

DISSERTATION/ DOCTORAL THESIS

Titel der Dissertation/Title of the Doctoral Thesis

Prokaryotic communities and plastic pollution in the ocean

verfasst von/ submitted by

Maria Gomes Ribeiro Teixeira Pinto

angestrebter akademischer Grad / in partial fulfilment of the requirements for the degree of

Doctor of Philosophy (PhD)

Wien, 2020 / Vienna, 2020

Studienkennzahl lt. Studienblatt / degree programme

code as it appears on the student record sheet:

A 794 685 437

Dissertationsgebiet lt. Studienblatt /field of study as it

appears on the student record sheet:

Biologie / Biology

Betreut von / Supervisor:

Univ.-Prof. Dr. Gerhard J. Herndl

ACKNOWLEDGEMENTS

I want to thank my supervisor Gerhard Herndl for the opportunity of doing this PhD and his continuous support over the last years. I want to thank Gerhard for always being available whenever needed, for the insightful discussions and advice, for trusting my work and for fostering my growth as a scientist.

I want to thank all my colleagues at the Division of Microbial Oceanography for all the inspiring discussions over the years and for all I have had the pleasure to learn from them. I thank Paula Polonia for all the great assistance in the lab and great company. I thank all my past and present office mates, Barbara, Paul, Alex, Eddie, Florian and Pavla for the great discussions and nice atmosphere in the office. I thank Zihao for his patience and availability to help whenever I had bioinformatic issues. I thank Fede for his constant moral support and for the good laughs we shared, Tinkara and Chie for always creating a great environment around them and Christian and Thomas for their questions and suggestions to my work. I thank Mili for her positivity, willingness to help and always having the ability of making me laugh. I want to give a special thanks to my friend and field work companion Teresa Langer for the great scientific discussions, her determination, remarkable work, the valuable help in sampling and laboratory work and for the amazing company throughout our many adventures.

I thank Barbara Mähnert, Christian Baranyi and Luca for maintaining the lab operational. I also thank Christian for all the laboratory techniques he taught me and for all the help in the lab and Barbara for all the assistance provided whenever needed, both in the lab and in identifying random species of plants and animals. I thank the Rovinj crew, Eva, Danielle, Paul, Lisi and Alice, for all the fun times we spent in Rovinj, for the great environment and for all the support in the lab and during sampling. I also thank all the people from the Ruđer Bošković Institute that accompanied us while we worked there, especially Mirjana, Marino, Paolo, Ingrid and of course captain Dario.

I sincerely thank Pedro Frade for always creating a pleasant atmosphere and for accepting to meet with me when I sent him an email asking if I could volunteer in the Microbial Oceanography group. None of this would have been possible if his answer would have been “no”. I want to thank Bettina for all the moral support while writing my PhD project and companionship.

I want to thank my friend Gabriela, whose positivity and good mood always uplifted me. Our regular lunches would always spark my motivation. I want to thank Miguel for his help with bioinformatics, for his friendship and availability for 5-minute walking breaks around the building.

I am sincerely thankful for my good friends in Vienna with whom I shared laughs, cries, excitement, struggles, ups and downs. Their patience, support, company, trust and friendship helped me keep a healthy and positive mindset over the last years.

I want to thank Valentin for everything. His strength and companionship over the last years kept me grounded in more stressful times and gave me confidence during the most frustrating ones. I am very grateful to have had you by my side.

Finally, I want to thank my family and my Portuguese friends that, despite being far, have always supported me whenever I needed. I want to thank my grandmother Anita, for her strength, my grandmother Milu for teaching me that it is possible to be strong and kind at the same time, and my grandfather Luís for his humour and personality and for being a constant source of inspiration. I want to especially thank my parents, who have always been my main inspiration, both personally and professionally. All I am and everything I have achieved was thanks to them.

Finalmente gostaria de agradecer à minha família e aos meus amigos portugueses, que apesar de longe, sempre me apoiaram e estiveram lá para mim quando eu precisava. Quero agradecer à minha avó Anita, pela sua força e espírito, à minha avó Milu por me mostrar que é possível ser-se forte e generosa ao mesmo tempo, e ao meu avô Luís pelo seu humor e personalidade e por ser uma constante fonte de inspiração. Quero agradecer especialmente aos meus pais, que sempre foram a minha maior inspiração, tanto a nível pessoal como a nível profissional. Tudo aquilo que sou e tudo aquilo que alcancei foi graças a eles.

OVERVIEW OF DISSERTATION

This thesis is presented as a cumulative dissertation, combining a general introduction about plastics and their impact in marine ecosystems, four chapters and a general discussion highlighting the main findings of the four chapters. Each chapter represents either a manuscript in review or published in an international scientific peer-reviewed journal. Hence, each chapter is presented in the format required by the journal to which the respective manuscript was submitted.

Taken together this thesis aims at shedding light on the interaction between prokaryotic communities and plastic pollution in the ocean. Chapter I investigates the influence of the type of plastic on the taxonomic composition of the prokaryotic community of the biofilm growing on different plastics, under both ambient and dim light conditions. Chapter II investigates the taxonomy and metabolism of three prokaryotic consortiums that can survive with low-density polyethylene (LDPE) as sole carbon source, enriched from the biofilm of polyethylene (PE) pieces collected from the environment. Chapter III investigates the presence of the prokaryotes studied in Chapter II on the biofilm of different plastics collected in different oceanic regions. Finally, Chapter IV investigates how compounds leaching from PE and polypropylene (PP) into the ambient seawater influence the dissolved organic carbon pool and microbial activity.

Table of contents

SUMMARY	1
ZUSAMENFASSUNG	3
INTRODUCTION	5
What is plastic?	5
Impact of plastic in marine ecosystems	6
Plastic biofilms in the ocean	8
Plastic biodegradation in the ocean	10
References	12
CHAPTER I	
The composition of bacterial communities associated with plastic biofilms differs between different polymers and stages of biofilm succession	17
Abstract	18
Introduction	18
Material and Methods	21
Results	25
Discussion	31
Conclusion	36
Acknowledgements	37
References	38
Supporting information	41
CHAPTER II	
Putative degraders of low-density polyethylene-derived compounds in the ocean	95
Abstract	96
Introduction	96
Results	99
Discussion	110
Material and Methods	114
Acknowledgments	119
References	120
Supporting information	124
References	165
CHAPTER III	
Putative degraders of low-density polyethylene-derived compounds are ubiquitous members of plastic-associated bacterial communities in the marine environment	168

Abstract	169
Introduction.....	169
Results	172
Discussion	180
Material and Methods.....	183
Acknowledgments	188
References.....	190
Supplementary Information	193
References	244
CHAPTER IV	
Dissolved organic carbon leaching from plastics stimulates microbial activity in the ocean	245
Abstract	246
Introduction.....	246
Results	248
Discussion	253
Material and Methods.....	256
Acknowledgements	259
References	260
GENERAL DISCUSSION	262
Plastic colonization by prokaryotes at the sea surface	262
Influence of plastic-derived compounds on marine microbial communities	264
Bacteria and metabolic pathways putatively involved in the degradation of LDPE-originating compounds	265
References	269

SUMMARY

Plastic pollution in the ocean has become one of the major environmental concerns of the last decades. Increase in plastic production and consequently waste has been accompanied with an increase in plastic debris in the ocean. The extent of the impact plastic pollution has on marine environments is still unclear, and the fate of plastic in the oceans is unknown. Understanding the influence of microbes on plastics and *vice versa* is essential to understand the lifecycle of plastics and their impact in the world's oceans. This thesis aimed at shedding light on the interaction between plastics and prokaryotic communities living in the seawater and attached to the plastics at the sea surface. Differences in prokaryotic colonization patterns under both dim and ambient light conditions on different plastics were studied. Bacteria and associated metabolic pathways putatively indicating degradation of low-density polyethylene (LDPE) and/or associated compounds were identified. The influence of plastic leachates on the dissolved organic carbon (DOC) pool and microbial activity in the seawater was also investigated.

Once in the ocean, plastics become colonized by a taxonomical diverse biofilm of prokaryotes and eukaryotes. The underlying factors determining plastic colonization are still to be understood. To determine whether different prokaryotic communities colonize different plastics under the same conditions, five different plastics and glass were incubated in the North Adriatic Sea over two months under both, dim and ambient light conditions. The prokaryotic community composition of their biofilm was then analyzed after one week and after one and two months via 16S rRNA gene analysis. The five plastics used in these experiments were LDPE, high-density polyethylene (HDPE), polypropylene (PP), polyvinyl chloride (PVC) with diisononyl phthalate (DINP) as an additive and PVC with bis(2-ethylhexyl) phthalate (DEHP) as an additive. Overall, the prokaryotic community composition of LDPE, HDPE, PP and glass was relatively similar between each other and different from those of the biofilm of the PVC. This difference was more pronounced after one week of incubation and decreased in later stages of biofilm development. At the same time, there were certain taxa that discriminated for certain plastics over the others and over glass, also especially after one-week incubation. Surface properties are known to influence biofilm establishment on surfaces and might have been the cause for the

observed differences between different plastics. The presence and concentration of additives could also play an important role in the biofilm development.

Three PE biofilms were incubated in artificial seawater with LDPE as the sole carbon source for two years. Metagenomic analysis was used to investigate the consortiums surviving with LDPE as sole carbon source after one- and two-years incubations. The analysis revealed an increase in the abundance of a taxonomically diverse consortium of bacteria with a predominant enrichment of members from the *Rhodobacteraceae* family, the *Planctomycetota* phylum and bacteria associated to the *Alcanivoraceae* family. Genomic analysis of metagenome assembled genomes (MAGs) of several of these bacteria revealed that the majority harbored genes encoding for the essential enzymes for alkane degradation, particularly genes encoding surfactants, alkane transporters, alcohol and aldehyde dehydrogenases and genes encoding enzymes responsible for the initial oxidation of alkanes such as genes *alkB*, *CYP153*, *LadA* and *AlmA*. Some of these genes also increased in relative abundance over time in all incubations. Several of the bacteria that were enriched in the LDPE incubations were also found to be ubiquitous on the biofilm of plastics collected in the North Atlantic, the Pacific and the North Adriatic. Furthermore, 16S rRNA gene analysis also revealed that members of the *Rhodobacteraceae* family enriched in LDPE-incubations discriminated for LDPE and PE in the in-situ incubations performed in the North Adriatic in comparison to PP and glass. Taken together, this indicates that some members of the biofilm of plastics in the ocean might have the potential to degrade the PE polymer or PE-associated compounds and that alkane degradation pathways might be involved.

ZUSAMENFASSUNG

Die Plastikverschmutzung der Ozeane ist eines der größten Umweltprobleme in den letzten Jahrzehnten. Der Anstieg der Plastikproduktion und des damit einhergehenden Abfalls hat zu einem Anstieg an Plastik in den Ozeanen geführt. Das Ausmaß der Auswirkung von Plastikverschmutzung auf marine Lebensräume ist noch nicht vollständig geklärt, und das Schicksal von Plastik in den Ozeanen ist unbekannt. Das Verstehen des Einflusses von Mikroben auf Plastik und vice versa, ist essentiell, um den Lebenszyklus des Plastiks und dessen Einfluss auf die Ozeane der Welt zu verstehen. Diese Arbeit versucht Aufschluss über die Interaktion zwischen Plastik und prokaryotischen Gemeinschaften, sowohl in der Wassersäule als auch auf Plastik an der Meeresoberfläche zu geben. Unterschiede im Besiedlungsmuster prokaryotischer Gemeinschaften unter unterschiedlichen Lichtverhältnissen, wurden in dieser Arbeit untersucht. Bakterien und deren Stoffwechselwege, die auf einen möglichen Abbau von Low-Density-Polyethylene (LDPE) und / oder zugehörigen Stoffen hinweisen, wurden identifiziert. Der Einfluss des Auswaschen von gelösten organischen Kohlenstoff auf die mikrobielle Aktivität im Meereswasser wurde ebenfalls untersucht.

Im Ozean wird Plastik von einem diversen Biofilm von Prokaryoten und Eukaryoten kolonisiert. Die grundlegenden Faktoren, die die Kolonialisierung von Plastik bestimmen, sind großteils noch unbekannt. Um zu untersuchen wie verschiedene prokaryotische Gemeinschaften verschiedene Arten von Plastik unter denselben Umständen kolonisieren, wurden fünf verschiedene Arten von Plastik und Glas für zwei Monate im nordadriatischen Meer abgedunkelt und in Umgebungslicht inkubiert. Die Zusammensetzung der prokaryotischen Gemeinschaften der diversen Biofilme wurde dann nach einer Woche, einem Monat und zwei Monaten via 16S rRNA Genanalyse untersucht. Die fünf Plastiktypen, die im Experiment verwendet wurden, waren LDPE, High-Density-Polyethylene (HDPE), Polypropylene (P), Polyvinylchlorid (PVC) mit di-isononyl Phthalate (DINP) als Zusatzstoff und PVC mit bis(2-ethylhexyl) Phthalate (DEHP) als Zusatzstoff. Insgesamt war die Zusammensetzung der prokaryotischen Gemeinschaft auf LDPE, HDPE, PP und Glas relativ ähnlich, und unterschiedlich zu der Zusammensetzung des Biofilms auf

PVC. Der Unterschied war deutlicher nach einer Woche der Inkubation, und nahm in den späteren Phasen der Biofilmentwicklung ab. Gleichzeitig gab es Taxa die bestimmte Typen von Plastik gegenüber den anderen Typen und Glas bevorzugt haben, speziell nach einer Woche Inkubation. Oberflächeneigenschaften sind ein bekannter Einflussfaktor bei Etablierung von Biofilmen auf Oberflächen und könnten der Grund für die beobachteten Unterschiede zwischen den verschiedenen Plastiktypen sein. Die Präsenz und Konzentration von Zusatzstoffen könnten auch eine wichtige Rolle in der Entwicklung von Biofilmen spielen.

Drei PE Biofilme wurden für zwei Jahre mit LDPE als einzige Kohlenstoffquelle in künstlichem Meerwasser inkubiert. Die Gemeinschaften die mit LDPE als einzige Kohlenstoffquelle überlebt haben, wurden nach einem und nach zwei Jahren mit metagenomischen Analysen untersucht. Die Analysen zeigten einen Anstieg der Häufigkeit einer taxonomisch diversen Gemeinschaft, mit einer vorherrschenden Anreicherung von Mitgliedern der Rhodobacteraceae, der Plantcomycetota und mit Repräsentanten der Alcanivoraceae. Genomische Analysen von Metagenome Assembled Genomes (MAGs) mehrerer dieser Bakterien zeigten, dass die Mehrheit der Bakterien Gene besitzen, die die essentiellen Enzyme zur Zersetzung von Alkanen kodieren, insbesondere Gene die Tenside kodieren, Alkan Transporter, Alkohol und Aldehyd-Dehydrogenase, und Gene die Enzyme kodieren welche verantwortlich für die initiale Oxidierung von Alkanen sind, wie die Gene *alkB*, *CYP153*, *LadA* und *AlmA*. Auch manche dieser Gene zeigten einen Anstieg in relativer Häufigkeit mit fortschreitender Inkubationsdauer in allen Inkubationen. Viele der Bakterien die in den LDPE Inkubationen angereichert wurden, waren allgegenwärtig auf Plastik welches im Nordatlantik, im Pazifik und im nordadriatischen Meer gesammelt wurde. Weiters zeigte die 16S rRNA Genanalyse, dass Mitglieder der Rhodobacteraceae, welche in LDPE Inkubationen angereichert wurden, LDPE und PE in den in-situ Inkubationen im nordadriatischen Meer gegenüber PP und Glas bevorzugten. Alles zusammengenommen deutet darauf hin, dass manche Mitglieder von Biofilmen auf Plastik in den Ozeanen das Potential zur Zersetzung von PE Polymer oder PE-verwandten Stoffen haben und dass Abbauwege von Alkanen beteiligt sein könnten.

