



# AquaBiomics Microbiome Test Report



## About this report

Generated on: Wed Jan 31 14:29:36 2024

This report summarizes an analysis of DNA from [Bacteria](#) and [Archaea](#) in an aquarium water sample. Thousands of individual DNA molecules from each sample were sequenced, and each DNA sequence compared with DNA databases to identify its origin. The report lists the different kinds of microbes in your sample, and their relative abundance, with a special focus on beneficial and harmful microbes for the saltwater aquarium.

Please check the links provided in each section for more information. If you have any questions about this report, please check the [FAQ](#).

## Information about the sample

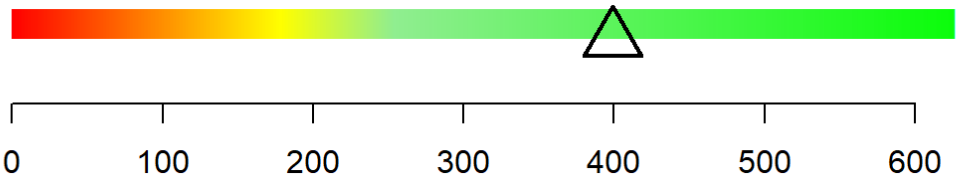
Sample ID	<a href="#">1002426</a>
Sample Name	29-Dec-23
Tank Name	IM 150
Sample Date	12/29/2023 20:15

## Diversity

This score is a measurement of the number of different types of Bacteria or Archaea in the sample. Read more about Microbial Diversity [here](#).

### Diversity Score (Percentile)

399 (90)



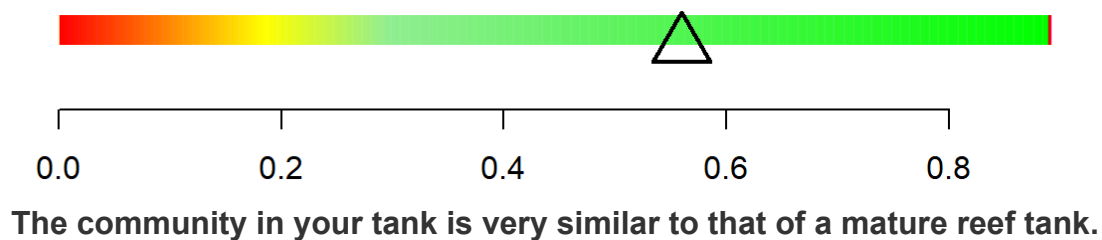
Your sample had a higher diversity than most tanks we've sampled. This is the kind of diversity we aim for in our tanks.

## Balance

This score compares the microbiome in your tank with that of a typical reef tank. High scores indicate a typical community, while low scores indicate an atypical community. Read more about this score [here](#).

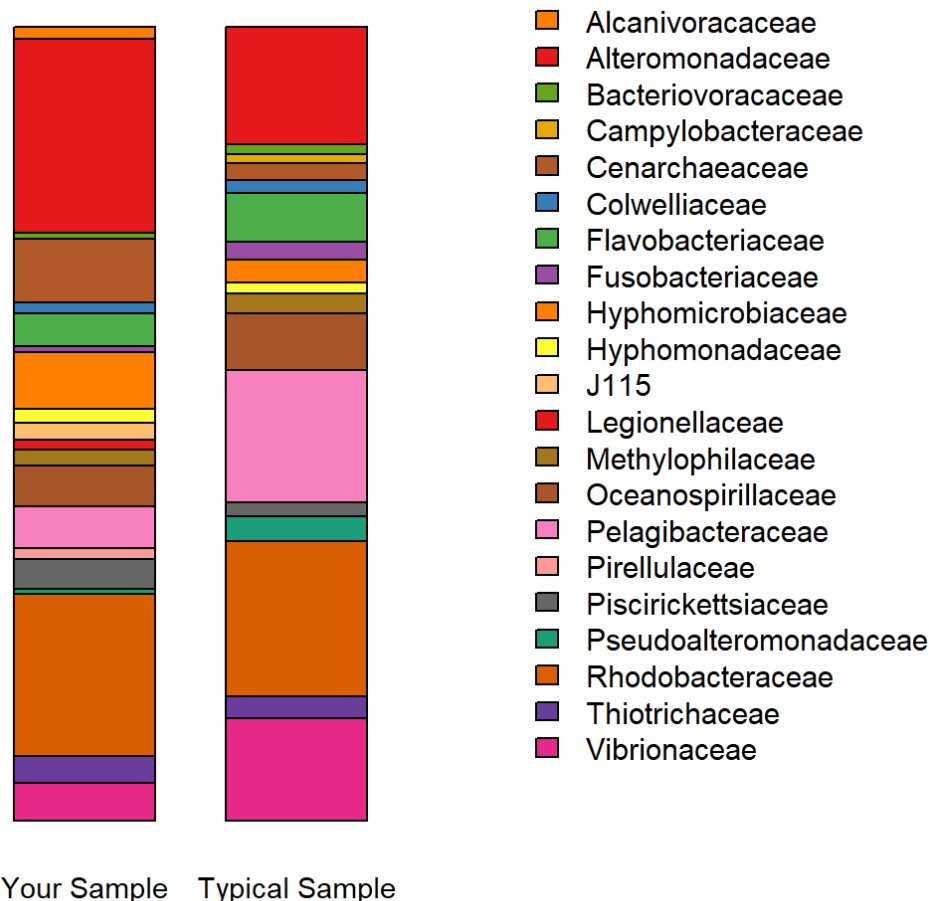
### Balance Score (Percentile)

