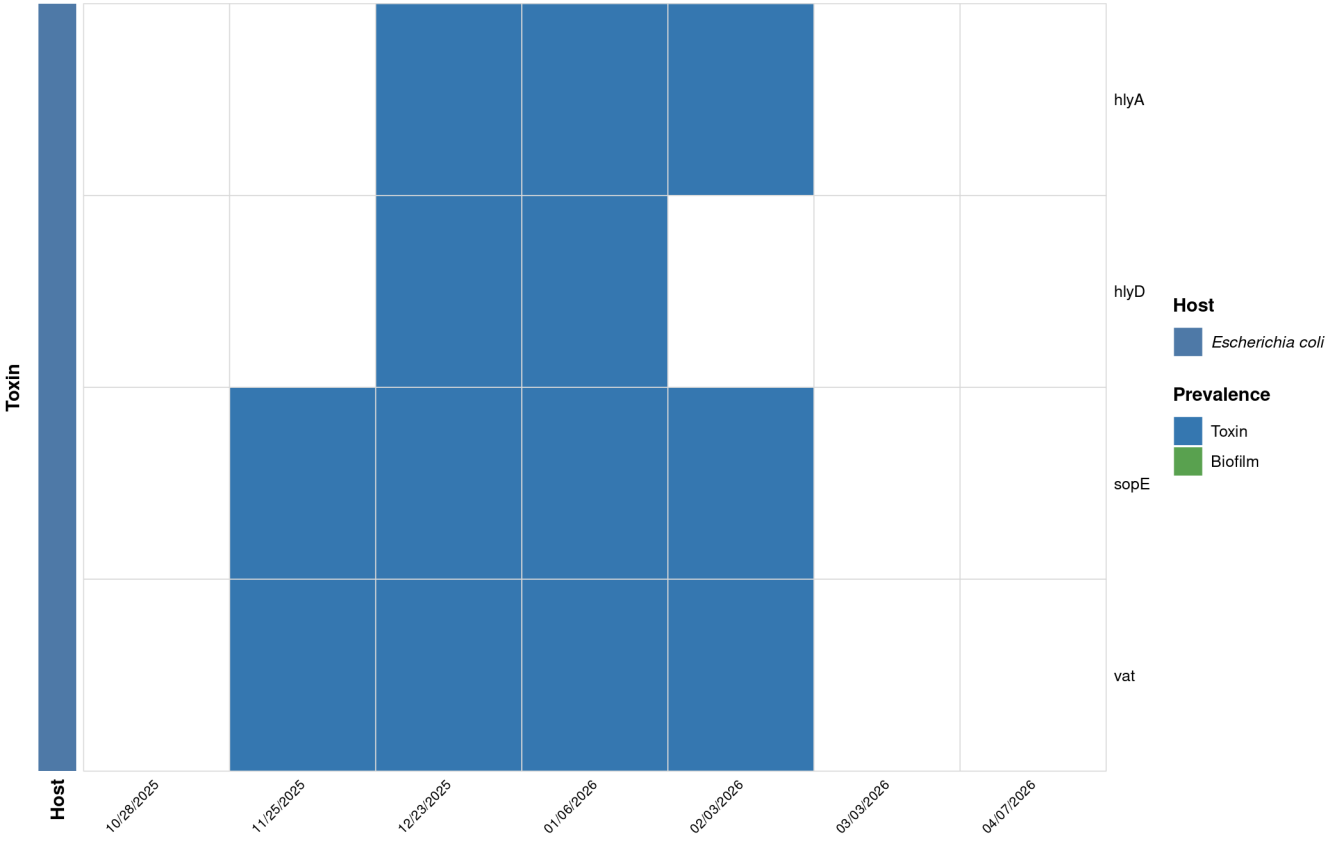
Total other eukaryota composition across samples with diversity scores and relative abundance by taxa; green shading indicates healthy range. The full eukaryota composition spreadsheet can be found HERE.

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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