INTRODUCTION

What is plastic?

Plastics refer to a variety of synthetic or semi-synthetic organic compounds that can be molded and shaped into different solid objects and used in a wide range of applications. In fact the word “plastic” comes from the Greek word “plastikos” which means capable of being shaped or molded (Liddel and Scott). They are polymers usually derived from fossil fuels, like natural gas and crude oil, but can also have renewable origins, like starch, sugar cane and vegetable oils, or mineral origins like salts.

There is evidence that humans have benefited from the use of natural polymers since 1600 BC, when ancient Mesoamericans used natural rubber to produce balls, bands and figurines (Hosler *et al.*, 1999). However it was not until the year 1909, that Bakelite, considered to be the first entirely synthetic manmade plastic, was created by Leo Hendrik Baekeland (Dodiuk and Goodman, 2013). Since then, plastic production has grown exponentially. Its low prices, ease of manufacturing, versatility and endurance made worldwide plastic demands rise exponentially over the last decades (Andrady and Neal, 2009), resulting in an 8.5% average annual production growth since 1950 (Chalmin, 2019). It is estimated that 359 million tons of plastic were produced worldwide in the year 2018 alone (PlasticsEurope).

There are several different types of plastic, depending on the source material and production processes. The different plastic types can be grouped in two main polymer groups: thermosets and thermoplastics. Thermoplastics are plastics that soften when heated and harden when cooled, with the most common being polyethylene (PE), polypropylene (PP), polystyrene (PS), polyvinyl chloride (PVC), polycarbonate (PC) and polyethylene terephthalate (PET). Thermosets are those which never soften once they have been molded, for example polyurethane (PUR), epoxide (EP), phenol-formaldehyde (PF), silicone and unsaturated polyester resins (UP) (PlasticsEurope). Thermoplastics, especially PE, PP and PVC are the most widely used plastics. In the year 2018, they amounted to approximately 60% of the total plastic demand (PlasticsEurope). The majority of plastics is used in packaging, construction, automotive industry, electronics and agriculture, having accounted for 39.9%, 19.8%, 9.9%, 6.2% and 3.4%, respectively, of the total plastic demand in Europe in the year 2018 (PlasticsEurope).

Most plastics are blended together with organic or inorganic compounds added during the manufacturing process to increase their performance (Lithner *et al.*, 2011). The most common types of plastic additives are plasticizers, flame retardants, antioxidants, acid scavengers, light and heat stabilizers, lubricants, pigments, antistatic agents, slip compounds and thermal stabilizers (Hahladakis *et al.*, 2018). In some PVCs, plastic additives, usually phthalates, can account for up to 60% of the plastic weight (Net *et al.*, 2015).

Due to their widespread use, durability, low recycling rates and poor waste management, a significant portion of the produced plastics ends up in marine ecosystems. Consequently, plastic debris has become one of the main environmental issues of the last decades.

Impact of plastic in marine ecosystems

Plastics are transported from land into the ocean via direct disposal of plastic waste by ships and people at the coast, riverine systems (Lebreton *et al.*, 2017), waste water discharges (Browne *et al.*, 2011), runoff and extreme weather events (Li *et al.*, 2016).

Even though there are reports of plastic in the ocean as early as the 1970s (Venrick *et al.*, 1973), until now, we do not know how much plastic there is in marine ecosystems. Conservative estimates put the number of plastic in the oceans at 5.25 trillion pieces in the year 2014 (Eriksen *et al.*, 2014). It was estimated that between 4.8 and 12.7 million tons entered the ocean in the year 2010 alone (Jambeck *et al.*, 2015), a number which is most likely increasing over time (Ostle *et al.*, 2019; Wilcox *et al.*, 2020). Positively buoyant plastics, like PE and PP, accumulate at the surface, mainly near the coast and oceanic gyres (Eriksen *et al.*, 2014). However, there is also a portion of plastics that sink deeper in the water column, either because they are denser, or because they become less buoyant. For example, plastic colonization by a biofilm can cause plastics to sink (Lobelle and Cunliffe, 2011). Additionally, buoyant plastics, like PE and PP, can also be vertically transported by marine snow (Porter *et al.*, 2018) and marine biota (Katija *et al.*, 2017) from the surface to deeper layers of the ocean, eventually reaching the seafloor (Van Cauwenberghe *et al.*, 2013). Plastics have even been discovered in abyssal zones (Chiba *et al.*, 2018), with recently observed microplastic concentrations reaching 71.1 items per kg dry weight of sediment in the Challenger Deep (Peng *et al.*, 2020).

Microplastics are plastics with an average diameter below 5 mm and are more abundant in the ocean than larger plastics (Eriksen *et al.*, 2014). Depending on their origin, microplastics are classified as either primary or secondary. Primary microplastics are already manufactured as such, usually used in cosmetics, textile and plastic industries. Secondary microplastics are a result of the fragmentation and degradation of larger plastic pieces. Microplastics can further degrade into smaller nanoplastics (Lambert and Wagner, 2016). Due to their smaller size, micro- and nanoplastics are more likely to be ingested by a higher number of organisms and can potentially have a stronger impact in marine ecosystems.

Plastics may pose several threats to marine ecosystems. By the year 2015 it was estimated that at least 690 marine species had encountered marine debris, most of it plastic, often with deadly outcomes (Gall and Thompson, 2015; Wilcox *et al.*, 2018). Direct physical harm to marine wildlife through entanglement and ingestion has been repeatedly reported in fish, marine mammals, seabirds, turtles and invertebrates (Moser and Lee, 1992; Moore *et al.*, 2009; Boerger *et al.*, 2010; Schuyler *et al.*, 2014; Lusher *et al.*, 2017). Microplastics can additionally be ingested by smaller organisms, such as bivalves, zooplankton and other invertebrates (Graham and Thompson, 2009; Cole *et al.*, 2013; Van Cauwenberghe and Janssen, 2014), and can negatively impact growth rates, fecundity and lifespan (Jeong *et al.*, 2016) and cause internal abrasion (Wright *et al.*, 2013). Exposure to higher concentrations of plastic has also been associated to an increase in likelihood of disease in corals (Lamb *et al.*, 2018). Additionally, plastics might be carriers of pathogens (Viršek *et al.*, 2017), like species of *Vibrio* sp. (Kirstein *et al.*, 2016) and of antibiotic resistance genes (Laganà *et al.*, 2019; Yang *et al.*, 2019).

There is also the concern that plastic-associated harmful compounds might enter food webs and be transferred through several trophic levels (Hermabessiere *et al.*, 2017; Diepens and Koelmans, 2018), potentially even reaching humans (Barboza *et al.*, 2018). Plastic additives have been detected in seawater globally in varying concentrations (Hermabessiere *et al.*, 2017). While these additives might have entered the ocean directly from diffuse sources, such as wastewater, atmospheric deposition and sewage discharges, there is growing evidence that plastics passively leach compounds into the ambient seawater and might be a source of additives in the ocean (Al-Odaini *et al.*, 2015; Paluselli *et al.*, 2018). Plastic additives, especially phthalates and PBDEs (polybrominated diphenyl ethers), have been detected in the tissues of a wide variety of marine organisms, such as bivalves (Johansson *et al.*, 2006), whales (de Boer *et al.*, 1998), seabirds (Tanaka *et al.*, 2013) zooplankton and fish (Mackintosh *et al.*,

2004). Even though the impact these chemicals exert on different organisms is largely unknown, there is evidence that they can impair ecophysiological functions (Browne *et al.*, 2013; Rochman *et al.*, 2013) and in some cases can be lethal to some animals (for a review see Hermabessiere *et al.*, 2017).

Plastics might also be a vector for hydrophobic organic compounds (HOCs), like the contaminants polychlorinated biphenyls (PCBs) adsorbed from seawater (Teuten *et al.*, 2007). However, exposure of the marine biota to these compounds via plastics might be negligible compared to other HOCs sources (Bakir *et al.*, 2016). In fact, there is some debate on whether ingestion of plastics by the marine biota might actually have a cleansing effect with regard to HOCs, due to the high affinity of plastics for these chemicals (Koelmans *et al.*, 2016).

Finally, plastics might influence biogeochemical cycles in the ocean by influencing the marine dissolved organic matter pool (Romera-Castillo *et al.*, 2018), by impacting microbe-mediated processes (Tetu *et al.*, 2019) and by altering the sinking properties of fecal pellets and therefore influencing the organic carbon export to the deep ocean (Cole *et al.*, 2016). There is growing evidence that plastics and associated compounds affect microbial communities in the surrounding environment. Plastic leachates can impair growth and photosynthesis of the probably most abundant primary producers, *Prochlorococcus* (Tetu *et al.*, 2019). Additionally, different types of microplastics might influence nitrogen cycling in sedimentary microbial communities (Seeley *et al.*, 2020).

Despite the increase of studies on the interaction between microbial communities and plastics in the ocean, the impact of the latter and that of their associated chemicals on marine biogeochemical cycles is highly understudied and their role in shaping microbial communities across different marine ecosystems is far from understood.

Plastic biofilms in the ocean

Biofilms are consortiums of one or multiple species of microorganisms that attach to each other or to a surface via an extracellular matrix composed of extracellular polymeric substances (EPS) (Flemming *et al.*, 2016). EPS usually include polysaccharides, lipids, extracellular DNA and proteins (Flemming and Wingender, 2010). Biofilms confer several advantages to their inhabitants, like higher nutrient availability (Liu *et al.*, 2017), protection against environmental stress and drugs (Kubota *et al.*, 2008) (Desai *et al.*, 2014), higher potential for horizontal gene transfer (Molin and Tolker-Nielsen, 2003) and provide a platform

for compound exchange with other members of the biofilm community. A shift of a microbe from a planktonic to a biofilm lifestyle is usually accompanied by phenotypic changes with genes involved in EPS production, chemotaxis, transport of substances and cell-cell communication being up-regulated (Costerton *et al.*, 1995).

Once in the sea, plastic rapidly becomes colonized by a biofilm like most other surfaces (Lobelle and Cunliffe, 2011). Initial colonization seems to follow the usual pattern of surface biofouling, with primary colonizers being comprised mostly of *Gamma*- and *Alphaproteobacteria* (Oberbeckmann *et al.*, 2015), followed by the establishment of a diverse community of prokaryotes and eukaryotes. This new habitat on plastics has been coined *plastisphere* (Zettler *et al.*, 2013). Until now, studies characterizing the community composition of the *plastisphere* have mostly focused on plastic colonization at the sea surface, and to a lesser extent at the seafloor (Harrison *et al.*, 2014). Diatoms and cyanobacteria are common *plastisphere* members and the main phototrophic representatives on plastic biofilms in the sunlit surface (Reisser *et al.*, 2014; Bryant *et al.*, 2016). Diatoms can be a dominant eukaryotic taxa in early stages of biofilm development (Eich *et al.*, 2015), however, decreasing in relative abundance with the appearance of new eukaryotic taxa in later stages such as dinoflagellates (Dudek *et al.*, 2020). Red, green, and brown algae, fungi, ciliates, metazoans and apicomplexans can also be found on plastic biofilms (Oberbeckmann *et al.*, 2016; De Tender *et al.*, 2017; Dudek *et al.*, 2020). Nevertheless, in comparison to the prokaryotic members, the eukaryotic component of the *plastisphere* is much less known.

The communities of plastic biofilms have been shown to be generally different from the ones in the surrounding seawater (Oberbeckmann *et al.*, 2014; Kettner *et al.*, 2017) and in organic particles (Dussud *et al.*, 2018). However, the main factors influencing the biofilm development on plastics remain unclear. While some studies suggest the existence of a plastic-specific community (Ogonowski *et al.*, 2018; Keszy *et al.*, 2019), others suggest the opposite, with plastic-associated microbial assemblages being similar to those of other surfaces. For example, after incubated for six weeks, the microbial community composition of PET biofilms was similar to the one on glass substrates (Oberbeckmann *et al.*, 2016). Similarly, when incubated for two weeks in a wastewater treatment plant, PE and PS harbored the same prokaryotic communities as wooden pellets (Oberbeckmann *et al.*, 2018). Interestingly, this contrasted with the results from that same study with samples incubated in marine and brackish water, in which the communities growing on PE and PS were distinct from the one

on wooden pellets. This leads us to suggest that plastic-specific communities only develop under certain environmental conditions.

The question has also been raised on whether plastics with different characteristics develop biofilms with different communities. Several studies have reported similar microbial community composition across different plastic types (e.g. PE, PP, PS, PET, etc.) collected in the same locations (Amaral-Zettler *et al.*, 2015; C Dussud *et al.*, 2018; Jiang *et al.*, 2018; Ogonowski *et al.*, 2018; Kesy *et al.*, 2019), while others detected distinct microbial assemblages between different plastics types (Oberbeckmann *et al.*, 2018; Dudek *et al.*, 2020). However, even in most cases in which the community composition between plastic types is similar, there are specific taxa that are more abundant in one type over the others (Woodall *et al.*, 2014). Surface properties, such as roughness, surface free energy and hydrophobicity are known to influence biofilm establishment in early stages of biofilm development (Taylor *et al.*, 1997; Ammar *et al.*, 2015). The influence of surface related properties is likely to decrease with thickening of the biofilm (Dussud *et al.*, 2018) with environmental factors and biofilm internal processes shaping further biofilm development (Oberbeckmann *et al.*, 2015). Therefore, it is not surprising that plastics with different characteristics develop biofilms with different taxonomic composition in early stages of biofilm development (Muthukrishnan *et al.*, 2019), becoming more similar in later stages (Hossain *et al.*, 2019). This results in the plastic-specific microorganisms being the ones in closer proximity to the plastic surface once the biofilm becomes thicker (Kirstein *et al.*, 2019).

Plastic biodegradation in the ocean

Fossil fuel-based plastics, due to their complex structure, presence of additives, high molecular weight and hydrophobicity, are considered to be highly resistant to degradation (Kale *et al.*, 2015). It is difficult to estimate for how long plastics have been in the sea, however, a recent study found plastics at the seafloor at 4150 m depth, estimated to have been there for over two decades with little to no signs of biodegradation (Krause *et al.*, 2020). It is even unsure if bio-degradable plastics are completely degradable or whether they are simply broken-down to micro- and nanoplastics.

Nevertheless, albeit at slow rates, plastics are altered by marine bacteria (Sudhakar *et al.*, 2008; Harshvardhan and Jha, 2013). In the natural environment, plastic degradation is most likely a result of the combined action of biotic and abiotic factors (Sivan, 2011).

Depending on the type of plastic, weathering by abiotic factors such as pH, UV radiation, temperature and the chemical properties of the water can cause polymer oxidation, cracking, fragmentation and loss of molecular weight (Gulmine *et al.*, 2003) facilitating microbial action (González-Pleiter *et al.*, 2019).

