Aquarium Microbiome Analysis Report

About this report

This report describes the results from DNA analysis of the following sample:

Sample ID	1000175
Sample Name	STN Sample − After Treatment
Tank Name	300g Reef
Sample Date	2020−04−05 04:15 PM
Report Date	04/21/2020 16:58

These data provide detailed information on the community of microbes living in your aquarium. Each type of microbe in your sample was identified by comparing DNA sequences from your sample with a database of DNA sequences from known types. The relative abundance of each sequence can be used to compare the relative abundance of each type across samples.

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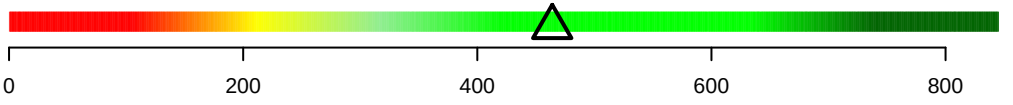
Part 1: Diversity and balance

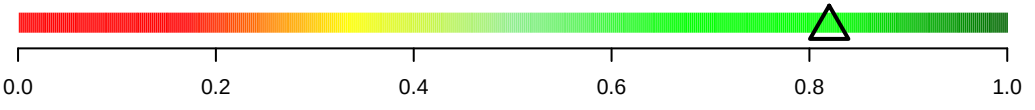
Number of Microbial Types

464



Diversity Score (Percentile)

0.82



Your tank's microbiome is among the least diverse of tanks we tested. *(<25th percentile)*	Your sample was less diverse than at least half the tanks we tested. *(25th to 50th percentile)*	Your sample was more diverse than most of the tanks we tested. *(>50th percentile)*
If you want to increase diversity, consider adding live rock or other natural sources of live microbes.	*Continue to monitor, or increase diversity by adding live microbes from natural sources.*	*Celebrate your success! The diversity of your aquarium's microbiome is higher than the average reef tank.*

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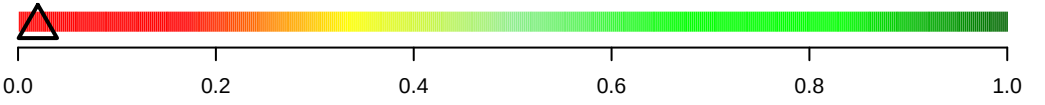
Balance Score (Correlation with Typical Abundance)

0.02



The balance between microbial types in your sample is very different than most reef tanks we tested. *(score < 0.25)* *Considering adjusting your tank's microbiome by changing the conditions, e.g., nutrient types / levels.*	The balance of microbial types in your sample shows both similarities and differences with the typical reef tank *(scores 0.25 to 0.5)* *Continue to monitor, or adjust by changing conditions in your tank.*	The balance of microbial types in your tank is very similar to a typical reef tank. *(scores above 0.5)* *Enjoy your healthy aquarium! Your tank's ecosystem has achieved a balance similar to that of established reef tanks.*

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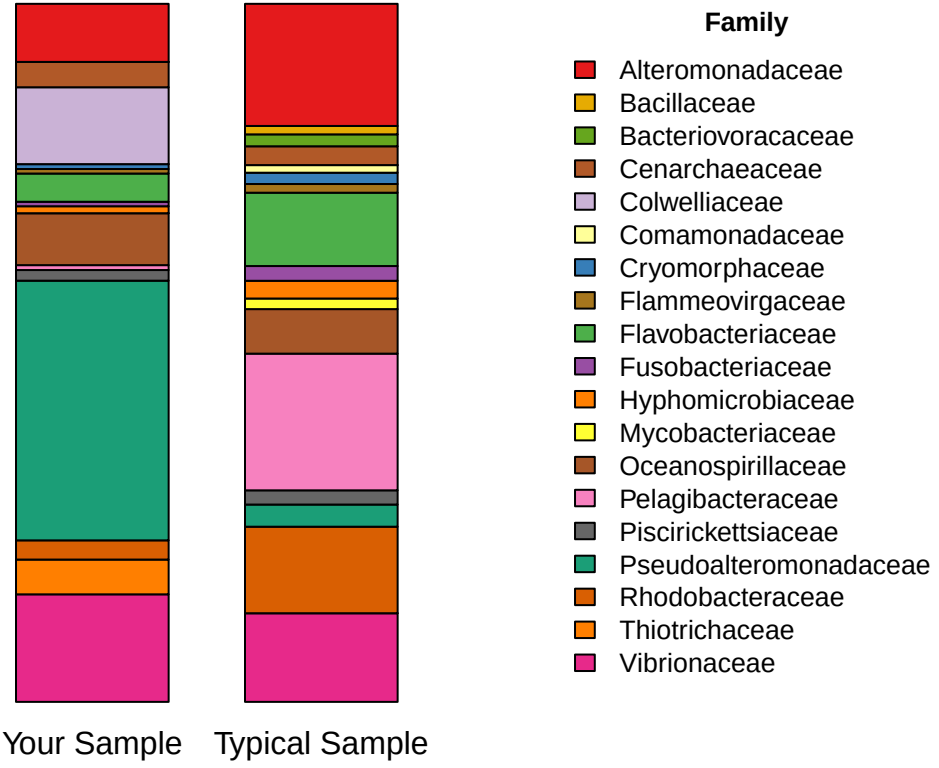
Part 2: Abundance of each family in your sample



Bars indicate the relative abundance of all microbial families accounting for at least 1% of the community either in your sample or the typical reef tank.

