

The environmental microbial composition and pathogen reduction capability of temperate  
seagrass beds

Corinne Klohmann

A thesis

Submitted in partial fulfillment of the  
Requirements for the degree of

Master of Science

University of Washington

2022

Committee:

Jacqueline L. Padilla-Gamiño

Drew Harvell

Jennifer Ruesink

Chelsea Wood

Program Authorized to Offer Degree:

School of Aquatic and Fishery Sciences

©Copyright 2022

Corinne Klohmann

University of Washington

**Abstract**

The environmental microbial composition and pathogen reduction capability of temperate  
seagrass beds

Corinne Klohmann

Chair of the Supervisory Committee:

Dr. Jacqueline L. Padilla-Gamiño

School of Aquatic and Fishery Sciences

Marine pathogens present serious challenges to aquaculture, fisheries productivity, and marine conservation requiring novel solutions to identify, control, and mitigate their effects. Several ecological habitats, such as mangroves and wetlands can recycle wastes and serve as aquatic filtration systems. In chapter 1 I review how mangroves, shellfish beds, seagrasses, and constructed wetlands can reduce pathogen pressure in coastal ecosystems. I identified mechanisms responsible for pathogen reduction in these ecosystems including sedimentation, biological/chemical filtration, and desalination. Protecting and restoring coastal ecosystems is key to maintaining pathogen filtration capacity, benefiting conservation efforts of threatened host populations, and mitigating large disease outbreaks. In chapter 2 I examine fecal indicator bacteria abundance and microbial community composition when the temperate eelgrass (*Zostera marina*) is present and absent in Puget Sound, Washington, USA. In one Indonesian study, seagrasses reduced the abundance of fecal indicator bacteria, *Enterococcus*, suggesting their ability to act as a natural pathogen reduction system. Eelgrass (*Zostera marina*) is a temperate

seagrass found around the globe that provides a variety of ecosystem services; however, it is not known whether eelgrass reduces bacterial abundance like its tropical counterparts. Additionally, it is not known how the bacterial community in the water column of eelgrass beds changes throughout the year. I found that there were strong differences in alpha and beta diversity between water samples collected during different seasons with higher alpha diversity in the spring and summer compared to the fall and winter. I did not find a consistent reduction of bacterial abundance associated with *Z. marina* beds or differences in microbial communities associated with *Z. marina* beds. I found that high *Enterococcus* abundance was correlated with high temperatures and low levels of pH, dissolved oxygen, salinity, and irradiance. We found the highest bacterial abundances during the summer months with several samples crossing the EPA single sample threshold of 104 CFUs/100mL. I detected *Vibrio*, *Pseudomonas*, and *Enterobacter*, potentially pathogenic bacteria that can all cause illness in human, fish, and marine mammals. My results suggest that seasonality, site, temperature, light and distance from shore are the best predictors of bacterial abundance and microbial community composition. This research has important implications for coastal management and human, animal, and environmental health.

## Table of contents

List of Figures .....	i
List of Tables .....	i

### Chapter 1: **Pathogen Filtration: An Untapped Ecosystem Service**

ABSTRACT.....	1
INTRODUCTION.....	2
<i>Mangroves</i> .....	6
<i>Shellfish beds</i> .....	10
<i>Seagrass beds</i> .....	12
<i>Pathogen reduction using constructed wetlands</i> .....	13
DISCUSSION.....	15

### Chapter 2: **Seasonal Changes in Microbial Community Composition in and around eelgrass (*Zostera marina*) meadows**

ABSTRACT.....	18
INTRODUCTION.....	19
MATERIALS AND METHODS.....	23
RESULTS.....	29
DISCUSSION.....	37
ACKNOWLEDGEMENTS.....	ii
REFERENCES.....	42
SUPPLEMENTARY MATERIALS .....	50

## List of Figures

<b>Fig 1.1</b> Marine diseases and ecosystems with potential filtration capacity.....	4
<b>Fig 1.2</b> Mechanisms involved in natural pathogen filtration.....	9
<b>Fig 2.1</b> Field site locations and descriptions.....	24
<b>Fig 2.2</b> Environmental characteristics in Puget Sound, Washington.....	30
<b>Fig 2.3</b> Monthly <i>Enterococcus</i> counts in Puget Sound, Washington .....	31
<b>Fig 2.4</b> Alpha diversity metrics of microbial communities .....	33
<b>Fig 2.5</b> Bacterial community composition.....	34
<b>Fig 2.6</b> Bray-Curtis dissimilarity and Jaccard emperor PCoA plots (month).....	36
<b>Fig S2.1</b> Map of the <i>Z. marina</i> bed at each field site.....	52
<b>Fig S2.2</b> Monthly average PAR levels at all field site.....	53
<b>Fig S2.3</b> <i>Enterococcus</i> single sample counts by depth .....	53
<b>Fig S2.4</b> PERMANOVA results testing for differences in beta diversity.....	54
<b>Fig S2.5</b> All bacterial genera detected through eDNA analysis.....	55
<b>Fig S2.6</b> Bray-Curtis dissimilarity and Jaccard emperor PCoA plots (site).....	65
<b>Fig S2.7</b> Bray-Curtis dissimilarity and Jaccard emperor PCoA plots (seagrass).....	65

## List of Tables

<b>Table 2.1</b> Time of field collections at study sites.....	25
<b>Table 2.2</b> GLM output showing significant predictors of <i>Enterococcus</i> abundance.....	32
<b>Table S2.1</b> Seasonal environmental conditions at all field sites.....	50
<b>Table S2.2</b> Alpha and beta diversity statistics.....	50
<b>Table S2.3</b> ANCOM results table showing differentially abundant bacterial genera.....	52

## **Acknowledgements**

Thank you to Jackie Padilla-Gamiño for your guidance and willingness to explore the eelgrass ecosystem with me. Many thanks to my committee members Drew Harvell, Jennifer Ruesink, and Chelsea Wood for their encouragement and support as well as many discussions about troublesome analysis and eelgrass ecology.

We would like to thank C. Tang and J. Macke for their help with field collections and laboratory experiments. We would also like to thank M. Groner for expert feedback and support of the project. A huge thank you to the Padilla-Gamiño lab members, M. Roethler, E. Bates, L. Lama, J. Axworthy, S. Tanja, C. Backstrom, N. Viladrich, and T. Brown, for many discussions on data analysis, lab techniques, or just questions like: “where do we keep the gloves”? It was a privilege to work with you all.

None of this work would have been possible without the immense support of my friends and family. John thank you for listening to me give almost the same presentation to you for the past three years and supporting me in every way possible. Dad and Nicole thank you for staying on the phone for hours listening to me when I was frustrated or excited, even when you didn't understand what I was talking about. A big thank you to the graduate student community at SAFS that continually strives to improve our department for those to come. To all of my friends, near and far that encouraged me to find joy in the big and small moments outside of school, thank you.

This project was funded by the Graduate Research Fellowship Program through the National Science Foundation, Sigma Xi, the Hall Conservation Genetics Grant (University of Washington), and by a fellowship from the University of Washington School of Aquatic and Fishery Sciences.

## **Dedication**

This thesis is dedicated to my grandmother, Dr. Klohmann. You continue to be my inspiration, may you read this among the stars.

# Chapter 1: Pathogen Filtration: An Untapped Ecosystem Service

C. A. Klohmann<sup>1</sup>, J. L. Padilla-Gamiño<sup>1</sup>

<sup>1</sup>University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA, USA

Published in *Frontiers in the Marine Science*

Citation: Klohmann CA and Padilla-Gamiño JL (2022) Pathogen Filtration: An Untapped Ecosystem Service. *Front. Mar. Sci.* 9:921451. doi: 10.3389/fmars.2022.921451

## Abstract

Marine pathogens present serious challenges to aquaculture, fisheries productivity, and marine conservation requiring novel solutions to identify, control, and mitigate their effects. Several ecological habitats, such as mangroves and wetlands can recycle wastes and serve as aquatic filtration systems. While nutrient cycling and other ecosystem services of these habitats have been well-studied, their potential to remove pathogens and mechanisms of filtration remain largely unstudied. Here, we review how mangroves, shellfish beds, seagrasses, and constructed wetlands can reduce pathogen pressure in coastal ecosystems. Mangroves may inhibit bacterial growth through phytochemicals in their leaves and remove viruses through desalination in their roots. Some bivalves remove pathogens by excreting pathogens through their pseudofeces and others concentrate pathogens within their tissues. Seagrasses slow flow rates, increase sedimentation rate and may reduce pathogens through allelopathy. Constructed wetlands decrease pathogens through a combination of mechanical, biological, and chemical filtration mechanisms. Protecting and restoring coastal ecosystems is key to maintaining pathogen filtration capacity, benefiting conservation efforts of threatened host populations, and mitigating large disease outbreaks.

## Introduction

Diseases, ubiquitous in the marine environment, are vital for healthy ecosystems but can be damaging when they impact fisheries, aquaculture, and ecosystem engineers (Burge and Hershberger 2020). Pathogens can influence the structure, function, and stability of food webs (Selakovic, de Ruiter, and Heesterbeek 2014) and they are critical to ecosystem dynamics as they play an important role in controlling host population densities and nutrient cycling (Carlson et al. 2020; Lafferty et al. 2008). At the Channel Islands National Park in California, sea urchin pathogens drove a community shift from desolate urchin-barrens toward biodiverse kelp forest assemblages (Behrens and Lafferty 2004). Pathogens can have a positive role in mitigating and controlling algal blooms (Bigalke et al. 2019). Algicidal bacteria limited the growth of three phytoplankton species, allowing other species to increase in abundance and thus have the potential to shift phytoplankton community structure (Bigalke et al. 2019). In New Zealand, nematode, trematode, and acanthocephalan parasites increased food chain length and food web complexity (Thompson, Mouritsen, and Poulin 2005).

High pathogen abundance can cause host population declines with implications for community structure, ecosystem dynamics, and fisheries and aquaculture production (Groner et al. 2016). This can be especially damaging in keystone and economically important species such as the long-spined sea urchin (*Diadema antillarum*) that declined by almost 98% in the 1980's in the Caribbean (Behrens and Lafferty 2004). The decline of this ecologically important grazer decreased herbivory of algae, contributing to coral reef deterioration in the region (Onufryk et al. 2018). Pathogens have the potential to severely compromise fisheries. Epizootic shell disease, caused by bacterial dysbiosis (Groner et al. 2016) (*Figure 1.1a*) substantially contributed to the

decline of one of the most profitable fisheries in the United States (US): the Southern New England lobster stock (Castro et al. 2012; Hoenig et al. 2017). The disease impact was two-fold in that it reduced the abundance of lobsters, with ovigerous females having somewhat higher mortality rates, and rendered the surviving lobsters unappealing for market sale (Lafferty et al. 2015). Another fishery impacted by disease is the black abalone (*Haliotis cracherodii*) along the West coast of the US (Raimondi et al. 2002). This population suffered major die-offs since the 1980's, accounting for total population losses of over 90%. These die-offs were caused by abalone withering syndrome, a chronic condition caused by a Rickettsiales-like organism (WS-RLO) that shrinks the mollusk's foot, preventing the animal from attaching to substrates (Raimondi et al. 2002) (*Figure 1.1a*). While efforts were made to rebuild the population, disease remains a hurdle to restoration and conservation efforts. Similarly, sea star wasting disease, hypothesized to be caused by a densovirus (SSaDV), caused a continental collapse of the sunflower star (*Pycnopodia helianthoides*), a keystone species, and impacted the abundance of 20 asteroid species along the West coast of the US (Harvell et al. 2019; Lamb et al. 2017). Warming ocean temperatures put additional physiological stress on sea stars, decimating wild populations and leading to unprecedented sea star mortality from Alaska to California (*Figure 1a*) (Harvell et al. 2019). Warming events, especially El Niño can trigger disease outbreaks such as the novel ulcerative skin disease that reduced ring-tailed damselfish (*Stegastes beebei*) and king angelfish (*Holocanthus passer*) populations by 78% and 86%, respectively in the Galapagos (Lamb et al. 2018).



Figure 1.1. a) Marine diseases known to severely impact host species including keystone species and ecosystem engineers. (Pictures courtesy of C. Harvell, NOAA Fisheries, AccessScience, O Graham and C Klohmann). Marine ecosystems with pathogen filtration capacity. b) Mangroves (left), seagrasses (middle), and shellfish beds (right). Pictures courtesy of Vecteezy, NOAA Photo Library, and Wikimedia commons.

Large die-offs of seagrass species over the last hundred years have also been attributed to pathogens. Eelgrass wasting disease, likely caused by the etiological agent *Labyrinthula zosterae*, created a large-scale blight in the Eelgrass (*Zostera marina*) population along the Atlantic coast of the US in the 1930s that has still not fully recovered (Figure 1.1a) (Rasmussen 1977). *L. zosterae* is causing outbreaks of disease in eelgrass from Europe to western North America (Groner et al. 2021; Bockelmann et al. 2013).

Pathogen pressure is an issue for human health. Humans can experience infections, gastrointestinal and respiratory diseases, and other health effects when exposed to viral and bacterial pathogens in the ocean (Graciaa et al. 2018; Griffin et al. 2003). We must look to innovative, sustainable, and creative solutions to manage ocean pathogens to limit their spread and effects. Filtration is an important ecosystem service to consider for removing and containing pathogens in the coastal environment. Filtration is defined as the reduction of pathogens in the water column by a variety of means including the reduction of water speed (i.e., flow rate), particle interception, biochemical transformation of nutrients and contaminants, absorption of water and nutrients, and sedimentation (Brauman et al. 2007; Kuehn and Mueller 2000; "Constructed Treatment Wetlands" 2004; Wu et al. 2016).

Natural filtration in coastal environments can occur by vegetation (i.e., via seagrass, salt marshes and mangroves) and shellfish beds (Burge et al. 2016; Lamb et al. 2017). However, these natural filtration services may be in danger as coastal ecosystems are threatened by habitat loss (Halpern et al. 2008), climate change (Harley et al. 2006), and disease (Rasmussen 1977). The planet has lost about 50% of its wetlands since 1900 (Davidson 2014) and seagrasses, salt marshes and mangroves are all declining globally (Halpern et al. 2008). Recent estimates indicate that mangroves and seagrass beds are declining annually by 0.13% and 7%, respectively (Evans et al. 2018; Goldberg et al. 2020). Bivalve populations tend to be more intensely managed since they are an important source of protein; however, it was estimated that globally, 85% of oysters reefs have been lost (Beck et al. 2011). Since the 1970's mussel (*Mytilus edulis*) populations declined by more than 60% in the gulf of Maine, USA (Sorte et al. 2017) and mussel bed communities declined by 58.9% along the West coast of the United States (Smith, Fong, and

Ambrose 2006). Bivalve populations have declined in Europe but are increasing in Asia (Wijsman et al. 2019).

New research seeks to bolster natural filtration systems to decrease pathogen pressure and improve human health. Investing in natural filtration systems is an affordable and low-maintenance option when compared to wastewater treatment facilities, which cost between \$250,000-\$10,000,000 USD for installation in the United States (“How Much Does an Industrial Water Treatment System Cost?” 2017). Restoring and protecting wetlands can sustainably reduce pathogen pressure in coastal ecosystems by supplementing existing wastewater treatment strategies. In terrestrial systems, forest cover and proximity to forested areas can decrease childhood diarrheal infections (Herrera et al. 2017), suggesting that conserving forests and riparian vegetation has the potential to limit disease. In Germany, riverbank filtration (water passed through the bank of the river) has been used for over 100 years to purify drinking water, providing approximately 16% of all German drinking water (Kuehn and Mueller 2000).

Despite recent efforts to better understand pathogen pressure in the ocean (Harvell and Lamb 2020; Tracy et al. 2019) we still have an incomplete understanding of how these pathogens are controlled in marine systems, and how they will impact marine and human health. So far studies suggest that disease is increasing in certain systems like corals reefs but may be declining in fishes and elasmobranchs (Tracy et al. 2019). It is also unclear whether the systems severely impacted by disease outbreak are lacking a filtration system or have one that has been impaired in some way. Here, we examine the role that coastal marine species, namely (1) mangroves, (2) shellfish beds (mussels and oysters), (3) seagrasses, and (4) constructed wetlands, play in pathogen filtration and the mechanisms that decrease pathogen loads.

### *Mangroves*

Mangrove forests are coastal ecosystems widespread in the intertidal zone in tropical and subtropical areas, covering 136,000 km<sup>2</sup> globally (*Figure 1.1b*) (Spalding and Maricé, 2021). These forests provide key ecosystem services such as carbon sequestration, nursery habitat for fish, and coastal protection. Mangroves reduce excess nutrients in coastal waters, including nitrogen and phosphorous (Lin and Dushoff 2004), and are resilient plants capable of exuding and expelling salts, enabling them to thrive in highly saline environments (Spalding and Maricé, 2021). Tropical shrimp farms utilize mangroves' natural biofiltration properties to efficiently remove excess nutrients (Buhmann and Papenbrock 2013). They are also the largest store of carbon in the coastal zone and can reduce ocean acidification (Lin and Dushoff 2004; Sippo et al. 2016). Mangrove trees buffer against acidic water using their roots by metabolizing organic matter from their carbon-rich and oxygen-poor soils and releasing alkaline water in return (Sippo et al. 2016). Mangroves are so efficient at this process that waters within mangrove forests can have a pH as high as 8.1, whereas the seawater measured outside of the forest usually has a pH of 7.3 (Sippo et al. 2016).

Human and fish pathogens are filtered by mangroves. The phytochemicals within mangrove leaves and fungi found in their root sediments may assist in killing bacterial pathogens (Sahoo et al. 2012; Thatoi, Behera, and Mishra 2013). Organic solvent extracts of leaves from five mangrove species in the Philippines inhibited growth of pathogenic fish bacteria (Choudhury et al. 2005). These extracts could be used in aquaculture facilities to reduce disease in fish (Choudhury et al. 2005). Mangrove leaf extracts inhibit the growth of human pathogens such as *Staphylococcus* and *Salmonella* (Sahoo et al. 2012). Another study inoculated compost with fungi isolated from mangrove sediments and found that plants grown in the fungal mangrove soil had higher disease defenses than plants without the fungi (Ameen and Al-

Homaidan 2021). Mangroves have also been referred to as “natural wastewater wetlands” (Wu et al. 2008) and considered as secondary wastewater treatment systems in China due to their filtration capabilities (Palacios et al. 2021)

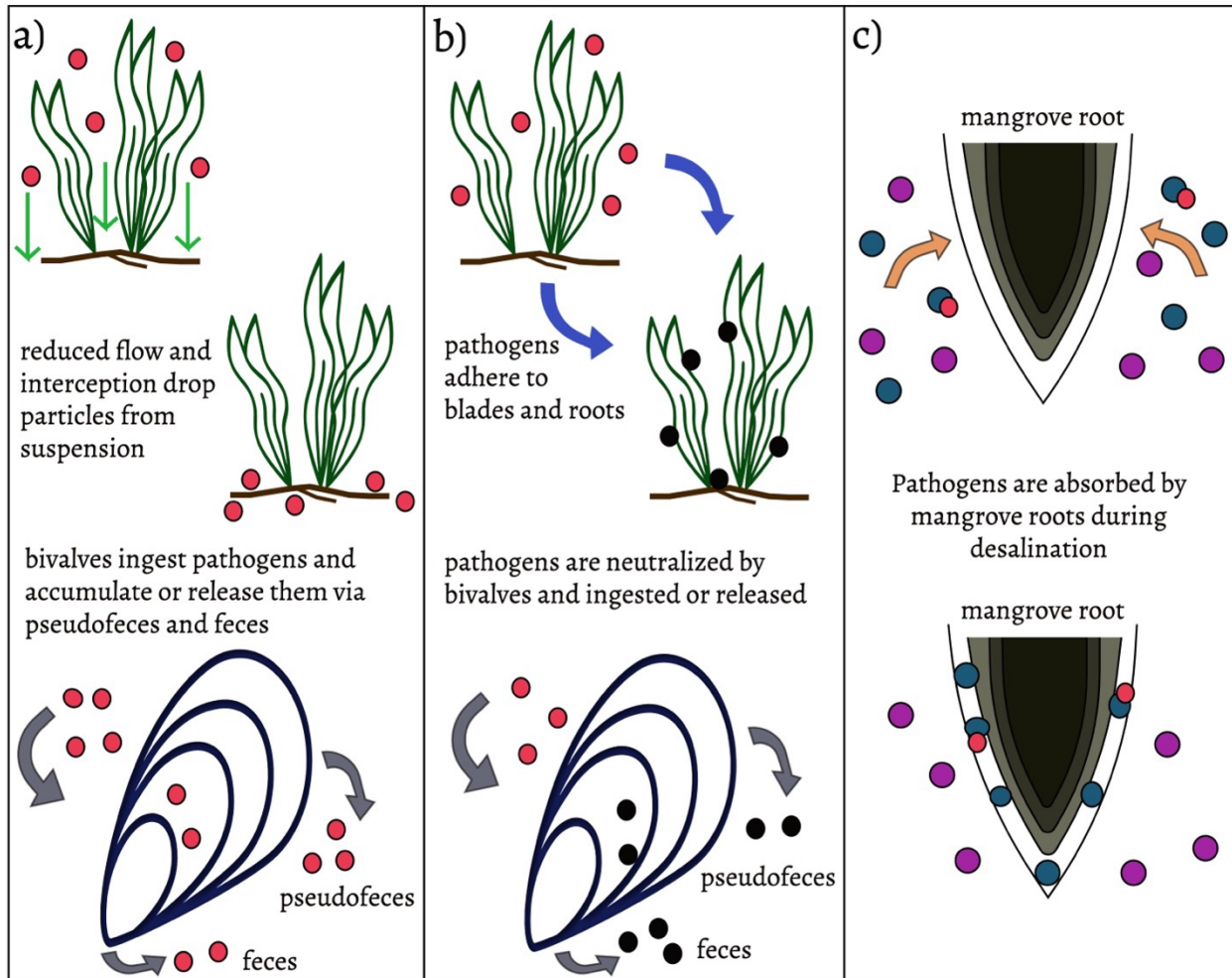
Mangrove roots, may reduce viral pathogens as they are efficient desalinators, removing up to 90% of sodium ions from seawater (Kim et al. 2016). The outermost root layer has a negative surface potential, attracting the positively charged sodium ions and repelling the negatively charged chlorine ions. These root potentials trap sodium ions in the first (outer) root layer, enabling fresh water to enter the inner roots (Kim et al. 2016) (*Figure 1.2c*). Mangrove desalination may be an important mechanism for pathogen filtration, as salts promote viral absorption due to their negative charge (Lukasik et al. 2000). This charge is hypothesized to increase hydrophobic interactions between viruses and the roots, which may lead to viral absorption by the mangroves (Lukasik et al. 2000).

For centuries, mangrove extracts were used to treat a variety of human health issues, and microbial compounds found in mangrove leaves and roots can kill antibiotic-resistant bacteria (Durai and Radhakrishnan 2016; Abeysinghe 2010; Saad et al. 2011; Alizadeh Behbahani et al. 2018; Audah 2020). These services could make mangrove forests very efficient pathogen filtration systems; however, more research is needed to better understand how we can best utilize mangroves to remove pathogens from coastal waters.

## Sedimentation

## Biological/Chemical

## Desalination



● Active pathogen ● Neutralized pathogen ● Na<sup>+</sup>ion ● Cl<sup>-</sup>ion

Figure 1.2. Mechanisms involved in natural pathogen filtration. a) Sedimentation – The removal of pathogens from suspension. This mechanism does not neutralize pathogens but removes them from the environment, it is utilized in seagrasses, bivalves, and constructed wetlands. b) Biological/Chemical filtration – the removal of pathogens through adhesion, consumption, and inhibition (allelopathy). Neutralizes pathogens and/or removes them from the environment. Utilized in seagrasses, bivalves, constructed wetlands, and mangroves. c) Desalination – the removal of sodium ion from salt water. Salt may promote viral absorption due to their negative charge, potentially removing viruses from the seawater. This mechanism is utilized by mangrove roots.

## *Shellfish beds*

Bivalves (Phylum Mollusca) are favorable pathogen filtration specialists due to their high filtration capacity, ubiquity in many ecosystems, tolerance for poor water quality, and abundance. An individual filter-feeding bivalve can filter 10-100 gallons of water a day using their gills (Burge et al. 2016). Bivalves feed by capturing particles from the water column, primarily phyto- and zooplankton, but they can also consume bacteria, viruses, and other organic matter in the process. Bivalves are selective feeders and particle capture depends on size, density and surface chemical compounds (Burge et al. 2016). Some pathogens may be killed within bivalve gills and gut tissue during ingestion and digestion, but most are likely expelled as feces or pseudofeces (*Figure 1.2*). These feces and pseudofeces remove pathogens through sedimentation, sinking out of the water column along with attached bacteria and viruses (Burge et al. 2016). For example, eelgrass plants had fewer lesions from wasting disease (*Labyrinthula zosterae*) when cocultured with oysters (Groner et al. 2018). Bivalves may also inhibit microbial growth through the production of peptides and polypeptides (Zannella et al. 2017). Additionally, mussels are used at aquaculture facilities to reduce bacterial and eukaryotic pathogen abundance in fish farms (Voudanta et al. 2016).

While bivalves may remove pathogens due to their filtration efficiency, they could also store them in their tissues. Some studies found concentrated pathogens within filter-feeder gill tissues, implicating bivalves as reservoirs for pathogens, and in some cases, amplification (Ben-Horin et al. 2015; Harvell and Lamb 2020). Accumulation occurs when pathogens do not degrade and instead build up inside the bivalve and can lead to transmission to species that consume the filter feeder (Burge et al. 2016). Specifically, clams and mussels can accumulate and transmit *Vibrio haemolyticus* to humans (Harvell and Lamb 2020). Mussels off the coast of

California have tested positive for *Toxoplasma gondii*, the causative agent of toxoplasmosis, the same strain known to infect sea otters in the region (Miller et al. 2008). This potential transmission renders bivalves a less sustainable option for natural filtration, as shellfish beds present an infection risk to their predators. However, recent research has shown that oyster aquaculture may reduce pathogens for wild oyster populations as long as aquaculture stocks are harvested before they can spread disease (Ben-Horin et al. 2018).