Dussud and Ghiglione (2014) summarized plastic biodegradation in four phases: bio-deterioration, bio-fragmentation, assimilation and mineralization. Bio-deterioration refers to chemical and physical changes of the plastic surface by the growing biofilm such as increase in pore size, cracking and weakening of the matrix structure. Bio-fragmentation is the result of extracellular enzymes produced by the microbes breaking the polymer down to smaller molecules. Assimilation is the transport of the smaller molecules through the semi-permeable cellular membrane into the cell, which can then be used as carbon and energy source (Gu, 2003). Finally, mineralization is the last phase of plastic biodegradation when the polymer molecules are mineralized resulting in completely oxidized metabolites (CO₂, N₂, CH₄, and H₂O).

There is growing evidence that there are microorganisms with the ability to degrade plastics (Jacquin *et al.*, 2019). Strains of fungi and bacteria have been shown to alter the physical and chemical properties of certain plastic types under laboratory conditions (Kale *et al.*, 2015). However, most of these studies were performed with isolated strains under controlled laboratory conditions. Whether these organisms would partially or completely degrade the same plastic surfaces in the environment remains unknown.

In the year 2006 a novel bacterium, *Ideonella sakaiensis*, capable of synthesizing an enzyme hydrolyzing PET, coined PETase, was isolated from sediments (Yoshida *et al.*, 2016). This is the only isolated and characterized enzyme isolated from a bacterium from the environment capable of completely degrading a common polymer.

While pathways for the degradation of other plastics have been suggested (Shah *et al.*, 2008), the organisms, enzymes and mechanisms involved in the assimilation and remineralization phases of plastic biodegradation in the ocean remain to be identified and characterized.

References

- Al-Odaini, N.A., Shim, W.J., Han, G.M., Jang, M., and Hong, S.H. (2015) Enrichment of hexabromocyclododecanes in coastal sediments near aquaculture areas and a wastewater treatment plant in a semi-enclosed bay in South Korea. *Sci Total Environ* **505**: 290–298.
- Amaral-Zettler, L.A., Zettler, E.R., Slikas, B., Boyd, G.D., Melvin, D.W., Morrall, C.E., et al. (2015) The biogeography of the Plastisphere: implications for policy. *Front Ecol Environ* **13**: 541–546.
- Ammar, Y., Swailes, D., Bridgens, B., and Chen, J. (2015) Influence of surface roughness on the initial formation of biofilm. *Surf Coatings Technol* **284**: 410–416.
- Andrady, A.L. and Neal, M.A. (2009) Applications and societal benefits of plastics. *Philos Trans R Soc B Biol Sci* **364**: 1977–1984.
- Bakir, A., O'Connor, I.A., Rowland, S.J., Hendriks, A.J., and Thompson, R.C. (2016) Relative importance of microplastics as a pathway for the transfer of hydrophobic organic chemicals to marine life. *Environ Pollut* **219**: 56–65.
- Barboza, L.G.A., Dick Vethaak, A., Lavorante, B.R.B.O., Lundebye, A.-K., and Guilhermino, L. (2018) Marine microplastic debris: An emerging issue for food security, food safety and human health. *Mar Pollut Bull* **133**: 336–348.
- de Boer, J., Wester, P.G., Klamer, H.J.C., Lewis, W.E., and Boon, J.P. (1998) Do flame retardants threaten ocean life? *Nature* **394**: 28–29.
- Boerger, C.M., Lattin, G.L., Moore, S.L., and Moore, C.J. (2010) Plastic ingestion by planktivorous fishes in the North Pacific Central Gyre. *Mar Pollut Bull* **60**: 2275–2278.
- Browne, M.A., Crump, P., Niven, S.J., Teuten, E., Tonkin, A., Galloway, T., and Thompson, R. (2011) Accumulation of Microplastic on Shorelines Worldwide: Sources and Sinks. *Environ Sci Technol* **45**: 9175–9179.
- Browne, M.A., Niven, S.J., Galloway, T.S., Rowland, S.J., and Thompson, R.C. (2013) Microplastic Moves Pollutants and Additives to Worms, Reducing Functions Linked to Health and Biodiversity. *Curr Biol* **23**: 2388–2392.
- Bryant, J.A., Clemente, T.M., Viviani, D.A., Fong, A.A., Thomas, K.A., Kemp, P., et al. (2016) Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. *mSystems* **1**: e00024-16.
- Van Cauwenberghe, L. and Janssen, C.R. (2014) Microplastics in bivalves cultured for human consumption. *Environ Pollut* **193**: 65–70.
- Van Cauwenberghe, L., Vanreusel, A., Mees, J., and Janssen, C.R. (2013) Microplastic pollution in deep-sea sediments. *Environ Pollut* **182**: 495–499.
- Chalmin, P. (2019) The history of plastics: from the Capitol to the Tarpeian Rock. *F Actions Sci Reports J F actions* 6–11.
- Chiba, S., Saito, H., Fletcher, R., Yogi, T., Kayo, M., Miyagi, S., et al. (2018) Human footprint in the abyss: 30 year records of deep-sea plastic debris. *Mar Policy* **96**: 204–212.
- Cole, M., Lindeque, P., Fileman, E., Halsband, C., Goodhead, R., Moger, J., and Galloway, T.S. (2013) Microplastic Ingestion by Zooplankton. *Environ Sci Technol* **47**: 6646–6655.
- Cole, M., Lindeque, P.K., Fileman, E., Clark, J., Lewis, C., Halsband, C., and Galloway, T.S. (2016) Microplastics Alter the Properties and Sinking Rates of Zooplankton Faecal Pellets. *Environ Sci Technol* **50**: 3239–3246.
- Costerton, J.W., Lewandowski, Z., Caldwell, D.E., Korber, D.R., and Lappin-Scott, H.M. (1995) MICROBIAL BIOFILMS. *Annu Rev Microbiol* **49**: 711–745.
- Desai, J. V, Mitchell, A.P., and Andes, D.R. (2014) Fungal biofilms, drug resistance, and recurrent infection. *Cold Spring Harb Perspect Med* **4**: a019729.
- Diepens, N.J. and Koelmans, A.A. (2018) Accumulation of Plastic Debris and Associated Contaminants

- in Aquatic Food Webs. *Environ Sci Technol* **52**: 8510–8520.
- Dodiuk, H. and Goodman, S.H. (2013) Handbook of thermoset plastics, William Andrew.
- Dudek, K.L., Cruz, B.N., Polidoro, B., and Neuer, S. (2020) Microbial colonization of microplastics in the Caribbean Sea. *Limnol Oceanogr Lett* 5–17.
- Dussud, C. and Ghiglione, J.-F. (2014) Bacterial degradation of synthetic plastics. In *CIESM Workshop Monogr.* pp. 49–54.
- Dussud, C., Hudec, C., George, M., Fabre, P., Higgs, P., Bruzard, S., et al. (2018) Colonization of Non-biodegradable and Biodegradable Plastics by Marine Microorganisms. *Front Microbiol* **9**: 1571.
- Dussud, C., Meistertzheim, A.L., Conan, P., Pujo-Pay, M., George, M., Fabre, P., et al. (2018) Evidence of niche partitioning among bacteria living on plastics, organic particles and surrounding seawaters. *Environ Pollut* **236**: 807–816.
- Eich, A., Mildenerger, T., Laforsch, C., and Weber, M. (2015) Biofilm and Diatom Succession on Polyethylene (PE) and Biodegradable Plastic Bags in Two Marine Habitats: Early Signs of Degradation in the Pelagic and Benthic Zone? *PLoS One* **10**: e0137201.
- Eriksen, M., Lebreton, L., Carson, H., Thiel, M., Moore, C., Borerro, J., et al. (2014) Plastic Pollution in the World's Oceans: More than 5 Trillion Plastic Pieces Weighing over 250,000 Tons Afloat at Sea. *PLoS One* **9**: e111913.
- Flemming, H.-C. and Wingender, J. (2010) The biofilm matrix. *Nat Rev Microbiol* **8**: 623–633.
- Flemming, H.-C., Wingender, J., Szewzyk, U., Steinberg, P., Rice, S.A., and Kjelleberg, S. (2016) Biofilms: an emergent form of bacterial life. *Nat Rev Microbiol* **14**: 563–575.
- Gall, S.C. and Thompson, R.C. (2015) The impact of debris on marine life. *Mar Pollut Bull* **92**: 170–179.
- González-Pleiter, M., Tamayo-Belda, M., Pulido-Reyes, G., Amariei, G., Leganés, F., Rosal, R., and Fernández-Piñas, F. (2019) Secondary nanoplastics released from a biodegradable microplastic severely impact freshwater environments. *Environ Sci Nano* **6**: 1382–1392.
- Graham, E.R. and Thompson, J.T. (2009) Deposit-and suspension-feeding sea cucumbers (Echinodermata) ingest plastic fragments. *J Exp Mar Bio Ecol* **368**: 22–29.
- Gu, J.-D. (2003) Microbiological deterioration and degradation of synthetic polymeric materials: recent research advances. *Int Biodeterior Biodegradation* **52**: 69–91.
- Gulmine, J. V., Janissek, P.R., Heise, H.M., and Akcelrud, L. (2003) Degradation profile of polyethylene after artificial accelerated weathering. *Polym Degrad Stab* **79**: 385–397.
- Hahladakis, J.N., Velis, C.A., Weber, R., Iacovidou, E., and Purnell, P. (2018) An overview of chemical additives present in plastics: Migration, release, fate and environmental impact during their use, disposal and recycling. *J Hazard Mater* **344**: 179–199.
- Harrison, J.P., Schratzberger, M., Sapp, M., and Osborn, a (2014) Rapid bacterial colonization of low-density polyethylene microplastics in coastal sediment microcosms. *BMC Microbiol* **14**: 232.
- Harshvardhan, K. and Jha, B. (2013) Biodegradation of low-density polyethylene by marine bacteria from pelagic waters, Arabian Sea, India. *Mar Pollut Bull* **77**: 100–106.
- Hermabessiere, L., Dehaut, A., Paul-Pont, I., Lacroix, C., Jezequel, R., Soudant, P., and Duflos, G. (2017) Occurrence and effects of plastic additives on marine environments and organisms: A review. *Chemosphere* **182**: 781–793.
- Hosler, D., Burkett, S.L., and Tarkanian, M.J. (1999) Prehistoric Polymers: Rubber Processing in Ancient Mesoamerica. *Science* **284**: 1988–1991.
- Hossain, M.R., Jiang, M., Wei, Q., and Leff, L.G. (2019) Microplastic surface properties affect bacterial colonization in freshwater. *J Basic Microbiol* **59**: 54–61.
- Jacquin, J., Cheng, J., Odobel, C., Pandin, C., Conan, P., Pujo-Pay, M., et al. (2019) Microbial Ecotoxicology of Marine Plastic Debris: A Review on Colonization and Biodegradation by the “Plastisphere”. *Front Microbiol* **10**: 865.
- Jambeck, J.R., Geyer, R., Wilcox, C., Siegler, T.R., Perryman, M., Andrady, A., et al. (2015) Plastic waste inputs from land into the ocean. *Science* **347**: 768–771.
- Jeong, C.-B., Won, E.-J., Kang, H.-M., Lee, M.-C., Hwang, D.-S., Hwang, U.-K., et al. (2016) Microplastic

- size-dependent toxicity, oxidative stress induction, and p-JNK and p-p38 activation in the monogonont rotifer (*Brachionus koreanus*). *Environ Sci Technol* **50**: 8849–8857.
- Jiang, P., Zhao, S., Zhu, L., and Li, D. (2018) Microplastic-associated bacterial assemblages in the intertidal zone of the Yangtze Estuary. *Sci Total Environ* **624**: 48–54.
- Johansson, I., Héas-Moisán, K., Guiot, N., Munschy, C., and Tronczyński, J. (2006) Polybrominated diphenyl ethers (PBDEs) in mussels from selected French coastal sites: 1981–2003. *Chemosphere* **64**: 296–305.
- Kale, S.K., Deshmukh, A.G., Dudhare, M.S., and Patil, V.B. (2015) Microbial degradation of plastic: a review. *J Biochem Technol* **6**: 952–961.
- Katija, K., Choy, C.A., Sherlock, R.E., Sherman, A.D., and Robison, B.H. (2017) From the surface to the seafloor: How giant larvaceans transport microplastics into the deep sea. *Sci Adv* **3**: e1700715.
- Kesy, K., Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2019) Spatial Environmental Heterogeneity Determines Young Biofilm Assemblages on Microplastics in Baltic Sea Mesocosms. *Front Microbiol* **10**: 1665.
- Kettner, M.T., Rojas-Jimenez, K., Oberbeckmann, S., Labrenz, M., and Grossart, H.-P. (2017) Microplastics alter composition of fungal communities in aquatic ecosystems. *Environ Microbiol* **19**: 4447–4459.
- Kirstein, I. V., Kirmizi, S., Wichels, A., Garin-Fernandez, A., Erler, R., Löder, M., and Gerdts, G. (2016) Dangerous hitchhikers? Evidence for potentially pathogenic *Vibrio* spp. on microplastic particles. *Mar Environ Res* **120**: 1–8.
- Kirstein, I.V., Wichels, A., Gullans, E., Krohne, G., and Gerdts, G. (2019) The Plastisphere – Uncovering tightly attached plastic “specific” microorganisms. *PLoS One* **14**: e0215859.
- Koelmans, A.A., Bakir, A., Burton, G.A., and Janssen, C.R. (2016) Microplastic as a Vector for Chemicals in the Aquatic Environment: Critical Review and Model-Supported Reinterpretation of Empirical Studies. *Environ Sci Technol* **50**: 3315–3326.
- Krause, S., Molari, M., Gorb, E. V., Gorb, S.N., Kossel, E., and Haeckel, M. (2020) Persistence of plastic debris and its colonization by bacterial communities after two decades on the abyssal seafloor. *Sci Rep* **10**: 1–15.
- Kubota, H., Senda, S., Nomura, N., Tokuda, H., and Uchiyama, H. (2008) Biofilm Formation by Lactic Acid Bacteria and Resistance to Environmental Stress. *J Biosci Bioeng* **106**: 381–386.
- Laganà, P., Caruso, G., Corsi, I., Bergami, E., Venuti, V., Majolino, D., et al. (2019) Do plastics serve as a possible vector for the spread of antibiotic resistance? First insights from bacteria associated to a polystyrene piece from King George Island (Antarctica). *Int J Hyg Environ Health* **222**: 89–100.
- Lamb, J.B., Willis, B.L., Fiorenza, E.A., Couch, C.S., Howard, R., Rader, D.N., et al. (2018) Plastic waste associated with disease on coral reefs. *Science* **359**: 460–462.
- Lambert, S. and Wagner, M. (2016) Characterisation of nanoplastics during the degradation of polystyrene. *Chemosphere* **145**: 265–268.
- Lebreton, L.C.M., van der Zwet, J., Damsteeg, J.-W., Slat, B., Andrady, A., and Reisser, J. (2017) River plastic emissions to the world’s oceans. *Nat Commun* **8**: 15611.
- Li, W.C., Tse, H.F., and Fok, L. (2016) Plastic waste in the marine environment: A review of sources, occurrence and effects. *Sci Total Environ* **566–567**: 333–349.
- Liddel, H.G. and Scott, R. A Greek-English Lexicon.
- Lithner, D., Larsson, Å., and Dave, G. (2011) Environmental and health hazard ranking and assessment of plastic polymers based on chemical composition. *Sci Total Environ* **409**: 3309–3324.
- Liu, J., Martinez-Corral, R., Prindle, A., Lee, D.D., Larkin, J., Gabalda-Sagarra, M., et al. (2017) Coupling between distant biofilms and emergence of nutrient time-sharing. *Science* **356**: 638–642.
- Lobelle, D. and Cunliffe, M. (2011) Early microbial biofilm formation on marine plastic debris. *Mar Pollut Bull* **62**: 197–200.
- Lusher, A.L., Welden, N.A., Sobral, P., and Cole, M. (2017) Sampling, isolating and identifying microplastics ingested by fish and invertebrates. *Anal Methods* **9**: 1346–1360.