DNA analysis conducted by AquaBiomics LLC.

https://aquabiomics.com/

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Part 3: Microbial groups of interest

Ammonia−oxidizing microbes

Group	Your.Frequency	Typical.Range
Ammonia−oxidizing community, total	0.00721	0.00151 − 0.04877
Nitrosococcus	0	0−0.00094
Nitrosomonadaceae	0	0−0.00141
Nitrososphaeraceae	0	0−0
Cenarchaeaceae	0.00721	0.00126−0.04777

Typical range describes the 10th to 90th percentiles.

- above 50th percentile
- between 10th and 50th percentile
- below 10th percentile

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Nitrite−oxidizing groups

Group	Your.Frequency	Typical.Range
Nitrite−oxidizing community, total	0.00056	0 − 0.005
Nitrobacter	0	0−0
Nitrococcus	0	0−0
Nitrotoga	0	0−0
Nitrospinaceae	0	0−0
Nitrospiraceae	0.00056	0−0.0035
Nitrolancea	0	0−0

Typical range describes the 10th to 90th percentiles.

- above 50th percentile
- between 10th and 50th percentile
- below 10th percentile

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Cyanobacteria, by family

Group	Your.Frequency	Typical.Range
Cyanobacteria, total	0.00094	0 – 0.005
Acaryochloridaceae	0	0–7e–04
Cyanobacteriaceae	0.00094	0–0
Phormidiaceae	0	0–0
Pseudanabaenaceae	0	0–0
Spirulinaceae	0	0–0
Synechococcaceae	0	0–0
Xenococcaceae	0	0–3e–04

Typical range describes the 10th to 90th percentiles.

- below 50th percentile
- between 50th and 90th percentile
- above 90th percentile

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Fish pathogens

Group	Your.Frequency	Typical.Range
Fish pathogens, total	0	0 – 0
Eubacterium tarantellae	0	0–0
Lactococcus garvieae	0	0–0
Enterococcus seriolicida	0	0–0
Streptococcus parauberis	0	0–0
Streptococcus iniae	0	0–0
Mycobacterium chelonei	0	0–0
Mycobacterium fortuitum	0	0–0
Mycobacterium marinum	0	0–0
Mycobacterium neoaurum	0	0–0
Nocardia asteroides	0	0–0
Nocardia salmonicida	0	0–0
Nocardia seriolae	0	0–0
Renibacterium salmoninarum	0	0–0
Aeromonas jandaei	0	0–0
Aeromonas salmonicida	0	0–0
Serratia liquefaciens	0	0–0
Chryseobacterium balustinum	0	0–0

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Fish pathogens (continued)

Group	Your.Frequency	Typical.Range
Chryseobacterium scophthalmum	0	0–0
Tenacibaculum maritimus	0	0–0
Tenacibaculum ovolyticus	0	0–0
Pasteurella skyensis	0	0–0
Pseudomonas anguilliseptica	0	0–0
Moritella marina	0	0–0
Moritella viscosa	0	0–0
Photobacterium damselae	0	0–0.0013
Shewanella putrefaciens	0	0–0
Vibrio alginolyticus	0	0–0
Vibrio cholerae	0	0–0
Vibrio fischeri	0	0–0
Vibrio furnissii	0	0–0
Vibrio harveyi	0	0–0
Vibrio carchariae	0	0–0
Vibrio trachuri	0	0–0
Vibrio ichthyoenteri	0	0–0
Vibrio logei	0	0–0

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Fish pathogens (continued)

Group	Your.Frequency	Typical.Range
Vibrio ordalii	0	0–0
Vibrio pelagius	0	0–0
Vibrio salmonicida	0	0–0
Vibrio splendidus	0	0–0
Halomonas cupida	0	0–0
Piscirickettsia salmonis	0	0–0

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Coral pathogens

Group	Your.Frequency	Typical.Range
Coral pathogens, total	0	0 – 0
Vibrio shiloi	0	0–0
Vibrio coralliilyticus	0	0–0
Vibrio harveyi	0	0–0
Aurantimonas coralicida	0	0–0
Vibrio rotiferianus	0	0–0
Vibrio alginolyticus	0	0–0
Vibrio proteolyticus	0	0–0
Vibrio charcharvina	0	0–0
Serratia marscens	0	0–0
Aquarickettsia rohweri	0	0–0