Bivalves grow in very dense clusters, potentially increasing their filtration ability (*Figure 1b*). Mussels (*Mytilus trossulus*) can reach densities of 35 individuals per 100 cm<sup>2</sup> in the intertidal zone and up to 90 individuals per 100 cm<sup>2</sup> at aquaculture facilities (Kirk, Esler, and Boyd 2007). Given the large distribution of bivalves, their filtration efficiency, and high densities, shellfish beds have the potential to reduce pathogen loads in coastal waters (Ben-Horin et al. 2015). Bivalves could also be used to monitor pathogens and have been used to monitor pollutants. In Poznan, Poland, clams are used as bioindicators to assess water quality: In the presence of even small concentrations of pollutants, the clams will close their shells as a defense mechanism to prevent ingesting harmful or lethal items. Sensors glued to clams are triggered when the bivalves close, which initiates a shutoff of the water supply. This biological sensor system provides a remarkable means of monitoring environmental pollutants at very little cost (Micu 2020). The National Oceanic and Atmospheric Administration's (NOAA) "Mussel Watch" program used bivalves as environmental indicators by establishing oysters in the Chesapeake Bay, Maryland to monitor environmental contamination. Scientists tested oyster tissues for pharmaceutical products, pesticides, and other contaminants, detecting 98 different contaminants using this ecosystem-based monitoring approach (Apeti et al 2018). Complementary monitoring methods can be developed with bivalves to filter, monitor and detect

pathogens in the natural environment. One example is an oyster fishery in Myanmar that detected pathogenic bacterial in bivalve tissues, illustrating the impacts of agricultural runoff on coastal ecosystems (Littman et al. 2020)

### *Seagrass beds*

Seagrass beds are another ecosystem hypothesized to remove pathogens and are one of the most important coastal ecosystems, providing \$1.9 trillion USD in nutrient cycling services annually (Waycott et al. 2009) (*Figure 1.1b*). Additionally, seagrasses act as a “nutrient pump” by absorbing nutrients from the soil and releasing these nutrients through their leaves (Fourqurean 2002). Seagrasses are estimated to cover 600,000 km<sup>2</sup> of the coastal floor from the Arctic circle to the tropics, and some beds are large enough to be seen from space, earning them the name “forests of the sea” (Cullen-Unsworth and Unsworth 2013).

While seagrasses are well studied, their ability to filter pathogens from the water column was only recently identified. In the tropics, researchers found that seagrass beds are associated with reduced abundances of human, fish, and invertebrate pathogens (Lamb et al. 2017). This reduction of pathogens not only improves human health but also benefits corals that have fewer diseases in seagrass beds (Lamb et al. 2017). To date, little is known about the underlying mechanisms involved in the reduction of these pathogens. However, it is likely that a combination of sedimentation, a decrease in water flow rate, and mechanical and chemical filtration contribute to seagrasses’ reduction of pathogens (S. Wu et al. 2016) (*Figure 1.2a and 1.2b*). Ocean flow rates are reduced by up to 40% within seagrass meadows, which may lead to pathogen particles dropping out of suspension (Lamb et al. 2017). In the South China Sea researchers found that one seagrass species, *Enhalus acroides*, trapped pathogens within its beds thus removing bacteria from the water (Deng et al. 2021). Phytochemicals within the seagrass

plants may also kill pathogens, but this mechanism is still unclear (Babuseviam et al. 2017).

*Thalassia hemprichii*, likely inhibited pathogens using antimicrobial chemical compounds such as phenol, flavonoid, and tannins (Deng et al. 2021).

Eelgrass (*Zostera marina*), a temperate seagrass that provides \$87,000 of ecosystem services per hectare annually (Babuseviam et al. 2017), has been shown to exclude harmful dinoflagellates (Jacobs-Palmer et al. 2020). Researchers discovered significantly lower dinoflagellate abundances inside and around the *Z. marina* bed, such that *Z. marina* can form a ‘halo’ of dinoflagellate exclusion, up to 16 meters beyond the extent of the meadow (Jacobs-Palmer et al. 2020). Other studies found reduced algal growth due to seagrass phenolic compounds (DellaGreca et al. 2000) and antilarval and antibacterial properties from ethanol extract from a seagrass species in the South China Sea (Qi et al. 2008). Allelopathic activity in seagrasses, the defensive release of chemicals, and biological interactions of the micro and macro epibionts may also play a role in pathogen filtration services in this important ecosystem (Jacobs-Palmer et al. 2020). The outbreaks of the unicellular protist *L. zosterae* (Sullivan et al. 2018) in eelgrass beds (M. Groner et al. 2021; Bockelmann et al. 2013) suggest that seagrass pathogens may also accumulate within the beds and that biological filtration may not only apply to pathogens that are non-infectious to seagrass. It is important to note that the decline of seagrass beds worldwide is attributed to both pathogens and anthropogenic factors such as ocean warming and eutrophication. More research is needed to fully understand the vulnerability and potential of these filtration mechanisms (Jacobs-Palmer et al. 2020) (*Figure 1.2*).

#### *Pathogen reduction using constructed wetlands*

Constructed wetlands are defined as treatment systems that improve water quality through natural processes involving wetland vegetation, soils, and associated microbial

assemblages (US EPA 2015). In the 1950s, constructed wetlands were developed to expand on the services that naturally-occurring wetlands provided, such as improving water quality from stormwater runoff, greywater, and wastewater (Wu et al. 2016). Constructed wetlands can vary in their design but are meant to remove heavy metals, nitrogen, phosphorous, and chemical pollutants from runoff and remove harmful pathogens (Wu et al. 2016).

Constructed wetlands are utilized in a wide variety of industries to filter wastes, such as in textiles, paper milling, agriculture, and mining (Buhmann and Papenbrock 2013). Recently, constructed wetlands were integrated into the aquaculture industry and have successfully been used to remove nutrients from catfish and rainbow trout aquaculture facilities (Buhmann and Papenbrock 2013). Vegetation in the constructed wetland removes excess nutrients and also reduces water flow, allowing solids to be taken up by their root systems (Buhmann and Papenbrock 2013). Constructed wetlands are excellent effluent removal options for land-locked aquaculture facilities because they can be implemented in both fresh and saline environments (Buhmann and Papenbrock 2013). Additionally, constructed wetlands decrease human pathogens from wastewater without the use of chlorine, which is a more sustainable and less damaging process than traditional chemical practices (Wu et al. 2016). Some constructed wetlands reduce water flow, allowing viruses in suspension to be killed by UV radiation (Wu et al. 2016).

Pathogens are removed from constructed wetlands by multiple mechanisms. The reduction of nutrients and pathogens depends on wetland type, size, and design and a combination of physical, chemical, and biological mechanisms (Wu et al. 2016). Some physical factors include mechanical filtration, sedimentation, and absorption of organic matter as well as CW design. Sedimentation, the removal of particles from suspension, is most effective against bacteria and coliforms such as fecal streptococcus due to these pathogens' larger size and faster

settling rate (Wu et al. 2016). Mechanical filtration (i.e., passing the water through a filter), included in some constructed wetlands, can effectively remove pathogenic microorganisms, particularly protozoans (Wu et al. 2016). One study in a constructed wetland (Redder et al. 2010) noted a 100-fold reduction in protozoan pathogens when using mechanical filtration. Mechanical filtration is also effective at removing fecal indicator bacteria such as *Enterococcus* and *E. coli* (Wu et al. 2016). Predation activity of nematodes, rotifers, protozoa, bacterivorous bacteria, and phages is also an important factor affecting the bacterial removal in CWs (Wu et al. 2016). Artificial and vegetative oxygenation increase dissolved oxygen in CWs and are correlated with pathogen die-offs, especially bacteria (Wu et al. 2016).

The need for sustainable and affordable wastewater treatment systems, such as CWs, will only continue to grow along with the global population and wastewater discharge (S. Wu et al. 2016). CWs are an excellent example of a sustainable investment that will lower the abundance and risk of pathogens. These systems may also provide some insight into the mechanisms associated with pathogen removal in natural ecosystems.

## **Discussion**

Marine diseases are challenging to manage because pathogen transmission is impacted by water chemistry, currents, and ecological dynamics. We need creative solutions to reduce pathogen pressure to limit catastrophic host population die-offs and other negative downstream impacts. Natural filtration systems are an appealing solution to reduce pathogen loads and supplement wastewater treatment due to (1) their cost compared to artificial filtration systems and/or water treatment plants and (2) because pathogen reduction is not contingent upon pathogen isolation. These benefits make natural filtration systems an excellent investment to

reduce novel, zoonotic diseases in marine environments with important consequences for human health (Sutton-Grier and Sandifer 2019).

Natural pathogen filtration has several inherent limitations. Natural filtration only has the potential to reduce infectious disease when transmission is a rate-limiting step for the epidemiology. Some marine pathogens are so ubiquitous that exposure and transmission are almost guaranteed. In other cases, such as epizootic shell disease in lobsters, many of the bacteria associated with this disease are found on the shell of healthy lobsters, but their role switches from commensal to pathogenic. Natural filtration may be unable to prevent or mitigate the effects of such pathogens on an ecologically significant scale.

In mangroves and seagrasses, filtration mechanisms are not fully understood; likewise, in shellfish beds, it is not clear which pathogens are removed and which pathogens concentrate within bivalve tissues. Similarly, the extent of pathogen removal is still being explored in constructed wetlands. Important aspects of each system need to be explored to take full advantage of their filtration properties, including optimal densities in filtering bivalve populations, the role of microbiomes and epiphytes on seagrasses and mangroves, allelopathic interactions, and climate change on filtration capability. Additionally, it is unclear what the impact of filtration is on the host organism and if it can affect its productivity, physiological performance and/or quality. Future work is needed to examine the interactions between pathogen and host in ecosystems with filtration potential and to answer the following questions: Can natural filters fail due to pathogen overload? How can we test and monitor filtration performance? How often do we need to replace natural filtration systems to maintain pathogen filtration efficiency? What are the impacts of extracellular and intracellular pathogens in

filtration performance? These are important questions as we consider the use of natural filtration systems to reduce pathogens in the coastal zone.

Coastal wetland ecosystems create habitats that facilitate high biodiversity, which may lead to lower pathogen pressure (Duffy et al. 2015; Johnson et al. 2013; Rahman et al. 2021). Despite the critical roles these ecosystems play, they are increasingly threatened by climate change, pollution, and anthropogenic activities. It is essential to protect them to maintain the services they provide. Conserving these natural areas may decrease pathogen transmission between wildlife and humans, leading to fewer zoonotic events (Keesing and Ostfeld 2021). We require further understanding of the mechanisms involved in pathogen filtration, its relation to other ecosystem services, and the role that other ecological factors play in pathogen reduction to implement these systems at their full potential.

## Chapter 2: Seasonal Changes in Microbial Community Composition in and around eelgrass (*Zostera marina*) meadows

C. A. Klohmann<sup>1</sup>, J. L. Padilla-Gamiño<sup>1</sup>

<sup>1</sup>University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA, USA

### Abstract

Seagrasses provide a variety of ecosystem services such as carbon sequestration, coastal protection, and nutrient cycling. Eelgrass (*Zostera marina*) is a temperate seagrass found around the globe that provides a variety of ecosystem services; however, it is unknown whether eelgrass reduces bacterial abundance like its tropical counterparts. Additionally, it is not known how the bacterial community in the water column of eelgrass beds changes throughout the year. Ocean microbial communities are in constant flux due to physical, chemical, and biological factors. In the coastal zone, runoff and other anthropogenic stressors can cause shifts in microbial community composition and in some cases increase harmful pathogens or microbes of public health concern. Runoff and other anthropogenic stressors can cause shifts in microbial community composition and increase harmful pathogens or microbes of public health concern. In this study, we examined differences in microbial community composition and abundance of fecal indicator bacteria (*Enterococcus*) in coastal waters in Puget Sound, Washington, USA. In this study we collected water samples in areas where *Z. marina* was present and absent and examined the spatial and seasonal differences in bacterial communities using environmental DNA (eDNA). We found that there were strong differences in alpha and beta diversity between water samples collected during different seasons with higher alpha diversity in the spring and summer compared to the fall and winter. We did not find differences in bacterial abundance or microbial composition in water collected inside or outside *Z. marina* beds. High *Enterococcus* abundance was correlated with high temperatures and low levels of pH, dissolved oxygen, salinity, and

irradiance. We found the highest bacterial abundances during the summer months with several samples crossing the EPA single sample threshold of 104 CFUs/100mL. We detected *Vibrio*, *Pseudomonas*, and *Enterobacter*, potentially pathogenic bacteria that can all cause illness in human, fish, and marine mammals at all field sites. The most abundant bacteria at all sites were alpha proteobacteria family *Rhodobacteraceae*, alphaproteobacteria of the SAR11 clade, and the gamma proteobacteria family *Alcaligenaceae*. Our results suggest that seasonality, site, light levels, and temperature combined are the best predictors of bacterial abundance and microbial community composition as well as distance from shore. This research has important implications for coastal management including timing beach closures to limit human illness and when to sample to detect pathogens.

## **Introduction**

Pathogenic microorganisms play important roles in coastal ecosystem structure and function (Selakovic, de Ruiter, and Heesterbeek 2014; Lafferty et al. 2008; Carlson et al. 2020) but they can also impact fisheries, aquaculture facilities, and ecosystem engineers (Burge and Hershberger 2020). The Southern New England lobster, one of the most profitable fisheries in the United States (Castro et al. 2012), declined due to epizootic shell disease, caused by bacterial dysbiosis (Groner et al. 2016). Along the west coast of the United States sea star wasting disease, originally thought to be caused by a densovirus (SSaDV) (Hewson et al. 2014) devastated the population of the sunflower star (*Pycnopodia helianthoides*), a key ecosystem engineer along with 20 other asteroid species (Harvell et al. 2019). *P. helianthoides* still have not recovered from this epizootic event and there are active captive breeding programs to help bolster wild populations (Hodin et al. 2021).

It is important to find sustainable and creative solutions to manage pathogen pressure in coastal environments in order to limit epizootic events. Natural pathogen filtration has the potential to remove and contain pathogens in the coastal environment. Mangroves, seagrasses, and bivalves may reduce pathogens by a variety of means including the reduction of water speed (i.e., flow rate), particle interception, biochemical transformation of nutrients and contaminants, absorption of water and nutrients, and sedimentation (Harvell and Lamb 2020; Klohmann and Padilla-Gamiño 2022).

In the tropics, seagrass beds can potentially act as natural filtration systems by decreasing the abundance of human, fish, and invertebrate pathogens (Lamb et al. 2017). In Indonesia, researchers found lower abundances of fecal indicator bacteria, *Enterococcus*, within seagrass beds when compared to bare areas. Additionally, they found lower relative abundances of specific pathogens such as *Vibrio* and *Pseudomonas* within seagrass beds using eDNA samples. This study also found that coral reefs adjacent to seagrass beds had 50% less disease than reefs without adjacent seagrass beds (Lamb et al. 2017).

Leaf extracts of three seagrass species, *Halophila stipulacea*, *Cymodocea serrulate*, and *Halodule pinifolia*, collected off the coast of India inhibited the growth of seven drug-resistant human pathogens (Babuselvam et al. 2017). Seagrasses may also reduce pathogen loads through a combination of sedimentation, chemical filtration, and water flow reduction. On the other hand, because pathogenic bacteria can be killed by UV-radiation (Davies-Colley, Bell, and Donnison 1994) shading from seagrasses could elevate bacterial levels within seagrass beds (Wallace et al. 2018). To date, little is known about the underlying mechanisms and the role seagrasses may play in removing or accumulating pathogens (Klohmann and Padilla-Gamiño 2022).

*Z. marina* (eelgrass) is a temperate seagrass that is ubiquitous along the Pacific Coast of the United States. Eelgrass beds are found in temperate coastal waters worldwide in both subtidal and intertidal habitats (Thom 1990) and provide nurseries for fish, shoreline protection, sediment stabilization, nutrient recycling and carbon sequestration (Alongi et al. 2016; Thom 1990). It is estimated that *Z. marina* alone provides \$87,000 of ecosystem services per hectare annually in Puget Sound, Washington where there are ~ 23,000 hectares (Wright 2017; Christiaen et al. 2022). However, it is not known whether eelgrass provides a pathogen filtration service.

Coastal microbial communities are dynamic and influenced by several physical, chemical and biological factors (Fuhrman, Cram, and Needham 2015). Coastal microbial communities are distinct to the open ocean communities and are more vulnerable to perturbations such as pollution since they are at the land-sea interface (Wallace et al. 2018; Harley et al. 2006). It is important to study the coastal microbiome to understand how these communities are changing and how these changes might impact human, animal, and environmental health.

Microbial abundance and diversity change seasonally across spatial scales (Fuhrman, Cram, and Needham 2015). Time series data in Bermuda showed strong seasonal changes in the coastal microbial communities due to stratification in the winter months (Morris et al. 2005). Contrastingly, microbial community analysis in Hawai'i indicated low seasonal variability and suggest that community dynamics and stratification had a higher impact on community composition than seasonality (Eiler, Hayakawa, and Rappé 2011). In Puget Sound, Washington there are strong seasonal differences in coastal microbial communities with pathogenic bacteria being more common in the summer (Wallace et al. 2018).

In this study we used *Enterococcus* assays and environmental DNA (eDNA) samples to examine the microbial community composition and fecal indicator bacterial abundance in areas where eelgrass beds are present and absent in Puget Sound. This location supports a large shellfish aquaculture industry that generates millions of dollars in annual revenue as well as thousands of jobs for Washington State residents (Washington Sea Grant, 2015).

*Enterococcus* is a genus of gram positive, primarily commensal bacteria known to colonize the intestinal tract of many mammals including humans, livestock and rodents, as well as some insects, birds and plants. While many species of *Enterococcus* live in the bodies of animals with no ill effects, a few species are known pathogens. These include *E. faecium*, *E. gallinarum*, and *E. raffinosus*, thus making them important indicators of water and soil contamination (Byappanahalli et al. 2012).

Our work addresses the following questions: (i) Are there spatial and seasonal differences in bacterial communities associated with *Z. marina* at specific sites in Puget Sound, Washington? (ii) Are there differences in bacterial communities and abundance associated with seagrass beds when compared to adjacent sites without seagrass present (i.e., Does eelgrass reduce pathogen abundance in the water column)? If eelgrass beds can reduce pathogens, we expect to detect lower bacterial abundance and diversity in the water column when eelgrass is present. We anticipate that seasonality will impact the microbial communities, with higher abundance and diversity during the summer months (Wallace et al. 2018). This work has important implications for human health, eelgrass ecosystem services, and coastal management in the Puget Sound region.

## **Materials and Methods**

### *Research sites and Field collections*

We collected water samples to examine microbial community composition in Puget Sound, which is a discrete, fjord-like estuary located in Washington state, east of the Olympic Mountains and west of Seattle. The estuary is the second largest in the United States and receives freshwater input from local streams and marine inflow from the Pacific Ocean (Moore et al. 2008). Puget Sound provides recreational activities, supports the economy, and is culturally important to the region (Chan et al., 2015.; Poe, Donatuto, and Satterfield 2016; Mojica and Fletcher 2020.).

We collected samples at three public beaches: Golden Gardens Park (-122.4040, 47.690), Smith's Cove (-122.385, 47.631), and Alki Beach (-122.401, 47.584) (*Figure 2.1*). We chose these sites because they are public beaches and have eelgrass beds with adjacent areas that are bare sediment. At each site we collected samples monthly between February 2020 and January 2021 in areas where *Z. marina* was present and in adjacent areas where *Z. marina* was absent (*Table 2.1, Figure S2.1*).

We collected monthly water samples at three field sites beginning in February of 2020 and ending in January of 2021. We missed collections in April and May due to the global COVID-19 pandemic and September due to unsafe weather conditions. We collected samples from the three field sites within two weeks of each other and between 10am and 2pm to sample during the hours with the most photosynthetically available radiation.

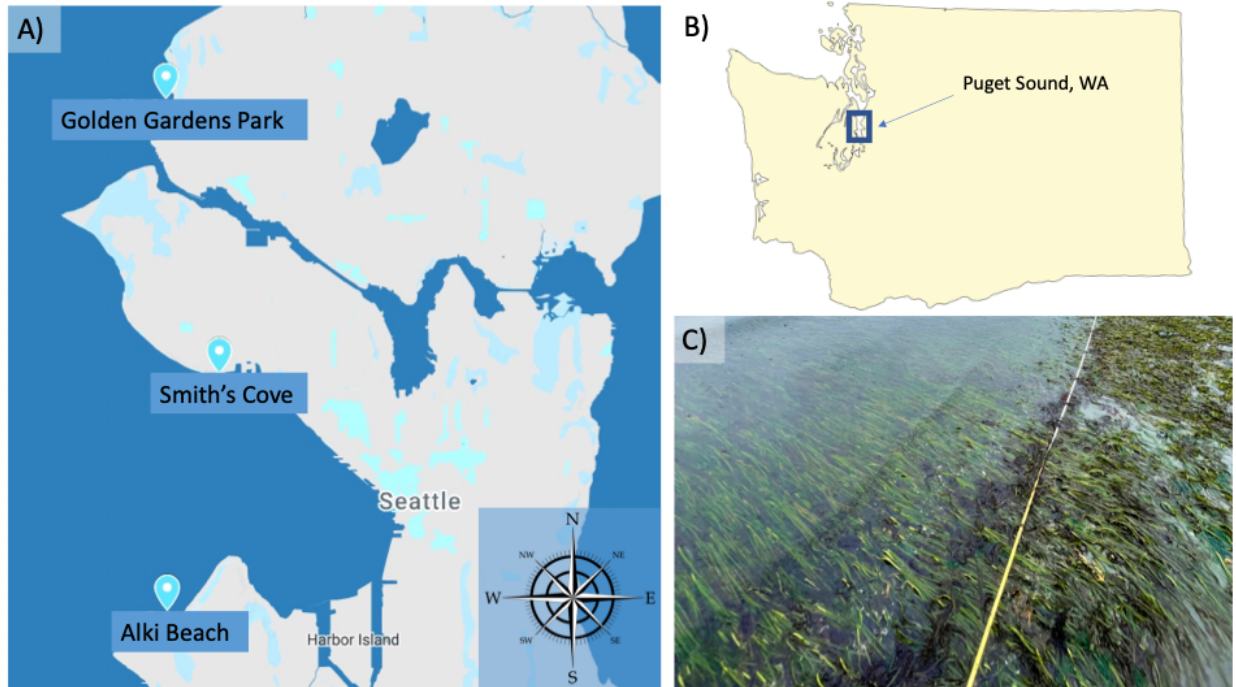


Figure 2.1. A) Field sites in Puget Sound, Washington with *Zostera marina* and confirmed detection of *Enterococcus*. B) Map of Washington State. Blue rectangle shows where field sites are located in Puget Sound. C) *Z. marina* plants at Golden Gardens field site.

At each site, we set two 100 m transects perpendicular from shore. One transect was over the *Z. marina* bed and the other over bare sediment. The bare sediment and seagrass bed were 195.9 meters apart at the Golden Gardens site, 140.5 meters apart at the Smith's Cove site, and 190.6 at the Alki Beach site. Along the transects we collected 100 mL water samples in triplicate every 20 meters starting at zero and ending at 100 meters to evaluate *Enterococcus* abundance. We collected 900 mL water samples for environmental DNA (eDNA) at the same intervals. We collected the samples by submerging sterile Nalgene bottles vertically from a kayak during a slack or receding high tide along two 100-meter transects, making sure no air bubbles remained in the bottles. For each collection, we recorded water quality measures (pH, temperature, dissolved oxygen, salinity) using a YSI professional series sonde and photosynthetically available radiation (PAR) using a LI-COR LI-250A light meter. In August 2021, we performed additional water collections at Golden Gardens Park using a Vandorn sampler to quantify the

vertical distribution of *Enterococcus* within the *Z. marina* bed and over bare sediment (0.5 and 4 m).

Table 2.1. Time of field collections at study sites

Site	Year	Month	Day	Time	Tidal Height (m)
Alki Beach	2020	Feb	2	10:00	10.9
		Mar	17	10:00	8.2
		Jun	29	10:00	6.1
		Aug	25	10:00	8.2
		Nov	15	10:00	5.5
		Dec	16	10:00	9.5
	2021	Jan	22	10:30	10.1
Golden Gardens	2020	Feb	16	12:00	11.5
		Mar	19	10:00	6.3
		Jul	9	10:00	5.5
		Aug	21	10:00	5.0
		Oct	16	10:00	3.2
		Nov	20	10:00	11.9
		Dec	21	10:30	11.9
	2021	Jan	29	10:30	8.2
Smith's Cove	2020	Feb	20	10:30	7.5
		Mar	17	12:30	7.5
		Jun	29	12:30	6.9
		Aug	25	12:30	8.1
		Oct	18	10:00	6.8
		Nov	25	10:00	6.3
		Dec	18	10:00	10.1
	2021	Jan	18	10:30	10.2

We quantified *Enterococcus* abundance using the World Health Organization's (WHO) standardized culture-based method for evaluating intestinal *Enterococci* (Water and Team 1999). The protocol included vacuum filtration of the water samples onto a 47 mm diameter and 0.45  $\mu\text{m}$  pore size cellulose acetate filter, plating the filters on petri dishes with m-*Enterococcus* agar medium, and incubating the plates at  $37.0 \pm 1.0$  °C for  $4.0 \pm 0.5$  hours followed by  $44.0 \pm 0.5$  °C for  $40 \pm 4$  hours. Fecal Indicator Bacteria are used to detect the presence of bacteria

associated with pathogenic bacteria and *Enterococcus spp.* is the most used Fecal Indicator Bacteria in Washington state waters (Washington State Department of Ecology, 2021). The United States Environmental Protection Agency's (EPA) single sample standard for *Enterococcus* is 104 colony forming units (CFUs) per 100 mL, samples that cross that threshold indicate unsafe water (US EPA 2013). This standard is used by the Washington Department of Ecology when they measure *Enterococcus* abundance at public beaches in Puget Sound, Washington (Washington State Department of Ecology, 2021).

#### *DNA extraction, sequencing, and quality control*

eDNA analysis is a molecular technique used to detect macro- and microorganisms in the aquatic environment by targeting the 16S ribosomal RNA (rRNA) genes (Hashizume et al. 2017). These are useful tools to study bacterial species diversity and distribution since the eDNA samples are easy to collect, affordable to sequence, and can detect thousands of species (Tang et al. 2015). In the past this technique has been successfully applied to examine bacterial communities associated with seagrass beds and detect pathogens such as trematodes, herpesviruses, and vibrio (Lamb et al. 2017; Hashizume et al. 2017).