- Mackintosh, C.E., Maldonado, J., Hongwu, J., Hoover, N., Chong, A., Ikonomou, M.G., and Gobas, F.A.P.C. (2004) Distribution of phthalate esters in a marine aquatic food web: comparison to polychlorinated biphenyls. *Environ Sci Technol* **38**: 2011–2020.
- Molin, S. and Tolker-Nielsen, T. (2003) Gene transfer occurs with enhanced efficiency in biofilms and induces enhanced stabilisation of the biofilm structure. *Curr Opin Biotechnol* **14**: 255–261.
- Moore, E., Lyday, S., Roletto, J., Litle, K., Parrish, J.K., Nevins, H., et al. (2009) Entanglements of marine mammals and seabirds in central California and the north-west coast of the United States 2001–2005. *Mar Pollut Bull* **58**: 1045–1051.
- Moser, M.L. and Lee, D.S. (1992) A Fourteen-Year Survey of Plastic Ingestion by Western North Atlantic Seabirds. *Colon Waterbirds* **15**: 83–94.
- Muthukrishnan, T., Al Khaburi, M., and Abed, R.M.M. (2019) Fouling Microbial Communities on Plastics Compared with Wood and Steel: Are They Substrate- or Location-Specific? *Microb Ecol* **78**: 361–374.
- Net, S., Sempéré, R., Delmont, A., Paluselli, A., and Ouddane, B. (2015) Occurrence, Fate, Behavior and Ecotoxicological State of Phthalates in Different Environmental Matrices. *Environ Sci Technol* **49**: 4019–4035.
- Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2018) Environmental Factors Support the Formation of Specific Bacterial Assemblages on Microplastics. *Front Microbiol* **8**: 2709.
- Oberbeckmann, S., Löder, M.G.J., and Labrenz, M. (2015) Marine microplastic-associated biofilms—a review. *Environ Chem* **12**: 551–562.
- Oberbeckmann, S., Loeder, M.G.J., Gerdts, G., and Osborn, A.M. (2014) Spatial and seasonal variation in diversity and structure of microbial biofilms on marine plastics in Northern European waters. *FEMS Microbiol Ecol* **90**: 478–492.
- Oberbeckmann, S., Osborn, A.M., and Duhaime, M.B. (2016) Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. *PLoS One* **11**: e0159289.
- Ogonowski, M., Motiei, A., Ininbergs, K., Hell, E., Gerdes, Z., Udekwu, K.I., et al. (2018) Evidence for selective bacterial community structuring on microplastics. *Environ Microbiol* **20**: 2796–2808.
- Ostle, C., Thompson, R.C., Broughton, D., Gregory, L., Wootton, M., and Johns, D.G. (2019) The rise in ocean plastics evidenced from a 60-year time series. *Nat Commun* **10**: 1622.
- Paluselli, A., Fauvelle, V., Galgani, F., and Sempéré, R. (2018) Phthalate Release from Plastic Fragments and Degradation in Seawater. *Environ Sci Technol* **53**: 166–175.
- Peng, G., Bellerby, R., Zhang, F., Sun, X., and Li, D. (2020) The ocean's ultimate trashcan: Hadal trenches as major depositories for plastic pollution. *Water Res* **168**: 115121.
- PlasticsEurope (2019). Plastics - the Facts 2019
- Porter, A., Lyons, B.P., Galloway, T.S., and Lewis, C. (2018) Role of Marine Snows in Microplastic Fate and Bioavailability. *Environ Sci Technol* **52**: 7111–7119.
- Reisser, J., Shaw, J., Hallegraeff, G., Proietti, M., Barnes, D.K.A., Thums, M., et al. (2014) Millimeter-Sized Marine Plastics: A New Pelagic Habitat for Microorganisms and Invertebrates. *PLoS One* **9**: e100289.
- Rochman, C.M., Hoh, E., Kurobe, T., and Teh, S.J. (2013) Ingested plastic transfers hazardous chemicals to fish and induces hepatic stress. *Sci Rep* **3**: 3263.
- Romera-Castillo, C., Pinto, M., Langer, T.M., Álvarez-Salgado, X.A., and Herndl, G.J. (2018) Dissolved organic carbon leaching from plastics stimulates microbial activity in the ocean. *Nat Commun* **9**: 1–7.
- Schuyler, Q., Hardesty, B.D., Wilcox, C., and Townsend, K. (2014) Global Analysis of Anthropogenic Debris Ingestion by Sea Turtles. *Conserv Biol* **28**: 129–139.
- Seeley, M.E., Song, B., Passie, R., and Hale, R.C. (2020) Microplastics affect sedimentary microbial communities and nitrogen cycling. *Nat Commun* **11**: 1–10.
- Shah, A.A., Hasan, F., Hameed, A., and Ahmed, S. (2008) Biological degradation of plastics: a

- comprehensive review. *Biotechnol Adv* **26**: 246–65.
- Sivan, A. (2011) New perspectives in plastic biodegradation. *Curr Opin Biotechnol* **22**: 422–426.
- Sudhakar, M., Doble, M., Murthy, P.S., and Venkatesan, R. (2008) Marine microbe-mediated biodegradation of low- and high-density polyethylenes. *Int Biodeterior Biodegradation* **61**: 203–213.
- Tanaka, K., Takada, H., Yamashita, R., Mizukawa, K., Fukuwaka, M., and Watanuki, Y. (2013) Accumulation of plastic-derived chemicals in tissues of seabirds ingesting marine plastics. *Mar Pollut Bull* **69**: 219–222.
- Taylor, G.T., Zheng, D., Lee, M., Troy, P.J., Gyananath, G., and Sharma, S.K. (1997) Influence of surface properties on accumulation of conditioning films and marine bacteria on substrata exposed to oligotrophic waters. *Biofouling* **11**: 31–57.
- De Tender, C., Devriese, L.I., Haegeman, A., Maes, S., Vangeyte, J., Cattrijse, A., et al. (2017) Temporal dynamics of bacterial and fungal colonization on plastic debris in the North Sea. *Environ Sci Technol* **51**: 7350–7360.
- Tetu, S.G., Sarker, I., Schrameyer, V., Pickford, R., Elbourne, L.D.H., Moore, L.R., and Paulsen, I.T. (2019) Plastic leachates impair growth and oxygen production in *Prochlorococcus*, the ocean's most abundant photosynthetic bacteria. *Commun Biol* **2**: 1–9.
- Teuten, E.L., Rowland, S.J., Galloway, T.S., and Thompson, R.C. (2007) Potential for Plastics to Transport Hydrophobic Contaminants. *Environ Sci Technol* **41**: 7759–7764.
- Venrick, E.L., Backman, T.W., Bartram, W.C., Platt, C.J., Thornhill, M.S., and Yates, R.E. (1973) Man-made Objects on the Surface of the Central North Pacific Ocean. *Nature* **241**: 271.
- Viršek, M.K., Lovšin, M.N., Koren, Š., Kržan, A., and Peterlin, M. (2017) Microplastics as a vector for the transport of the bacterial fish pathogen species *Aeromonas salmonicida*. *Mar Pollut Bull* **125**: 301–309.
- Wilcox, C., Hardesty, B.D., and Law, K.L. (2020) Abundance of Floating Plastic Particles Is Increasing in the Western North Atlantic Ocean. *Environ Sci Technol* **54**: 790–796.
- Wilcox, C., Puckridge, M., Schuyler, Q.A., Townsend, K., and Hardesty, B.D. (2018) A quantitative analysis linking sea turtle mortality and plastic debris ingestion. *Sci Rep* **8**: 12536.
- Woodall, L.C., Sanchez-Vidal, A., Canals, M., Paterson, G.L.J., Coppock, R., Sleight, V., et al. (2014) The deep sea is a major sink for microplastic debris. *R Soc Open Sci* **1**: 140317.
- Wright, S.L., Thompson, R.C., and Galloway, T.S. (2013) The physical impacts of microplastics on marine organisms: a review. *Environ Pollut* **178**: 483–492.
- Yang, Y., Liu, G., Song, W., Ye, C., Lin, H., Li, Z., and Liu, W. (2019) Plastics in the marine environment are reservoirs for antibiotic and metal resistance genes. *Environ Int* **123**: 79–86.
- Yoshida, S., Hiraga, K., Takehana, T., Taniguchi, I., Yamaji, H., Maeda, Y., et al. (2016) A bacterium that degrades and assimilates poly(ethylene terephthalate). *Science* **351**: 1196–1199.
- Zettler, E.R., Mincer, T.J., and Amaral-Zettler, L. (2013) Life in the “plastisphere”: Microbial communities on plastic marine debris. *Environ Sci Technol* **47**: 7137–7146.

CHAPTER I

The composition of bacterial communities associated with plastic biofilms differs between different polymers and stages of biofilm succession

Maria Pinto^{1,2*}, Teresa M. Langer¹, Thorsten Huffer^{2,3}, Thilo Hofmann^{2,3}, Gerhard J. Herndl^{1,2,4}

¹ Department of Limnology and Bio-Oceanography, Center of Functional Ecology, University of Vienna, Vienna, Austria

² Research Platform 'Plastics in the Environment and Society', University of Vienna, Vienna, Austria

³ Department of Environmental Geosciences, Center for Microbiology and Environmental Systems Science, University of Vienna, Vienna, Austria

⁴ NIOZ, Department of Marine Microbiology and Biogeochemistry, Royal Netherlands Institute for Sea Research, Utrecht University, Den Burg, The Netherlands

*Corresponding author

Email: maria.pinto@univie.ac.at

Published in PLOS ONE

Abstract

Once in the ocean, plastics are rapidly colonized by complex microbial communities. Factors affecting the development and composition of these communities are still poorly understood. Additionally, whether there are plastic-type specific communities developing on different plastics remains enigmatic. We determined the development and succession of bacterial communities on different plastics under ambient and dim light conditions in the coastal Northern Adriatic over the course of two months using scanning electron microscopy and 16S rRNA gene analyses. Plastics used were low- and high-density polyethylene (LDPE and HDPE, respectively), polypropylene (PP) and polyvinyl chloride with two typical additives (PVC DEHP and PVC DINP). The bacterial communities developing on the plastics clustered in two groups; one group was found on PVC and the other group on all the other plastics and on glass, which was used as an inert control. Specific bacterial taxa were found on specific surfaces in essentially all stages of biofilm development and in both ambient and dim light conditions. Differences in bacterial community composition between the different plastics and light exposures were stronger after an incubation period of one week than at the later stages of the incubation. Under both ambient and dim light conditions, one part of the bacterial community was common on all plastic types, especially in later stages of the biofilm development, with families such as *Flavobacteriaceae*, *Rhodobacteraceae*, *Planctomycetaceae* and *Phyllobacteriaceae* presenting relatively high relative abundances on all surfaces. Another part of the bacterial community was plastic-type specific. The plastic-type specific fraction was variable among the different plastic types and was more abundant after one week of incubation than at later stages of the succession.

Introduction

Between 4.8 and 12.7 million metric tons of plastic are estimated to enter the ocean every year (Jambeck *et al.*, 2015). When plastics enter aquatic systems, a microbial biofilm rapidly develops on the plastic surface. The microbial community composition of this biofilm is typically different from that in the ambient water (Lobelle and Cunliffe, 2011) and might play an important role in the fate of plastics in the ocean (Rummel *et al.*, 2017). Biofilm development or biofouling can cause previously positively buoyant plastics to eventually sink into the water column (Van Cauwenberghe *et al.*, 2013; Fazey and Ryan, 2016). Also, the

biofilm might include individual microbial species or consortia capable of degrading plastics (Debroas *et al.*, 2017). Also, invasive and pathogenic species might be transported over large distances by plastic debris (Kirstein *et al.*, 2016). The composition of these plastic associated microbial communities is affected by spatial and temporal variations in environmental parameters (Amaral-Zettler *et al.*, 2015; Oberbeckmann *et al.*, 2016). Comparative studies, however, following the development of the microbial biofilm on different plastic types in the same environment are scarce (Oberbeckmann *et al.*, 2014, 2016).

Studies on the early biofilm formation (9-72h) on plastic surfaces have reported a community succession with typical biofilm primary colonizers of the *Proteobacteria* phylum, such as the genera *Alteromonas* (Gammaproteobacteria class) and *Roseobacter* (Alphaproteobacteria class) (Dang and Lovell, 2000; Lee *et al.*, 2008), followed by members of the phyla *Bacteroidetes*, *Acidobacteria*, *Actinobacteria*, *Cyanobacteria*, *Firmicutes*, *Planctomycetes* and *Verrucomicrobia* (Salta *et al.*, 2013).

Zettler *et al.* (2013) used the term “plastisphere” to describe the specific microbial community developing on plastics collected in the surface waters of the North Atlantic and comprising microbes different from those found in the ambient water. Since then, several studies reported the existence of this plastic-specific microbial community in aquatic systems (McCormick *et al.*, 2016; De Tender *et al.*, 2017; Hoellein *et al.*, 2017; Kettner *et al.*, 2017; Harrison *et al.*, 2018; Kirstein *et al.*, 2018; Miao *et al.*, 2019). For instance, the fungal community composition of the biofilm developing on submerged wood differed from that on two plastic types (polyethylene-PE and polypropylene-PP) (Kettner *et al.*, 2017). Also the bacterial community developing on PE sheets differed from that developing on a dolly rope at the seafloor (De Tender *et al.*, 2017). Furthermore, a recent study using polystyrene (PS), PP and PE showed that the bacterial communities developing on the different plastic polymers were distinct from each other after two weeks and different from the communities developing on glass and cellulose (Ogonowski *et al.*, 2018). This suggests that the type of polymers also influences the microbial community composition of the plastic associated biofilm.

It appears, however, that a specific plastic community does not always develop. Oberbeckmann *et al.* (2016) found that a biofilm with a similar bacterial community composition was established on both PET bottles and glass slides incubated in three different seasons and locations. This suggests that typical biofouling processes were the main drivers for the biofilm formation rather than the type of surface. More recently, a study has shown that plastic-specific microbial communities only develop under particular environmental

conditions (Oberbeckmann *et al.*, 2018). Nevertheless, even in cases where no major differences in the microbial community composition between different surfaces were found, plastic-specific taxa were identified. Examples of plastic-specific taxa are members of the families *Alcanivoracaceae* and *Cryomorphaceae* being specifically enriched on PET surfaces in comparison to glass (Oberbeckmann *et al.*, 2016), and members of the families *Hyphomonadaceae* and *Erythrobacteraceae* dominating on PE and PS surfaces over wood pellets (Oberbeckmann *et al.*, 2018). The reasons for the occasional preferential attachment of certain taxa to plastic or specific plastic types remain enigmatic. Also, the role of environmental factors and physico-chemical properties of the plastics on biofilm formation is largely unknown.

