



## Certificate of Analysis

### About this report

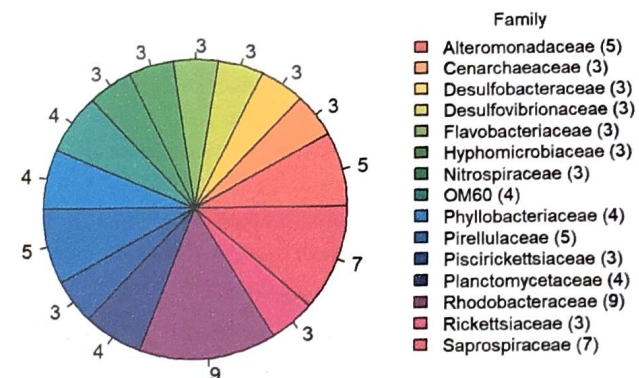
This report summarizes the results from DNA analysis of the community growing in and on a batch of live rock rubble. Universal genetic markers were amplified from microbial (prokaryotic) and other (eukaryotic) DNA in the sample, and thousands of individual DNA molecules from this mixture were sequenced. Each sequence was then compared with public DNA databases to identify its origin. This report summarizes the kinds of organisms detected in the sample, with a focus on beneficial microbes, pathogens, and parasites.

### Information about this sample

Sample ID rock7.2  
Batch Name 1833157-2  
Sample Date 2021-05-31 07:30 AM

### Microbial Diversity

This sample contained DNA from 447 different types of microbes.



This pie chart shows the diversity of each microbial family found in the sample. The size of each slice is proportional to the number of different types (labels on each slice). For clarity, only families containing 3 or more types are shown here. Unidentified sequences lacking any match in public databases are not shown.

### Nitrifying Community

#### Ammonia-Oxidizing Microbes

##### Nitrosomonadaceae

Type	Percent of Community	Genus	Species
46720	0.25	Unknown	Unknown

##### Nitrososphaeraceae

Type	Percent of Community	Genus	Species
4288	0.05	Candidatus	Unknown

##### Cenarchaeaceae

Type	Percent of Community	Genus	Species
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Type	Percent of Community	Genus	Species
73	1.29	Nitrosopumilus	Unknown
2860	0.60	Nitrosopumilus	Unknown
9677	0.43	Nitrosopumilus	Unknown

### Nitrite-Oxidizing Bacteria

#### Nitrospinaeae

Type	Percent of Community	Genus	Species
71549	0.05	Nitrospina	Unknown

#### Nitrospiraceae

Type	Percent of Community	Genus	Species
1603	0.52	Unknown	Unknown
25186	0.17	Unknown	Unknown
71041	0.05	Unknown	Unknown

The nitrifying community in this sample included 9 different types of microbes.

### Bacterial Pathogens

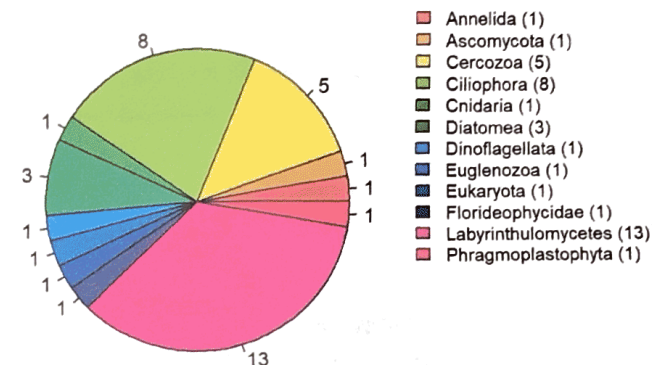
None found.

