



# AquaBiomics Microbiome Test Report



## About this report

Generated on: Sat Nov 19 14:54:54 2022

These data provide detailed information on the community of microbes ( [Bacteria](#) and [Archaea](#)) living in your aquarium. For this analysis we extracted DNA from microbes sampled from water and biofilm communities. Universal primers were used to amplify a genetic marker from this combined sample, and thousands of individual DNA molecules from this mixture were sequenced. Each sequence was then compared with public DNA databases to identify its origin.

This report summarizes 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 industry and hobby.

## Information about the sample

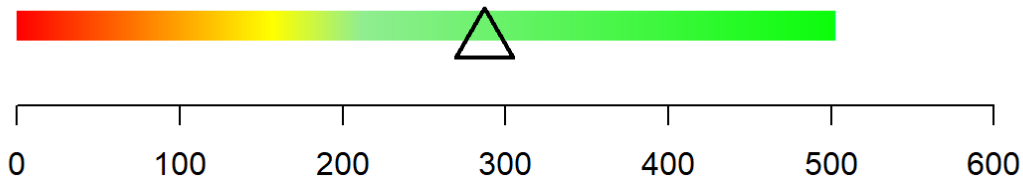
Sample ID	<a href="#">1001189</a>
Sample Name	Cycled Rocks
Tank Name	Rocks that have been cycled in dark for over a year
Sample Date	10/15/2022 11:30am PST

## 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)

287 (83)



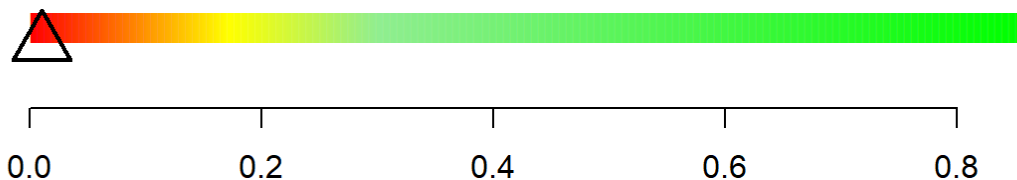
**Your sample had a higher diversity than most tanks we've sampled. This is the kind of diversity we aim for in our tanks.**

## 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)

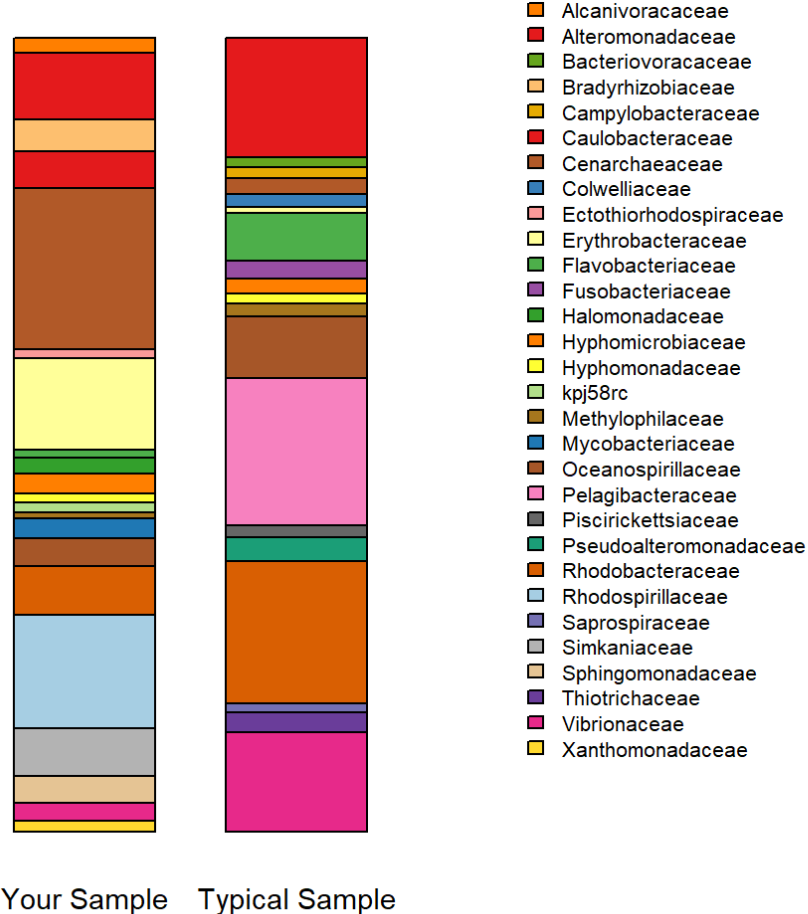
0.01 (2)



**The composition of your tank's community is very different than most tanks we've tested. If you're interested in increasing this score, please see [these notes](#).**

## 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.**

### Higher than typical

[Simkaniaceae](#)