We used 16S rRNA gene amplicon sequencing from eDNA samples to compare bacterial diversity when *Z. marina* is present and absent and in different seasons. After water collection we filtered the samples under vacuum pressure through a 47 mm diameter and 0.45 mm pore size cellulose acetate filters and stored them at room temperature in Longmire's buffer (Renshaw et al. 2015). To extract DNA from the filters (n = 144) we used a phenol:chloroform:isoamyl alcohol extraction protocol using half of the cellulose filter (Renshaw et al. 2015). The protocol included the Qiagen ATL buffer as a lysis buffer, incubation 65 °C for 10-15 minutes, and the

addition of phenol/chloroform and chloroform, as well as an overnight incubation in ethanol and NaCl at 20 °C. After extraction, the samples were stored in TE Buffer at room temperature, and we quantified the DNA concentrations and quality using a Nanodrop 2000C spectrophotometer. We sent DNA samples to Molecular Research LP (Mr. DNA) for 16S ribosomal RNA gene amplicon sequencing on the Illumina MiSeq.

The V4 variable region of 16S rRNA gene was amplified using the 515/806 primer sets. Barcodes on the forward primer were used in a 30 cycle PCR using the HotStarTaq Plus Master Mix Kit (Qiagen, USA) under the following conditions: 94 °C for 3 minutes, followed by 30 cycles of 94 °C for 30 seconds, 53 °C for 40 seconds and 72 °C for 1 minute, after which a final elongation step at 72 °C for 5 minutes was performed. After amplification, PCR products were checked in 2% agarose gel to determine the success of amplification and the relative intensity of bands. Multiple samples were pooled together (e.g., 100 samples) in equal proportions based on their molecular weight and DNA concentrations. Pooled samples are purified using calibrated Ampure XP beads. Then the pooled and purified PCR product was used to prepare the Illumina DNA library.

After receiving the sequencing data, we removed barcodes and secondary adapter sequences. We assembled the raw reads and demultiplexed them using a FastQ processor provided by Molecular Research LP in command line. All processing steps and outputs are available on GitHub (<https://github.com/cklohmann/microbial-methods>). First, we trimmed the forward and reverse sequences at 290 base pairs based on data quality scores. We removed any data that did not have a quality score of 8 or greater. We used the qiime2 dada2 denoise-pyro method to denoise and chimera-check the sequences to generate amplicon sequence variants

(ASVs) (Callahan et al. 2016). We then assigned taxonomy to the sequences using the Silva 132 species assignment database (Bolyen et al. 2019; Yilmaz et al. 2014).

### *Statistical analysis*

In order to analyze the field data, we used a fixed effects generalized linear model with a negative binomial distribution. We chose this model and distribution based on the large number of zeros in our data set due to no *Enterococcus* abundance. In order to find the best model fit, we calculated AIC values for all combinations of the environmental parameters, including the interaction effects and chose the model with the lowest AIC value. Model selection was completed in R (version 1.3.1093) using the `glm.nb()` function from the MASS package. The full model included seagrass presence, distance from shore, site, Julian date, dissolved oxygen, PAR, temperature, and salinity as fixed effect predictors and *Enterococcus* abundance as the response variable. We chose to use Julian date to standardize the dataset as one sampling was done in 2021 while the rest were conducted in 2020. To examine the vertical distribution of bacterial abundance in the water column we used a t-test.

We generated alpha- and beta-diversity using the qiime2 diversity core-metrics phylogenetic method after rarefaction to 400 sequences per sample (the sequencing depth of the shallowest sample). Although rarefaction reduces statistical power it protects against false-positive results due to unequal sequencing depth between samples without needing to make assumptions about the distribution of microbial species within samples (Weiss et al. 2017). We evaluated alpha diversity using phylogenetic diversity (Faith's PD) which uses phylogenetic distance to calculate the diversity of a given sample and the Shannon's diversity index (which combines richness and evenness). We looked at overall differences in alpha diversity and tested

using Kruskal-Wallis tests. Post hoc comparisons were performed automatically in QIIME2 (via a procedure that produces equivalent  $p$ -values to a Mann-Whitney  $U$  post hoc test). We assessed beta diversity between samples using Weighted UniFrac distances and Bray-Curtis dissimilarities. The differences in beta-diversity between field sites were examined using PERMANOVA (Anderson 2001). We tested for differential microbial abundances using ANCOM (Mandal et al. 2015).

## Results

### *Environmental characteristics*

The environmental data show seasonal fluctuations in water characteristics at all field sites (*Figure 2.2*). The warmest temperatures were found in summer. The average summer temperatures were 14.2 °C, 13.3 °C, and 13.1 °C at the Golden Gardens, Alki Beach, and Smith's Cove field sites, respectively. We found the coolest mean temperatures in the spring at Golden Gardens (8.2 °C), Alki beach (8.0 °C) and Smith's Cove (7.2 °C) (Table S2.1, *Fig. 2.2a*). Average seasonal pH values were highest during the spring at all field sites with values of 8.67, 9.00, and 8.79 at Golden Gardens, Alki Beach, and Smith's Cove, respectively. The lowest pH values were recorded in the winter months. We found average values of 8.27, 8.27, and 8.12 at Golden Gardens, Alki Beach, and Smith's Cove, respectively (Table S1, *Fig. 2.2b*). Dissolved oxygen had the highest average levels in the spring at Golden Gardens (10.6 mg/L), Alki Beach (9.63 mg/L) and Smith's Cove (9.81 mg/L). The lowest DO values were recorded in the fall at Golden Gardens (6.65 mg/L), Alki Beach (7.01 mg/L), and Smith's Cove (7.28 mg/L) (Table S1, *Fig. 2.2c*) with one site, Golden Gardens, measuring 5.50 mg/L, bordering on anoxic conditions of 2-3 mg/L (Council 2000). Seasonal variation in environmental characteristics was very

consistent across sites, except for salinity. The salinity at Alki beach was higher than the salinities at the other two sites and was very consistent throughout the year. In contrast, the salinity at Golden Gardens and Smith's Cove was variable throughout the year (Table S2.1, *Fig. 2.2d*). PAR levels showed seasonal fluctuations at all field sites and varied between 1-40  $\mu\text{mol}/\text{m}^2/\text{sec}$  (*Figure S2.1*).

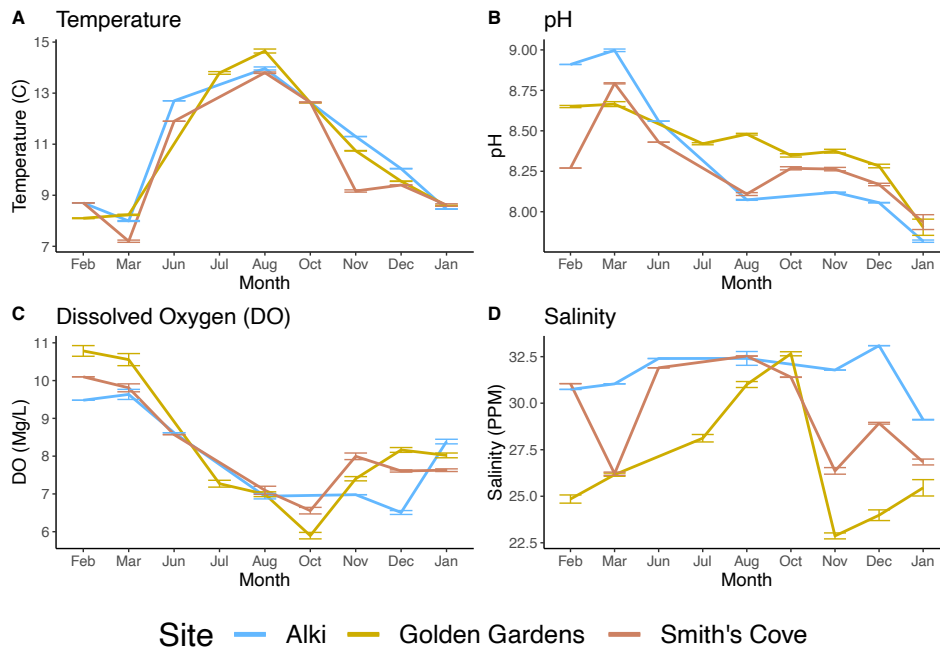


Figure 2.2. Environmental characteristics in Puget Sound, Washington from January 2020-January 2021. Graphs show mean monthly values and standard error.

### *Enterococcus* abundance

The *Enterococcus* field data showed seasonal fluctuations in *Enterococcus* abundance at all sites (*Figure 2.3*). The lowest abundances of *Enterococcus* were seen in January and February with average counts ranging from 5-55 CFUs/100mL. We observed the highest counts during June and July at all field sites with average counts ranging from 20-150 CFUs/100 mL. It is also important to note that multiple samples from Golden Garden's (June) and Smith's cove (June and July) crossed the EPA single sample threshold of 104 CFUs/100 mL while no samples from

Alki beach did. Results from the vertical sampling at Golden Gardens Park (0.5 - 4 m) indicated that the number of bacteria in the surface water and water close to the seafloor within *Z. marina* beds did not differ ( $p = 0.110$ ) (Figure S2.3).

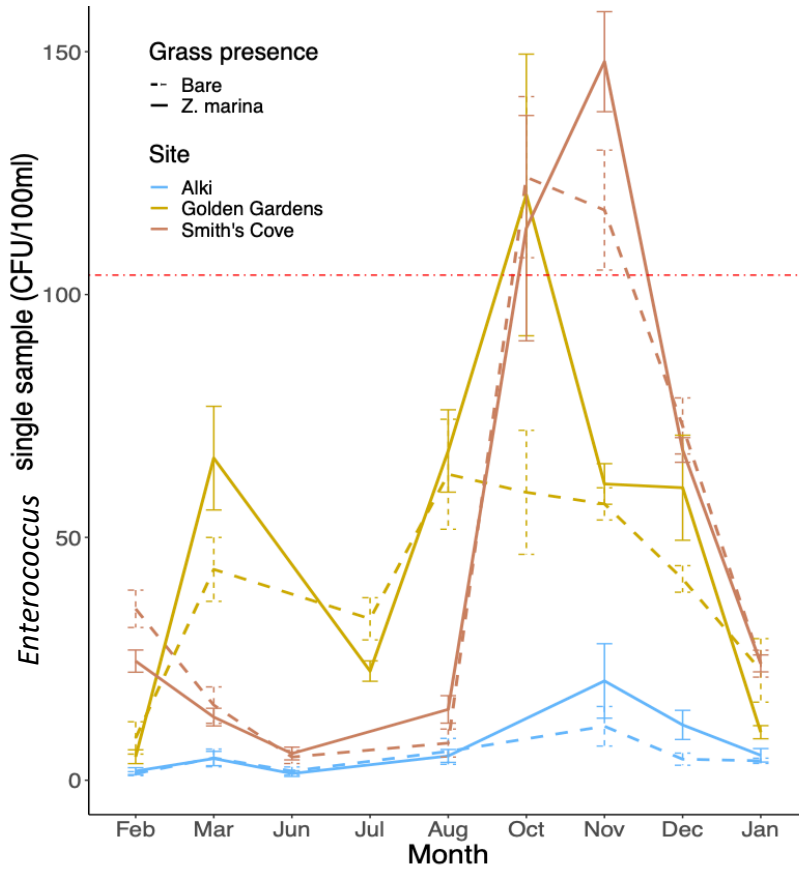


Figure 2.3. Monthly Enterococcus counts in Puget Sound, Washington (2020-2021). Colors indicate different field sites. Solid lines are locations where *Z. marina* is present and dotted lines are locations where *Z. marina* is absent. The horizontal line indicates the EPA single sample threshold (104 CFU/100 mL) that indicates unsafe water.

The GLM indicated that there was not a significant effect of *Z. marina* on bacterial abundance during the months that we sampled ( $p = 0.248$ ) and there was not a significant interaction between sampling date and *Z. marina* presence (Table 2.2). There were higher amounts of bacteria present at the Golden Gardens ( $p < 0.001$ ) and Smith's Cove ( $p < 0.001$ ) field sites compared to Alki beach between February 2020 and January 2021 (Figure 2.4). The

GLM predicted significant decreases in *Enterococcus* abundance as distance from shore ( $p < 0.001$ ), PAR ( $p = 0.024$ ), and temperature ( $p = 0.007$ ) increased (Figure 2.4). Although not significant, the GLM predicted that as dissolved oxygen levels increased *Enterococcus* abundance decreased ( $p = 0.576$ ) (Figure 2.4). The inverse was true for salinity, as salinity increased so did *Enterococcus* abundance although this relationship was not significant ( $p = 0.099$ ) (Figure 2.4).

Table 2.2. GLM output showing significant predictors of *Enterococcus* abundance and test statistics

Predictors	<i>Enterococcus</i> abundance										
	Incidence Rate Ratios	std. Error	std. Beta	standardized std. Error	CI	standardized CI	Statistic	std. Statistic	p	std. p	
(Intercept)	3.81	2.96	4.72	0.40	0.85 – 17.24	4.01 – 5.58	1.73	18.22	0.084	<b>&lt;0.001</b>	
<i>Z. marina</i> presence	0.93	0.13	1.05	0.04	0.70 – 1.23	0.97 – 1.13	-0.54	1.16	0.589	0.248	
Distance from shore (m)	0.99	0.00	0.83	0.03	0.99 – 1.00	0.77 – 0.89	-4.93	-4.93	<b>&lt;0.001</b>	<b>&lt;0.001</b>	
Site: Golden Gardens	9.48	1.25	9.48	1.25	7.36 – 12.25	7.36 – 12.25	17.02	17.02	<b>&lt;0.001</b>	<b>&lt;0.001</b>	
Site: Smith's Cove	8.59	0.88	8.59	0.88	7.01 – 10.53	7.01 – 10.53	21.06	21.05	<b>&lt;0.001</b>	<b>&lt;0.001</b>	
Julian Date	1.00	0.00	1.69	0.09	1.00 – 1.00	1.52 – 1.88	7.48	9.93	<b>&lt;0.001</b>	<b>&lt;0.001</b>	
Dissolved Oxygen (mg/L)	0.97	0.05	0.96	0.07	0.88 – 1.08	0.83 – 1.11	-0.56	-0.56	0.576	0.576	
Photosynthetically available radiation ( $\mu\text{mol}/\text{m}^2/\text{s}$ )	0.99	0.00	0.88	0.05	0.98 – 1.00	0.78 – 0.99	-2.26	-2.26	<b>0.024</b>	<b>0.024</b>	
Temperature ( $^{\circ}\text{C}$ )	0.92	0.03	0.83	0.06	0.87 – 0.99	0.72 – 0.97	-2.71	-2.71	<b>0.007</b>	<b>0.007</b>	
Salinity (ppt)	1.03	0.02	1.11	0.07	0.99 – 1.07	0.98 – 1.25	1.65	1.65	0.099	0.099	
Julian date* <i>Z. marina</i> presence	1.00	0.00	1.06	0.04	1.00 – 1.00	0.98 – 1.14	1.42	1.42	0.154	0.154	
Observations	807										
R <sup>2</sup>	0.689										
Nagelkerke											

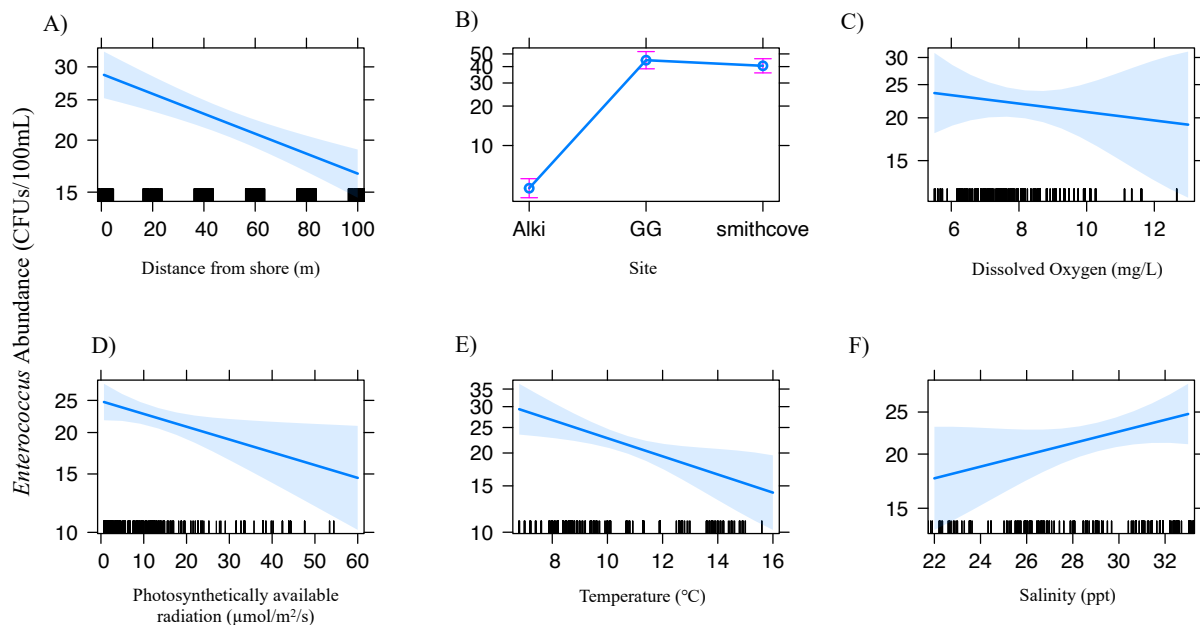


Figure 2.4. Effect plots generated from GLM output showing the influence of A) Distance from shore, B) Site, C) Dissolved Oxygen, D) Photosynthetically available radiation, E) Temperature, and F) Salinity on *Enterococcus* abundance.

### Community Composition

#### Richness and Evenness

We found that there was not a difference in alpha diversity based on seagrass presence ( $p = 0.591$ ) or field site ( $p = 0.902$ ); however, we found significant differences in the alpha diversity based on the sampling month ( $p < 0.001$ ) (Table S2.2). We observed lower alpha diversity in November and December with species richness (Faith's PD) mean values of 4 and 2, respectively. Species richness was higher in August with a mean value of 15 and the highest diversity was found in March with a mean value of 19 (Figure 2.5A). Evenness (Pielou evenness) did not change based on seagrass presence ( $p = 0.474$ ) or site ( $p = 0.145$ ). Again, month was a significant predictor of evenness ( $p < 0.001$ ), however; the November samples had the lowest evenness (mean = 0.81) when compared to August (mean = 0.89), December (mean =

0.91), and March (mean = 0.94) (Figure 2.5B). We did not find a difference in beta diversity based on seagrass presence ( $p = 0.973$ ) (Figure S2.3b), but we did see significant differences based on sampling month ( $p = 0.001$ ) (Figure S2.3b).

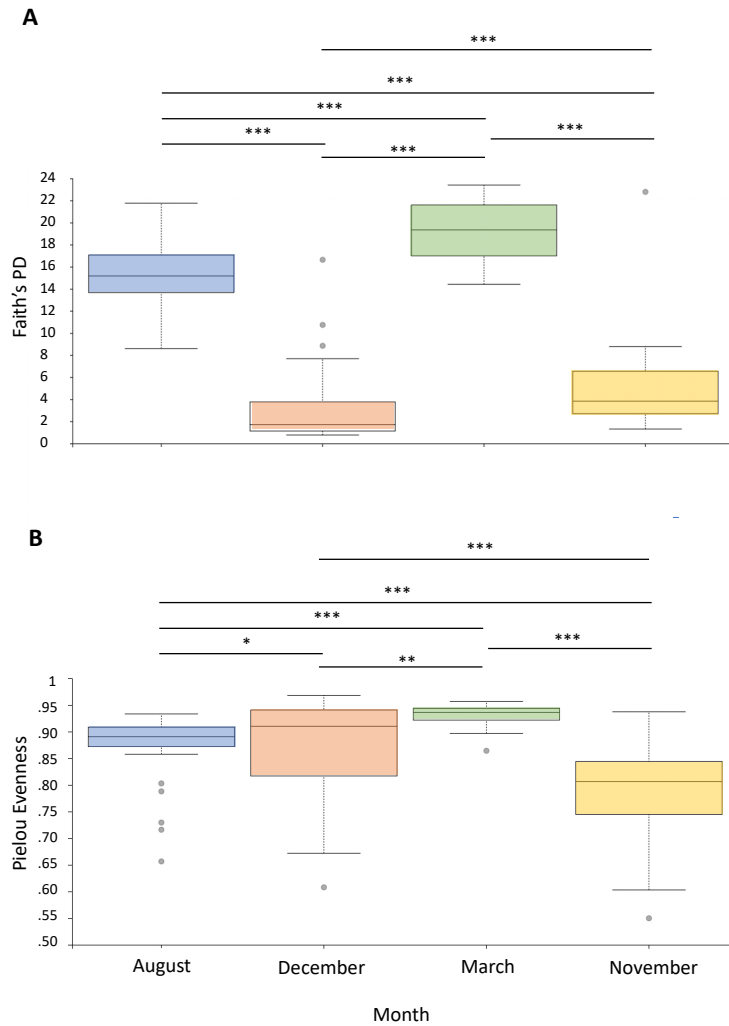


Figure 2.5. Alpha diversity metrics of microbial communities in Puget Sound water in different seasons. A) Richness metric, Faith's PD and B) Pielou evenness. Asterisks in boxplots represent significant difference, where \* indicates  $p > 0.05$ , \*\* indicates  $p > 0.01$ , and \*\*\* indicates  $p > 0.001$ .

### Community analysis

Sequencing of the amplicon library on the Illumina MiSeq generated 6,041,511 high-quality reads ( $n = 144$  samples, median 40,572 reads). We detected 8,077 unique sequences and were able to assign taxonomy to all sequences (Figure 2.6). The most abundant bacteria in the

samples from August were SAR11\_clade of alphaproteobacteria, *Rhodobacteria*, and *cyanobacteria*. In March the most frequent were *Rickettsiales*, *Rhodobacteracea*, *Flavobacteriaceae* and *Ulvibacter*. In November and December the most frequent bacteria were *Pseudomonas*, *Vibrio*, *Enterobacterales -Yersiniaceae -Serratia*, and *Ochrobactrum*. We found differences in the microbial communities based on the sampling month. We saw that samples collected in November and December were the most closely related to each other and the samples collected in March and August were more closely related to each other (*Figure 2.7*) while site (*Figure S2.6*) and seagrass presence (*Figure S2.7*) did not impact relatedness. Additionally, we found that hgcI clade of Sporichthyaceae, Cyanobium PCC of the family Cyanobiaceae, and Glaciecola of the family Alteromonadaceae were differentially abundant over bare sediment the Golden gardens field site with median reads of 95.5, 64.5, and 68.5, respectively (Table S2.3). The hgcI clade of Sporichthyaceae and Cyanobium PCC of the family Cyanobiaceae were also differentially abundant inside of the *Z. marina* bed with median reads of 122 and 37.5, respectively (Table S2.3).

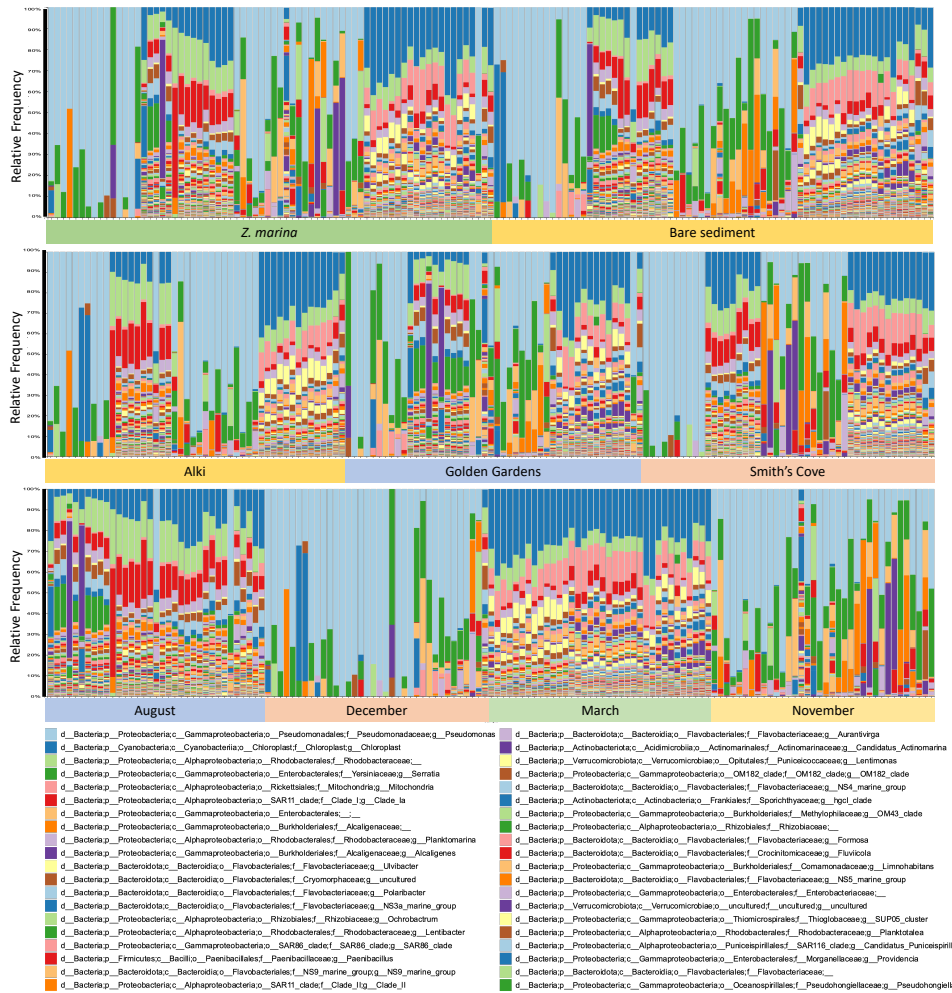


Figure 2.6. Bacterial community composition across *Z. marina* presence, site, and month. Unique OTUs were summarized at the genus level and the representation of taxonomic groups within each sample are plotted. A limited number of the most abundant genera are represented to remove visual clutter. The full list can be found in figure S2.5.