Solar radiation has direct and indirect effects on marine microbial communities, usually suppressing bacterial activity and growth (Elasri and Miller, 1999; Davidson and Belbin, 2002). In surface waters, direct effects result from the deleterious effects of ultraviolet (UV) radiation on DNA, proteins and other macromolecules (World Health Organization, 1994; Benner and Biddanda, 1998). Indirect effects of solar radiation are UV-induced changes in the bioavailability of near-surface dissolved organic matter (DOM) due to photochemical transformations (Herndl *et al.*, 1993; Obernosterer *et al.*, 1999). Bacterial communities in marine biofilms are impaired by solar radiation (Herndl *et al.*, 1993; Davidson and Belbin, 2002). Partial plastic photo-oxidation typically precedes biotic plastic degradation by changing surface properties of the polymers such as roughness, topography and chemistry (Rummel *et al.*, 2017). Hence, one might assume that the development of biofouling communities on marine plastics is also affected by solar radiation.

Solar radiation, particularly UV, generates free radicals during plastic photo-degradation processes and thereby changes the polymer properties (Singh and Sharma, 2008) which, in turn, facilitates biodegradation processes (for a review on biological degradation of plastics see Shah *et al.*, 2008). A recent study shows that plastics leach dissolved organic carbon into the surrounding seawater, regardless whether exposed to solar radiation or kept in the dark, stimulating heterotrophic microbial activity (Romera-Castillo *et al.*, 2018). Furthermore, Royer *et al.* (2018) reported the production of methane and ethylene if PE is exposed to natural solar radiation. Hence, solar radiation is likely affecting biofilm development directly via its effect on cellular constituents and indirectly by its effect on the plastics and organic matter.

In this study we addressed the question whether there is a general “plastisphere”, i.e., a plastic-associated microbial community independent of the plastic type, or whether there is a plastic type-specific community. Furthermore, we studied how biofilm successional stages and exposure to solar radiation might affect these plastic-associated microbial communities.

Material and Methods

In situ incubations of different plastics at the sea surface

Virgin polyvinylchloride (PVC) pellets with approximately 5 mm diameter, containing two plasticizers, di(2-ethylhexyl) phthalate (DEHP) and di-isononyl phthalate (DINP), 4 cm² sized pieces of virgin polypropylene (PP), LDPE and HDPE, with approximately 0.5 mm thickness, and glass slides of 1 cm², with approximately 1 mm thickness, were mounted on a floating frame (Fig. S1) in the Northern Adriatic, approximately 500m off the coast of Rovinj, Croatia (Fig. S2) over a three-month period (November 2016 - January 2017). LDPE, PP and PVC were purchased from Goodfellow Cambridge Ltd., while the HDPE consisted of pieces cut from an empty sodium chloride chemical container (Sigma-Aldrich Co. LLC). The glass pieces were cut from microscope slides (Carl Roth GmbH) and used as an inert control. Prior to incubating the plastics on the floating frame, all plastic and glass pieces were rinsed with 70% ethanol and Milli-Q water.

To assess the influence of solar radiation on the development and structure of the biofilm community, two different treatments were established. One set of plastic types and glass slides were exposed to the full range of solar radiation, while the other set of plastic surfaces and glass slides were held under dim light conditions. All the plastics and the glass slides were mounted on a custom-made rectangular floating frame of 1.5m x 0.5m (for a scheme see Fig. S1). The frame supported four metal wires where the plastic pieces and the glass slides were attached by a thin nylon string thread through a small hole on the tip of each piece of plastics or glass. To study microbes from approximately the same surface area of each material, we mounted four 1 cm² glass slides on each string. These four pieces were regarded and treated as one single sample. For all the PVC samples, 10 pellets were considered as one sample. For the other plastics, one piece was considered as one sample. The different plastics and glass slides were equally distributed between the metal wires, with a spacing of around 8 cm between them. To achieve dim light conditions, two of the four wires supported two grey

tubes (10 cm inner diameter) that shielded off the plastics and glass slides from direct solar radiation. The metal wire ran through the center of each tube and care was taken to ensure that the different surfaces did not touch the tube walls or each other. The tubes were open on both sides to allow water exchange and maintaining dim light conditions. The frame was connected to a single main float and therefore, oriented itself to the direction of the currents, allowing constant water flow through the tubes.

Three samples of each plastic type and glass from each treatment were collected after one week (November 2016), one month (December 2016) and two months (January 2017) of incubation. To remove organisms not part of the biofilm, samples were carefully rinsed 4 times with 0.2 μm freshly filtered seawater. Two of the three samples collected from the same wire were immediately frozen at -80°C for DNA extraction. The third sample was immersed in 2% glutaraldehyde for 10 min and then stored at -80°C for scanning electron microscopy (SEM). For comparison, surface water samples were also taken in close vicinity to the floating frame at each sampling day. Seawater was filtered in duplicates (two times two L) onto 0.2 μm pore-size Millipore (Merck KGaA, 47 mm filter diameter) GTTP filters and stored at -80°C for DNA extraction. Additionally, plastics from the dark treatment were also collected to measure DEHP and DINP concentrations in the plastics. Additive measurements were done as described in the Supporting Information (S1).

DNA extraction and amplification

DNA from plastic and glass pieces and filters (for ambient water) was extracted using a modified bead-beating approach in combination with the Puregene Tissue DNA extraction kit (Qiagen, Valencia, CA) (as described in S2 of the supporting information) (Debeljak *et al.*, 2017). To compare the bacterial community of the biofilm with that of the ambient water, PCR amplification of the 16S rRNA V3-V4 hypervariable region was used with the primer pair 341F (5'- CCT ACG GGN GGC WGC AG - 3') and 802R (5'- TAC HVG GGT ATC TAA TCC - 3') resulting in fragments of ~460 bp. Each PCR was performed in a total volume of 52 μL containing 25 μL Library Amplification Ready Mix 2xMM (Kapa Biosystems), 1 μL of each 25 μM primer, 23 μL of sterile water and 2 μL of extracted DNA. Amplification was done on a Mastercycler Pro (Eppendorf AG, Germany). The conditions consisted of an initial denaturation at 95°C for 3 min, followed by 20 cycles at 98°C for 20 s, at 56°C for 30 s and at 72°C for 30 s, and a final elongation at 72°C for 5 min.

PCR products were then purified in a 96-well plate using the Agencourt® AMPure® XP Purification kit and protocol (Beckman Coulter Life Sciences). These purified PCR products were barcoded and an additional 10-cycle PCR was done, followed by paired-end next-generation amplicon sequencing (2 x 250 bp) using Illumina MiSeq technology at Microsynth AG, Switzerland. All raw sequence files have been submitted to the NCBI Sequence Read Archive (SRA) database (BioProject: PRJNA515271).

Processing of sequence data

Sequence data were processed with Usearch tools by merging paired reads, quality filtering (max. error 1 in 100 nucleotides), eliminating singletons, chimera filtering, mapping, and operational taxonomic unit (OTU) clustering. OTU clustering was performed using the UPARSE OTU clustering Algorithm with USEARCH command lines (Edgar, 2013). For taxonomy assignment blastn and the SILVA_123_SSURef reference database were used (97% similarity between query and target sequences as threshold). Furthermore, the merging of taxonomy and OTU reads was done in Python. After quality filtering and phylogenetic classification, samples with less than 1000 reads were excluded from further analysis (one PVC DINP sample of the dim light treatment collected after one month and one after two months of incubation, one LDPE sample of the dim light treatment and one seawater sample both collected after two months of incubation).

Phylogenetic diversity analysis

Shannon and Simpson diversity and OTU richness indexes were calculated through the iNext package in R (Hsieh *et al.*, 2016) using coverage based rarefaction to a coverage of 97%. Analysis of variance (ANOVA) for each index was performed to identify differences between surface type, time points and treatments (n=74, degree of replication=2). To decipher differences in bacterial community composition between the different plastic types and seawater, post-hoc Tukey tests for each index were performed.

Analysis of the bacterial community composition

OTU read numbers per sample were converted into relative abundances. Permutational multivariate analysis of variance (PERMANOVA) was used to compare the community composition between different surface types, time points and treatments (n=74, degree of replication=2). To understand whether the exposure treatment or the type of

polymer influenced the presence and relative abundance of specific bacterial taxa, we performed PERMANOVA analysis using the Jaccard index and Bray-Curtis dissimilarity as distance measurements, respectively. The seawater samples were excluded from these analyses.

Non-Metric Multidimensional Scaling (NMDS) with Bray-Curtis Dissimilarity as a distance measurement was conducted for a visual representation of the similarity of the bacterial community composition between samples. To determine differences in the community composition of heterotrophic bacteria between the treatments and plastic types, the PERMANOVA and NMDS analyses were repeated after excluding *Cyanobacteria*.

Determining surface discrimination of specific bacterial taxa

To identify bacterial taxa discriminating specific surfaces, we performed a linear discriminant analysis size effect (LEfSe) for each month. The analysis was performed on the online Galaxy framework. Treatment was used as a subclass in the analysis to assure that differences between the surface types were consistent within each treatment. The default settings were used for all other parameters, for data formatting and LDA effect size analysis. Individual LEfSe analyses were also performed to identify bacterial families discriminating for each of the plastics compared to glass. Treatment was also used as a subclass in these analyses, but due to the large difference in relative abundance of the different families between the ambient and dim light treatments growing on the same surface, the alpha value for the factorial Kruskal-Wallis test among classes was set to 0.5. The default settings were used for all other parameters.

To determine the most abundant bacterial families discriminating a specific plastic type in comparison to glass, we applied the following formula for all families with a relative abundance of > 5% of the total community in at least one of the samples:

$$i_F = \left(\frac{P_F - G_F}{P_F + G_F} \right) * 100$$

Where P_F is the relative abundance of family F on plastic type P and G_F is the relative abundance of family F on glass. i_F , the discrimination factor of family F , was calculated separately for each treatment and each month. All non-identified cyanobacterial families were grouped in one single *Cyanobacteria* group.

Statistical analysis

All statistical tests and plots were conducted using R Studio Version 1.0.153 (RStudio, Inc. 2009-2017) unless stated otherwise.

SEM analysis

SEM samples were dehydrated in an ethanol dilution series of 30%, 50%, 70%, 80%, 90%, 95% each for 10 min and three times in 100% absolute ethanol for 10 min. The dehydrated samples were CO₂ critical point dried with a CPD 300 auto critical point dryer (Leica Microsystems). The dried pieces were gold-coated using a JFC-2300HR sputter coater (JEOL Ltd.) for 80s. Pictures were taken using a secondary electron detector with a JEOL JSM-IT300 scanning electron microscope at 150x, 450x, 2000x magnification, 15kV acceleration voltage in ultra-high vacuum.

Results

After one week of incubation, the surface of PVCs exhibited a more developed biofilm in both the ambient and dim light treatment compared to the other plastics and the glass slides (Fig. S3, A-F), with a larger area of their surface covered by a biofilm matrix and individual cells. After two months of incubation, all plastics and glass surfaces were patchily covered with a biofilm (Fig. S3, A-F). Diatoms were found on all plastics of the ambient light treatment throughout the incubation period. Although diatoms were also found in the biofilm on all the plastic and glass surfaces even under dim light conditions, they appeared to be considerably less abundant in the latter (Fig. S3, A-F). The concentrations of DINP in the PVC DINP pellets ranged between 33% and 37% (w/w) over the incubation period, while the concentration of DEHP in the PVC DEHP pellets was around 41% throughout the incubation. LDPE, HDPE and PP did not contain measurable phthalate concentrations.

A total of 4823 OTUs was classified and used for comparative analyses, from which 3303 OTUs were present after one week of incubation, 4277 OTUs after one month and 3921 OTUs after two months of the incubation. OTU richness and diversity varied among light treatments, sampling time and surface type (Table S1). In the ambient light treatment, OTU diversity and richness of the biofilm communities were similar among all plastic surfaces and glass. In the dim light treatment, both PVCs exhibited a high OTU richness but low diversity in all sampling months. PP and glass exhibited the highest bacterial diversity after one week and

one month of incubation, indicated by both the Shannon and Simpson index, but after two months of incubation LDPE and HDPE exhibited a higher bacterial diversity than the other surfaces (Fig. 1, Table S2-S4).

OTU richness and diversity were significantly higher in the dim than the ambient light treatment (Table S1) over the two months of incubation (PERMANOVA: $F=3.176$, $p=0.001$) (Fig. 1).

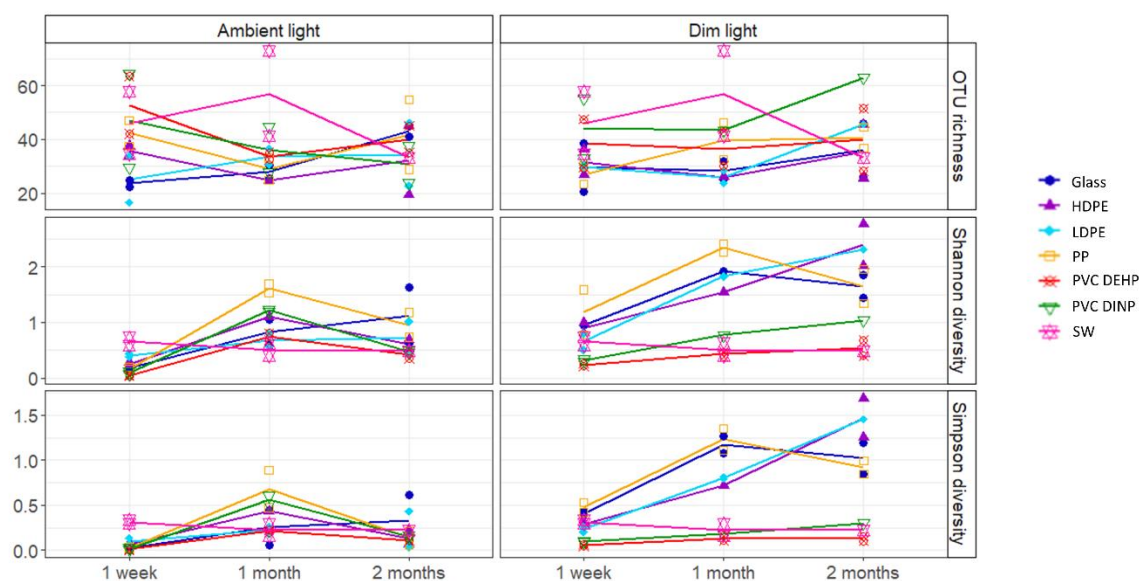


Fig. 1 – OTU richness and diversity of the bacterial community of the biofilm of all plastics, glass and water samples after one week, one month and two months of incubation. Each symbol represents a sample. Duplicate samples from the individual surfaces and seawater were collected except LDPE after one month incubation under dim light conditions, seawater after two months incubation and PVC DINP under dim light conditions after one and two months of incubation. The lines connect the middle value between the duplicates of the different sampling points. In cases where there were no duplicates, the lines connect to the value of the single sample.