0.56 (91)



## Community Composition

This figure shows the reasons for your balance score. Compare your sample with the typical community to identify families that are unusually high or low in your sample. Read more about the major families of microbes in reef tanks [here](#).



The size of each bar indicates the relative abundance of each microbial family, coded by color. For clarity, only the families accounting for at least 1% of either community are shown here.

**Your sample showed differences in the relative abundance of one or more of the major microbial families, compared with the typical reef tank. Learn more about these families [here](#) or at the links below.**

#### Excess families (higher than typical)

[Hyphomicrobiaceae](#)

[Cenarchaeaceae](#)

▼ Additional details on excess families

#### Hyphomicrobiaceae

Type	Name (Family)	Your level (Percentile)	Prevalence
104	unclassified (Hyphomicrobiaceae)	1.13% (81)	52.3%
955	unclassified (Hyphomicrobiaceae)	0.74% (79)	62.3%
200	unclassified (Hyphomicrobiaceae)	0.53% (84)	33.4%
4524	unclassified (Hyphomicrobiaceae)	0.26% (88)	24.7%
3746	unclassified (Hyphomicrobiaceae)	0.25% (88)	19.6%
1679	unclassified (Hyphomicrobiaceae)	0.23% (89)	15.2%

2169	unclassified (Hyphomicrobiaceae)	0.21% (89)	21.7%
9772	unclassified (Hyphomicrobiaceae)	0.19% (94)	10.6%
25362	unclassified (Hyphomicrobiaceae)	0.16% (98)	2.9%
98646	unclassified (Hyphomicrobiaceae)	0.02% (99)	2.2%
118808	unclassified (Hyphomicrobiaceae)	0.01% (99)	1.2%
139589	unclassified (Hyphomicrobiaceae)	0.01% (96)	6%
139789	<a href="#">Hyphomicrobium sp.</a> (Hyphomicrobiaceae)	0.01% (98)	2.9%
144656	<a href="#">Hyphomicrobium sp.</a> (Hyphomicrobiaceae)	0.01% (99)	1.1%
151388	unclassified (Hyphomicrobiaceae)	0.01% (100)	0.6%
190765	unclassified (Hyphomicrobiaceae)	0.01% (100)	0.2%
194974	unclassified (Hyphomicrobiaceae)	0.01% (100)	0.1%

### Cenarchaeaceae

Type	Name (Family)	Your level (Percentile)	Prevalence
760	<a href="#">Nitrosopumilus sp.</a> (Cenarchaeaceae)	2.09% (84)	58.1%
73	<a href="#">Nitrosopumilus sp.</a> (Cenarchaeaceae)	0.77% (89)	43.8%
9655	<a href="#">Nitrosopumilus sp.</a> (Cenarchaeaceae)	0.71% (88)	22.8%
338	<a href="#">Nitrosopumilus sp.</a> (Cenarchaeaceae)	0.54% (89)	18.6%

### Deficient families (lower than typical)

[Vibrionaceae](#)

[Pelagibacteraceae](#)

## Nitrifying Community

These communities include ammonia-oxidizing Bacteria (AOB), ammonia-oxidizing Archaea (AOA), and nitrite-oxidizing Bacteria (NOB). Although present at detectable levels in most tanks, there turns out to be more variation in the levels of these groups than many aquarists expected.