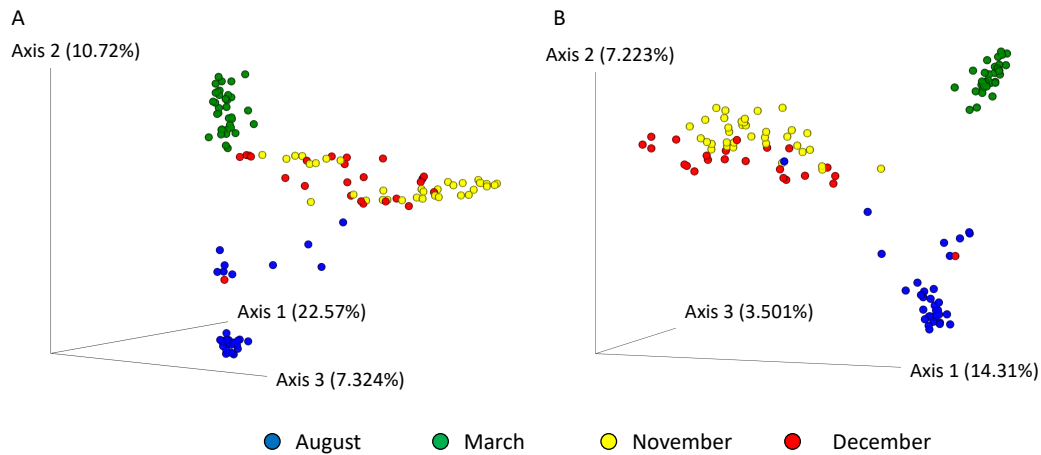


Figure 2.7. A) Bray-curtis dissimilarity and B) Jaccard emperor PCoA plots showing maximum dissimilarity between samples. Axis 1 represents the maximum dissimilarity between samples followed by axis 2, and 3. Colors and shapes indicate different months (Blue = August, Red = December, Green = March, Yellow = November).

## Discussion

In this study we found no differences in levels of indicator and pathogenic bacteria inside eelgrass meadows (*Z. marina*) compared to paired nearby bare areas. The coastal microbial community composition was heavily influenced by the season but not by seagrass presence. This contrasts with other studies that found reduced bacterial abundance within tropical seagrass beds (Lamb et al. 2017) or increased bacterial abundance within temperate seagrass beds (Deng et al. 2021). One explanation for this could be the difference in sampling methods. We collected samples at multiple time points whereas Lamb et al. collected at one time point. Additionally, Lamb et al. recorded much higher bacterial counts at the shore compared to the counts that we found at our field sites. It is possible that the filtration service is only detectable at very high bacterial abundances.

It is possible that seagrass beds provide shade for bacteria, reducing the likelihood that they will be damaged or killed by UV radiation and creating an environment for them to thrive (Chang et al. 1985). This is supported by the fact that eelgrass bed densities and growth rates

tend to increase in the spring and summer months, potentially increasing shading (Thom et al. 2008). A recent study shows that seagrass beds impact pathogen abundance in coastal waters by concentrating bacteria within their beds. In the South China Sea researchers found higher abundances of *Vibrio* spp. and *Salmonella* spp. within the bed of seagrass *Enhalus acoroides* when compared to bare areas (Deng et al. 2021).

We showed the spatial and temporal variability of *Enterococcus* abundance and the microbial community composition in areas associated with seagrass beds in Puget Sound. Our work found strong seasonal differences in the diversity and relative abundance of microbial communities. This result is consistent with another study examining the seasonal microbial community in Puget Sound, Washington. Wallace et al. (2018) found seasonal changes in diversity and community structure using metagenomics. We saw similar results in that samples collected close to shore showed dramatic decreases in alpha diversity during the winter months. We also found similar bacteria such as *Rhodobacter* but it was not as predominant in our samples. There is a need for more research to fully understand the coastal microbial community ecology as it relates to *Z. marina* presence.

We detected potentially pathogenic bacterial genera in certain eDNA samples. *Vibrio*, *Pseudomonas*, and *Enterobacter* can all cause illness in human, fish, and marine mammals if ingested or if they come in contact with open wounds. *Vibrio* infections can cause diarrhea, stomach cramps, fevers, and chills (New York Department of Health, 2017). *Pseudomonas* infections can cause rashes, swelling, joint pain, headaches, and diarrhea (Centers for Disease Control and Prevention, 2019). Lastly, *Enterobacter* can cause lower respiratory tract infections, skin infections, and urinary tract infections (Ramirez and Giron 2022).

*Pseudomonas* and *Enterobacter* were primarily found during the winter months at all field sites when dissolved oxygen and pH values were the highest and the temperature was the coolest. In fact, the samples from November and December were dominated by *Pseudomonas* and four samples from December (two from Golden Gardens and two from Smith's Cove) only contained these bacteria. This species is common in marine environments and is frequently detected as bacterioplankton in seawater as well as sediments and in aquaculture facilities (Isnansetyo and Kamei 2009). In contrast, *Vibrio* was seen at all field sites year-round and did not seem to be impacted by the varying environmental conditions. *Enterococcus* abundance was highest in the summer months when salinity varied the most (32.5 - 22.5 ppm), temperature was high (11-13 °C), and dissolved oxygen was the lowest (6-7 mg/L). The decrease in salinity at Golden Gardens and Smith's cove during from June to August may indicate a high volume of freshwater input that could be carrying bacteria from runoff or possibly from the West Point wastewater Treatment Plant. High *Enterococcus* abundance also coincided with times of the year when there is high recreation, potentially due to recreators, and therefore more possibility of illness. This data indicates seasonal patterns in certain potentially pathogenic bacteria and can help inform coastal management of recreational sites and conservation efforts.

We found several bacteria that were differentially abundant at the three field sites. We found *hgcI* clade of the *Sporichthyaceae* family, *Cyanobium PCC* of the family *Cyanobiaceae*, and *Glaciecola* of the family *Alteromonadaceae* were more abundant at Golden Gardens Park when *Z. marina* was absent. The median number of sequences assigned to the *hgcI* clade, *Cyanobium PCC*, and *Cyanobiaceae* were 95.5, 64.5, and 23.5 respectively while the median for the other sites was one. Within *Z. marina* beds *Cyanobium PCC* and the *hgcI* clade were also more abundant at Golden Gardens with median reads of 122 and 37.5, respectively (Table S2.3).

Golden Gardens is located next to a large marina and West Point wastewater treatment plant which could help explain the differences in bacterial abundances that we found at this site.

We detected several bacteria that were common at all field sites throughout the year. This includes the alpha proteobacteria family *Rhodobacteraceae*, alphaproteobacteria of the SAR11 clade, and the gamma proteobacteria family *Alcaligenaceae*. The *Rhodobacteraceae* family is incredibly common in the marine environment, especially the pelagic zone and algal-associated biofilms, has high ecological and phenotypic diversity, and remains uncultured (Pohlner et al. 2019). SAR11 is a highly abundant group of alphaproteobacteria in the ocean globally (Giovannoni et al. 1990). This group plays an important role in the ocean carbon cycle and makes up a quarter of the bacteria in the open ocean as well as estuaries and coastal areas (Rusch et al. 2007; Biers, Sun, and Howard 2009). The *Alcaligenaceae* family of the order *Burkholderiales* is abundant in the terrestrial and marine environment and includes animal and human pathogens such as *Bordetella pertussis* from whooping cough (Austin 2014). Some species in the genus *Alcaligenes* have biotechnological applications, such as bioremediation and biocontrol (Durán et al. 2019).

Our results show that overall bacterial abundance decreased as we sampled further from the shoreline. We found an average decrease of 7 bacterial colonies over the 100 m transect. We can attribute this to the fact that most bacterial pollution in the Puget Sound comes from runoff and other land-based sources such as wastewater and boat waste discharge, stormwater, sewage overflows, and faulty septic systems (Washington State Department of Ecology, 2021). This result is the same as the findings in a tropical system where bacterial abundances significantly decreased as distance from shore increased (Lamb et al. 2017).

Not all microbes will interact equally with seagrass beds. A previous study found that *Z. marina* excluded harmful dinoflagellates (Jacobs-Palmer et al. 2020). Researchers discovered significantly lower dinoflagellate abundances inside and around the *Z. marina* bed, such that *Z. marina* can form a ‘halo’ of dinoflagellate exclusion, up to 16 meters beyond the extent of the meadow (Jacobs-Palmer et al. 2020). Allelopathic activity, the defensive release of chemicals, and biological interactions of the micro and macro epibionts can also affect the microbial diversity and abundance within the bed (Jacobs-Palmer et al. 2020). Additional research is still needed to fully understand the physical and chemical filtration mechanisms that *Z. marina* can possess to exclude certain bacteria through allelopathy and remove others by reducing flow and/or intercepting particles.

To learn more about the microbial dynamics in coastal communities associated with seagrass beds it is important to consider the microbiome of leaves, roots and seagrass sediments (Ettinger et al. 2017; Martin et al. 2020). While previous research indicates that the microbiome of *Z. marina* leaves is distinct from the surrounding seawater, they may contribute and interact with microbial communities in the water column (Hurtado-McCormick et al. 2019). More research is needed to better understand the role that microbes play in the physiology and health of seagrass beds and the ecology and biogeochemistry of seagrass habitats.

This study provides insight into the seasonal changes in fecal indicator bacteria and the microbial community composition in Puget Sound, Washington as they relate to *Z. marina* beds. This research can help inform recreational site managers about the best time to close public beaches to limit the risk of exposure to pathogenic bacteria. This work also highlights the need for further research into the mechanisms that seagrasses use to reduce pathogens and particles and how they influence the microbial communities around them.

## References

- Abeysinghe, P. D. 2010. "Antibacterial Activity of Some Medicinal Mangroves against Antibiotic Resistant Pathogenic Bacteria." *Indian Journal of Pharmaceutical Sciences* 72 (2): 167–72. <https://doi.org/10.4103/0250-474X.65019>.
- Alizadeh Behbahani, Behrooz, Farideh Tabatabaei Yazdi, Fakhri Shahidi, Hamid Noorbakhsh, Alireza Vasiee, and Ali Alghooneh. 2018. "Phytochemical Analysis and Antibacterial Activities Extracts of Mangrove Leaf against the Growth of Some Pathogenic Bacteria." *Microbial Pathogenesis* 114 (January): 225–32. <https://doi.org/10.1016/j.micpath.2017.12.004>.
- Alongi, D. M., D. Murdiyarsa, J. W. Fourqurean, J. B. Kauffman, A. Hutahaean, S. Crooks, C. E. Lovelock, et al. 2016. "Indonesia's Blue Carbon: A Globally Significant and Vulnerable Sink for Seagrass and Mangrove Carbon." *Wetlands Ecology and Management* 24 (1): 3–13. <https://doi.org/10.1007/s11273-015-9446-y>.
- Ameen, Fuad, and Ali A. Al-Homaidan. 2021. "Compost Inoculated with Fungi from a Mangrove Habitat Improved the Growth and Disease Defense of Vegetable Plants." *Sustainability* 13 (1): 124. <https://doi.org/10.3390/su13010124>.
- Anderson, Marti J. 2001. "A New Method for Non-Parametric Multivariate Analysis of Variance." *Austral Ecology* 26 (1): 32–46. <https://doi.org/10.1111/j.1442-9993.2001.01070.pp.x>.
- Audah, Kholis A. 2020. "Antibacterial Screening of Mangrove Extract Library Showed Potential Activity against *Escherichia Coli* and *Staphylococcus Aureus*," May.
- Babuselvam, M., A. Panneerselvam, K. Kanimozhi, and G. Kavitha. 2017. "Antibacterial Potential of Actinomycetes from Seagrass against Human and Aquaculture Pathogens." *Journal of Microbiology and Biotechnology Research* <https://www.semanticscholar.org/paper/Antibacterial-potential-of-actinomycetes-from-human-Babuselvam-Panneerselvam/e2bb6e6ac37c81b256547d86e50f527a1291e06b>.
- "Bacteria - Washington State Department of Ecology." n.d. *Monitoring bacteria in Puget Sound*. Accessed June 5, 2022. <https://ecology.wa.gov/Water-Shorelines/Puget-Sound/Issues-problems/Bacteria>.
- Beck, Michael W., Robert D. Brumbaugh, Laura Airoidi, Alvar Carranza, Loren D. Coen, Christine Crawford, Omar Defeo, et al. 2011. "Oyster Reefs at Risk and Recommendations for Conservation, Restoration, and Management." *BioScience* 61 (2): 107–16. <https://doi.org/10.1525/bio.2011.61.2.5>.
- Ben-Horin, Tal, Gorka Bidegain, Lauren Huey, Diego A. Narvaez, and David Bushek. 2015. "Parasite Transmission through Suspension Feeding." *Journal of Invertebrate Pathology* 131 (October): 155–76. <https://doi.org/10.1016/j.jip.2015.07.006>.
- Ben-Horin, Tal, Colleen A. Burge, David Bushek, Maya L. Groner, Dina A. Proestou, Lauren I. Huey, Gorka Bidegain, and Ryan B. Carnegie. 2018. "Intensive Oyster Aquaculture Can Reduce Disease Impacts on Sympatric Wild Oysters." *Aquaculture Environment Interactions* 10 (December): 557–67. <https://doi.org/10.3354/aei00290>.
- Bockelmann, Anna-Christina, Verena Tams, Jana Ploog, Philipp R. Schubert, and Thorsten B. H. Reusch. 2013. "Quantitative PCR Reveals Strong Spatial and Temporal Variation of the Wasting Disease Pathogen, *Labyrinthula Zosteriae* in Northern European Eelgrass (*Zostera Marina*) Beds." *PLOS ONE* 8 (5): e62169. <https://doi.org/10.1371/journal.pone.0062169>.

- Bolyen, Evan, Jai Ram Rideout, Matthew R. Dillon, Nicholas A. Bokulich, Christian C. Abnet, Gabriel A. Al-Ghalith, Harriet Alexander, et al. 2019. "Reproducible, Interactive, Scalable and Extensible Microbiome Data Science Using QIIME 2." *Nature Biotechnology* 37 (8): 852–57. <https://doi.org/10.1038/s41587-019-0209-9>.
- Brauman, Kate A., Gretchen C. Daily, T. Ka'eo Duarte, and Harold A. Mooney. 2007. "The Nature and Value of Ecosystem Services: An Overview Highlighting Hydrologic Services." *Annual Review of Environment and Resources* 32 (1): 67–98. <https://doi.org/10.1146/annurev.energy.32.031306.102758>.
- Buhmann, Anne, and Jutta Papenbrock. 2013. "Biofiltering of Aquaculture Effluents by Halophytic Plants: Basic Principles, Current Uses and Future Perspectives." *Environmental and Experimental Botany*, Sustainable cultivation and exploitation of halophyte crops in a salinizing world, 92 (August): 122–33. <https://doi.org/10.1016/j.envexpbot.2012.07.005>.
- Burge, Colleen A., Collin J. Closek, Carolyn S. Friedman, Maya L. Groner, Cody M. Jenkins, Amanda Shore-Maggio, and Jennifer E. Welsh. 2016. "The Use of Filter-Feeders to Manage Disease in a Changing World." *Integrative and Comparative Biology* 56 (4): 573–87. <https://doi.org/10.1093/icb/icw048>.
- Byappanahalli, Muruleedhara N., Meredith B. Nevers, Asja Korajkic, Zachery R. Staley, and Valerie J. Harwood. 2012. "Enterococci in the Environment." *Microbiology and Molecular Biology Reviews : MMBR* 76 (4): 685–706. <https://doi.org/10.1128/MMBR.00023-12>.
- Callahan, Benjamin J., Paul J. McMurdie, Michael J. Rosen, Andrew W. Han, Amy Jo A. Johnson, and Susan P. Holmes. 2016. "DADA2: High-Resolution Sample Inference from Illumina Amplicon Data." *Nature Methods* 13 (7): 581–83. <https://doi.org/10.1038/nmeth.3869>.
- Carlson, Colin J., Skylar Hopkins, Kayce C. Bell, Jorge Doña, Stephanie S. Godfrey, Mackenzie L. Kwak, Kevin D. Lafferty, et al. 2020. "A Global Parasite Conservation Plan." *Biological Conservation* 250 (October): 108596. <https://doi.org/10.1016/j.biocon.2020.108596>.
- Chan, Kai, Mollie Chapman, Cheryl Chen, Noah Enelow, Taylor Hesselgrave, and Sarah Klain. 2015. *The Values of Place: Recreation and Cultural Ecosystem Services in Puget Sound* "Report to the Puget Sound Institute," 116.
- Choudhury, S, A Sree, S. Mukherjee, P Pattnaik, and Bapuji Maringanti. 2005. "In Vitro Antibacterial Activity of Extracts of Selected Marine Algae and Mangroves against Fish Pathogens." *Asian Fisheries Science* 18 (2005): 285-294 *Asian Fisheries Society, Manila, Philippines* 18 (December). <https://doi.org/10.33997/j.afs.2005.18.3.009>.
- Christiaen B, Ferrier L, Dowty P, Gaeckle J, Berry H (2022). Puget Sound Seagrass Monitoring Report, monitoring year 2018-2020. Nearshore Habitat Program. Washington State Department of Natural Resources, Olympia, WA.
- Cullen-Unsworth, Leanne, and Richard Unsworth. 2013. "Seagrass Meadows, Ecosystem Services, and Sustainability." *Environment Science and Policy for Sustainable Development* 55 (May): 14–28. <https://doi.org/10.1080/00139157.2013.785864>.
- Davidson, Nick. 2014. "How Much Wetland Has the World Lost? Long-Term and Recent Trends in Global Wetland Area." *Marine and Freshwater Research* 65 (January): 936–41. <https://doi.org/10.1071/MF14173>.

- DellaGreca, Marina, Antonio Fiorentino, Marina Isidori, Pietro Monaco, and Armando Zarrelli. 2000. "Antialgal *Ent-Labdane Diterpenes* from *Ruppia Maritima*." *Phytochemistry* 55 (8): 909–13. [https://doi.org/10.1016/S0031-9422\(00\)00253-3](https://doi.org/10.1016/S0031-9422(00)00253-3).
- Deng, Yiqin, Songlin Liu, Juan Feng, Yunchao Wu, and Can Mao. 2021. "What Drives Putative Bacterial Pathogens Removal within Seagrass Meadows?" *Marine Pollution Bulletin* 166 (May): 112229. <https://doi.org/10.1016/j.marpolbul.2021.112229>.
- Duffy, J. Emmett, Pamela L. Reynolds, Christoffer Boström, James A. Coyer, Mathieu Cusson, Serena Donadi, James G. Douglass, et al. 2015. "Biodiversity Mediates Top-down Control in Eelgrass Ecosystems: A Global Comparative-Experimental Approach." *Ecology Letters* 18 (7): 696–705. <https://doi.org/10.1111/ele.12448>.
- Durai, Saravanan, and Manikkam Radhakrishnan. 2016. "Antimicrobial Activity of Mangrove Leaves against Drug Resistant Pathogens" 9 (January): 141–46.
- Eiler, Alexander, Darin Hayakawa, and Michael Rappé. 2011. "Non-Random Assembly of Bacterioplankton Communities in the Subtropical North Pacific Ocean." *Frontiers in Microbiology* 2. <https://www.frontiersin.org/article/10.3389/fmicb.2011.00140>.
- Ettinger, Cassandra L., Sofie E. Voerman, Jenna M. Lang, John J. Stachowicz, and Jonathan A. Eisen. 2017. "Microbial Communities in Sediment from *Zostera Marina* Patches, but Not the *Z. Marina* Leaf or Root Microbiomes, Vary in Relation to Distance from Patch Edge." *PeerJ* 5: e3246. <https://doi.org/10.7717/peerj.3246>.
- Evans, Suzanna M., Kingsley J. Griffin, Ray A. J. Blick, Alistair G. B. Poore, and Adriana Vergés. 2018. "Seagrass on the Brink: Decline of Threatened Seagrass *Posidonia Australis* Continues Following Protection." *PLOS ONE* 13 (4): e0190370. <https://doi.org/10.1371/journal.pone.0190370>.
- Fourqurean, James W. 2002. "HEMMINGA, M. A., AND C. M. DUARTE. 2000. Seagrass Ecology. Cambridge University Press. Xi+298 p. US\$80. ISBN 0-521-66184-6." *Limnology and Oceanography* 47 (2): 611–611. <https://doi.org/10.4319/lo.2002.47.2.0611>.
- Fuhrman, Jed A., Jacob A. Cram, and David M. Needham. 2015. "Marine Microbial Community Dynamics and Their Ecological Interpretation." *Nature Reviews Microbiology* 13 (3): 133–46. <https://doi.org/10.1038/nrmicro3417>.
- Goldberg, Liza, David Lagomasino, Nathan Thomas, and Temilola Fatoyinbo. 2020. "Global Declines in Human-Driven Mangrove Loss." *Global Change Biology* 26 (10): 5844–55. <https://doi.org/10.1111/gcb.15275>.
- Graciaa, Daniel S., Jennifer R. Cope, Virginia A. Roberts, Bryanna L. Cikesh, Amy M. Kahler, Marissa Vigar, Elizabeth D. Hilborn, et al. 2018. "Outbreaks Associated with Untreated Recreational Water - United States, 2000-2014." *MMWR. Morbidity and Mortality Weekly Report* 67 (25): 701–6. <https://doi.org/10.15585/mmwr.mm6725a1>.
- Griffin, Dale W., Kim A. Donaldson, John H. Paul, and Joan B. Rose. 2003. "Pathogenic Human Viruses in Coastal Waters." *Clinical Microbiology Reviews* 16 (1): 129–43. <https://doi.org/10.1128/CMR.16.1.129-143.2003>.
- Groner, Maya L., Colleen A. Burge, Ruth Cox, Natalie D. Rivlin, Mo Turner, Kathryn L. Van Alstyne, Sandy Wyllie-Echeverria, John Bucci, Philip Staudigel, and Carolyn S. Friedman. 2018. "Oysters and Eelgrass: Potential Partners in a High PCO<sub>2</sub> Ocean." *Ecology* 99 (8): 1802–14. <https://doi.org/10.1002/ecy.2393>.
- Groner, MI, Me Eisenlord, Rm Yoshioka, Ea Fiorenza, Pd Dawkins, Oj Graham, M Winningham, et al. 2021. "Warming Sea Surface Temperatures Fuel Summer Epidemics

- of Eelgrass Wasting Disease.” *Marine Ecology Progress Series* 679 (November): 47–58. <https://doi.org/10.3354/meps13902>.
- Halpern, Benjamin S., Shaun Walbridge, Kimberly A. Selkoe, Carrie V. Kappel, Fiorenza Micheli, Caterina D’Agrosa, John F. Bruno, et al. 2008. “A Global Map of Human Impact on Marine Ecosystems.” *Science*, February. <https://doi.org/10.1126/science.1149345>.
- Harley, Christopher D. G., A. Randall Hughes, Kristin M. Hultgren, Benjamin G. Miner, Cascade J. B. Sorte, Carol S. Thornber, Laura F. Rodriguez, Lars Tomanek, and Susan L. Williams. 2006. “The Impacts of Climate Change in Coastal Marine Systems.” *Ecology Letters* 9 (2): 228–41. <https://doi.org/10.1111/j.1461-0248.2005.00871.x>.
- Harvell, C. Drew, and Joleah B. Lamb. 2020. “Disease Outbreaks Can Threaten Marine Biodiversity.” In *Marine Disease Ecology*. Oxford: Oxford University Press. <https://doi.org/10.1093/oso/9780198821632.003.0008>.
- Herrera, Diego, Alicia Ellis, Brendan Fisher, Christopher D. Golden, Kiersten Johnson, Mark Mulligan, Alexander Pfaff, Timothy Treuer, and Taylor H. Ricketts. 2017. “Upstream Watershed Condition Predicts Rural Children’s Health across 35 Developing Countries.” *Nature Communications* 8 (1): 811. <https://doi.org/10.1038/s41467-017-00775-2>.
- Hewson, Ian, Jason B. Button, Brent M. Gudenkauf, Benjamin Miner, Alisa L. Newton, Joseph K. Gaydos, Janna Wynne, et al. 2014. “Densovirus Associated with Sea-Star Wasting Disease and Mass Mortality.” *Proceedings of the National Academy of Sciences* 111 (48): 17278–83. <https://doi.org/10.1073/pnas.1416625111>.
- Hodin, J., A. Pearson-Lund, F. P. Anteau, P. Kitaeff, and S. Cefalu. 2021. “Progress Toward Complete Life-Cycle Culturing of the Endangered Sunflower Star, *Pycnopodia helianthoides*.” *The Biological Bulletin* 241 (3): 243–58. <https://doi.org/10.1086/716552>.
- “How Much Does an Industrial Water Treatment System Cost?” 2017. *Samco Tech* (blog). September 22, 2017. <https://www.samcotech.com/how-much-does-an-industrial-water-treatment-system-cost/>.
- Hurtado-McCormick, Valentina, Tim Kahlke, Katherina Petrou, Thomas Jeffries, Peter J. Ralph, and Justin Robert Seymour. 2019. “Regional and Microenvironmental Scale Characterization of the *Zostera muelleri* Seagrass Microbiome.” *Frontiers in Microbiology* 10. <https://www.frontiersin.org/article/10.3389/fmicb.2019.01011>.
- Jacobs-Palmer, Emily, Ramón Gallego, Ana Ramón-Laca, Emily Kunselman, Kelly Cribari, Micah Horwith, and Ryan P. Kelly. 2020. “A Halo of Reduced Dinoflagellate Abundances in and around Eelgrass Beds.” *PeerJ* 8: e8869. <https://doi.org/10.7717/peerj.8869>.
- Johnson, Pieter T. J., Daniel L. Preston, Jason T. Hoverman, and Katherine L. D. Richgels. 2013. “Biodiversity Decreases Disease through Predictable Changes in Host Community Competence.” *Nature* 494 (7436): 230–33. <https://doi.org/10.1038/nature11883>.
- Keesing, Felicia, and Richard S. Ostfeld. 2021. “Impacts of Biodiversity and Biodiversity Loss on Zoonotic Diseases.” *Proceedings of the National Academy of Sciences* 118 (17). <https://doi.org/10.1073/pnas.2023540118>.
- Kim, Kiwoong, Hyejeong Kim, Jae Hong Lim, and Sang Joon Lee. 2016. “Development of a Desalination Membrane Bioinspired by Mangrove Roots for Spontaneous Filtration of Sodium Ions.” *ACS Nano* 10 (12): 11428–33. <https://doi.org/10.1021/acsnano.6b07001>.
- Kirk, Molly, Daniel Esler, and W. Sean Boyd. 2007. “Morphology and Density of Mussels on Natural and Aquaculture Structure Habitats: Implications for Sea Duck Predators.”