Bacterial community composition

The composition of the bacterial community differed between the type of surface (i.e., different plastic types and glass) (PERMANOVA: $F=16.11$, $p=0.001$), light regime (PERMANOVA: $F=39.33$, $p=0.001$) and duration of incubation (PERMANOVA: $F=48.07$, $p=0.001$) when considering both, the entire bacterial community and solely the heterotrophic bacterial community (Table S5). The influence of exposure and polymer type on the bacterial community composition was significant (p -values < 0.05) after one week, one month and two months of incubation, both in terms of presence/absence of organisms (Table S6) and their relative abundances (Table S7). Even though we only had duplicate data per sampling, the NMDS analysis (Fig. 2) and the relative abundances of the most abundant families (Fig. 3)

indicate a clustering of the samples in three groups with different bacterial community composition. The community developing on the PVCs formed a distinct group and the communities developing on the other surfaces (glass, LDPE, HDPE and PP) formed another cluster. This clustering was stronger after one week of incubation and overall, in the dim light treatment. After one month of incubation all samples from the ambient light treatment exhibited relatively similar communities (Figs. 2, 3).

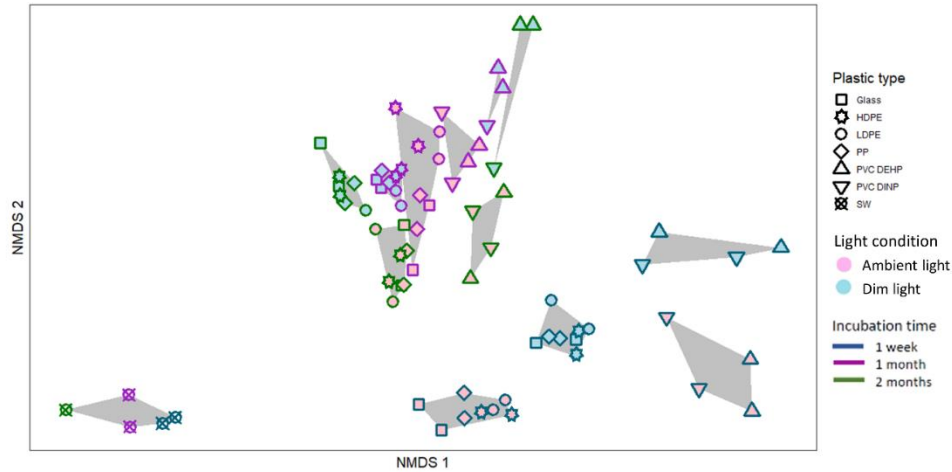


Fig. 2 – NMDS representation of the similarity between the bacterial community composition of the biofilm on different surfaces and seawater. Bray-Curtis Dissimilarity was used as the distance measurement. Each point represents one sample. The grey polygons connect groups of samples from each time point exposed to the same light conditions.

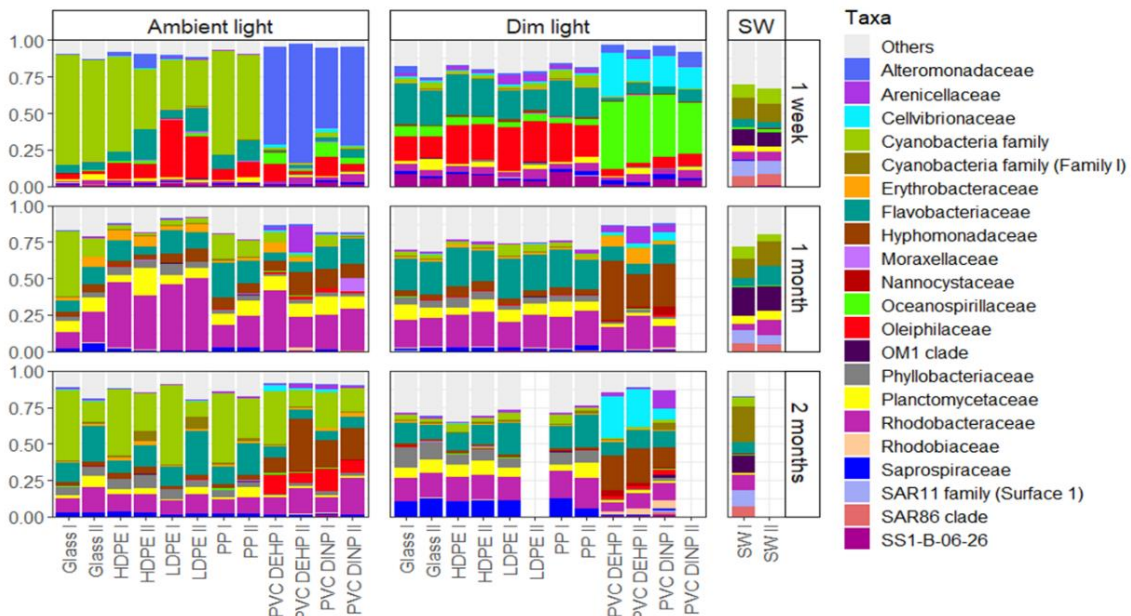


Fig. 3 – Relative abundances of the bacterial families representing at least 5% of the total bacterial community in at least one sample. Families representing < 5% of the total bacterial community were grouped into the category “Others”.

Moreover, all the bacterial communities associated with plastic and glass surfaces were different from that of the ambient water (Fig. 2, Fig. S4).

After one and two months of incubation, the communities developing on LDPE, HDPE, PP and glass were more different from each other when exposed to ambient solar radiation than under dim light conditions (Fig. 2). This difference appeared to be diminished, however, when considering only the heterotrophic bacterial community (Fig. S4).

Community composition after one week

Differences between the bacterial communities associated with the PVC and the other plastic and glass surfaces were most pronounced after one week of incubation under both dim and ambient light conditions, and decreased with increasing duration of the incubation (Fig. 3). After one week of incubation, PVC surfaces were highly dominated by families of Gammaproteobacteria, mainly *Alteromonadaceae*, *Cellvibrionaceae* and *Oceanospirillaceae*. The other plastic surfaces were mainly dominated by members of the phylum Cyanobacteria and of the families *Flavobacteriaceae* and *Oleiphilaceae* (Fig. 3).

Under ambient light conditions, the community associated with the PVCs was dominated by one OTU affiliated to the genus *Alteromonas* with relative abundances ranging from 54% to 81% of the total 16S rRNA gene abundance (Fig. S5). Under dim light conditions, this OTU was present in much lower relative abundance on PVC reaching at most 7% in one of the PVC DINPs. On all other surfaces, this OTU was present only in very low relative abundances. These non-PVC surfaces were dominated by Cyanobacteria reaching relative abundances of 75% of the total 16S rRNA gene abundance on glass slides, while an uncultured bacterium of the *Oleiphilus* genus showed a clear discrimination for LDPE with relative abundances of up to 39% of the total bacterial community (Fig. S5).

The bacterial community of the PVCs in the dim light treatment was dominated by four OTUs, two were affiliated with the family *Cellvibrionaceae* and two with the family *Oceanospirillaceae*. One of the *Cellvibrionaceae* OTUs, classified as the genus *Aestuariicela* (OTU 15), was relatively more abundant on the PVC DINP than on other surfaces (Fig. S5), with a relative abundance of approximately 1% of the total 16S rRNA gene. Nevertheless, all three families, *Oceanospirillaceae*, *Cellvibrionaceae* and *Alteromonadaceae*, exhibited a relatively higher abundance on PVCs than on glass in both light treatments (Fig. 4, Table S8). In contrast, most of the other families, including *Planctomycetaceae*, *Flavobacteriaceae*, *Cryomorphaceae* among many others, discriminated for glass over either one of the PVCs (Table S8). While families discriminating for both PVCs over glass were the same in both dim and ambient light treatments, families that discriminated for any of the other plastics (PEs and PP) over glass

were different between the dim and ambient light communities. *Oleiphilaceae* and *Arenicellaceae* families discriminated for LDPE, HDPE and PP over glass in both light treatments, while other families discriminated for one of the surfaces in only one of the treatments. For example, the *Alcanivoracaceae* family was relatively more abundant on the LDPE than on glass when exposed to dim light while when exposed to ambient light, discrimination for LDPE was not apparent (Fig. 4).

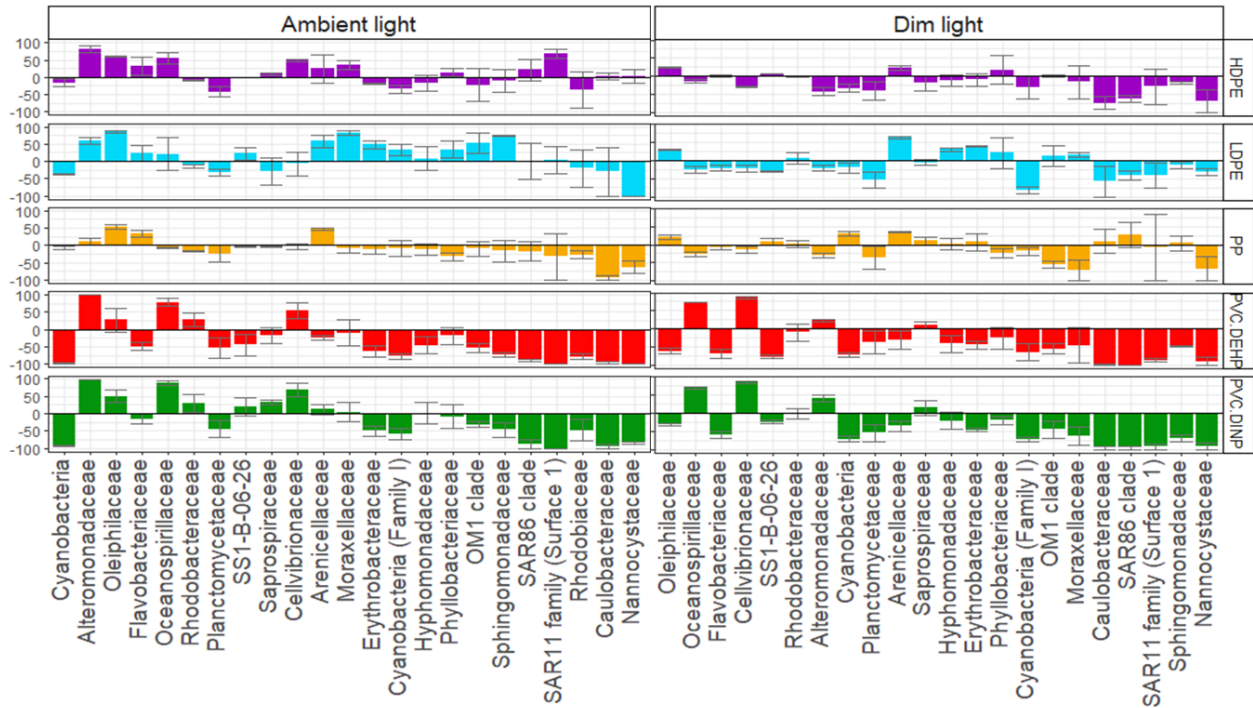


Fig. 4 – Values of i_F representing the discrimination of the most abundant bacterial families (with >5% relative abundance in at least one of the samples) for either one of the plastics or glass after one week under ambient and dim light conditions. Positive values indicate discrimination for a specific plastic type over glass, negative values indicate discrimination for glass over a specific plastic type. Bacterial families are ordered from high (left) to low (right) relative abundance. Total abundance was determined per treatment and time point. The LEfSe analysis identifying discriminating families of either glass or of any of the polymers after one week of incubation can be found in Table S8.

After one week, the phyla *Lentisphaerae* and *Actinobacteria* and the class *Deltaproteobacteria* were favoring glass against all other surfaces. The phyla *Flavobacteria* and *Verrucomicrobiae* significantly discriminated for PP and the order *Sphingomonadales* and the family *Oleiphilaceae* for LDPE (Fig. 5).

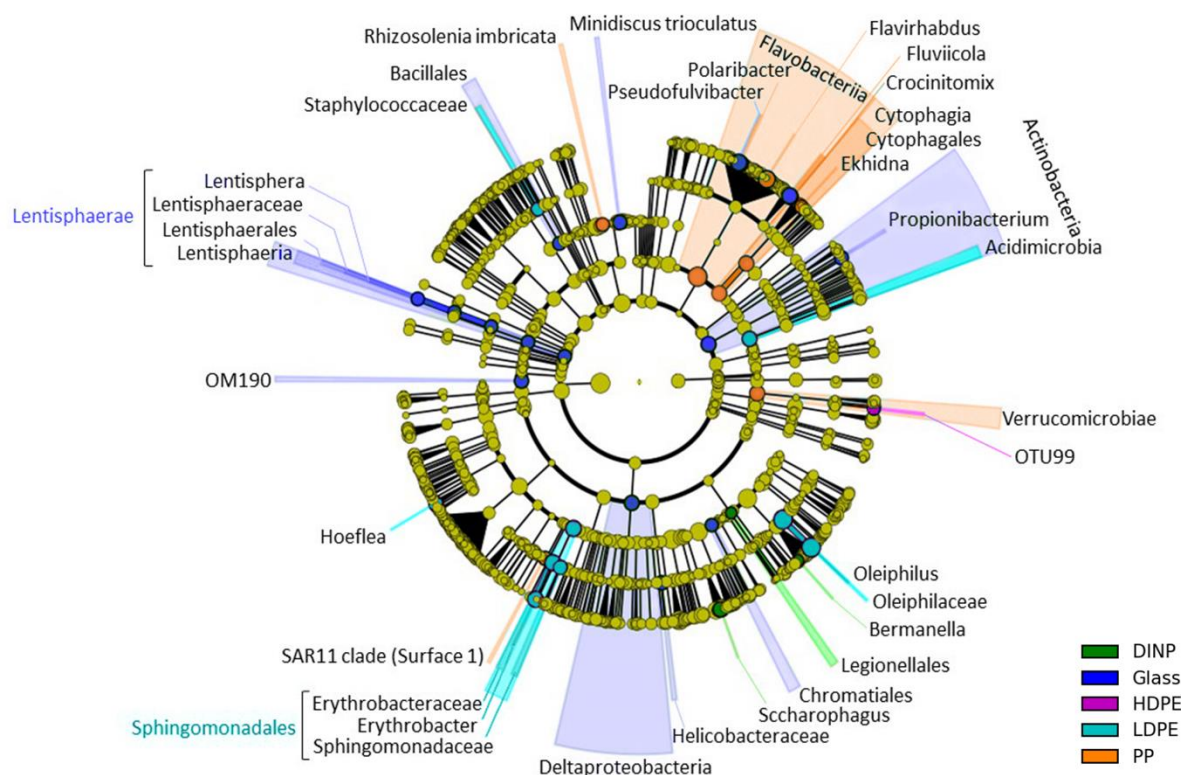


Fig. 5 – Taxa that discriminated for one of the surfaces over all other surfaces considering both light treatments and determined by the discriminant linear analysis (LEfSe) after one week of incubation. The results of the LEfSe analysis can be found in Table S11.

Community composition after one month

After one month of incubation, differences between the community compositions among the different surfaces decreased, with the families *Hyphomonadaceae*, *Flavobacteriaceae*, *Rhodobacteraceae*, *Planctomycetaceae* dominating all surfaces.