### Ammonia-Oxidizing Microbes

Group	Your Level	Typical Range
<b>Total</b>	<b>0.04214</b>	<b>0.00071 - 0.06042</b>
<a href="#">Nitrosococcus</a>	0	0 - 0
<a href="#">Nitrosomonadaceae</a>	0	0 - 0.00087
<a href="#">Nitrososphaeraceae</a>	0.00096	0 - 0
<a href="#">Cenarchaeaceae</a>	0.04118	0.00071 - 0.05955

*Note:*

Typical range is between the 10th and 90th percentiles. High levels (>50th percentile) are color coded green, intermediate levels (between 10th and 50th percentiles) are coded yellow, and low levels (< 10th percentile) are coded red.

### Nitrite-Oxidizing Bacteria

Group	Your Level	Typical Range
<b>Total</b>	<b>0.00138</b>	<b>0 - 0.00289</b>
<a href="#">Nitrobacter</a>	0	0 - 0
Nitrococcus	0	0 - 0
Nitrotoga	0	0 - 0
<a href="#">Nitrospinaceae</a>	0	0 - 0
<a href="#">Nitrospiraceae</a>	0.00138	0 - 0.00289
Nitrolancea	0	0 - 0

*Note:*

Typical range is between the 10th and 90th percentiles. High levels (>50th percentile) are color coded green, intermediate levels (between 10th and 50th percentiles) are coded yellow, and low levels (< 10th percentile) are coded red.

**Your sample showed a healthy nitrifying community with levels similar to a typical reef tank.**

### Cyanobacteria

Group	Your Level	Typical Range
<b>Total</b>	<b>0</b>	<b>0 - 0</b>
<a href="#">Acaryochloridaceae</a>	0	0 - 0
<a href="#">Chlorarachniophyceae</a>	0	0 - 0
<a href="#">Cyanobacteriaceae</a>	0	0 - 0
<a href="#">Nostocaceae</a>	0	0 - 0
<a href="#">Oscillatoriaceae</a>	0	0 - 0
Phormidiaceae	0	0 - 0
<a href="#">Prochloraceae</a>	0	0 - 0
<a href="#">Pseudanabaenaceae</a>	0	0 - 0
<a href="#">Rivulariaceae</a>	0	0 - 0
<a href="#">Spirulinaceae</a>	0	0 - 0
<a href="#">Schizotrichaceae</a>	0	0 - 0
<a href="#">Scytonemataceae</a>	0	0 - 0
<a href="#">Synechococcaceae</a>	0	0 - 0
<a href="#">Xenococcaceae</a>	0	0 - 0

*Note:*

Typical range is between the 10th and 90th percentiles. High levels (>90th percentile) are color coded red, intermediate levels (between 50th and 90th percentiles) are coded yellow, and low levels (< 50th percentile) are coded green.

**Your sample showed little or no evidence of Cyanobacteria.**

## Fish Pathogens

Type	Name	Your level	Average level	Typical range	Prevalence
<b>188</b>	<a href="#">Vibrio fortis</a>	<b>0.289</b>	<b>0.4</b>	<b>0 - 1.5</b>	<b>43.9</b>

*Note:*

Levels are expressed as percent of DNA sequences matching each type. Prevalence indicates the fraction of samples tested that contained each type, expressed as a percent. Type is an arbitrary ID number assigned to each unique sequence found in our database.

Your sample contained one or more Bacterial pathogens of fish. To read more about whether this is a concern, and how you might address it, please see [these notes](#).

► View the full table

## Coral Pathogens

Type	Name	Your level	Average level	Typical range	Prevalence
192531	<a href="#">Serratia_marcescens</a>	0.021	0	0 - 0	0.2

*Note:*

Levels are expressed as percent of DNA sequences matching each type. Prevalence indicates the fraction of samples tested that contained each type, expressed as a percent. Type is an arbitrary ID number assigned to each unique sequence found in our database.

Your sample contained one or more Bacterial pathogens of corals. To read more about whether this is a concern, and how you might address it, please see [these notes](#).

► View the full table

Your sample contained one or more suspected pathogens of corals. To read more about whether this is a concern, and how you might address it, please see [these notes](#).

Type	Name	Your level	Average level	Typical range	Prevalence
438	SCTLD-associated Planktotellea sp.	0.158	0.3	0 - 1.1	25.8
1110	SCTLD-associated Shimia sp.	0.365	0.1	0 - 0.5	22.5

*Note:*

Levels are expressed as percent of DNA sequences matching each type. Prevalence indicates the fraction of samples tested that contained each type, expressed as a percent. Type is an arbitrary ID number assigned to each unique sequence found in our database.

DNA analysis conducted by [AquaBiomics LLC](#).