- Marine Ecology Progress Series* 346 (September): 179–87.  
<https://doi.org/10.3354/meps07046>.
- Klohmann, C. A., and J. L. Padilla-Gamiño. 2022. “Pathogen Filtration: An Untapped Ecosystem Service.” *Frontiers in Marine Science* 9.  
<https://www.frontiersin.org/articles/10.3389/fmars.2022.921451>.
- Kuehn, Wolfgang, and Uwe Mueller. 2000. “Riverbank Filtration: An Overview.” *Journal AWWA* 92 (12): 60–69. <https://doi.org/10.1002/j.1551-8833.2000.tb09071.x>.
- Lafferty, Kevin D, Stefano Allesina, Matias Arim, Cherie J Briggs, Giulio De Leo, Andrew P Dobson, Jennifer A Dunne, et al. 2008. “Parasites in Food Webs: The Ultimate Missing Links.” *Ecology Letters* 11 (6): 533–46. <https://doi.org/10.1111/j.1461-0248.2008.01174.x>.
- Lamb, Joleah, Jeroen Van de Water, David Bourne, Craig Altier, Margaux Hein, Evan Fiorenza, Nur Abu, Jamaluddin Jompa, and Catherine Harvell. 2017. “Seagrass Ecosystems Reduce Exposure to Bacterial Pathogens of Humans, Fishes, and Invertebrates.” *Science* 355 (February): 731. <https://doi.org/10.1126/science.aal1956>.
- Lin, Brenda, and Jonathan Dushoff. 2004. “Mangrove Filtration of Anthropogenic Nutrients in the Rio Coco Solo, Panama.” *Management of Environmental Quality: An International Journal* 15 (April): 131–42. <https://doi.org/10.1108/14777830410523071>.
- Littman, Raechel A., Evan A. Fiorenza, Amelia S. Wenger, Kathryn L. E. Berry, Jeroen A. J. M. van de Water, Lily Nguyen, Soe Tint Aung, et al. 2020. “Coastal Urbanization Influences Human Pathogens and Microdebris Contamination in Seafood.” *Science of The Total Environment* 736 (September): 139081. <https://doi.org/10.1016/j.scitotenv.2020.139081>.
- Lukasik, Jerzy, Troy M. Scott, Diane Andryshak, and Samuel R. Farrah. 2000. “Influence of Salts on Virus Adsorption to Microporous Filters.” *Applied and Environmental Microbiology* 66 (7): 2914–20. <https://doi.org/10.1128/AEM.66.7.2914-2920.2000>.
- Mandal, Siddhartha, Will Van Treuren, Richard A. White, Merete Eggesbø, Rob Knight, and Shyamal D. Peddada. 2015. “Analysis of Composition of Microbiomes: A Novel Method for Studying Microbial Composition.” *Microbial Ecology in Health and Disease* 26: 27663. <https://doi.org/10.3402/mehd.v26.27663>.
- Martin, Belinda C, Marta Sanchez Alarcon, Deirdre Gleeson, Jen A Middleton, Matthew W Fraser, Megan H Ryan, Marianne Holmer, Gary A Kendrick, and Kiernyn Kilminster. 2020. “Root Microbiomes as Indicators of Seagrass Health.” *FEMS Microbiology Ecology* 96 (2): fiz201. <https://doi.org/10.1093/femsec/fiz201>.
- Micu, Alexander “In Poznan, Poland, Eight Clams Get to Decide If People in the City Get Water or Not.” 2020. *ZME Science* (blog). December 28, 2020.  
<https://www.zmescience.com/science/poznan-mussel-water-plants-892524/>.
- Miller, M. A., W. A. Miller, P. A. Conrad, E. R. James, A. C. Melli, C. M. Leutenegger, H. A. Dabritz, et al. 2008. “Type X *Toxoplasma Gondii* in a Wild Mussel and Terrestrial Carnivores from Coastal California: New Linkages between Terrestrial Mammals, Runoff and Toxoplasmosis of Sea Otters.” *International Journal for Parasitology* 38 (11): 1319–28. <https://doi.org/10.1016/j.ijpara.2008.02.005>.
- Mojica, J., Fletcher, A., 2020. Economic Analysis of Outdoor Recreation in Washington State, 2020 Update. *Earth Economics*. Tacoma, WA
- Morris, Robert M., Kevin L. Vergin, Jang-Cheon Cho, Michael S. Rappé, Craig A. Carlson, and Stephen J. Giovannoni. 2005. “Temporal and Spatial Response of Bacterioplankton Lineages to Annual Convective Overturn at the Bermuda Atlantic Time-Series Study

- Site.” *Limnology and Oceanography* 50 (5): 1687–96.  
<https://doi.org/10.4319/lo.2005.50.5.1687>.
- “NOAA Mussel Watch Program: An Assessment of Contaminants of Emerging Concern in Chesapeake Bay, MD, and Charleston Harbor, SC.” n.d. NCCOS Coastal Science Website. Accessed January 24, 2022. <https://coastalscience.noaa.gov/project/mussel-watch-program-assessment-chesapeake-bay-charleston-harbor/>.
- Palacios, Oskar A., Jaime Raúl Adame-Gallegos, Blanca Estela Rivera-Chavira, and Guadalupe Virginia Nevarez-Moorillon. 2021. “Antibiotics, Multidrug-Resistant Bacteria, and Antibiotic Resistance Genes: Indicators of Contamination in Mangroves?” *Antibiotics* 10 (9): 1103. <https://doi.org/10.3390/antibiotics10091103>.
- Poe, Melissa R., Jamie Donatuto, and Terre Satterfield. 2016. “‘Sense of Place’: Human Wellbeing Considerations for Ecological Restoration in Puget Sound.” *Coastal Management* 44 (5): 409–26. <https://doi.org/10.1080/08920753.2016.1208037>.
- Qi, Shu-Hua, Si Zhang, Pei-Yuan Qian, and Bin-Gui Wang. 2008. “Antifeedant, Antibacterial, and Antilarval Compounds from the South China Sea Seagrass *Enhalus Acoroides*” 51 (5): 441–47. <https://doi.org/10.1515/BOT.2008.054>.
- Rahman, Md Mizanur, Martin Zimmer, Imran Ahmed, Daniel Donato, Mamoru Kanzaki, and Ming Xu. 2021. “Co-Benefits of Protecting Mangroves for Biodiversity Conservation and Carbon Storage.” *Nature Communications* 12 (1): 3875. <https://doi.org/10.1038/s41467-021-24207-4>.
- Rasmussen, E. 1977. *Seagrass Ecosystems: A Scientific Perspective*. New York: Marcel Dekker, Inc.
- Redder, Andreas, Matthias Dürr, Georg Daeschlein, Oliver Baeder-Bederski, Christoph Koch, Roland Müller, Martin Exner, and Marianne Borneff-Lipp. 2010. “Constructed Wetlands—Are They Safe in Reducing Protozoan Parasites?” *International Journal of Hygiene and Environmental Health* 213 (1): 72–77. <https://doi.org/10.1016/j.ijheh.2009.12.001>.
- Renshaw, Mark A., Brett P. Olds, Christopher L. Jerde, Margaret M. McVeigh, and David M. Lodge. 2015. “The Room Temperature Preservation of Filtered Environmental DNA Samples and Assimilation into a Phenol-Chloroform-Isoamyl Alcohol DNA Extraction.” *Molecular Ecology Resources* 15 (1): 168–76. <https://doi.org/10.1111/1755-0998.12281>.
- Saad, Shahbudin, Muhammad Taher, Deny Susanti, Haitham Qaralleh, and Nurul Afifah Binti Abdul Rahim. 2011. “Antimicrobial Activity of Mangrove Plant (*Lumnitzera Littorea*).” *Asian Pacific Journal of Tropical Medicine* 4 (7): 523–25. [https://doi.org/10.1016/S1995-7645\(11\)60138-7](https://doi.org/10.1016/S1995-7645(11)60138-7).
- Sahoo, G., N. S. S. Mulla, Z. A. Ansari, and C. Mohandass. 2012. “Antibacterial Activity of Mangrove Leaf Extracts against Human Pathogens.” *Indian Journal of Pharmaceutical Sciences* 74 (4): 348–51. <https://doi.org/10.4103/0250-474X.107068>.
- Selakovic, Sanja, Peter C. de Ruiter, and Hans Heesterbeek. 2014. “Infectious Disease Agents Mediate Interaction in Food Webs and Ecosystems.” *Proceedings of the Royal Society B: Biological Sciences* 281 (1777): 20132709. <https://doi.org/10.1098/rspb.2013.2709>.
- Sippo, James Z., Damien T. Maher, Douglas R. Tait, Ceylena Holloway, and Isaac R. Santos. 2016. “Are Mangroves Drivers or Buffers of Coastal Acidification? Insights from Alkalinity and Dissolved Inorganic Carbon Export Estimates across a Latitudinal Transect.” *Global Biogeochemical Cycles* 30 (5): 753–66. <https://doi.org/10.1002/2015GB005324>.

- Smith, Jayson R., Peggy Fong, and Richard F. Ambrose. 2006. "Dramatic Declines in Mussel Bed Community Diversity: Response to Climate Change?" *Ecology* 87 (5): 1153–61. [https://doi.org/10.1890/0012-9658\(2006\)87\[1153:DDIMBC\]2.0.CO;2](https://doi.org/10.1890/0012-9658(2006)87[1153:DDIMBC]2.0.CO;2).
- Sorte, Cascade J. B., Victoria E. Davidson, Marcus C. Franklin, Kylla M. Benes, Meredith M. Doellman, Ron J. Etter, Robyn E. Hannigan, Jane Lubchenco, and Bruce A. Menge. 2017. "Long-Term Declines in an Intertidal Foundation Species Parallel Shifts in Community Composition." *Global Change Biology* 23 (1): 341–52. <https://doi.org/10.1111/gcb.13425>.
- Spalding, Mark D and Leal, Maricé (editors), 2021 The State of the World's Mangroves 2021. Global Mangrove Alliance. Designed and produced by MSQ Sustain.
- Sullivan, Brooke K., Stacey M. Trevathan-Tackett, Sigrid Neuhauser, and Laura L. Govers. 2018. "Review: Host-Pathogen Dynamics of Seagrass Diseases under Future Global Change." *Marine Pollution Bulletin*, Securing a future for seagrass, 134 (September): 75–88. <https://doi.org/10.1016/j.marpolbul.2017.09.030>.
- Sutton-Grier, Ariana E., and Paul A. Sandifer. 2019. "Conservation of Wetlands and Other Coastal Ecosystems: A Commentary on Their Value to Protect Biodiversity, Reduce Disaster Impacts, and Promote Human Health and Well-Being." *Wetlands* 39 (6): 1295–1302. <https://doi.org/10.1007/s13157-018-1039-0>.
- Thatoi, Hrudayanath, Bikash C. Behera, and Rashmi R. Mishra. 2013. "Ecological Role and Biotechnological Potential of Mangrove Fungi: A Review." *Mycology* 4 (1): 54–71. <https://doi.org/10.1080/21501203.2013.785448>.
- Thom, R. M. 1990. "Spatial and Temporal Patterns in Plant Standing Stock and Primary Production in a Temperate Seagrass System" 33 (6): 497–510. <https://doi.org/10.1515/botm.1990.33.6.497>.
- Tracy, Allison M., Madeline L. Pielmeier, Reyn M. Yoshioka, Scott F. Heron, and C. Drew Harvell. 2019. "Increases and Decreases in Marine Disease Reports in an Era of Global Change." *Proceedings of the Royal Society B: Biological Sciences* 286 (1912): 20191718. <https://doi.org/10.1098/rspb.2019.1718>.
- US EPA, OW. 2013. "Indicators: Enterococci." Overviews and Factsheets. December 4, 2013. <https://www.epa.gov/national-aquatic-resource-surveys/indicators-enterococci>.
- . 2015. "Constructed Wetlands." Overviews and Factsheets. September 23, 2015. <https://www.epa.gov/wetlands/constructed-wetlands>.
- Voudanta, Eleni, Konstantinos Ar Kormas, Sebastián Monchy, Alice Delegrange, Dorothée Vincent, Savvas Genitsaris, and Urania Christaki. 2016. "Mussel Biofiltration Effects on Attached Bacteria and Unicellular Eukaryotes in Fish-Rearing Seawater." *PeerJ* 4 (March): e1829. <https://doi.org/10.7717/peerj.1829>.
- Wallace, James C., Jessica E. Youngblood, Jesse A. Port, Alison C. Cullen, Marissa N. Smith, Tomomi Workman, and Elaine M. Faustman. 2018. "Variability in Metagenomic Samples from the Puget Sound: Relationship to Temporal and Anthropogenic Impacts." *PLOS ONE* 13 (2): e0192412. <https://doi.org/10.1371/journal.pone.0192412>.
- Water, World Health Organization, and Sanitation and Health Team. 1999. "Health Based Monitoring of Recreational Waters : The Feasibility of a New Approach (the 'Annapolis Protocol') : Outcome of an Expert Consultation, Annapolis, USA." WHO/SDE/WSH/99.1. World Health Organization. <https://apps.who.int/iris/handle/10665/66477>.

- Waycott, Michelle, Carlos M. Duarte, Tim J. B. Carruthers, Robert J. Orth, William C. Dennison, Suzanne Olyarnik, Ainsley Calladine, et al. 2009. "Accelerating Loss of Seagrasses across the Globe Threatens Coastal Ecosystems." *Proceedings of the National Academy of Sciences* 106 (30): 12377–81. <https://doi.org/10.1073/pnas.0905620106>.
- Weiss, Sophie, Zhenjiang Zech Xu, Shyamal Peddada, Amnon Amir, Kyle Bittinger, Antonio Gonzalez, Catherine Lozupone, et al. 2017. "Normalization and Microbial Differential Abundance Strategies Depend upon Data Characteristics." *Microbiome* 5 (1). <https://doi.org/10.1186/s40168-017-0237-y>.
- Wijisman, J. W. M., K. Troost, J. Fang, and A. Roncarati. 2019. "Global Production of Marine Bivalves. Trends and Challenges." In *Goods and Services of Marine Bivalves*, edited by Aad C. Smaal, Joao G. Ferreira, Jon Grant, Jens K. Petersen, and Øivind Strand, 7–26. Cham: Springer International Publishing. [https://doi.org/10.1007/978-3-319-96776-9\\_2](https://doi.org/10.1007/978-3-319-96776-9_2).
- Wright, Nikki 2017. "Eelgrass." *Ocean Watch*. Howe Sound Edition. <https://oceanwatch.ca/howesound/wp-content/uploads/sites/2/2016/12/OceanWatch-HoweSoundReport-Eelgrass.pdf>
- Wu, Shubiao, Pedro N. Carvalho, Jochen A. Müller, Valsa Remony Manoj, and Renjie Dong. 2016. "Sanitation in Constructed Wetlands: A Review on the Removal of Human Pathogens and Fecal Indicators." *The Science of the Total Environment* 541 (January): 8–22. <https://doi.org/10.1016/j.scitotenv.2015.09.047>.
- Wu, Y., A. Chung, N. F. Y. Tam, N. Pi, and M. H. Wong. 2008. "Constructed Mangrove Wetland as Secondary Treatment System for Municipal Wastewater." *Ecological Engineering* 34 (2): 137–46. <https://doi.org/10.1016/j.ecoleng.2008.07.010>.
- Yilmaz, Pelin, Laura Wegener Parfrey, Pablo Yarza, Jan Gerken, Elmar Pruesse, Christian Quast, Timmy Schweer, Jörg Peplies, Wolfgang Ludwig, and Frank Oliver Glöckner. 2014. "The SILVA and 'All-Species Living Tree Project (LTP)' Taxonomic Frameworks." *Nucleic Acids Research* 42 (D1): D643–48. <https://doi.org/10.1093/nar/gkt1209>.
- Zannella, Carla, Francesco Mosca, Francesca Mariani, Gianluigi Franci, Veronica Folliero, Marilena Galdiero, Pietro Giorgio Tiscar, and Massimiliano Galdiero. 2017. "Microbial Diseases of Bivalve Mollusks: Infections, Immunology and Antimicrobial Defense." *Marine Drugs* 15 (6): 182. <https://doi.org/10.3390/md15060182>.

**Supplementary materials**

*Table S2.1. Seasonal environmental conditions at all field sites in Puget Sound, Washington*

Field Site	Season	pH				Temperature (C°)				Dissolved Oxygen (mg/L)			
		mean	min	max	CV	mean	min	max	CV	mean	min	max	CV
Golden Gardens	Summer	8.45	8.36	8.53	0.005	14.2	13.0	15.6	0.041	7.13	6.62	9.00	0.068
	Fall	8.36	8.28	8.50	0.008	11.7	10.7	12.7	0.081	6.65	5.50	8.09	0.131
	Winter	8.27	7.72	8.86	0.043	8.74	8.0	9.6	0.070	8.99	7.47	11.6	0.156
	Spring	8.67	8.48	8.74	0.010	8.2	8.0	8.4	0.017	10.6	9.91	12.7	0.091
Alki Beach	Summer	8.31	8.05	8.56	0.030	13.3	8.4	14.6	0.052	7.78	6.41	8.62	0.115
	Fall	8.41	8.12	8.83	0.004	11.3	10.5	12.0	0.009	7.01	6.98	7.90	0.103
	Winter	8.27	7.76	8.91	0.057	9.1	8.4	10.1	0.078	8.08	6.25	9.48	0.160
	Spring	9.00	8.91	9.05	0.005	8.0	7.9	8.2	0.013	9.63	9.06	11.3	0.083
Smith's Cove	Summer	8.23	8.05	8.43	0.020	13.1	11.9	14.2	0.072	7.68	6.20	8.57	0.115
	Fall	8.27	8.18	8.39	0.007	10.9	8.9	12.9	0.162	7.28	6.16	8.92	0.122
	Winter	8.12	7.80	8.83	0.026	8.9	7.9	9.4	0.044	8.45	7.32	10.1	0.140
	Spring	8.79	8.77	8.82	0.002	7.2	6.8	7.6	0.036	9.81	9.33	11.1	0.064

Field Site	Season	Salinity (ppm)				PAR ( $\mu\text{mol m}^{-2}\text{s}^{-1}$ )			
		mean	min	max	CV	mean	min	max	CV
Golden Gardens	Summer	24.5	29.6	32.6	0.074	19.0	4.14	54.4	0.904
	Fall	27.8	21.9	33.3	0.180	2.86	0.67	11.6	0.953
	Winter	24.8	21.7	29.3	0.082	17.8	1.15	62.4	1.17
	Spring	26.2	25.5	26.9	0.019	22.6	10.7	43.9	0.655
Alki Beach	Summer	32.4	25.1	33.1	0.048	15.07	5.07	38.6	0.611
	Fall	31.4	31.1	32.2	0.003	18.2	6.45	37.1	0.312
	Winter	31.1	29.0	33.1	0.053	17.4	1.67	44.3	0.927
	Spring	31.0	31.0	31.1	0.001	15.8	9.45	31.6	0.500
Smith's Cove	Summer	32.3	31.9	32.6	0.010	18.4	8.44	35.8	0.405
	Fall	28.9	25.0	31.4	0.091	2.65	1.21	5.08	0.394
	Winter	29.0	25.6	31.1	0.063	15.8	0.96	37.8	1.01
	Spring	26.2	25.3	26.8	0.020	14.1	12.5	16.9	0.102

*Table S2.2. Alpha and beta diversity statistics. Alpha diversity (Faith's PD and Pielou evenness) was determined using Kruskal-Wallis tests and pairwise comparisons. Beta diversity was determined using PERMANOVA and pairwise comparisons.*

*Alpha Diversity*

<b>Faith's PD (richness)</b>				
<i>Group 1</i>	<i>Group 2</i>	<i>H</i>	<i>p-value</i>	<i>q-value</i>
<i>Z. marina</i>		0.2888	0.591	
<i>Z. marina</i>	sand	0.2888	0.591	0.591

Month		95.84	$1.22e^{-20}$	
August	December	35.05	$3.21e^{-09}$ ***	$4.81e^{-09}$
August	March	25.41	$4.63e^{-07}$ ***	$5.55e^{-07}$
August	November	45.97	$1.20e^{-11}$ ***	$3.60e^{-11}$
December	March	40.01	$2.52e^{-10}$ ***	$5.05e^{-10}$
December	November	7.739	$0.0054$ **	$0.0054$
March	November	47.97	$4.32e^{-12}$ ***	$2.59e^{-11}$
Site		0.2052	0.9025	
Alki	Golden Gardens	0.0353	0.851	0.851
Alki	Smith's Cove	0.2292	0.6321	0.851
Golden Gardens	Smith's Cove	0.0486	0.8255	0.851

### ***Pielou Evenness***

<i>Group 1</i>	<i>Group 2</i>	<i>H</i>	<i>p-value</i>	<i>q-value</i>
<i>Z. marina</i>		0.5134	0.4737	
<i>Z. marina</i>	sand	0.5134	0.4737	0.4737
Month		56.41	$4.10e^{-14}$ ***	
August	December	0.5358	$0.0464$ *	0.4642
August	March	34.8	$3.66e^{-09}$ ***	$1.10e^{-08}$
August	November	26.01	$3.40e^{-07}$ ***	$6.80e^{-07}$
December	March	5.363	$0.0206$ *	0.0247
December	November	10.86	$0.00098$ ***	0.00148
March	November	50.02	$1.52e^{-12}$ ***	$9.12e^{-12}$
Site		3.858	0.1452	
Alki	Golden Gardens	0.6761	0.4109	0.4109
Alki	Smith's Cove	3.788	0.0516	0.1548
Golden Gardens	Smith's Cove	1.373	0.2414	0.362

### ***Beta Diversity***

<i>Group 1</i>	<i>Group 2</i>	<i>Sample size</i>	<i>Permutations</i>	<i>pseudo-F</i>	<i>p-value</i>	<i>q-value</i>
August	December	57	999	29.36	$0.001$ **	0.001
August	March	70	999	20.15	$0.001$ **	0.001
August	November	70	999	29.9	$0.001$ **	0.001
December	March	59	999	43.24	$0.001$ **	0.001
December	November	59	999	5.268	$0.001$ **	0.001
March	November	72	999	43.42	$0.001$ **	0.001
<i>Z. marina</i>	sand	129	999	0.4797	0.973	0.973

Table S2.3. ANCOM results table showing bacterial genera that were differentially abundant at the three field sites within and outside of *Z. marina* beds.

Bacteria	Site			W statistic	<i>Z. marina</i> presence
	Alki Beach	Golden Gardens	Smith's Cove		
	Median Sequences Assigned				
<i>hgcl</i> clade of <i>Sporichthyaceae</i>	1	122	1	709	Y
	1	95.5	1	659	N
<i>Cyanobium</i> PCC of the family <i>Cyanobiaceae</i>	1	37.5	1	702	Y
	1	64.5	1	658	N
<i>Glaciecola</i> of the family <i>Alteromonadaceae</i>	1	68.5	1	601	N

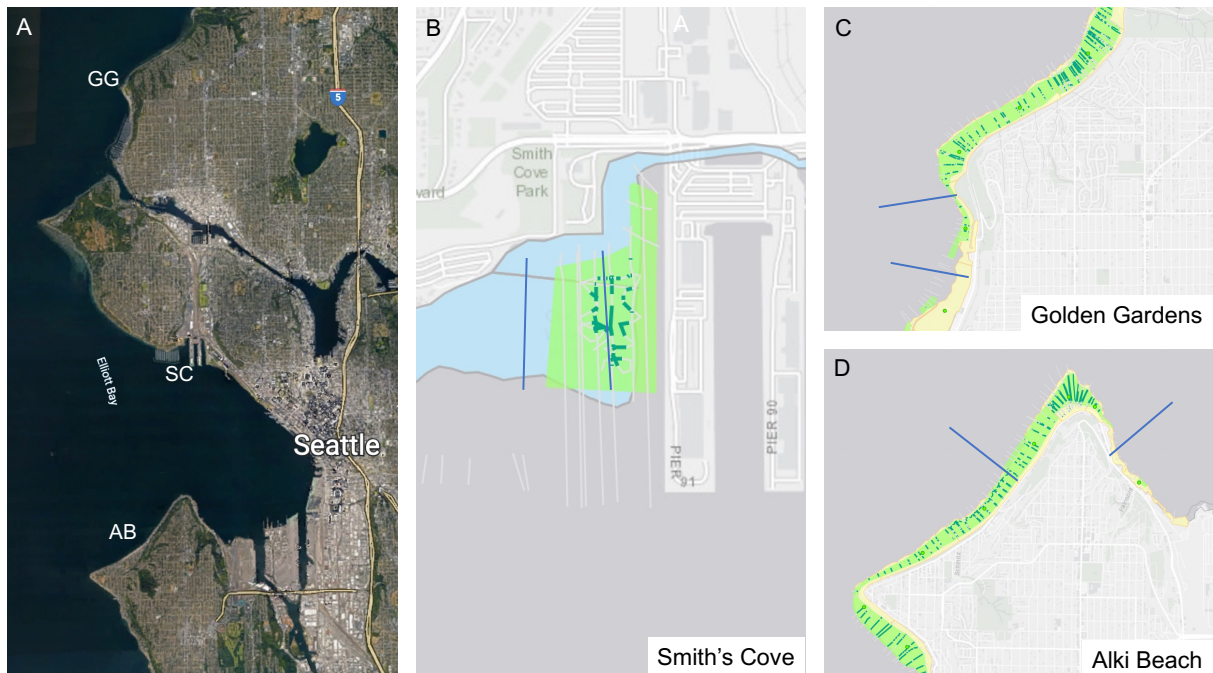


Figure S2.1. Study sites in Seattle, Washington. A) Satellite (Google Earth) image of Seattle, showing Golden Gardens (GG), Smith's Cove (SC), and Alki Beach (AB). B-D) Images of eelgrass beds at each field site. Maps courtesy of the Washington Department of Natural Resources (WA DNR). Green indicates *Z. marina* presence. Blue lines indicate field transects.

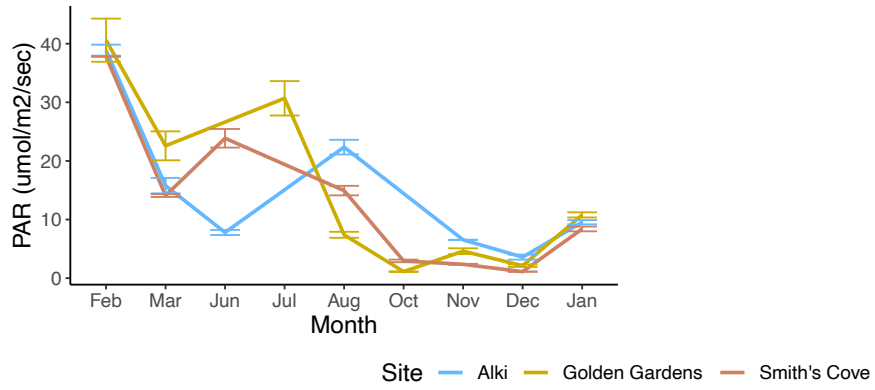


Figure S2.2. Monthly average PAR levels at all field sites in Puget Sound, Washington from January 2020-January 2021. Graphs show the mean monthly values and Standard Error.