Additionally, Cyanobacteria were relatively abundant on glass and PP in the ambient light treatment. Both LDPE and HDPE exhibited relatively high abundances of OTUs affiliated with the genus *Loktanella* (OTU 9) and *Ruegeria* (OTU 12) (Fig. S5). The relatively abundant *Rhodobacteraceae* family discriminated for HDPE and *Sphingomonadaceae* for LDPE over glass in both light treatments, while all the other families showed no discrimination for either HDPE, LDPE or PP in comparison to glass (Fig. S6A, Table S9). Contrary to the previous month, *Oleiphilaceae* discriminated for PVC DINP instead of LDPE (Fig. S7A). Some fairly abundant families, however, did show discrimination for glass in only one of the light treatments over one of the three plastics. For instance, the families *Saprospiraceae* and *Rubritaleaceae* discriminated for glass over LDPE in the ambient light treatment (Fig. S7A). Some families, however, still showed a strong discrimination for the PVCs over glass and *vice versa*. From the most abundant families, *Hyphomonadaceae*, *Oleiphilaceae*, and *Cellvibrionaceae* discriminated for both types of PVC over glass and additionally, *Alteromonadaceae* and

Sphingomonadaceae also discriminated for PVC DEHP over glass. *Phyllobacteriaceae*, *Saprospiraceae*, Cyanobacteria, the OM1 clade and *Thiotrichaceae* discriminated for glass over both PVCs (Fig. S6A, Table S9). Additionally, the OCS116 clade also discriminated for glass over PVC DEHP. The relatively abundant family *Rhodobacteraceae* discriminated for HDPE over glass (Table S9), especially in the ambient light treatment (Fig. S6A).

Community composition after two months

After two months of incubation, most of the taxa showing discrimination for a specific plastic type were relatively low in abundance, except for the abundant *Flavobacteria* discriminating for LDPE (Fig. S7B).

Under ambient and dim light conditions both PVCs exhibited a higher relative abundance of the family *Hyphomonadaceae* and a lower relative abundance of the family *Phyllobacteriaceae* than the other surfaces. On both PVCs in the dim light treatment, the family *Cellvibrionaceae* were more abundant than on the other surfaces (Fig. 3).

After two months of incubation, the families *Hyphomonadaceae* and *Oleiphilaceae* still discriminated for both PVCs over glass in both light treatments and, similar to after one month of incubation, *Cellvibrionaceae* and *Oceanospirillaceae* maintained the discrimination for PVC DEHP over glass (Fig. 3). The family *Nannocystaceae* discriminated for glass over HDPE and PP, and the family *Arenicillaceae* discriminated for glass over HDPE (Fig. S6B, Table S10).

Discussion

Role of plastic type in determining bacterial community composition

Apparently, the surface type has a stronger influence on the initial bacterial colonization and consequently, on the bacterial community composition, than on late successional stages (Figs. 2, 3). This is indicated by the more pronounced differences in bacterial community composition between polymer surfaces at the beginning of the incubation experiment than after one and two months of incubation (Figs. 2, 3). In the later successional stages of biofilm development, such as after one month and two months in our experiment, the bacterial community was likely more influenced by internal biofilm processes than by surface-related characteristics. The initial colonizers are in direct contact with the surface and hence are more likely to be influenced by its physico-chemical properties than bacteria embedded in an already developed biofilm.

Physico-chemical properties of surfaces, such as roughness, hydrophobicity, topography, surface free energy, charge and electrostatic interactions are known to influence the attachment of initial colonizers and biofilm development (Characklis and G, 1990; Donlan, 2002; Teughels *et al.*, 2006; Rummel *et al.*, 2017). Hydrophobicity has been shown to determine initial bacterial attachment, with bacteria preferentially attaching to more hydrophilic surfaces (Characklis and G, 1990; Donlan, 2002; Teughels *et al.*, 2006). Glass is highly hydrophilic compared to plastics, however, bacterial OTU richness and diversity of the communities developing on glass appear similar to those of plastics throughout our incubations (Fig. 1). Actually, in the dim light treatment after one week of incubation, the glass biofilm appears to exhibit a higher bacterial diversity than both PVCs (Fig. 1). Even though the bacterial biofilm was more developed on the PVCs after one week of incubation than on the other surfaces, this was not the case for the other plastic surfaces compared to glass. As we did not measure surface hydrophobicity, we cannot exclude that it might have influenced the biofilm bacterial community, however, our results suggest that there are other important factors affecting initial biofilm development on plastics.

When in contact with seawater, surfaces sorb organic and inorganic substances creating a conditioning layer that might attract or repel microorganisms (Rummel *et al.*, 2017). The chemical composition of this layer is influenced by the properties of the solid surface. Rochman *et al.* (Rochman *et al.*, 2013) found that HDPE, LDPE and PP sorbed higher concentrations of organic pollutants than PVC and PET over a 12-month period. It also appears that the chemical composition of this conditioning layer is more relevant for initial bacterial attachment than other surface-related properties such as roughness and hydrophobicity (Lorite *et al.*, 2011). The large differences in bacterial community composition after one week of incubation between the PVCs and the other surfaces might be an indication that differences in the chemical composition of the conditioning layer of the different surfaces play a selective role in the attachment of bacterial populations.

While OTU richness of the bacterial community on PVCs was higher than that of the other surface communities in both light treatments (Fig. 1), OTU diversity was lower. This high richness and low diversity can be explained by the presence of very dominant OTUs, such as the genus *Alteromonas* in the biofilm of both PVCs under ambient light conditions, and OTUs belonging to the *Cellvibrionaceae* and *Oceanospirillaceae* families in the biofilm under dim light conditions.

Phthalates, such as DINP and DEHP are known to impact bacterial growth and development (Staples *et al.*, 2009). Iwaki *et al.* (2012) found that bacteria closely related to the families *Alteromonadaceae* and *Oceanospirillaceae* were capable of growing on phthalates, while other bacterial taxa have been shown to be inhibited by certain phthalates (Staples *et al.*, 2009). These two families discriminated for the two PVCs over glass after one week of incubation and the latter family discriminated for PVC DEHP over glass throughout the entire duration of the experiment (Tables S8-S10). Thus, phthalates might act as a selection factor in the development of bacterial biofilms on PVCs (Kapanen *et al.*, 2007). This could also explain why the bacterial community composition in the PVC-associated biofilm remained different from that on glass even after one and two months of incubation (Fig. 2), with some bacterial taxa discriminating for either one of the surfaces (Fig. 4, Tables S8-S10). For example, relatively abundant taxa such as Cyanobacteria, and families *Phyllobacteriaceae*, *Planctomycetaceae* and *Saprospiraceae* showed a consistent discrimination for glass over PVC in almost all samples (Fig. 4, S6, Tables S8-S10). It has been suggested that surface properties are a selective factor for microbial biofilm initiation, hence surface degrading taxa are only selected during the initial successional stages of bacterial aggregate formation (Datta *et al.*, 2016). As the biofilm develops, the community is more structured via the dynamic interactions within the biofilm community, rather than by the selective pressure caused by the properties of the colonized surface (Datta *et al.*, 2016). This might explain the higher relative abundance of potential phthalate degraders after one week than after one and two months of incubation (Fig. 3).

It is important to note, however, that our knowledge on the effect of DEHP and DINP on the above-mentioned bacterial taxa and on marine microbial communities is generally rather limited. Furthermore, whether members of the *Alteromonadaceae* and *Oceanospirillaceae* families as prominent members of these biofilms are indeed taking up phthalates is unknown and other plastic type related properties as discussed above might be responsible for their high abundance. We did not investigate the presence of other additives in the plastics we used. Different polymer types have typically different additives. Thus, differences in the composition and concentration of additives might have also be partly responsible for the compositional differences in the bacterial community composition on the different plastic types.

Oberbeckmann *et al.* (2016) found that *Flavobacteria* and *Crocinitomix* discriminated for PET over glass after 5-6 weeks of incubation in the North Sea. In our study, *Flavobacteria*

and *Crocinitomix* were discriminating for PP over all other surfaces after one week of incubation (Fig. 5). *Flavobacterium* sp. has been associated with PP degradation (Khanna *et al.*, 2010), and *Cryomorphaceae*, to which *Crocinitomix* is affiliated, are known to degrade hydrocarbons (Rodrigues *et al.*, 2018). *Oleiphilus* clearly discriminated for LDPE and is capable of degrading hydrocarbons (Golyshin *et al.*, 2002) thriving in the presence of oil (Hazen *et al.*, 2010). *Erythrobacter*, also discriminating for LDPE over all other surfaces, is also known to thrive in the presence of hydrocarbons (Röling *et al.*, 2002). This indicates that the polymer type and additives might play a regulatory role in the initial attachment and development of specific bacterial taxa on certain plastics.

Some studies report the existence of a plastic-specific community different from that in the surrounding seawater (Zettler *et al.*, 2013; Amaral-Zettler *et al.*, 2015; C Dussud *et al.*, 2018; Dussud *et al.*, 2018) and on detrital particles (C Dussud *et al.*, 2018; Ogonowski *et al.*, 2018). In contrast, other studies have not found any significant differences between communities developing on different plastics and other organic and inorganic surfaces (Oberbeckmann *et al.*, 2016; Dussud *et al.*, 2018). In our study, the lack of major differences in the bacterial community composition between glass, HDPE, LDPE and PP is in agreement with studies comparing the development of the biofilm on plastics and other surfaces (Oberbeckmann *et al.*, 2014, 2016) that suggest that general biofilm processes rather than polymer-type associated characteristics are the main drivers of biofilm establishment and development in late biofilm development stages. Our study, however, also suggests that there is a small fraction of the bacterial community which is polymer type-specific particularly in the initial phase of the biofilm succession. These findings are in agreement with a recent study (Kirstein *et al.*, 2018) where only a small percentage of the prokaryotic community developing on plastic polymers was different from that on glass, while a common core community dominated on all surfaces.

Even though we only studied duplicates, not allowing a more thorough statistical analysis, a consistent difference between the PVCs and the other surfaces is obvious throughout the entire incubation period, especially in the dim light treatment (Figs. 2, 3). Thus, polymer characteristics apparently influence the bacterial community composition to a certain extent.

Influence of solar radiation on the microbial community composition

As expected, one of the major differences in bacterial community composition between the two light treatments was the high abundance of autotrophs, mainly Cyanobacteria, in the ambient light treatment in contrast to their very low abundance in the dim light treatment (Fig. 3) (Bengtsson *et al.*, 2018). Moreover, SEM analysis revealed that eukaryotic autotrophs such as diatoms and algae were also less abundant in the dim than in the ambient light treatment. Heterotrophic bacterial metabolism is tightly linked to the composition and availability of organic matter (Roman and Sabater, 1999). Wagner *et al.* (2015) suggested a shift in organic matter utilization by the bacterial community of a stream biofilm with changing light intensity, shifting from the utilization of photoautotrophically derived organic matter at high light intensities to more complex organic matter under low light availability. Furthermore, it appears that under low light conditions biofilm communities utilize mostly allochthonous organic carbon while shifting to autochthonous carbon at high light intensity (Wagner *et al.*, 2017).

The interaction between the direct effect of light on the availability of autochthonous organic carbon and the differences in relative abundance of photoautotrophs between the two light treatments might have contributed to the differences in bacterial community composition between the two light treatments.

Members of the *Alteromonadaceae*, such as *Marinobacter* and *Alteromonas*, known to thrive under solar radiation in the presence of oil (Agogué *et al.*, 2005; Bacosa *et al.*, 2015), were highly abundant on the PVCs after one week in the ambient light treatment (Fig. 3). Their relative resistance to UV radiation together with their potential ability to degrade hydrocarbons could have given them a selective advantage over other bacteria in the ambient light treatment. However, whether these organisms do indeed degrade PVC in the environment remains to be shown. Furthermore, the indirect effect of solar radiation on the plastic associated biofilm and the influence of potentially different eukaryotic communities in the two light treatments, both not addressed in this study, might have also contributed to the observed differences in the biofilms developing under dim and ambient light conditions.

Solar radiation can have different effects on different types of plastics (Singh and Sharma, 2008). For instance, emission rates of hydrocarbon gases are higher from LDPE than from HDPE, PP, polyethylene terephthalate (PET), polycarbonate (PC), acrylic (AC) and polystyrene (PS), when exposed to solar radiation (Royer *et al.*, 2018). This can indirectly affect the community composition attached to different plastics. Romero-Castillo *et al.* (2018) report

higher release rates of dissolved organic carbon from HDPE, LDPE and PP when exposed to solar radiation as compared to plastics held in the dark. Furthermore, in the same study, the plastic leachates influenced bacterial abundance and activity differently, depending on the type of plastics and light conditions. Also, Paluselli *et al.* (2018) noted differences in the leaching of additives from different plastics kept under different light conditions and in the presence or absence of microorganisms. This supports the idea that solar radiation has a significant impact on microbial communities by indirectly affecting compounds released from different polymers.

Solar, particularly ultraviolet (UV), radiation is also known to exert varying effects on different microorganisms (Fernández Zenoff *et al.*, 2006). The decreasing differences in the composition of the bacterial communities developing under ambient and dim light conditions after one month of incubation compared to after one week of incubation might be the result of the increase in biofilm thickness, shielding off harmful UV radiation from a substantial part of the community.

The impact of light exposure on biofilm communities in the marine environment is highly understudied, and to our knowledge this is the first study shedding light onto the impact of solar radiation on the biofilm developing on plastics. Most likely the community composition of plastics biofilm is shaped by an interaction between indirect effects of solar radiation on plastics and organic matter and direct effects on biofilm associated microbes.

Conclusion

Based on our data, we conclude that there is no specific plastic associated bacterial community, recently coined “plastisphere”, but rather there is a part of the bacterial community, which is influenced by the characteristics of the individual plastic polymers and potentially their additives. This plastic type-specific bacterial community might be more abundant, as we found on the PVCs or less abundant, as in LDPE, HDPE and PP, probably depending, besides the composition of the additives, on other physico-chemical characteristics and environmental factors. Furthermore, differences in the composition of bacterial communities associated with different plastic surfaces appear to be higher in the initial than in later successional stages of biofilm formation. In the later stages of the biofilm formation these differences were more pronounced when samples were kept under dim light than under ambient light conditions. Taken together, this study reveals different

colonization patterns by the microbial community depending on plastic-related properties, exposure to solar radiation, and most likely its additives.

Acknowledgements

We thank the Ruđer Bošković Institute at Rovinj, Croatia, for all the support and help whenever needed, especially Mirjana Najdek, Dario and Paolo Paliaga for keeping an eye on the *in situ* deployment during our absence. We would also like to thank Eva Sintes and Paul Steiner for their help during sampling. Daniela Gruber's help with electron microscopy is gratefully acknowledged.