Complete list of pathogens we screened for:

Eubacterium tarantellae, Lactococcus garvieae, Enterococcus seriolicida, Streptococcus parauberis, Streptococcus iniae, Mycobacterium chelonae, Mycobacterium fortuitum, Mycobacterium marinum, Mycobacterium neoaurum, Nocardia asteroides, Nocardia salmonicida, Nocardia seriolae, Renibacterium salmoninarum, Aeromonas jandaei, Aeromonas salmonicida, Serratia liquefaciens, Chryseobacterium balustinum, Chryseobacterium scophthalmum, Tenacibaculum maritimum, Tenacibaculum ovolyticum, Pasteurella skyensis, Pseudomonas anguilliseptica, Moritella marina, Moritella viscosa, Photobacterium damsela, Shewanella putrefaciens, Vibrio alginolyticus, Vibrio cholerae, Vibrio fischeri, Vibrio furnissii, Vibrio harveyi, Vibrio carchariae, Vibrio trachuri, Vibrio ichthyenteri, Vibrio logei, Vibrio ordalii, Vibrio pelagius, Vibrio salmonicida, Vibrio splendidus, Halomonas cupida, Piscirickettsia salmonis, Vibrio shiloi, Vibrio coralliilyticus, Vibrio harveyi, Aurantimonas corallicida, Vibrio rotiferianus, Vibrio alginolyticus, Vibrio proteolyticus, Vibrio charcharvina, Serratia marscens, Aquarickettsia rohweri

### Eukaryotic Biodiversity

This sample contained DNA from 37 different Eukaryotic sources.



This pie chart shows the diversity of each Eukaryotic Phylum detected in the sample. The size of each slice is proportional to the number of different types from each phylum. Unidentified sequences lacking any match in public databases are not shown.

### Parasites

None of the DNA sequences from this sample matched known parasites.

Group	Description	Percent of eDNA
Amyloodinium	Dinoflagellate parasites responsible for the fish disease Marine Velvet	0
Cryptocaryon	Ciliate parasites responsible for the fish disease Ich	0
Brooklynella	Ciliate parasites responsible for the fish disease Brook	0
Uronema	Ciliate parasites responsible for a fish disease called by the same name	0
Phestilla	Montipora-eating Nudibranchs	0
Amakusaplana	Acropora-eating Flatworms	0
Ancyrocephalidae	Flatworms often called Flukes that parasitize fish	0
Gyrodactylidae	Flatworms often called Flukes that parasitize fish	0
Capsalidae	Flatworms often called Flukes that parasitize fish	0
Turbonilla	Snails in the family Pyramidellidae that parasitize giant clams	0

Group	Description	Percent of eDNA
Trichodina	A ciliated protozoan parasite of fish	0

## Other Animal Pests

None of the DNA sequences from this sample matched known animal pests.

Group	Description	Percent of eDNA
Aiptasia	The glass anemone, a ubiquitous pest	0
Thylacodes	Vermelid snails	0
Asterina	A group of sea stars that includes coral predators	0

## Complete list of Eukaryotes identified

This list includes all Eukaryotes (Animals, Protists, and anything else besides Bacteria or Archaea) that were detected in the sample and identified based on comparison with public DNA sequence databases. DNA sequences that lacked any matches in public datasets could not be identified, and are not shown here. The list is sorted by abundance, from highest to lowest.

Exogone dispar (Annelida), Humulus lupulus (Ascomycota), Gromia oviformis (Cercozoa), Gromia oviformis (Cercozoa), Vampyrellida sp. (Cercozoa), uncultured marine 5327 (Cercozoa), uncultured eukaryote 5405 (Cercozoa), uncultured marine 4872 (Ciliophora), Vorticella oceanica (Ciliophora), Apokeronopsis sinica (Ciliophora), Dysteria procera (Ciliophora), metagenome (Ciliophora), Moneuplotes minuta (Ciliophora), Protocruzia adherens (Ciliophora), Dysteria procera (Ciliophora), Rhodactis indosinensis (Cnidaria), uncultured marine 4812 (Diatomea), Entomoneis sp. (Diatomea), Entomoneis sp. (Diatomea), Dinophyceae sp. (Dinoflagellata), Hemistasiidae sp. (Euglenozoa), Paramoeba branchiphila (Eukaryota), Peyssonnelia rubra (Florideophycidae), uncultured eukaryote 426 (Labyrinthulomycetes), uncultured eukaryote 4942 (Labyrinthulomycetes), uncultured eukaryote 269 (Labyrinthulomycetes), Thraustochytrium multirudimentale (Labyrinthulomycetes), uncultured eukaryote 1120 (Labyrinthulomycetes), uncultured eukaryote 72 (Labyrinthulomycetes), uncultured marine 5243 (Labyrinthulomycetes), Labyrinthula sp. (Labyrinthulomycetes), Thraustochytrium multirudimentale (Labyrinthulomycetes), Thraustochytrium multirudimentale (Labyrinthulomycetes), Thraustochytrium multirudimentale (Labyrinthulomycetes), Thraustochytrium multirudimentale (Labyrinthulomycetes), Oblongichytrium sp. (Labyrinthulomycetes), Festuca arundinacea (Phragmoplastophyta)