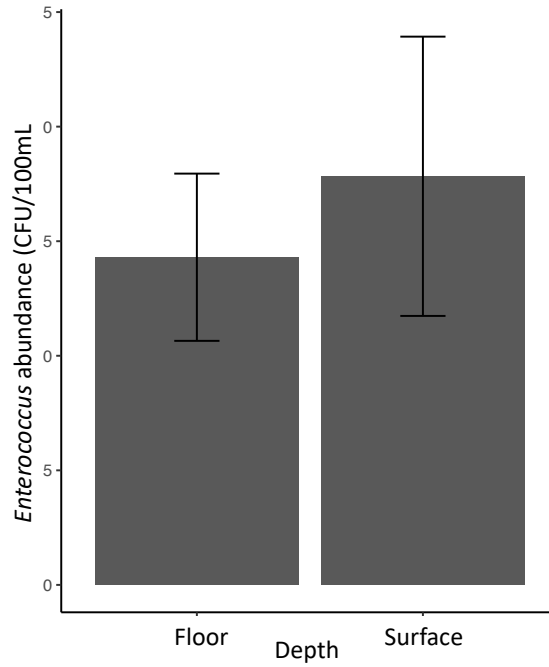


Figure S2.3. Enterococcus single sample counts by depth (0.5m and 4m) at Golden Gardens. Error bars indicate +/- 1 SD,  $p = 0.11$ . Includes all field samples ( $n = 66$ ).

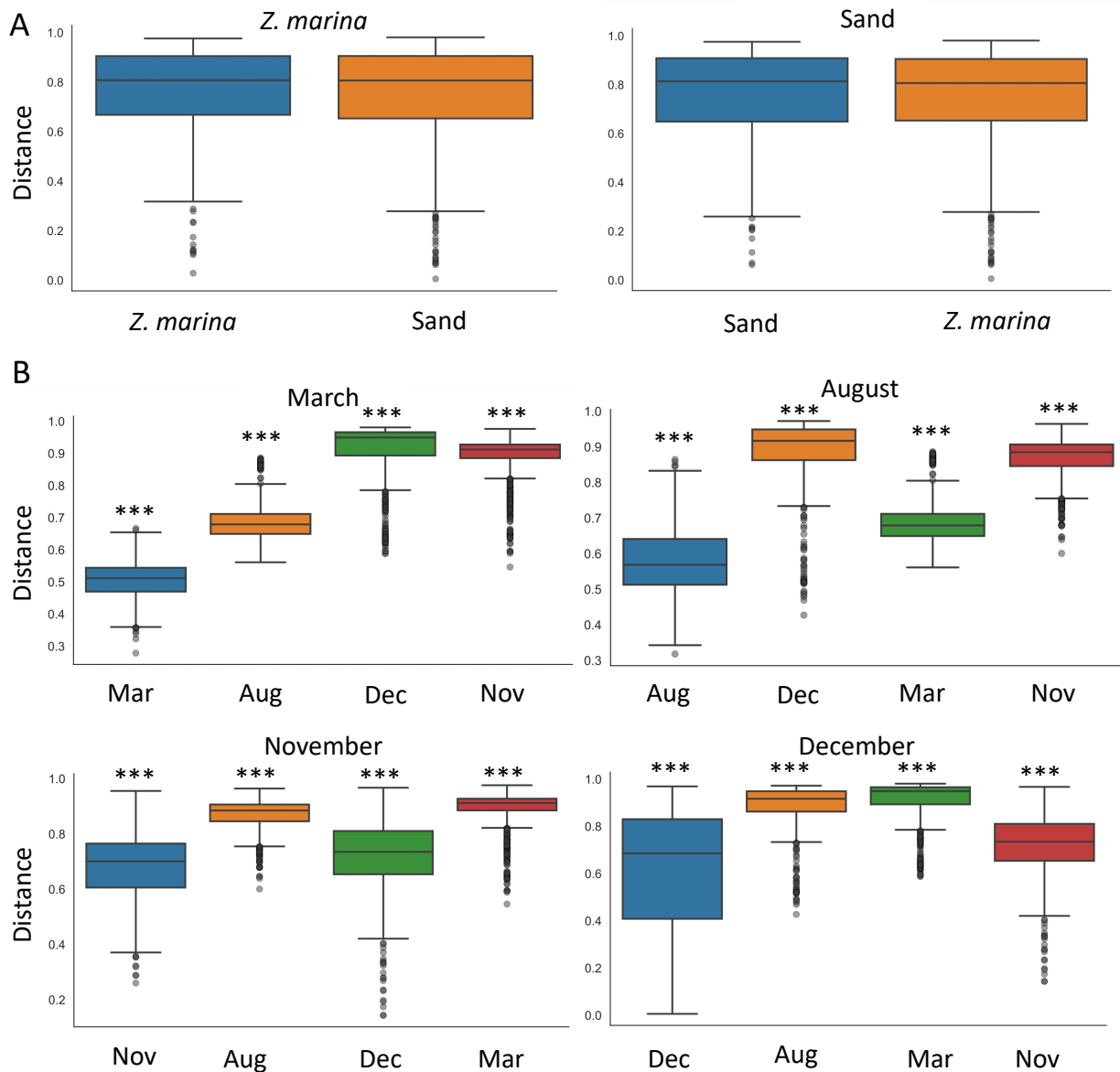


Figure S2.4. PERMANOVA (999 permutations) results testing for differences in beta diversity. A) Group significance plots from pairwise comparisons with respect to *Z. marina* presence ( $p = 0.973$ ). B) Group significant plots from pairwise comparisons with respect to each month (March, August, November, and December) ( $p = 0.001$ ).

d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Pseudomonadales;f\_Pseudomonadaceae;g\_Pseudomonas  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteriia;o\_Chloroplast;f\_Chloroplast;g\_Chloroplast  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Yersiniaceae;g\_Serratia  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rickettsiales;f\_Mitochondria;g\_Mitochondria  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_SAR11\_clade;f\_Clade\_I;g\_Clade\_Ia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Alcaligenaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Planktomarina  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Alcaligenaceae;g\_Alcaligenes  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Ulvibacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Cryomorphaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Polaribacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_NS3a\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Ochrobactrum  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Lentibacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_SAR86\_clade;f\_SAR86\_clade;g\_SAR86\_clade  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Paenibacillales;f\_Paenibacillaceae;g\_Paenibacillus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_NS9\_marine\_group;g\_NS9\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_SAR11\_clade;f\_Clade\_II;g\_Clade\_II  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Aurantivirga  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteriia;o\_Actinomarinales;f\_Actinomarinaceae;g\_Candidatus\_Actinomarina  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opitutales;f\_Puniceicoccaceae;g\_Lentimonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_OM182\_clade;f\_OM182\_clade;g\_OM182\_clade  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_NS4\_marine\_group  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteriia;o\_Frankiales;f\_Sporichthyaceae;g\_hgcl\_clade  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Methylophilaceae;g\_OM43\_clade  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Formosa  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Crocinitomicaceae;g\_Fluviicola  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Limnochthobacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_NS5\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Enterobacteriaceae;g\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_uncultured;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiomicrospirales;f\_Thioglobaceae;g\_SUP05\_cluster  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Planktotalea  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Puniceispirillales;f\_SAR116\_clade;g\_Candidatus\_Puniceispirillum  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Morganellaceae;g\_Providencia  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Pseudohongiellaceae;g\_Pseudohongiella  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Alteromonadaceae;g\_Glaciecola  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Puniceispirillales;f\_SAR116\_clade;g\_SAR116\_clade  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;g\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_uncultured  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Bacillales;f\_Bacillaceae;g\_Bacillus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Flavobacterium  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Rhodoferrax  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Aeromonadales;f\_Aeromonadaceae;g\_Aeromonas  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Yoonia-Loktanella  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Vibrionales;f\_Vibrionaceae;g\_Vibrio  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_RS62\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_Thalassospiraceae;g\_Thalassospira  
d\_Bacteria;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Tateyamaria  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Colwelliaceae;g\_Colwellia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Yersiniaceae;g\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Algibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Sulfitobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Porticococcaceae;g\_SAR92\_clade  
d\_Bacteria;p\_Planktomycetota;c\_Planktomyces;o\_Pirellulales;f\_Pirellulaceae;g\_Blastopirellula  
d\_Bacteria;p\_Marinimicrobia(SAR406\_clade);c\_Marinimicrobia(SAR406\_clade);o\_Marinimicrobia(SAR406\_clade);f\_Marinimicrobia(SAR406\_clade);g\_Marinimicrobia(SAR406\_clade)  
d\_Bacteria;p\_Planktomycetota;c\_OM190;g\_OM190;f\_OM190;g\_OM190  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteriia;o\_Synechococcales;f\_Cyanobiaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Shewanellaceae;g\_Shewanella  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Erwiniaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Enterobacteriaceae;g\_Citrobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Alcaligenaceae;g\_Bordetella  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteriia;o\_Synechococcales;f\_Cyanobiaceae;g\_Cyanobium\_PCC-6307  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Haliellaceae;g\_Luminiphilus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Puniceispirillales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Litreibacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Spirosomaceae;g\_Pseudarcicella  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Octadecabacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_SAR11\_clade;f\_Clade\_III;g\_Clade\_III  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Sphingobacteriales;f\_NS11-12\_marine\_group;g\_NS11-12\_marine\_group  
d\_Bacteria;p\_Nitrospina;c\_Nitrospina;o\_Nitrospinales;f\_Nitrospinaeae;g\_LS-NOB  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Rubritaleaceae;g\_Roseibacillus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacterales;f\_Morganellaceae;g\_Morganella  
d\_Bacteria;p\_Planktomycetota;c\_Planktomyces;o\_Pirellulales;f\_Pirellulaceae;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteriia;o\_Streptomycetales;f\_Streptomycetaceae;g\_Streptomyces  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Bacillales;f\_Planococcaceae;g\_Lysinibacillus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Changchengzhania

d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;g\_Sporichthyaceae  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Nitricolaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Nitrosococcales;f\_Methylophagaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Cryomorphaceae;g\_NS10\_marine\_group  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteriia;o\_Synechococcales;f\_Cyanobiaceae;g\_Synechococcus\_CC9902  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Methylophilaceae;g\_Methylotenera  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_NS2b\_marine\_group  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opitutales;f\_Punicicoccaceae;g\_MB11C04\_marine\_group  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Pirellulales;f\_Pirellulaceae;g\_Rubripirellula  
d\_Bacteria;p\_Patescibacteria;c\_Gracilibacteria;o\_JGI\_0000069-P22;f\_JGI\_0000069-P22;g\_JGI\_0000069-P22  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Granulosicoccales;f\_Granulosicoccaceae;g\_Granulosicoccus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Saprosiraceae;g\_Lewinella  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Planctomycetales;f\_Gimesiaceae;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_Microtrichales;f\_Microtrichaceae;g\_Sva0996\_marine\_group  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Paenibacillales;f\_Paenibacillaceae;g\_Cohnella  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Nitrosococcales;f\_Methylophagaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Jannaschia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Burkholderiaceae;g\_Polynucleobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Litoricolaceae;g\_Litoricola  
Unassigned;\_:;\_:;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Parvibaculales;f\_OCS116\_clade;g\_OCS116\_clade  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Aquibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Thalassobaculales;f\_Nisaeaceae;g\_OM75\_clade  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Haliaceae;g\_OM60(NOR5)\_clade  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Saprosiraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_UBA10353\_marine\_group;f\_UBA10353\_marine\_group;g\_UBA10353\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium  
d\_Bacteria;p\_Proteobacteria;\_:;\_:;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_Magnetospiraceae;g\_uncultured  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Rubritaleaceae;g\_Persicirhabdus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Cyclobacteriaceae;g\_Marinoscillum  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;\_:;\_:;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_KI89A\_clade;f\_KI89A\_clade;g\_KI89A\_clade  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;\_:;\_:;\_  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Gemmatales;f\_Gemmataceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Salinisphaerales;f\_Salinisphaeraceae;g\_Salinisphaera  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Crocinitomiacae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Polaromonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Pseudoalteromonadaceae;g\_Pseudoalteromonas  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Algitalea  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Cryomorphaceae;g\_Vicingus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Parvibaculales;f\_PS1\_clade;g\_PS1\_clade  
d\_Bacteria;p\_Chloroflexi;c\_Dehalococcoidia;o\_SAR202\_clade;f\_SAR202\_clade;g\_SAR202\_clade  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Methylococcales;f\_Methylomonadaceae;g\_Crenothrix  
d\_Bacteria;p\_NB1-j;c\_NB1-j;o\_NB1-j;f\_NB1-j;g\_NB1-j  
d\_Bacteria;p\_SAR324\_clade(Marine\_group\_B);c\_SAR324\_clade(Marine\_group\_B);o\_SAR324\_clade(Marine\_group\_B);f\_SAR324\_clade(Marine\_group\_B);g\_SAR324\_clade(Mar  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_Microtrichales;f\_Illumatobacteraceae;g\_Illumatobacter  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Planctomycetales;f\_Rubinisphaeraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Kordiimonadales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;g\_Candidatus\_Planktophila  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Tenderiales;f\_Tenderiaceae;g\_Candidatus\_Tenderia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Haliaceae;g\_Halioglobus  
d\_Bacteria;p\_Planctomycetota;c\_Phycisphaerae;o\_Phycisphaerales;f\_Phycisphaeraceae;g\_CL500-3  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Chitinophagaceae;g\_Ferruginibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Pseudahrensia  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Maribacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Defluviococcales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Winogradskyella  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Methylophilaceae;g\_Candidatus\_Methylolpumulis  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Yersiniaceae;g\_Rahnella1  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Chitinophagaceae;g\_Sediminibacterium  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Chitinophagaceae;g\_  
d\_Bacteria;p\_Campylobacterota;c\_Campylobacteria;o\_Campylobacteriales;f\_Arcobacteraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Nitrosomonadaceae;g\_JS-44  
d\_Bacteria;p\_Chloroflexi;c\_Anaerolineae;o\_Anaerolineales;f\_Anaerolineaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_AEGEAN-169\_marine\_group;g\_AEGEAN-169\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Nitrosococcales;f\_Methylophagaceae;g\_Marine\_Methylotrophic\_Group\_3  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_Rhodoluna  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Crocinitomiacae;g\_Crocinitomix  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;\_:;\_:;\_  
d\_Bacteria;p\_Nitrospina;c\_Nitrospina;o\_Nitrospinales;f\_Nitrospinaeae;g\_Nitrospina  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiomicrospirales;f\_Thioglobaceae;g\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_DEV007;g\_DEV007  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Pirellulales;f\_Pirellulaceae;g\_Rhodopirellula  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteriia;o\_Cyanobacteriales;f\_Xenococcaceae;g\_Pleurocapsa\_PCC-7319  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Alcaligenaceae;g\_GKS98\_freshwater\_group  
d\_Bacteria;p\_Acidobacteriota;c\_Holophagae;o\_Holophagales;f\_Holophagaceae;g\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Methylococcales;f\_Methylomonadaceae;g\_Milano-WF1B-03  
d\_Bacteria;p\_Bdellovibrionota;c\_Bdellovibrionia;o\_Bdellovibrionales;f\_Bdellovibrionaceae;g\_OM27\_clade  
d\_Bacteria;p\_Dadabacteria;c\_Dadabacteriia;o\_Dadabacteriales;f\_Dadabacteriales;g\_Dadabacteriales  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Morganeliaceae;g\_Proteus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Primsoskiyibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sphingomonadales;f\_Sphingomonadaceae;g\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidiales;f\_Marinifilaceae;g\_uncultured

d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Staphylococcales;f\_Staphylococcaceae;g\_Staphylococcus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Colwelliaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiotrichales;f\_Thiotrichaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_NS7\_marine\_group;g\_NS7\_marine\_group  
d\_Bacteria;p\_Chloroflexi;o\_SL56\_marine\_group;o\_SL56\_marine\_group;f\_SL56\_marine\_group;g\_SL56\_marine\_group  
d\_Bacteria;p\_Fibrobacterota;c\_Fibrobacteria;o\_Fibrobacteriales;f\_Fibrobacteraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sphingomonadales;f\_Sphingomonadaceae;g\_Sphingorhabdus  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Paenibacillales;f\_Paenibacillaceae;\_  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_PeM15;f\_PeM15;g\_PeM15  
d\_Bacteria;p\_Plantcomycetota;c\_Plantcomycetes;o\_Plantcomycetales;f\_Rubinisphaeraceae;g\_Plantmicrobium  
d\_Bacteria;p\_Actinobacteriota;\_:\_;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Lutimonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Saccharospirillaceae;g\_Reinekea  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;\_:\_;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Nitrosoomonadaceae;g\_Nitrosomonas  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;\_:\_;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Haliaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Xanthobacteraceae;g\_Ancylobacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Pseudorhodobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Psychromonadaceae;g\_Psychromonas  
d\_Bacteria;p\_Campilobacterota;c\_Campylobacteria;o\_Campylobacteriales;f\_Sulfurovaceae;g\_Sulfurovum  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;g\_Marinagarivorans  
d\_Bacteria;p\_Gemmatimonadota;c\_BD2-11\_terrestrial\_group;o\_BD2-11\_terrestrial\_group;f\_BD2-11\_terrestrial\_group;g\_BD2-11\_terrestrial\_group  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Enterobacteriaceae;g\_Enterobacteriaceae  
d\_Bacteria;p\_Verrucomicrobiota;c\_Lentisphaeria;o\_Lentisphaerales;f\_Lentisphaeraceae;g\_Lentisphaera  
d\_Bacteria;p\_Campilobacterota;c\_Campylobacteria;o\_Campylobacteriales;f\_Sulfurimonadaceae;g\_Sulfurimonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Marinomonadaceae;g\_Marinomonas  
d\_Bacteria;p\_Fusobacteriota;c\_Fusobacteriia;o\_Fusobacteriales;f\_Fusobacteriaceae;g\_Psychrilyobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Methylococcales;f\_Methylomonadaceae;g\_Methylobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Coxiellales;f\_Coxiellaceae;g\_Coxiella  
d\_Bacteria;p\_Bdellovibrionota;\_:\_;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Sphingobacteriales;f\_env.OPS\_17;g\_env.OPS\_17  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_HOC36;f\_HOC36;g\_HOC36  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Tenacibaculum  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiotrichales;f\_Thiotrichaceae;g\_Thiothrix  
d\_Bacteria;p\_Plantcomycetota;c\_Plantcomycetes;o\_Plantcomycetales;f\_Rubinisphaeraceae;\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opitutales;f\_Opitutaceae;g\_Opitutus  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Pedosphaerales;f\_Pedosphaeraceae;g\_SCGC\_AAA164-E04  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Pseudomonadales;f\_Pseudomonadaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Enterobacteriaceae;g\_Lelliottia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Ga0077536;f\_Ga0077536;g\_Ga0077536  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Caulobacteriales;f\_Hyphomonadaceae;g\_Litorimonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Vibrionales;f\_Vibrionaceae;g\_Aliivibrio  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;\_:\_;\_  
d\_Bacteria;p\_Plantcomycetota;c\_Pla3\_lineage;o\_Pla3\_lineage;f\_Pla3\_lineage;g\_Pla3\_lineage  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Caulobacteriales;f\_Hyphomonadaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Prolixibacteraceae;g\_Roseimarinus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Nereida  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Saccharospirillaceae;g\_Oleispira  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Sphingobacteriales;f\_Sphingobacteriaceae;g\_Solitalea  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sphingomonadales;f\_Sphingomonadaceae;g\_Altererythrobacter  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Bacillales;f\_Bacillaceae;g\_Anaerobacillus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Rhodobacteraceae  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteriia;o\_Cyanobacteriales;f\_Xenococcaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Lacimonas  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Parvibaculales;f\_Parvibaculaceae;g\_uncultured  
d\_Bacteria;p\_Fusobacteriota;c\_Fusobacteriia;o\_Fusobacteriales;f\_Fusobacteriaceae;g\_Propionigenium  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Zobellia  
d\_Bacteria;p\_Plantcomycetota;c\_Plantcomycetes;o\_Isosphaerales;f\_Isosphaeraceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;\_:\_;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Crocinitomicaceae;g\_Salinirepens  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Alteromonadaceae;g\_Paraglaciicola  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Reyranellales;f\_Reyranellaceae;g\_Reyranella  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Paracoccus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Ectothiorhodospirales;f\_Ectothiorhodospiraceae;g\_uncultured  
d\_Bacteria;p\_Fibrobacterota;c\_Chitinivibrionia;o\_Chitinivibrionales;f\_Chitinivibrionaceae;g\_possible\_genus\_03  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Chitinophagaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Ahrensia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Yersiniaceae;g\_Yersinia  
d\_Bacteria;p\_Fusobacteriota;c\_Fusobacteriia;o\_Fusobacteriales;f\_Fusobacteriaceae;g\_Fusobacterium  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_Candidatus\_Aquiluna  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micromonosporales;f\_Micromonosporaceae;g\_Stackebrandtia  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidetes\_VC2.1\_Bac22;f\_Bacteroidetes\_VC2.1\_Bac22;g\_Bacteroidetes\_VC2.1\_Bac22  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Nonlabens  
d\_Bacteria;p\_Chloroflexi;\_:\_;\_  
d\_Bacteria;p\_Nitrospirota;c\_Nitrospira;o\_Nitrospirales;f\_Nitrospiraceae;g\_Nitrospira  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Profundibacterium  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_SAR11\_clade;\_:\_;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Rhodobacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Puniceispirillales;f\_SAR116\_clade;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Beijerinckiaceae;g\_alpha\_cluster  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;\_:\_;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Hydrogenophaga

d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Pedosphaerales;f\_Pedosphaeraeae;g\_SH3-11  
d\_Bacteria;p\_Desulfobacterota;c\_Desulfobulbia;o\_Desulfobulbales;f\_Desulfocapsaceae;g\_Desulfurhopalus  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Rubritaleae;g\_Rubritalea  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Nitrosococcales;f\_Nitrosococcaceae;g\_Cm1-21  
d\_Bacteria;p\_Chloroflexi;c\_TK10;o\_TK10;f\_TK10;g\_TK10  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Dokdonia  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Actibacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Lacinutrix  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Olleya  
d\_Bacteria;p\_Campilobacterota;c\_Campylobacteria;o\_Campylobacteriales;f\_Arcobacteraceae;g\_Pseudarcobacter  
d\_Bacteria;p\_Patescibacteria;c\_Gracilibacteria;o\_Absconditabacteriales\_(SR1);f\_Absconditabacteriales\_(SR1);g\_Absconditabacteriales\_(SR1)  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_EPR3968-O8a-Bc78;f\_EPR3968-O8a-Bc78;g\_EPR3968-O8a-Bc78  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_KF-JG30-B3;g\_KF-JG30-B3  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Erwiniaecae;g\_Erwinia  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Synechococcales;f\_Cyanobiaceae;g\_Prochlorococcus\_MIT9313  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Phormidismiales;f\_Phormidismiaceae;g\_Phormidismis\_ANT.LACV5.1  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Spirosomaceae;g\_Emticia  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Crocinitomicaceae;\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Kiritimatiellae;o\_Kiritimatiellales;f\_Kiritimatiellaceae;g\_R76-B128  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Bacillales;f\_Planococcaceae;g\_Sporosarcina  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Celeribacter  
d\_Bacteria;p\_Verrucomicrobiota;c\_Omnitrophia;o\_Omnitrophales;f\_Omnitrophaceae;g\_Candidatus\_Omnitrophus  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opituales;f\_Opituaceae;g\_Lacunisphaera  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Planctomycetales;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Rhodocyclaceae;g\_Sulfuritalea  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Hafniaceae;g\_Hafnia-Obesumbacterium  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_SAR11\_clade;f\_Clade\_l;g\_Clade\_lb  
d\_Bacteria;p\_Actinobacteriota;c\_Thermoleophila;o\_Gaiellales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Patescibacteria;c\_Gracilibacteria;o\_Gracilibacteria;f\_Gracilibacteria;g\_Gracilibacteria  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Marinifilaceae;g\_Marinifilum  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opituales;f\_Puniciceocccaceae;g\_Pelagicoccus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Chthoniobacteriales;f\_Terrimicrobiaceae;g\_Terrimicrobium  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Pseudoruegeria  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_Magnetospiraceae;g\_Magnetospira  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Pirellulales;f\_Pirellulaceae;\_  
d\_Bacteria;p\_PAUC34f;c\_PAUC34f;o\_PAUC34f;f\_PAUC34f;g\_PAUC34f  
d\_Bacteria;p\_AncK6;c\_AncK6;o\_AncK6;f\_AncK6;g\_AncK6  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Bejerinckiaceae;\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opituales;f\_Opituaceae;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_Candidatus\_Planktoluna  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Flavobacteriaceae  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Alteromonadaceae;g\_Alliiglaciecola  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Pseudomonadales;f\_Moraxellaceae;g\_Psychrobacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Planctomycetales;f\_Schlesneriaceae;g\_Schlesneria  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Caulobacteriales;f\_Hyphomonadaceae;g\_Hellea  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Pectobacteriaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Aquimarina  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Cryomorphaeae;g\_Phaeocystidibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Micavibrionales;f\_Micavibrionaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Gallionellaceae;g\_Gallionella  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Pedosphaerales;f\_Pedosphaeraeae;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Sphingobacteriales;f\_Sphingobacteriaceae;g\_Pedobacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Lutibacter  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Planctomycetales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Prevotellaceae;g\_Prevotella  
d\_Bacteria;p\_Hydrogenedentes;c\_Hydrogenedentia;o\_Hydrogenedentiales;f\_Hydrogenedensaceae;g\_Hydrogenedensaceae  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Halocynthiibacter  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_Microtrichales;f\_Illumatobacteraceae;g\_CL500-29\_marine\_group  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Legionellales;f\_Legionellaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriales;f\_Enterobacteriaceae;g\_Enterobacter  
d\_Bacteria;p\_Chloroflexi;c\_JG30-KF-CM66;o\_JG30-KF-CM66;f\_JG30-KF-CM66;g\_JG30-KF-CM66  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Methylococcales;f\_Methylomonadaceae;g\_uncultured  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opituales;f\_Opituaceae;\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Omnitrophia;o\_Omnitrophales;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_Undibacterium  
d\_Bacteria;p\_Planctomycetota;c\_Planctomycetes;o\_Pirellulales;f\_Pirellulaceae;g\_Pir4\_lineage  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Cyanobacteriales;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Micavibrionales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_Aurantimicrobium  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Punicispirillales;f\_EF100-94H03;g\_EF100-94H03  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Lactobacillales;f\_Aerococcaceae;g\_Abiotrophia  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Bacteroidaceae;g\_Bacteroides  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Lactobacillales;f\_Streptococcaceae;g\_Streptococcus  
d\_Bacteria;p\_Actinobacteriota;c\_Thermoleophila;o\_Solirubrobacteriales;f\_Solirubrobacteraceae;g\_Conexibacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Steroidobacteriales;f\_Woeseiaceae;g\_Woeseia  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Cyanobacteriales;f\_Microcystaceae;g\_Snowella\_OTU37504  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_IMCC26256;f\_IMCC26256;g\_IMCC26256  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Moritellaceae;g\_Moritella  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Flavicella  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Corynebacteriales;f\_Mycobacteriaceae;g\_Mycobacterium  
d\_Bacteria;p\_Desulfobacterota;c\_Desulfurmonadia;o\_Bradymonadales;f\_Bradymonadales;g\_Bradymonadales  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Chthoniobacteriales;f\_Chthoniobacteraceae;g\_Chthoniobacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Kiloniellales;f\_Kiloniellaceae;g\_Kiloniella  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiales\_Incertae\_Sedis;g\_Bauldia  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Aquamicrobium  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_Microbacteriaceae

