

<b>Patient Name:</b>	<b>Health Status:</b>	<b>Account #:</b>
<b>Owner's Name:</b>	<b>Ordered by:</b>	<b>Internal ID:</b>
<b>Breed:</b>	<b>Email:</b>	<b>Sample Type:</b> Feces
<b>Age:</b>	<b>Hospital:</b>	<b>Received Date:</b>
<b>Species:</b> Dog	<b>Location:</b>	<b>Report Date:</b>

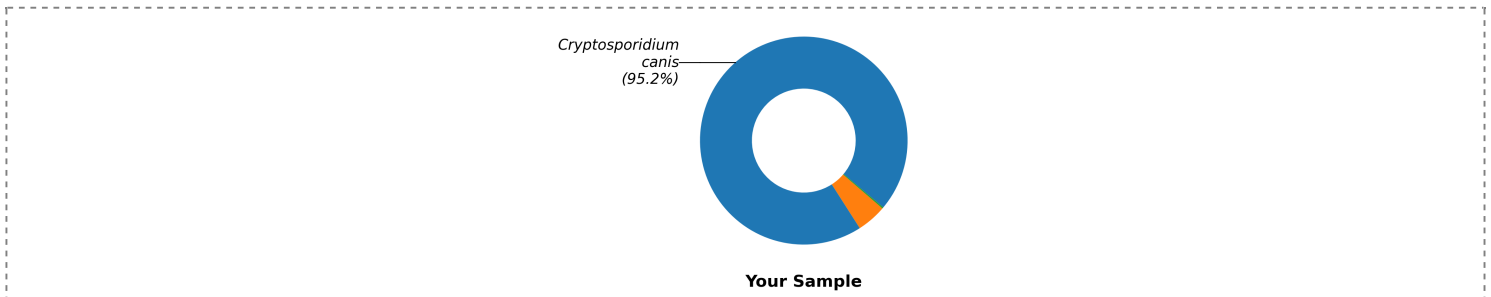
## Potential Clinically Relevant Microbes Detected:

Top 5 potential Bacterial and Eukaryotic pathogens are listed. The comprehensive list of all microbes are shown in page 3.

### Parasites

Species Detected	AID*	Percentage	Cells per Sample	Normal Range	Inferred Status
<a href="#">Cryptosporidium canis</a> [1][2][3]	<a href="#">[Link]</a>	95.2 %	7,700	NA	NA
<a href="#">Cryptosporidium sp.</a> [1][2][3]	<a href="#">[Link]</a>	4.6 %	370	NA	NA
<a href="#">Giardia duodenalis</a> [4]	<a href="#">[Link]</a>	0.2 %	17	NA	NA

### Eukaryota (Excluding Fungi) Composition



Species Detected	AID*	Percentage	Cells per Sample	Normal Range	Inferred Status
<a href="#">Cryptosporidium canis</a> [1][2][3]	<a href="#">[Link]</a>	95.2 %	7,700	NA	NA
<a href="#">Cryptosporidium sp.</a> [1][2][3]	<a href="#">[Link]</a>	4.6 %	370	NA	NA
<a href="#">Giardia duodenalis</a> [4]	<a href="#">[Link]</a>	0.2 %	17	NA	NA

\* AID stands for Animal Infection Database. It is a resource center to provide more information for microbes in animal microbiome settings.

## Download Links of Intermediate Tables

No AMR genes were detected.

## References

1. Carpenter, James W., and Chris Marion. Exotic Animal Formulary-E-Book. Elsevier Health Sciences, 2017.
2. Wallach, Joel D., and William J. Boever. Diseases of exotic animals. Medical and surgical management. WB Saunders Co., 1983.
3. Ballard, Bonnie, and Ryan Cheek, eds. Exotic animal medicine for the veterinary technician. John Wiley & Sons, 2016.
4. Ryan, U., & Cacci<sup>2</sup>, S. M. (2013). Zoonotic potential of Giardia. *International journal for parasitology*, 43(12-13), 943-956.

## Methods

The MiDOG<sup>®</sup> 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 microbial 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<sup>®</sup> 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 patients individual clinical presentation. The information in the MiDOG<sup>®</sup> report has not been evaluated by the FDA.

## Customer Support

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