## Complete List of Microbes Identified

This list includes all microbes (Bacteria & Archaea) that were detected in the sample and identified based on comparison with public DNA sequence databases. DNA sequences that lacked any matches in public datasets could not be identified, and are not shown here. The list is sorted by abundance, from highest to lowest.

Unclassified Bacteria 67347, Unclassified Phyllobacteriaceae 52061, Unclassified Hyphomicrobiaceae 273, Pseudidiomarina sp., Unclassified Desulfovibrionaceae 96, Unclassified Coxiellaceae 67363, Unclassified Rhodobacteraceae 428, Unclassified Piscirickettsiaceae 761, Hirschia baltica, Unclassified Oleiphilaceae 3600, Unclassified Oleiphilaceae 175, Nitrosopumilus sp., Unclassified Bacteria 7624, Unclassified

Pelagibacteraceae 316, Francisella sp., BD2-13 sp., Pseudidiomarina homiensis, Arcobacter sp., Unclassified Bacteria 1697, Unclassified Hyphomicrobiaceae 2583, Curtobacterium sp., Desulfofrigus sp., Unclassified J115 635, Unclassified Bacteria 67743, Unclassified Rhodobacteraceae 694, Unclassified Desulfobacteraceae 57166, Unclassified Rickettsiaceae 67796, Unclassified Bacteria 67824, Coraliomargarita sp., Unclassified Pseudoalteromonadaceae 13962, Unclassified Bacteria 67861, Nautella sp., Alcanivorax sp., Unclassified Phyllobacteriaceae 1255, Shewanella sp., Unclassified Bacteria 1156, Unclassified Bacteria 878, Unclassified Bacteria 26609, Unclassified Cryomorphaceae 11825, Unclassified Bacteria 378, Unclassified [Amoebophilaceae] 1322, Unclassified Bacteria 58483, Unclassified Bacteria 4270, WH1-8 sp., Unclassified Nitrospiraceae 1603, Unclassified Kiloniellaceae 2300, Bacteriovorax sp., Unclassified Rickettsiaceae 43149, Unclassified Phyllobacteriaceae 1520, Unclassified Erythrobacteraceae 1911, Unclassified Pirellulaceae 11291, Plesiocystis sp., Unclassified Victivallaceae 68887, Unclassified Flavobacteriaceae 1191, Unclassified Bacteria 50216, Unclassified Bacteria 69128, Unclassified Desulfovibrionaceae 69129, Unclassified Kiloniellaceae 422, Unclassified wb1\_P06 69393, Unclassified Pelagibacteraceae 1, Unclassified Cryomorphaceae 275, Unclassified Bacteria 29757, Planctomyces sp., Candidatus sp., Unclassified Rhodospirillaceae 67794, Unclassified Bacteria 69733, Unclassified JTB36 69734, Unclassified Hyphomonadaceae 69735, Marinicella sp., Unclassified Desulfovibrionaceae 67547, Unclassified Pirellulaceae 70185, Unclassified Marinilabiaceae 70187, Sulfurimonas sp., Unclassified Bacteria 70189, Unclassified Saprospiraceae 364, Unclassified Bacteria 70778, Unclassified Legionellaceae 70785, Unclassified Bacteria 67417, Spirochaeta sp., Unclassified C111 71543, Nitrospina sp., Unclassified Helicobacteraceae 8029, Unclassified Bacteria 72594, Unclassified Bacteria 72600, Unclassified Bacteria 72602, Unclassified Bacteria 72604, Unclassified Peptostreptococcaceae 72608, Unclassified Clostridiaceae 59431, Unclassified Haloplasmataceae 71073, Unclassified Bacteria 73981, Unclassified Bacteria 73983, Unclassified Bacteria 73993, Unclassified PAUC26f 74002

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