[Rhodospirillaceae](#)

[Erythrobacteraceae](#)

[Cenarchaeaceae](#)

### Lower than typical

[Vibrionaceae](#)

[Rhodobacteraceae](#)

[Pelagibacteraceae](#)

[Oceanospirillaceae](#)

[Flavobacteriaceae](#)

## 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 Frequency	Typical Range
<b>Total</b>	<b>0.02662</b>	<b>0.00058 - 0.05248</b>
<a href="#">Nitrosococcus</a>	0	0 - 0
<a href="#">Nitrosomonadaceae</a>	0	0 - 0.0011
<a href="#">Nitrososphaeraceae</a>	6e-04	0 - 0
<a href="#">Cenarchaeaceae</a>	0.02602	0.00058 - 0.05137

*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 Frequency	Typical Range
<b>Total</b>	<b>0</b>	<b>0 - 0.00302</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	0 - 0.00302
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 Frequency	Typical Range
<b>Total</b>	<b>0</b>	<b>0 - 2e-04</b>
<a href="#">Acaryochloridaceae</a>	0	0 - 2e-04
<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

None of the DNA sequences from this sample matched known fish pathogens.

▼ View the full table

Group	Your Frequency	Typical Range
<b>Total</b>	<b>0</b>	<b>0 - 0.01095</b>
Eubacterium tarantellae	0	0 - 0
<a href="#">Lactococcus garvieae</a>	0	0 - 0
Enterococcus seriolicida	0	0 - 0
Streptococcus parauberis	0	0 - 0
<a href="#">Streptococcus iniae</a>	0	0 - 0
<a href="#">Mycobacterium chelonae</a>	0	0 - 0
<a href="#">Mycobacterium fortuitum</a>	0	0 - 0
<a href="#">Mycobacterium marinum</a>	0	0 - 0
<a href="#">Mycobacterium neoaurum</a>	0	0 - 0
<a href="#">Nocardia asteroides</a>	0	0 - 0
Nocardia salmonicida	0	0 - 0
Nocardia seriolae	0	0 - 0
<a href="#">Renibacterium salmoninarum</a>	0	0 - 0
<a href="#">Aeromonas jandaei</a>	0	0 - 0
<a href="#">Aeromonas salmonicida</a>	0	0 - 0
<a href="#">Serratia liquefaciens</a>	0	0 - 0
<a href="#">Chryseobacterium balustinum</a>	0	0 - 0
<a href="#">Chryseobacterium scophthalmum</a>	0	0 - 0
Tenacibaculum maritimus	0	0 - 0
Tenacibaculum ovolyticus	0	0 - 0
Pasteurella skyensis	0	0 - 0
<a href="#">Pseudomonas anguilliseptica</a>	0	0 - 0
Moritella marina	0	0 - 0
Moritella viscosa	0	0 - 0

Photobacterium damsela	0	0 - 0.00265
<a href="#">Shewanella putrefaciens</a>	0	0 - 0
<a href="#">Vibrio alginolyticus</a>	0	0 - 0
<a href="#">Vibrio cholerae</a>	0	0 - 0
<a href="#">Vibrio fischeri</a>	0	0 - 0
Vibrio fortis	0	0 - 0.0083
<a href="#">Vibrio furnissii</a>	0	0 - 0
<a href="#">Vibrio harveyi</a>	0	0 - 0
<a href="#">Vibrio carchariae</a>	0	0 - 0
<a href="#">Vibrio trachuri</a>	0	0 - 0
Vibrio ichthyenteri	0	0 - 0
Vibrio logei	0	0 - 0
<a href="#">Vibrio ordalii</a>	0	0 - 0
<a href="#">Vibrio pelagius</a>	0	0 - 0
Vibrio salmonicida	0	0 - 0
Vibrio splendidus	0	0 - 0
<a href="#">Halomonas cupida</a>	0	0 - 0
<a href="#">Piscirickettsia salmonis</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.

## Coral Pathogens

None of the DNA sequences from this sample matched known coral pathogens.

▼ View the full table

Group	Your Frequency	Typical Range
<b>Total</b>	<b>0</b>	<b>0 - 0</b>
Vibrio shiloi	0	0 - 0

<a href="#">Vibrio coralliilyticus</a>	0	0 - 0
<a href="#">Vibrio harveyi</a>	0	0 - 0
<a href="#">Aurantimonas coralicida</a>	0	0 - 0
Vibrio rotiferianus	0	0 - 0
<a href="#">Vibrio alginolyticus</a>	0	0 - 0
Vibrio proteolyticus	0	0 - 0
Vibrio charcharvina	0	0 - 0
<a href="#">Serratia marcescens</a>	0	0 - 0
Aquarickettsia rohweri	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.

**None of the DNA sequences from this sample matched suspected coral pathogens.**

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