d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Aeromonadales;f\_Aeromonadaceae;g\_Tolomonas  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;\_:;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Saprospiraceae;g\_Aureispira  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_TRA3-20;g\_TRA3-20  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiales\_Incertae\_Sedis;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_Microtrichales;f\_Microtrichaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Pelagicola  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Pasteurellales;f\_Pasteurellaceae;g\_Haemophilus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;g\_Cellvibrio  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_Rhodospirillaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Arenicellales;f\_Arenicellaceae;g\_Arenicella  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Bacillales;f\_Bacillaceae;\_  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Blautia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Cyclobacteriaceae;g\_Algoriphagus  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Cyanobacteriales;f\_Xenococcaceae;g\_Chroococciopsis\_PCC-6712  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Pseudohongiellaceae;g\_Bly10  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sphingomonadales;f\_Sphingomonadaceae;g\_Sphingomonas  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Hoeflea  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Stappiaceae;\_  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Phormidesmiales;f\_Phormidesmiaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Xanthobacteraceae;g\_Bradyrhizobium  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;\_:;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Hyphomicrobiaceae;g\_Filomicrobium  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Pseudoalteromonadaceae;\_  
d\_Bacteria;p\_Patescibacteria;c\_Gracilbacteria;o\_Candidatus\_Peribacteria;f\_Candidatus\_Peribacteria;g\_Candidatus\_Peribacteria  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Gammaproteobacteria\_Incertae\_Sedis;f\_Unknown\_Family;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;\_:;\_  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Rubritaleaceae;g\_Haloferula  
d\_Bacteria;p\_Campilobacterota;c\_Campylobacteria;o\_Campylobacteriales;f\_Arcobacteraceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Devosiaceae;g\_Devosia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Saccharospirillaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Milano-WF1B-44;f\_Milano-WF1B-44;g\_Milano-WF1B-44  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Endozoicomonadaceae;g\_Endozoicomonas  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_Actinomarinales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Sphaerotilus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Cyclobacteriaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Pseudoalteromonadaceae;g\_Psychrosphaera  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Acetobacterales;f\_Acetobacteraceae;g\_Roseomonas  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiaceae;g\_Lentilitoribacter  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Anaerostipes  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Malikia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Porticocccaceae;g\_Porticoccus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Pseudophaeobacter  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Defluviitaleaceae;g\_Defluviitaleaceae\_UCG-011  
d\_Bacteria;p\_Margulisbacteria;c\_Margulisbacteria;o\_Margulisbacteria;f\_Margulisbacteria;g\_Margulisbacteria  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Legionellales;f\_Legionellaceae;g\_Legionella  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Rubritaleaceae;g\_Luteolibacter  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Agathobacter  
d\_Bacteria;p\_Verrucomicrobiota;\_:;\_:;\_  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;g\_Sporichthya  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;\_:;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_Duganella  
d\_Bacteria;p\_Desulfobacterota;c\_Desulfobulbia;o\_Desulfobulbiales;f\_Desulfocapsaceae;\_  
d\_Bacteria;p\_Acidobacteriota;c\_Vicinamibacteria;o\_Vicinamibacteriales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Chitinophagaceae;g\_Terrimonas  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Paenibacillales;f\_Paenibacillaceae;g\_Paenibacillaceae  
d\_Bacteria;p\_Bdellovibrionota;c\_Oligoflexia;o\_Oligoflexales;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Myxococcota;c\_Polyangia;o\_Polyangiales;f\_Sandaracinaceae;g\_uncultured  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;\_:;\_:;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Robiginitalea  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micromonosporales;f\_Micromonosporaceae;g\_Verrucospora  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Alteromonadaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Piscirickettsiales;f\_Piscirickettsiaceae;g\_Candidatus\_Endoecteinascidia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiotrichales;f\_Thiotrichaceae;g\_Leucothrix  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;\_:;\_  
d\_Bacteria;p\_Spirochaetota;c\_Leptospirae;o\_Leptospirales;f\_Leptospiraceae;g\_Turneriella  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Kordia  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rickettsiales;f\_Rickettsiaceae;g\_Candidatus\_Megaira  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;\_:;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Psychromonadaceae;g\_Agarivorans  
d\_Bacteria;p\_WPS-2;c\_WPS-2;o\_WPS-2;f\_WPS-2;g\_WPS-2  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Psychroserpens  
d\_Bacteria;p\_Bdellovibrionota;c\_Bdellovibrionia;o\_Bacteriovoracales;f\_Bacteriovoracaceae;g\_Halobacteriovorax  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Caulobacterales;f\_Caulobacteraceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_JTB23;f\_JTB23;g\_JTB23  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Lactobacillales;f\_Carnobacteriaceae;g\_Granulicatella  
d\_Eukaryota;\_:;\_:;\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Cyclobacteriaceae;g\_Reichenbachiella  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Neisseriaceae;g\_uncultured  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Fusicatenibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Hyphomicrobiaceae;g\_Hyphomicrobium  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Opitutales;f\_Puniceococcaceae;g\_A714019  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Acetobacterales;f\_Acetobacteraceae;g\_Acidocella  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Nitrincolaceae;g\_Profundimonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Psychromonadaceae;\_  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Lactobacillales;f\_Streptococcaceae;g\_Lactococcus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_Massilia

d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Vibrionales;f\_\_Vibrionaceae;g\_\_Photobacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Nitrosococcales;f\_\_Nitrosococcaceae;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_AT-s3-44;f\_\_AT-s3-44;g\_\_AT-s3-44  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Weeksellaceae;g\_\_Chryseobacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Spongiibacteraceae;g\_\_BD1-7\_clade  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Sphingobacteriales;f\_\_AKYH767;g\_\_AKYH767  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Hyunsoonleella  
d\_Bacteria;p\_\_Patescibacteria;c\_\_Gracilibacteria;\_;;\_  
d\_Bacteria;p\_\_Gemmatimonadota;c\_\_Gemmatimonadetes;o\_\_Gemmatimonadales;f\_\_Gemmatimonadaceae;\_  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Rhodothermia;o\_\_Rhodothermales;f\_\_Rhodothermaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Methylophilaceae;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Rhodobacteraceae;g\_\_Limimanicola  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Neisseriaceae;g\_\_Neisseria  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Fusibacteraceae;g\_\_Fusibacter  
d\_Bacteria;p\_\_Desulfobacterota;c\_\_Desulfobulbia;o\_\_Desulfobulbales;f\_\_Desulfocapsaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Achromobacter  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Chitinophagales;f\_\_Chitinophagaceae;g\_\_Dinghuibacter  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Chitinophagales;f\_\_Saprosiraceae;\_  
d\_Bacteria;p\_\_Chloroflexi;c\_\_Anaerolineae;o\_\_Ardenticatenales;f\_\_Ardenticatenaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_T34;g\_\_T34  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Arenicellales;f\_\_Arenicellaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_Alteromonadaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Bdellovibrionota;c\_\_Bdellovibrionia;o\_\_Bacteriovorales;f\_\_Bacteriovoraceae;g\_\_Peredibacter  
d\_Bacteria;p\_\_Bdellovibrionota;c\_\_Bacteroidia;o\_\_Chitinophagales;f\_\_Chitinophagaceae;g\_\_Taibaella  
d\_Bacteria;p\_\_Desulfobacterota;c\_\_Desulfobulbia;o\_\_Desulfobulbales;f\_\_Desulfocapsaceae;g\_\_Desulfopila  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Methylococcales;f\_\_Methylomonadaceae;\_  
d\_Bacteria;p\_\_Planctomycetota;c\_\_vadinHA49;o\_\_vadinHA49;f\_\_vadinHA49;g\_\_vadinHA49  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Propionibacteriales;f\_\_Propionibacteriaceae;g\_\_Cutibacterium  
d\_Bacteria;p\_\_Gemmatimonadota;c\_\_Gemmatimonadetes;o\_\_Gemmatimonadales;f\_\_Gemmatimonadaceae;g\_\_Gemmatimonas  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Micrococcales;f\_\_Microbacteriaceae;g\_\_Microbacterium  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Verrucomicrobiae;o\_\_Arctic97B-4\_marine\_group;f\_\_Arctic97B-4\_marine\_group;g\_\_Arctic97B-4\_marine\_group  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Verrucomicrobiae;o\_\_Opitutales;f\_\_Opitutaceae;g\_\_Diplosphaera  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Chitinibacteraceae;g\_\_Deefgea  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Kapabacteria;o\_\_Kapabacteriales;f\_\_Kapabacteriales;g\_\_Kapabacteriales  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Caulobacteraceae;g\_\_Brevundimonas  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Anaerovoracaceae;g\_\_Anaerovorax  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Rhodocyclaceae;g\_\_C39  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Streptosporangiales;f\_\_Streptosporangiaceae;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Caulobacteraceae;g\_\_Phenylobacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Halomonadaceae;g\_\_Salinicola  
d\_Bacteria;p\_\_Campilobacterota;c\_\_Campylobacteria;o\_\_Campylobacteriales;f\_\_Arcobacteraceae;g\_\_Arcobacter  
d\_Bacteria;p\_\_Bdellovibrionota;c\_\_Bdellovibrionia;o\_\_Bacteriovorales;f\_\_Bacteriovoraceae;g\_\_uncultured  
d\_Bacteria;p\_\_Acidobacteriota;c\_\_Viciniabacteria;o\_\_Viciniabacteriales;f\_\_Viciniabacteriaceae;g\_\_Viciniabacteriaceae  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Nitriocolaceae;g\_\_Marinobacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Rhodobacteraceae;g\_\_Roseobacter\_clade\_CHAB-I-5\_lineage  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Pseudomonadales;f\_\_Moraxellaceae;g\_\_Acinetobacter  
d\_Bacteria;p\_\_Planctomycetota;c\_\_Planctomycetes;o\_\_Pirellulales;f\_\_Pirellulaceae;g\_\_Bythopirellula  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Comamonas  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Paracaedibacteriales;f\_\_Paracaedibacteriaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Lentisphaeria;o\_\_P.palmC41;f\_\_P.palmC41;g\_\_P.palmC41  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Rhodocyclaceae;\_  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Corynebacteriales;f\_\_Corynebacteriaceae;g\_\_Corynebacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Nitrosomonadaceae;g\_\_MND1  
d\_Bacteria;p\_\_Firmicutes;c\_\_Negativicutes;o\_\_Veillonellales-Selenomonadales;f\_\_Veillonellaceae;g\_\_Veillonella  
d\_Bacteria;p\_\_Planctomycetota;c\_\_Phycisphaerae;o\_\_Phycisphaerales;f\_\_Phycisphaeraceae;g\_\_FS140-16B-02\_marine\_group  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Kordiimonadales;f\_\_Kordiimonadaceae;g\_\_Kordiimonas  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rickettsiales;\_;;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Gammaproteobacteria\_Incertae\_Sedis;f\_\_Unknown\_Family;g\_\_Marinicella  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Euzeybiales;f\_\_Euzeybiaceae;g\_\_Euzeybia  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Arcticflavibacter  
d\_Bacteria;p\_\_Myxococcota;c\_\_Polyangia;o\_\_MidBa8;f\_\_MidBa8;g\_\_MidBa8  
d\_Bacteria;p\_\_Planctomycetota;\_;;\_  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Pseudofulvibacter  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Rhizobacter  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Bacteroidales;f\_\_Porphyromonadaceae;g\_\_Porphyromonas  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Aquabacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Rhodobacteraceae;g\_\_Marivita  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_SAR11\_clade;f\_\_Clade\_I;\_  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Flavirhabdus  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Lentisphaeria;o\_\_Victivallales;f\_\_BD2-3;g\_\_BD2-3  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Rhizobiales\_Incertae\_Sedis;g\_\_Andersenella  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Acetobacteriales;f\_\_Acetobacteraceae;g\_\_Acidiphilium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rickettsiales;f\_\_Fokiniaaceae;g\_\_MD3-55  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Parvularculaceae;g\_\_Parvularcula  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Gallionellaceae;g\_\_Sideroxydans  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Peptostreptococcales-Tissierellales;g\_\_JT215  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_uncultured;f\_\_uncultured;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Cellvibrionaceae;g\_\_Agarilytica  
d\_Bacteria;p\_\_Chloroflexi;c\_\_Anaerolineae;o\_\_Ardenticatenales;f\_\_uncultured;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Cellvibrionaceae;g\_\_Gilvimirinus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodospirillales;f\_\_Terasakiellaceae;g\_\_Terasakiella  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Enterobacteriales;f\_\_Enterobacteriaceae;g\_\_Escherichia-Shigella  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_B2M28;f\_\_B2M28;g\_\_B2M28  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Acidimicrobia;o\_\_Microtrichales;\_;;\_  
d\_Bacteria;p\_\_Deinococcota;c\_\_Deinococci;o\_\_Deinococcales;f\_\_Deinococcaceae;g\_\_Deinococcus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Thiotrichales;f\_\_Thiotrichaceae;g\_\_Cocleimonas  
d\_Bacteria;p\_\_Patescibacteria;c\_\_Parcubacteria;\_;;\_

d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Novosphingobium  
d\_Bacteria;p\_\_Spirochaetota;c\_\_Spirochaetia;o\_\_Spirochaetales;f\_\_Spirochaetaceae;g\_\_Spirochaeta\_2  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Verrucomicrobiae;o\_\_Opitutales;f\_\_Puniceococcaceae;g\_\_Verruc-01  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Cellulophaga  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Diplorickettsiales;f\_\_Diplorickettsiaceae;g\_\_  
d\_Bacteria;p\_\_Fusobacteriota;c\_\_Fusobacteria;o\_\_Fusobacteriales;f\_\_Leptotrichiaceae;g\_\_Hyphocyclicus  
d\_Bacteria;p\_\_Patenscibacteria;c\_\_Parcubacteria;o\_\_Candidatus\_Kaiserbacteria;f\_\_Candidatus\_Kaiserbacteria;g\_\_Candidatus\_Kaiserbacteria  
d\_Bacteria;p\_\_Desulfobacterota;c\_\_Desulfuromonadia;o\_\_PB19;f\_\_PB19;g\_\_PB19  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rickettsiales;f\_\_Rickettsiaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Arenicellales;f\_\_Arenicellaceae;g\_\_Arenicellaceae  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodospirillales;f\_\_Terasakiellaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacterales;f\_\_Hyphomonadaceae;g\_\_Hyphomonas  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Muriicola  
d\_Bacteria;p\_\_Chloroflexi;c\_\_Anaerolineae;o\_\_SBR1031;f\_\_A4b;g\_\_A4b  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Beijerinckiaceae;g\_\_Methylobacterium-Methylorubrum  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Rhodobacteraceae;g\_\_Litorimicrobium  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Lactobacillales;f\_\_Lactobacillaceae;g\_\_Lactobacillus  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;g\_\_Lachnoanaerobaculum  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Paucibacter  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Glycomycetales;f\_\_Glycomycetaceae;g\_\_Glycomyces  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;g\_\_[Ruminococcus]\_torques\_group  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Omnitrophia;o\_\_Omnitrophales;f\_\_Omnitrophales;g\_\_Omnitrophales  
d\_Bacteria;p\_\_Myxococcota;c\_\_Polyangia;o\_\_Polyangiales;f\_\_;  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Rhodobacteraceae;g\_\_Pelagimonas  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Spongiibacteraceae;g\_\_uncultured  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Bacteroidales;f\_\_Prolixibacteraceae;g\_\_Draconibacterium  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Methyloligellaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Desulfobacterota;c\_\_Desulfobacteria;o\_\_Desulfobacterales;f\_\_Desulfosarcinaceae;g\_\_Desulfosarcina  
d\_Bacteria;p\_\_Campylobacterota;c\_\_Campylobacteria;o\_\_Campylobacterales;f\_\_Arcobacteraceae;g\_\_Poseidonibacter  
d\_Bacteria;p\_\_Patenscibacteria;f\_\_;  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Sphingobacteriales;f\_\_KD3-93;g\_\_KD3-93  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Corynebacteriales;f\_\_Corynebacteriaceae;g\_\_Lawsonella  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Diplorickettsiales;f\_\_Diplorickettsiaceae;g\_\_Rickettsiella  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Rhodothermia;o\_\_Rhodothermales;f\_\_Rhodothermaceae;g\_\_Rubricoccus  
d\_Bacteria;p\_\_Bdellovibrionota;c\_\_Bdellovibrionia;o\_\_Bdellovibrionales;f\_\_Bdellovibrionaceae;g\_\_Bdellovibrio  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Francisellales;f\_\_Francisellaceae;g\_\_Francisella  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Mycoplasmatales;f\_\_Mycoplasmataceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Xanthomonadales;f\_\_Rhodanobacteraceae;g\_\_Aquimonas  
d\_Bacteria;p\_\_Myxococcota;f\_\_;  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Neisseriaceae;g\_\_Eikenella  
d\_Bacteria;p\_\_Verrucomicrobiota;c\_\_Verrucomicrobiae;o\_\_Opitutales;f\_\_Puniceococcaceae;g\_\_Cerasicoccus  
d\_Bacteria;p\_\_Fusobacteriota;c\_\_Fusobacteria;o\_\_Fusobacteriales;f\_\_Leptotrichiaceae;g\_\_Leptotrichia  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Arenicellales;f\_\_Arenicellaceae;g\_\_HTCC5015  
d\_Bacteria;p\_\_Bdellovibrionota;c\_\_Oligoflexia;o\_\_Oligoflexales;f\_\_Oligoflexales;g\_\_Oligoflexus  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Postechiella  
d\_Bacteria;p\_\_Patenscibacteria;c\_\_ABY1;o\_\_Candidatus\_Magasanikbacteria;f\_\_Candidatus\_Magasanikbacteria;g\_\_Candidatus\_Magasanikbacteria  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Maritimimonas  
d\_Bacteria;p\_\_Patenscibacteria;c\_\_Saccharimonadia;o\_\_Saccharimonadales;f\_\_Saccharimonadales;g\_\_Saccharimonadales  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Micrococcales;f\_\_;  
d\_Bacteria;p\_\_Chloroflexi;c\_\_Anaerolineae;o\_\_RBG-13-54-9;f\_\_RBG-13-54-9;g\_\_RBG-13-54-9  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Nitriliruptorales;f\_\_Nitriliruptoraceae;g\_\_YC-ZSS-LKJ90  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Gillisia  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Cytophagales;f\_\_Cyclobacteriaceae;g\_\_  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Bacteroidales;f\_\_Paludibacteraceae;g\_\_uncultured  
d\_Bacteria;p\_\_Patenscibacteria;c\_\_Parcubacteria;o\_\_Candidatus\_Staskawiczbacteria;f\_\_Candidatus\_Staskawiczbacteria;g\_\_Candidatus\_Staskawiczbacteria  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Acidimicrobia;o\_\_Microtrichales;f\_\_uncultured;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Xanthobacteraceae;g\_\_  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Bacteroidales;f\_\_Bacteroidetes\_BD2-2;g\_\_Bacteroidetes\_BD2-2  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Spongiibacteraceae;g\_\_Oceanicoccus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Nitrincolaceae;g\_\_Neptunomonas  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Frankiales;f\_\_Nakamurellaceae;g\_\_Nakamurella  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Lactobacillales;f\_\_Carnobacteriaceae;g\_\_Trichococcus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Nitrincolaceae;g\_\_Amphritea  
d\_Bacteria;p\_\_Desulfobacterota;c\_\_Desulfuromonadia;o\_\_Sva1033;f\_\_Sva1033;g\_\_Sva1033  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Jejuia  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Streptosporangiales;f\_\_Streptosporangiaceae;g\_\_Streptosporangium  
d\_Bacteria;p\_\_Planctomycetota;c\_\_Phycisphaerae;o\_\_Phycisphaerales;f\_\_Phycisphaeraeae;g\_\_Phycisphaera  
d\_Bacteria;p\_\_Myxococcota;c\_\_Polyangia;o\_\_Polyangiales;f\_\_Blrii41;g\_\_Blrii41  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Eudoraea  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;g\_\_Lachnospiraceae\_NK4A136\_group  
d\_Bacteria;p\_\_Cyanobacteria;c\_\_Cyanobacteriia;f\_\_;  
d\_Bacteria;p\_\_Patenscibacteria;c\_\_Gracilibacteria;o\_\_Candidatus\_Peregrinibacteria;f\_\_Candidatus\_Peregrinibacteria;g\_\_Candidatus\_Peregrinibacteria  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Wenylingzhuangia  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Nitrosomonadaceae;g\_\_GOUTA6  
d\_Bacteria;p\_\_Planctomycetota;c\_\_Planctomycetes;o\_\_Pirellulales;f\_\_Pirellulaceae;g\_\_Pirellula  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Cytophagales;f\_\_Microscillaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_Alteromonadaceae;g\_\_Alteromonas  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Bacillales;f\_\_Bacillaceae;g\_\_Oceanobacillus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Salinisphaerales;f\_\_Solimonadaceae;g\_\_Nevskia  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Rhodothermia;o\_\_Rhodothermales;f\_\_Rhodothermaceae;g\_\_Rubrivirga  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Bacillales;f\_\_Bacillaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;g\_\_Coproccoccus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Devosiaceae;g\_\_Maritalea  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Gallionellaceae;g\_\_  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Micrococcales;f\_\_Intrasporangiaceae;g\_\_Knoellia  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Xanthomonadales;f\_\_Xanthomonadaceae;g\_\_Arenimonas  
d\_Bacteria;p\_\_Planctomycetota;c\_\_Planctomycetes;o\_\_Pirellulales;f\_\_Pirellulaceae;g\_\_Pir1\_lineage  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rickettsiales;f\_\_AB1;g\_\_AB1

d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Enterobacteriales;f\_\_Erwiniaceae;g\_\_Pantoea  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Parvibaculales;\_:\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Spongiibacteraceae;\_  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Cytophagales;f\_\_Cyclobacteriaceae;g\_\_Fulvivirga  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Hyphomonadaceae;g\_\_Algimonas  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Gaetbulibacter  
d\_Bacteria;p\_\_Planctomycetota;c\_\_Phycisphaerae;o\_\_MSBL9;f\_\_SG8-4;g\_\_SG8-4  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Cytophagales;f\_\_Spirosomaceae;g\_\_Lacihabitus  
d\_Bacteria;p\_\_Patescibacteria;c\_\_Parcubacteria;o\_\_Candidatus\_Adlerbacteria;f\_\_Candidatus\_Adlerbacteria;g\_\_Candidatus\_Adlerbacteria  
d\_Bacteria;p\_\_Cyanobacteria;c\_\_Cyanobacteriia;o\_\_Cyanobacteriales;f\_\_Microcystaceae;g\_\_Microcystis\_PCC-7914  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_Pseudalteromonadaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Rhizobiaceae;g\_\_Aureimonas  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Thermicanales;f\_\_Thermicaceae;g\_\_Thermicanus  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Clostridiaceae;\_  
d\_Bacteria;p\_\_Sva0485;c\_\_Sva0485;o\_\_Sva0485;f\_\_Sva0485;g\_\_Sva0485  
d\_Bacteria;p\_\_Planctomycetota;c\_\_SGST604;o\_\_SGST604;f\_\_SGST604;g\_\_SGST604  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Chromatiales;f\_\_Chromatiaceae;g\_\_Candidatus\_Thiobios  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Oxalobacteraceae;g\_\_CM1G08  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Acetobacteriales;f\_\_Acetobacteraceae;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Sandarakinorhabdus  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Caulobacteraceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_SAR11\_clade;f\_\_Clade\_I;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Ectothiorhodospirales;f\_\_Ectothiorhodospiraceae;g\_\_Thiogranum  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Micrococcales;f\_\_Micrococcales\_Incertae\_Sedis;g\_\_Timonella  
d\_Bacteria;p\_\_Patescibacteria;c\_\_Parcubacteria;o\_\_Candidatus\_Nomurabacteria;f\_\_Candidatus\_Nomurabacteria;g\_\_Candidatus\_Nomurabacteria  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_B1-7BS;g\_\_B1-7BS  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Parasphingopyxis  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;g\_\_Ruminococcus\_gauvreuii\_group  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Micrococcales;f\_\_Micrococcales;g\_\_Paeniglutamibacter  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Streptosporangiales;f\_\_Streptosporangiaceae;g\_\_Nonomuraea  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacteriales;f\_\_Rhodobacteraceae;g\_\_Cognatiyoonia  
d\_Bacteria;p\_\_Cyanobacteria;c\_\_Cyanobacteriia;o\_\_Cyanobacteriales;f\_\_Nostocaceae;g\_\_Dolichospermum\_NIES41  
d\_Bacteria;p\_\_Fibrobacterota;c\_\_Fibrobacteria;o\_\_Fibrobacteriales;f\_\_Fibrobacteraceae;g\_\_Fibrobacter  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Thermoleophilia;o\_\_Solirubrobacteriales;f\_\_67-14;g\_\_67-14  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Rhodocyclaceae;g\_\_Ferribacterium  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Sphingobacteriales;f\_\_Sphingobacteriaceae;g\_\_Mucilagibacter  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Xanthobacteraceae;g\_\_Xanthobacter  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Zetaproteobacteria;o\_\_Mariprofundales;f\_\_Mariprofundaceae;g\_\_Mariprofundus  
d\_Bacteria;p\_\_Elusimicrobiota;c\_\_Elusimicrobia;o\_\_Lineage\_IV;f\_\_Lineage\_IV;g\_\_Lineage\_IV  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Micrococcales;f\_\_Microbacteriaceae;g\_\_Lysinimonas  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Lachnospirales;f\_\_Lachnospiraceae;g\_\_Lachnospiraceae\_ND3007\_group  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Mycoplasmatales;f\_\_Mycoplasmataceae;g\_\_Candidatus\_Bacilloplasma  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Cellvibrionaceae;g\_\_Umboniibacter  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_Xanthomonadales;f\_\_Xanthomonadaceae;g\_\_Stenotrophomonas  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Chitinibacteraceae;g\_\_Iodobacter  
d\_Bacteria;p\_\_Patescibacteria;c\_\_Microgenomatia;o\_\_Candidatus\_Woesebacteria;f\_\_Candidatus\_Woesebacteria;g\_\_Candidatus\_Woesebacteria  
d\_Bacteria;p\_\_Patescibacteria;c\_\_Parcubacteria;o\_\_Parcubacteria;f\_\_Parcubacteria;g\_\_Parcubacteria  
d\_Bacteria;p\_\_Actinobacteriota;c\_\_Actinobacteria;o\_\_uncultured;f\_\_uncultured;g\_\_uncultured  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Cryomorphaceae;g\_\_Luteibaculum  
d\_Bacteria;p\_\_Planctomycetota;c\_\_BD7-11;o\_\_BD7-11;f\_\_BD7-11;g\_\_BD7-11  
d\_Bacteria;p\_\_Myxococcota;c\_\_Polyangia;o\_\_Polyangiales;f\_\_Eel-36e1D6;g\_\_Eel-36e1D6  
d\_Bacteria;p\_\_Chloroflexi;c\_\_Anaerolineae;o\_\_Caldilineales;f\_\_Caldilineaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Acidobacteriota;c\_\_Subgroup\_26;o\_\_Subgroup\_26;f\_\_Subgroup\_26;g\_\_Subgroup\_26  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rickettsiales;f\_\_SM2D12;g\_\_SM2D12  
d\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Erysipelotrichales;f\_\_Erysipelotrichaceae;g\_\_Erysipelothrix  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Xanthobacteraceae;g\_\_Tardiphaga  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Hyphomonadaceae;g\_\_SWB02  
d\_Bacteria;p\_\_Chloroflexi;c\_\_KD4-96;o\_\_KD4-96;f\_\_KD4-96;g\_\_KD4-96  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacteriales;f\_\_Rhodobacteraceae;g\_\_Cereibacter  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Burkholderiales;f\_\_Rhodocyclaceae;g\_\_Dechlorosoma  
d\_Bacteria;p\_\_Cyanobacteria;c\_\_Cyanobacteriia;o\_\_Cyanobacteriales;f\_\_Oscillatoriaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Erythrobracter  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Spongiibacterium  
d\_Bacteria;p\_\_Myxococcota;c\_\_Myxococcia;o\_\_Myxococcales;f\_\_Myxococcaceae;g\_\_P30B-42  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Vibrionales;f\_\_Vibrionaceae;g\_\_Enterovibrio  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Oleiphilaceae;g\_\_Oleiphilus  
d\_Bacteria;p\_\_Fusobacteriota;c\_\_Fusobacteriia;o\_\_Fusobacteriales;f\_\_Fusobacteriaceae;g\_\_Cetobacterium  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Bacteroidales;f\_\_Paludibacteraceae;g\_\_Paludibacter  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Cytophagales;f\_\_Spirosomaceae;g\_\_Taeseokella  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Peptostreptococaceae;g\_\_Romboutsia  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Peptostreptococaceae;\_  
d\_Bacteria;p\_\_Dependentiae;c\_\_Babeliae;o\_\_Babeliales;\_:\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Tistrellales;f\_\_Geminococcaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Flavobacteriales;f\_\_Flavobacteriaceae;g\_\_Mesoflavibacter  
d\_Bacteria;p\_\_Latescibacterota;\_:\_;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Pseudomonadales;f\_\_Moraxellaceae;\_  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Cellvibrionales;f\_\_Halieaceae;g\_\_Congregibacter  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_Alteromonadaceae;g\_\_Rheinheimera  
d\_Bacteria;p\_\_Desulfobacterota;c\_\_Desulfobacteria;o\_\_Desulfobacteriales;f\_\_Desulfolunaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Oscillospirales;f\_\_Oscillospiraceae;g\_\_Oscillibacter  
d\_Bacteria;p\_\_Chloroflexi;c\_\_Chloroflexia;o\_\_Chloroflexales;f\_\_Herpetosiphonaceae;g\_\_Herpetosiphon  
d\_Bacteria;p\_\_Bacteroidota;c\_\_Bacteroidia;o\_\_Chitinophagales;f\_\_Chitinophagaceae;g\_\_Edaphobaculum  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Oceanospirillaceae;g\_\_Oceanospirillum  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Peptostreptococaceae;g\_\_Intestinibacter  
d\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Peptostreptococcales-Tissierellales;f\_\_Anaerovoracaceae;g\_\_uncultured  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacteriales;f\_\_Caulobacteraceae;g\_\_Caulobacter  
d\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Beijerinckiaceae;g\_\_Microvirga  
d\_Bacteria;p\_\_Cyanobacteria;c\_\_Vampirivibrionia;o\_\_Gastranaerophilales;f\_\_Gastranaerophilales;g\_\_Gastranaerophilales

d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_Leucobacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Saprosiraceae;g\_Portibacter  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Dorea  
d\_Bacteria;p\_Chloroflexi;c\_Dehalococcoidia;o\_Dehalococcoidia;f\_Dehalococcoidia;g\_Dehalococcoidia  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micrococcales;f\_Microbacteriaceae;g\_ML602J-51  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Cyanobacteriales;f\_Chroococcidiopsaceae;g\_Alterella  
d\_Bacteria;p\_Acidobacteriota;c\_Aminicenantia;o\_Aminicenantales;f\_Aminicenantales;g\_Aminicenantales  
d\_Bacteria;p\_Dependentiae;c\_Babeliae;o\_Babeliales;f\_UBA12409;g\_UBA12409  
d\_Bacteria;p\_Zixibacteria;c\_Zixibacteria;o\_Zixibacteria;f\_Zixibacteria;g\_Zixibacteria  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Clostridia;f\_Hungateiclostridiaceae;g\_uncultured  
d\_Bacteria;p\_Firmicutes;c\_Negativicutes;o\_Veillonellales-Selenomonadales;f\_Veillonellaceae;g\_Dialister  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_uncultured;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Clostridiales;f\_Clostridiaceae;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Shewanellaceae;g\_Psychrobium  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Tannerellaceae;g\_Macelibacteroides  
d\_Bacteria;p\_Chloroflexi;c\_Chloroflexia;o\_Chloroflexales;f\_Roseiflexaceae;g\_uncultured  
d\_Bacteria;p\_Myxococcota;c\_bacteriap25;o\_bacteriap25;f\_bacteriap25;g\_bacteriap25  
d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Entomoplasmatales;f\_Spiroplasmataceae;g\_Spiroplasma  
d\_Bacteria;p\_Acidobacteriota;c\_Blastocatellia;o\_Blastocatellales;f\_Blastocatellaceae;g\_Blastocatella  
d\_Bacteria;p\_Cyanobacteria;c\_Vampirivibronia;o\_Caenarcaniphilales;f\_Caenarcaniphilales;g\_Caenarcaniphilales  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Methyloligellaceae;g\_Methyloceanibacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Albimonas  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Xanthomonadales;f\_Xanthomonadaceae;g\_Lysobacter  
d\_Bacteria;p\_Chloroflexi;c\_Anaerolineae;o\_uncultured;f\_uncultured;g\_uncultured  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Gemmobacter  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Muribaculaceae;g\_Muribaculaceae  
d\_Bacteria;p\_Patescibacteria;c\_CPR2;o\_CPR2;f\_CPR2;g\_CPR2  
d\_Bacteria;p\_Plantcymycetota;c\_Plantcymycetes;o\_Plantcymycetales;f\_Rubinispheeraceae;g\_Fuerstia  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Ruminococcus\_gnavus\_group  
d\_Bacteria;p\_Firmicutes;c\_Negativicutes;o\_Veillonellales-Selenomonadales;f\_Selenomonadaceae;g\_Megamonas  
d\_Bacteria;p\_Plantcymycetota;c\_Plantcymycetes;\_:\_:\_  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Pseudozobellia  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Nitriincolaceae;g\_Motiliproteus  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sphingomonadales;f\_Sphingomonadaceae;g\_uncultured  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Propionibacteriales;f\_Propionibacteriaceae;g\_uncultured  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Oscillospirales;f\_Ruminococcaceae;g\_CAG-352  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Sphingobacteriales;f\_Lentimicrobiaceae;g\_Lentimicrobiaceae  
d\_Bacteria;p\_Plantcymycetota;c\_Plantcymycetes;o\_Plantcymycetales;f\_Rubinispheeraceae;g\_SH-PL14  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Aquaspirillaceae;g\_Rivicola  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Prevotellaceae;\_  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_CH2b56;f\_CH2b56;g\_CH2b56  
d\_Bacteria;p\_Patescibacteria;c\_Microgenomatia;o\_Candidatus\_Gottesmanbacteria;f\_Candidatus\_Gottesmanbacteria;g\_Candidatus\_Gottesmanbacteria  
d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Oscillospirales;f\_Oscillospiraceae;g\_UCG-002  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Rhodocyclaceae;g\_Zoogloea  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Cyanobacteriales;f\_Nostocaceae;g\_Rivularia\_PCC-7116  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;\_  
d\_Bacteria;p\_Armatimonadota;c\_Fimbriimonadia;o\_Fimbriimonadales;f\_Fimbriimonadaceae;g\_Fimbriimonadaceae  
d\_Bacteria;p\_Cyanobacteria;c\_Cyanobacteria;o\_Limnotrachales;f\_Limnotrachaceae;g\_Limnotrach  
d\_Bacteria;p\_Dependentiae;c\_Babeliae;o\_Babeliales;f\_Vermiphilaceae;g\_Vermiphilaceae  
d\_Bacteria;p\_Actinobacteriota;c\_Thermoleophila;o\_Solirubrobacteriales;f\_Solirubrobacteraceae;g\_Solirubrobacter  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_SAR11\_clade;f\_Clade\_IV;g\_Clade\_IV  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Colwelliaceae;g\_Thalassotalea  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Bacteroidetes\_vadinHA17;g\_Bacteroidetes\_vadinHA17  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;g\_Pseudomarcuscurvus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Pseudomonadales;f\_Moraxellaceae;g\_Alkanindiges  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Oceanospirillales;f\_Kangiellaceae;g\_Aliikangiella  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Weeksellaceae;g\_Ornithobacterium  
d\_Bacteria;p\_Acidobacteriota;c\_Holophagae;o\_Holophagales;f\_Holophagaceae;g\_Geothrix  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiomicrospirales;f\_Thiomicrospiraceae;g\_endosymbionts  
d\_Bacteria;p\_Patescibacteria;c\_Parcubacteria;o\_Candidatus\_Zambryskibacteria;f\_Candidatus\_Zambryskibacteria;g\_Candidatus\_Zambryskibacteria  
d\_Bacteria;p\_Plantcymycetota;c\_Plantcymycetes;o\_Isosphaerales;f\_Isosphaeraceae;\_  
d\_Bacteria;p\_TA06;c\_TA06;o\_TA06;f\_TA06;g\_TA06  
d\_Bacteria;p\_Patescibacteria;c\_Parcubacteria;o\_Candidatus\_Yanofskybacteria;f\_Candidatus\_Yanofskybacteria;g\_Candidatus\_Yanofskybacteria  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;g\_Candidatus\_Endobugula  
d\_Bacteria;p\_Cloacimonadota;c\_Cloacimonadia;o\_Cloacimonadales;f\_MSBL8;g\_MSBL8  
d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobia;o\_Microtrichales;f\_Microtrichaceae;g\_IMCC26207  
d\_Bacteria;p\_Fusobacteriota;c\_Fusobacteriales;o\_Fusobacteriales;\_:\_:\_  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Nitriiliruptorales;f\_Nitriiliruptoraceae;g\_Nitriiliruptoraceae  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Acidovorax  
d\_Bacteria;p\_Acidobacteriota;c\_Acidobacteriales;o\_Bryobacteriales;f\_Bryobacteraceae;g\_Bryobacter  
d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Corynebacteriales;f\_Nocardiaceae;g\_Rhodococcus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Chromatiales;f\_Chromatiaceae;g\_Lamprocystis  
d\_Bacteria;p\_Latescibacterota;c\_Latescibacteria;o\_Latescibacteriales;f\_Latescibacteraceae;g\_Candidatus\_Latescibacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Sulfuricellaceae;g\_Sulfuricella  
d\_Bacteria;p\_Bdellovibrionota;c\_Oligoflexia;o\_0319-6G20;f\_0319-6G20;g\_0319-6G20  
d\_Bacteria;p\_Thermotogota;c\_Thermotogae;o\_Petrotogales;f\_Petrotogaceae;g\_SCI103  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Xanthomonadales;f\_Rhodanobacteraceae;g\_Dyella  
d\_Bacteria;p\_Actinobacteriota;c\_Coriobacteriales;o\_Coriobacteriales;f\_Eggerthellaceae;g\_Senegalimassilia  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Hyphomicrobiaceae;\_  
d\_Bacteria;p\_Patescibacteria;c\_ABY1;\_:\_:\_  
d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Acetobacteriales;f\_Acetobacteraceae;g\_Rhodovastum  
d\_Bacteria;p\_Desulfobacterota;c\_Desulfovibronia;o\_Desulfovibroniales;f\_Desulfovibronaceae;g\_Desulfovibrio  
d\_Bacteria;p\_Bdellovibrionota;c\_Bdellovibrionia;o\_Bacteriovoracales;f\_Bacteriovoracaceae;\_  
d\_Bacteria;p\_Actinobacteriota;c\_WCHB1-81;o\_WCHB1-81;f\_WCHB1-81;g\_WCHB1-81  
d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Verrucomicrobiaceae;g\_Prosthecobacter  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Thiomicrospirales;f\_Thiomicrospiraceae;g\_Thiomicrohabdus  
d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Ectothiorhodospirales;f\_Thioalkalipsiraceae;g\_Thiohalophilus  
d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Marinilabiliaceae;g\_uncultured

d\_Bacteria;p\_Myxococcota;c\_Polyangia;o\_Nannocystales;f\_Nannocystaceae;g\_Nannocystaceae  
 d\_Bacteria;p\_Elusimicrobiota;c\_Lineage\_Ila;o\_Lineage\_Ila;f\_Lineage\_Ila;g\_Lineage\_Ila  
 d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micromonosporales;f\_Micromonosporaceae;g\_Micromonospora  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Croceitalea  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Chitinophagales;f\_Saprosiraceae;g\_Rubidimonas  
 d\_Bacteria;p\_Nitrospirota;c\_Thermodesulfobionria;o\_uncultured;f\_uncultured;g\_uncultured  
 d\_Bacteria;p\_Bacteroidota;c\_Kryptonia;o\_Kryptoniales;f\_BSV26;g\_BSV26  
 d\_Bacteria;p\_Bacteroidota;c\_Ignavibacteria;o\_Ignavibacteriales;f\_PHOS-HE36;g\_PHOS-HE36  
 d\_Bacteria;p\_Dependentiae;c\_Babeliae;o\_Babeliales;f\_Babeliales;g\_Babeliales  
 d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_MBAE14;f\_MBAE14;g\_MBAE14  
 d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Cellvibrionales;f\_Cellvibrionaceae;g\_Saccharophagus  
 d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_SZB50;f\_SZB50;g\_SZB50  
 d\_Bacteria;p\_Spirochaetota;c\_Spirochaetia;o\_Spirochaetales;f\_Spirochaetaceae;g\_Salinispira  
 d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Pedosphaerales;f\_Pedosphaeraceae;g\_uncultured  
 d\_Bacteria;p\_Desulfobacterota;c\_Desulfobulbia;o\_Desulfobulbales;f\_Desulfocapsaceae;g\_Desulfotalea  
 d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Lachnospiraceae\_FCS020\_group  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Marinifilaceae;g\_Odoribacter  
 d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Propionibacteriales;f\_Nocardioidaceae;g\_Aeromicrobium  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Cytophagales;f\_Spirosomaceae;g\_Arcicella  
 d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Arenicellales;f\_Arenicellaceae;g\_uncultured  
 d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Diplorickettsiales;f\_Diplorickettsiaceae;g\_uncultured  
 d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Clostridiales;f\_Caloramatoraceae;g\_Fonticella  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Cryomorpaceae;g\_Owenweekia  
 d\_Bacteria;p\_Patescibacteria;c\_Microgenomatia;o\_Candidatus\_Curtissbacteria;f\_Candidatus\_Curtissbacteria;g\_Candidatus\_Curtissbacteria  
 d\_Bacteria;p\_Cyanobacteria;\_:\_:\_  
 d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_LD1-PB3;f\_LD1-PB3;g\_LD1-PB3  
 d\_Bacteria;p\_Elusimicrobiota;c\_Lineage\_Ilb;o\_Lineage\_Ilb;f\_Lineage\_Ilb;g\_Lineage\_Ilb  
 d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Propionibacteriales;f\_Nocardioidaceae;g\_Marmoricola  
 d\_Bacteria;p\_Myxococcota;c\_Polyangia;o\_Polyangiales;f\_Polyangiaceae;g\_Pajaroellobacter  
 d\_Bacteria;p\_Spirochaetota;c\_Spirochaetia;o\_Spirochaetales;f\_Spirochaetaceae;g\_Sphaerochaeta  
 d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Corynebacteriales;f\_Nocardiaceae;g\_Williamsia  
 d\_Bacteria;p\_Patescibacteria;c\_Microgenomatia;o\_Candidatus\_Amesbacteria;f\_Candidatus\_Amesbacteria;g\_Candidatus\_Amesbacteria  
 d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodospirillales;f\_Rhodospirillaceae;g\_Haematospirillum  
 d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Xanthobacteraceae;g\_Pseudolabrys  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Sphingobacteriales;f\_Sphingobacteriaceae;g\_uncultured  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Pricia  
 d\_Bacteria;p\_Campilobacterota;c\_Campylobacteria;o\_Campylobacterales;f\_Sulfurimonadaceae;g\_Sulfuricum  
 d\_Bacteria;p\_Bdellovibrionota;c\_Oligoflexia;o\_Oligoflexales;f\_Oligoflexales;g\_Pseudobacteriovorax  
 d\_Bacteria;p\_Desulfobacterota;c\_Syntrophia;o\_Syntrophales;f\_Syntrophaceae;g\_Syntrophus  
 d\_Bacteria;p\_Plantcymycetota;c\_Phycisphaerae;\_:\_:\_  
 d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Peptostreptococcales-Tissierellales;\_:\_  
 d\_Bacteria;p\_Desulfobacterota;c\_Desulfobacteria;o\_Desulfobacterales;f\_Desulfosarcinaceae;g\_uncultured  
 d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Clostridia;f\_Hungateiclostridiaceae;g\_Saccharofermentans  
 d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Actinomycetales;f\_Actinomycetaceae;g\_Actinomycetes  
 d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sneathiellales;f\_Sneathiellaceae;g\_Sneathiella  
 d\_Bacteria;p\_Armatimonadota;c\_Chthonomonadetes;o\_Chthonomonadales;f\_Chthonomonadales;g\_Chthonomonadales  
 d\_Bacteria;p\_Plantcymycetota;c\_Plantcymycetes;o\_Plantcymycetales;f\_Schlesneriaceae;g\_Plantcyporus  
 d\_Bacteria;p\_Plantcymycetota;c\_Plantcymycetes;o\_Isosphaerales;f\_Isosphaeraceae;g\_Aquisphaera  
 d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Entomoplasmatales;f\_Entomoplasmatales\_Incertae\_Sedis;g\_Candidatus\_Hepatoplasma  
 d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Verrucomicrobiaceae;g\_uncultured  
 d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacteriales;f\_Rhodobacteraceae;g\_Limibaculum  
 d\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Beggiatoales;f\_Beggiatoaceae;g\_uncultured  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Psychroflexus  
 d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Eubacterium\_fissicatena\_group  
 d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_RF39;f\_RF39;g\_RF39  
 d\_Bacteria;p\_Myxococcota;c\_Polyangia;o\_Haliangiales;f\_Haliangiaceae;g\_Haliangium  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Zeaxanthinibacter  
 d\_Bacteria;p\_Plantcymycetota;c\_Phycisphaerae;o\_Phycisphaerales;f\_Phycisphaeraceae;g\_SM1A02  
 d\_Bacteria;p\_Cyanobacteria;c\_Sericytochromatia;o\_Sericytochromatia;f\_Sericytochromatia;g\_Sericytochromatia  
 d\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Lachnospira  
 d\_Bacteria;p\_Acidobacteriota;c\_Holophagae;o\_Subgroup\_7;f\_Subgroup\_7;g\_Subgroup\_7  
 d\_Bacteria;p\_Acidobacteriota;c\_Thermoanaerobaculia;o\_Thermoanaerobaculiales;f\_Thermoanaerobaculiales;g\_Subgroup\_10  
 d\_Bacteria;p\_Chloroflexi;c\_Chloroflexia;o\_Thermomicrobiales;f\_JG30-KF-CM45;g\_JG30-KF-CM45  
 d\_Bacteria;p\_Sumerlaeota;c\_Sumerlaeae;o\_Sumerlaeales;f\_Sumerlaeaceae;g\_Sumerlaea  
 d\_Bacteria;p\_Actinobacteriota;c\_Acidimicrobiia;o\_Microtrichales;f\_Iamiaceae;g\_Iamia  
 d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Rhizobiales\_Incertae\_Sedis;g\_Phreatobacter  
 d\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Micromonosporales;f\_Micromonosporaceae;g\_uncultured  
 d\_Bacteria;p\_Bacteroidota;c\_Bacteroidia;o\_Bacteroidales;f\_Rikenellaceae;g\_Alistipes  
 d\_Bacteria;p\_Desulfobacterota;c\_Desulfuromonadia;o\_Desulfuromonadia;f\_Desulfuromonadaceae;g\_uncultured  
 d\_Bacteria;p\_Verrucomicrobiota;c\_Verrucomicrobiae;o\_Chthoniobacteriales;f\_Chthoniobacteriaceae;g\_uncultured  
 d\_Bacteria;p\_Patescibacteria;c\_Microgenomatia;o\_Candidatus\_Shapirobacteria;f\_Candidatus\_Shapirobacteria;g\_Candidatus\_Shapirobacteria  
 d\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Acetobacteriales;f\_Acetobacteraceae;g\_uncultured  
 d\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Izemoplasmatales;f\_Izemoplasmatales;g\_Izemoplasmatales

Figure S2.5. All bacterial genera detected through eDNA analysis

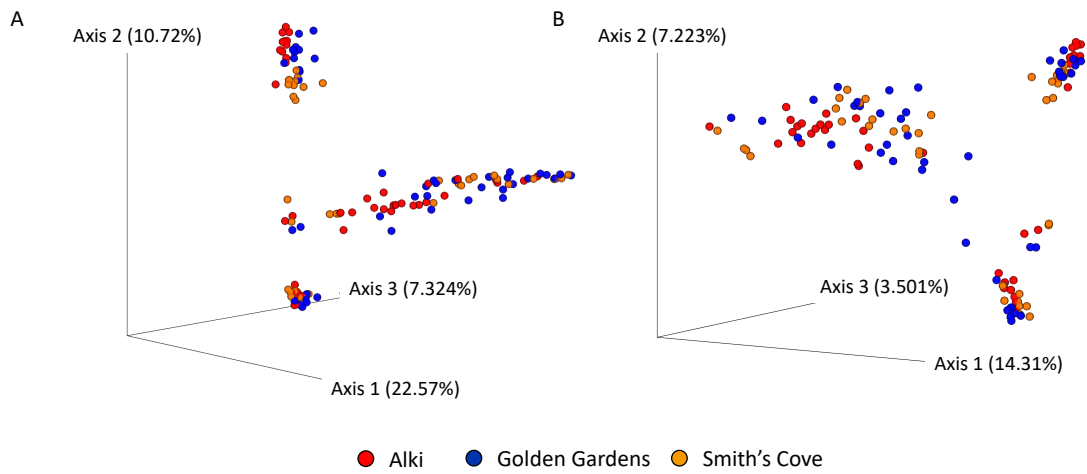


Figure S2.6. A) Bray-Curtis dissimilarity and B) Jaccard emperor PCoA plots showing maximum dissimilarity between samples. Axis 1 represents the maximum dissimilarity between samples followed by axis 2, and 3. Colors indicate different site (Red = Alki, Blue = Golden Gardens, Orange = Smith's Cove).

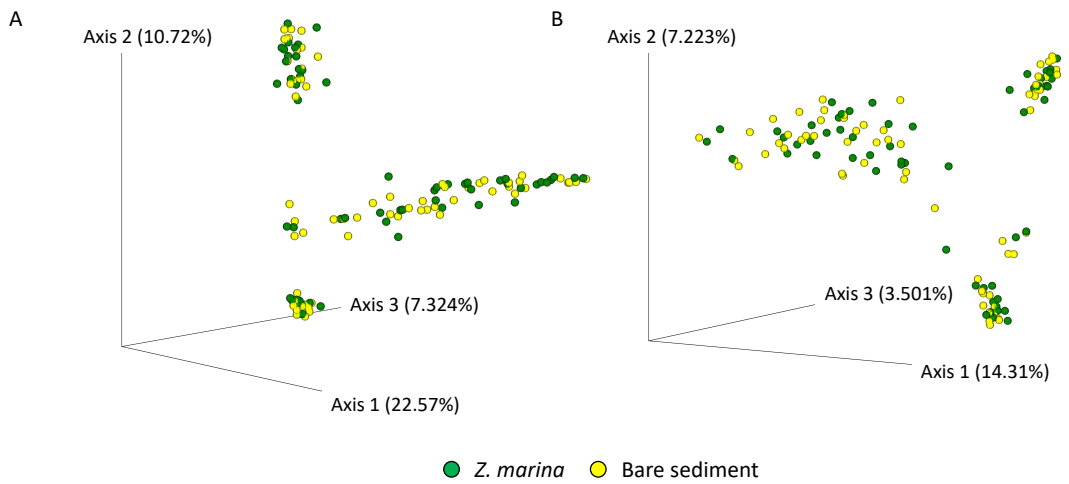


Figure S2.7. A) Bray-Curtis dissimilarity and B) Jaccard emperor PCoA plots showing maximum dissimilarity between samples. Axis 1 represents the maximum dissimilarity between samples followed by axis 2, and 3. Colors indicate seagrass presence (Green = *Z. marina*, Yellow = bare sediment).