References

- Agogu , H., Joux, F., Obernosterer, I., and Lebaron, P. (2005) Resistance of Marine Bacterioneuston to Solar Radiation. *Appl Environ Microbiol* **71**: 5282–5289.
- Amaral-Zettler, L.A., Zettler, E.R., Slikas, B., Boyd, G.D., Melvin, D.W., Morrall, C.E., et al. (2015) The biogeography of the Plastisphere: implications for policy. *Front Ecol Environ* **13**: 541–546.
- Bacosa, H.P., Liu, Z., and Erdner, D.L. (2015) Natural sunlight shapes crude oil-degrading bacterial communities in Northern Gulf of Mexico surface waters. *Front Microbiol* **6**: 1325.
- Bengtsson, M.M., Wagner, K., Schwab, C., Urich, T., and Battin, T.J. (2018) Light availability impacts structure and function of phototrophic stream biofilms across domains and trophic levels. *Mol Ecol* **27**: 2913–2925.
- Benner, R. and Biddanda, B. (1998) Photochemical transformations of surface and deep marine dissolved organic matter: effects on bacterial growth. *Limnol Oceanogr* **43**: 1373–1378.
- Van Cauwenberghe, L., Vanreusel, A., Mees, J., and Janssen, C.R. (2013) Microplastic pollution in deep-sea sediments. *Environ Pollut* **182**: 495–499.
- Characklis, W. and G (1990) Physiological ecology in biofilm systems. *Biofilms*.
- Dang, H. and Lovell, C.R. (2000) Bacterial primary colonization and early succession on surfaces in marine waters as determined by amplified rRNA gene restriction analysis and sequence analysis of 16S rRNA genes. *Appl Environ Microbiol* **66**: 467–475.
- Datta, M.S., Sliwerska, E., Gore, J., Polz, M.F., and Cordero, O.X. (2016) Microbial interactions lead to rapid micro-scale successions on model marine particles. *Nat Commun* **7**: 11965.
- Davidson, A. and Belbin, L. (2002) Exposure of natural Antarctic marine microbial assemblages to ambient UV radiation: effects on the marine microbial community. *Aquat Microb Ecol* **27**: 159–174.
- Debeljak, P., Pinto, M., Proietti, M., Reisser, J., Ferrari, F.F., Abbas, B., et al. (2017) Extracting DNA from ocean microplastics: a method comparison study. *Anal Methods* **9**: 1521–1526.
- Debroas, D., Mone, A., and Ter Halle, A. (2017) Plastics in the North Atlantic garbage patch: A boat-microbe for hitchhikers and plastic degraders. *Sci Total Environ* **599–600**: 1222–1232.
- Donlan, R.M. (2002) Biofilms: Microbial Life on Surfaces. *Emerg Infect Dis* **8**: 881–890.
- Dussud, C., Hudec, C., George, M., Fabre, P., Higgs, P., Bruzaud, S., et al. (2018) Colonization of Non-biodegradable and Biodegradable Plastics by Marine Microorganisms. *Front Microbiol* **9**: 1571.
- Dussud, C, Meistertzheim, A.L., Conan, P., Pujo-Pay, M., George, M., Fabre, P., et al. (2018) Evidence of niche partitioning among bacteria living on plastics, organic particles and surrounding seawaters. *Environ Pollut* **236**: 807–816.
- Edgar, R.C. (2013) UPARSE: highly accurate OTU sequences from microbial amplicon reads. *Nat Meth* **10**: 996–998.
- Elasri, M.O. and Miller, R. V (1999) Study of the response of a biofilm bacterial community to UV radiation. *Appl Environ Microbiol* **65**: 2025–2031.
- Fazey, F.M.C. and Ryan, P.G. (2016) Biofouling on buoyant marine plastics: An experimental study into the effect of size on surface longevity. *Environ Pollut* **210**: 354–360.
- Fern andez Zenoff, V., Si eriz, F., and Far as, M.E. (2006) Diverse Responses to UV-B Radiation and Repair Mechanisms of Bacteria Isolated from High-Altitude Aquatic Environments. *Appl Environ Microbiol* **72**: 7857–7863.
- Golyshin, P.N., Chernikova, T.N., Abraham, W.-R., L nsdorf, H., Timmis, K.N., and Yakimov, M.M. (2002) Oleiphilaceae fam. nov., to include Oleiphilus messinensis gen. nov., sp. nov., a novel marine bacterium that obligately utilizes hydrocarbons. *Int J Syst Evol Microbiol* **52**: 901–911.
- Harrison, J.P., Hoellein, T.J., Sapp, M., Tagg, A.S., Ju-Nam, Y., and Ojeda, J.J. (2018) Microplastic-associated biofilms: a comparison of freshwater and marine environments. In *Freshwater Microplastics*. Springer, Cham, pp. 181–201.
- Hazen, T.C., Dubinsky, E.A., DeSantis, T.Z., Andersen, G.L., Piceno, Y.M., Singh, N., et al. (2010) Deep-

- Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. *Science* **330**: 204–208.
- Herndl, G.J., Müller-Niklas, G., and Frick, J. (1993) Major role of ultraviolet-B in controlling bacterioplankton growth in the surface layer of the ocean. *Nature* **361**: 717–719.
- Hoellein, T.J., McCormick, A.R., Hittie, J., London, M.G., Scott, J.W., and Kelly, J.J. (2017) Longitudinal patterns of microplastic concentration and bacterial assemblages in surface and benthic habitats of an urban river. *Freshw Sci* **36**: 491–507.
- Hsieh, T.C., Ma, K.H., and Chao, A. (2016) iNEXT : an R package for rarefaction and extrapolation of species diversity (Hill numbers). 1451–1456.
- Iwaki, H., Nishimura, A., and Hasegawa, Y. (2012) Isolation and characterization of marine bacteria capable of utilizing phthalate. *World J Microbiol Biotechnol* **28**: 1321–1325.
- Jambeck, J.R., Geyer, R., Wilcox, C., Siegler, T.R., Perryman, M., Andrady, A., et al. (2015) Plastic waste inputs from land into the ocean. *Science* **347**: 768–771.
- Kapanen, A., Stephen, J.R., Brüggemann, J., Kiviranta, A., White, D.C., and Itävaara, M. (2007) Diethyl phthalate in compost: ecotoxicological effects and response of the microbial community. *Chemosphere* **67**: 2201–2209.
- Kettner, M.T., Rojas-Jimenez, K., Oberbeckmann, S., Labrenz, M., and Grossart, H.-P. (2017) Microplastics alter composition of fungal communities in aquatic ecosystems. *Environ Microbiol* **19**: 4447–4459.
- Khanna, N.D., Kaur, I., Bhalla, T.C., and Gautam, N. (2010) Effect of biodegradation on thermal and crystalline behavior of polypropylene–gelatin based copolymers. *J Appl Polym Sci* **118**: 1476–1488.
- Kirstein, I. V., Kirmizi, S., Wichels, A., Garin-Fernandez, A., Erler, R., Löder, M., and Gerds, G. (2016) Dangerous hitchhikers? Evidence for potentially pathogenic *Vibrio* spp. on microplastic particles. *Mar Environ Res* **120**: 1–8.
- Kirstein, I. V., Wichels, A., Krohne, G., and Gerds, G. (2018) Mature biofilm communities on synthetic polymers in seawater - Specific or general? *Mar Environ Res* **142**: 147–154.
- Lee, J.-W., Nam, J.-H., Kim, Y.-H., Lee, K.-H., and Lee, D.-H. (2008) Bacterial communities in the initial stage of marine biofilm formation on artificial surfaces. *J Microbiol* **46**: 174–182.
- Lobelle, D. and Cunliffe, M. (2011) Early microbial biofilm formation on marine plastic debris. *Mar Pollut Bull* **62**: 197–200.
- Lorite, G.S., Rodrigues, C.M., de Souza, A.A., Kranz, C., Mizaikoff, B., and Cotta, M.A. (2011) The role of conditioning film formation and surface chemical changes on *Xylella fastidiosa* adhesion and biofilm evolution. *J Colloid Interface Sci* **359**: 289–295.
- McCormick, A.R., Hoellein, T.J., London, M.G., Hittie, J., Scott, J.W., and Kelly, J.J. (2016) Microplastic in surface waters of urban rivers: concentration, sources, and associated bacterial assemblages. *Ecosphere* **7**: e01556.
- Miao, L., Wang, P., Hou, J., Yao, Y., Liu, Z., Liu, S., and Li, T. (2019) Distinct community structure and microbial functions of biofilms colonizing microplastics. *Sci Total Environ* **650**: 2395–2402.
- Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2018) Environmental Factors Support the Formation of Specific Bacterial Assemblages on Microplastics. *Front Microbiol* **8**: 2709.
- Oberbeckmann, S., Loeder, M.G.J., Gerds, G., and Osborn, A.M. (2014) Spatial and seasonal variation in diversity and structure of microbial biofilms on marine plastics in Northern European waters. *FEMS Microbiol Ecol* **90**: 478–492.
- Oberbeckmann, S., Osborn, A.M., and Duhaime, M.B. (2016) Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. *PLoS One* **11**: e0159289.
- Obernosterer, I., Reitner, B., and Herndl, G.J. (1999) Contrasting effects of solar radiation on dissolved organic matter and its bioavailability to marine bacterioplankton. *Limnol Oceanogr* **44**: 1645–1654.
- Ogonowski, M., Motiei, A., Ininbergs, K., Hell, E., Gerdes, Z., Udekwu, K.I., et al. (2018) Evidence for selective bacterial community structuring on microplastics. *Environ Microbiol* **20**: 2796–2808.

- World Health Organization. (1994). Ultraviolet radiation. *Environmental health criteria* (160).
- Paluselli, A., Fauvelle, V., Galgani, F., and Sempéré, R. (2018) Phthalate Release from Plastic Fragments and Degradation in Seawater. *Environ Sci Technol* **53**: 166–175.
- Rochman, C.M., Hoh, E., Hentschel, B.T., and Kaye, S. (2013) Long-term field measurement of sorption of organic contaminants to five types of plastic pellets: implications for plastic marine debris. *Environ Sci Technol* **47**: 1646–1654.
- Rodrigues, E.M., Morais, D.K., Pylro, V.S., Redmile-Gordon, M., de Oliveira, J.A., Roesch, L.F.W., et al. (2018) Aliphatic Hydrocarbon Enhances Phenanthrene Degradation by Autochthonous Prokaryotic Communities from a Pristine Seawater. *Microb Ecol* **75**: 688–700.
- Röling, W.F.M., Milner, M.G., Jones, D.M., Lee, K., Daniel, F., Swannell, R.J.P., and Head, I.M. (2002) Robust Hydrocarbon Degradation and Dynamics of Bacterial Communities during Nutrient-Enhanced Oil Spill Bioremediation. *Appl Environ Microbiol* **68**: 5537–5548.
- Roman, A.M. and Sabater, S. (1999) Effect of primary producers on the heterotrophic metabolism of a stream biofilm. *Freshw Biol* **41**: 729–736.
- Romera-Castillo, C., Pinto, M., Langer, T.M., Álvarez-Salgado, X.A., and Herndl, G.J. (2018) Dissolved organic carbon leaching from plastics stimulates microbial activity in the ocean. *Nat Commun* **9**: 1–7.
- Royer, S.-J., Ferrón, S., Wilson, S.T., and Karl, D.M. (2018) Production of methane and ethylene from plastic in the environment. *PLoS One* **13**: e0200574.
- Rummel, C.D., Jahnke, A., Gorokhova, E., Kühnel, D., and Schmitt-Jansen, M. (2017) Impacts of biofilm formation on the fate and potential effects of microplastic in the aquatic environment. *Environ Sci Technol Lett* **4**: 258–267.
- Salta, M., Wharton, J.A., Blache, Y., Stokes, K.R., and Briand, J.-F. (2013) Marine biofilms on artificial surfaces: structure and dynamics. *Environ Microbiol* **15**: 2879–2893.
- Shah, A.A., Hasan, F., Hameed, A., and Ahmed, S. (2008) Biological degradation of plastics: a comprehensive review. *Biotechnol Adv* **26**: 246–265.
- Singh, B. and Sharma, N. (2008) Mechanistic implications of plastic degradation. *Polym Degrad Stab* **93**: 561–584.
- Staples, C.A., Adams, W.J., Parkerton, T.F., Gorsuch, J.W., Biddinger, G.R., and Reinert, K.H. (2009) Aquatic toxicity of eighteen phthalate esters. *Environ Toxicol Chem* **16**: 875–891.
- De Tender, C., Devriese, L.I., Haegeman, A., Maes, S., Vangeyte, J., Cattijssse, A., et al. (2017) Temporal dynamics of bacterial and fungal colonization on plastic debris in the North Sea. *Environ Sci Technol* **51**: 7350–7360.
- Teughels, W., Van Assche, N., Sliepen, I., and Quirynen, M. (2006) Effect of material characteristics and/or surface topography on biofilm development. *Clin Oral Implants Res* **17**: 68–81.
- Wagner, K., Bengtsson, M.M., Findlay, R.H., Battin, T.J., and Ulseth, A.J. (2017) High light intensity mediates a shift from allochthonous to autochthonous carbon use in phototrophic stream biofilms. *J Geophys Res Biogeosciences* **122**: 1806–1820.
- Wagner, K., Besemer, K., Burns, N.R., Battin, T.J., and Bengtsson, M.M. (2015) Light availability affects stream biofilm bacterial community composition and function, but not diversity. *Environ Microbiol* **17**: 5036–5047.
- Zettler, E.R., Mincer, T.J., and Amaral-Zettler, L. (2013) Life in the “plastisphere”: Microbial communities on plastic marine debris. *Environ Sci Technol* **47**: 7137–7146.

Supporting information

S1 – Additive measurements protocol.

S2 – DNA extraction protocol.

Table S1 – Results of the ANOVA tests comparing diversity and richness indexes of the bacterial communities between the different sampling times (Month), different surfaces and water (Type) and the two exposure treatments (Exposure).

Table S2- Results of the post-hoc Tukey tests performed on the ANOVA comparing Shannon indexes (Table 1).

Table S3- Results of the post-hoc Tukey tests performed on the ANOVA comparing Simpson indexes (Table 1).

Table S4- Results of the post-hoc Tukey tests performed on the ANOVA comparing OTU richness (Table 1).

Table S5 – Results of the PERMANOVA comparing bacterial community composition between the different sampling times (Month), different surfaces (plastics + glass + water) (Type) and the two exposure treatments (Exposure), with and without autotrophs.

Table S6 – Results of the PERMANOVA comparing bacterial community composition between the different surfaces (plastics + glass) (Type) and the two light exposure treatments (Exposure) for after one week, one month and two months of incubation.

Tables S7 - Results of the PERMANOVA comparing bacterial community composition between the different surfaces (plastics + glass) (Type) and the two light exposure treatments (Exposure) for after one week, one month and two months of incubation.

Table S8 – Results of the LEfSe analysis identifying taxa (down to the family level) discriminating for either glass or either one of the plastics after one week of incubation.

Table S9 – Results of the LEfSe analysis identifying taxa (down to the family level) discriminating for either glass or either one of the plastics after one month of incubation.

Table S10 – Results of the LEfSe analysis identifying taxa (down to the family level) discriminating for either glass or either one of the plastics after two months incubation.

Table S11 – Results of the LEfSe analysis for each incubation time. It shows all OTUs that significantly discriminated for a specific surface at each sampling point.

Fig. S1 – Scheme of the structure used to incubate the plastics and glass.

Fig. S2 – Map of the location where the *in-situ* incubation was carried out.

Fig. S3 – SEM images of: (A) glass, (B) PP, (C) HDPE, (D) LDPE, (E) PVC DINP and (F) PVC DEHP incubated under both ambient and dim light conditions for one week, one month and two months.

Fig. S4 – NMDS representation of the similarity between the bacterial community composition of the biofilm on different surfaces and seawater, when excluding the autotrophic component, i.e., Cyanobacteria.

Fig. S5 – Stack plot representing the relative abundances of the OTUs representing > 5% of the total bacterial community in each sample.

Fig. S6 -Values of i_F representing the discrimination of the most abundant bacterial families (with 5% or more relative abundance in at least one of the samples) for either one of the plastics or glass and under the two different light conditions after (A) one month and (B) two months incubation.

Fig. S7- Representation of the bacterial taxa which discriminated for one of the surfaces over all the others (considering both light treatments) determined by the discriminant linear analysis (LEfSe) after (A) one month and (B) two months of incubation.

S1- To determine the concentration of DEHP and DINP in the plastics throughout the experiment, phthalate concentrations in the samples were measured for all plastic types kept under ambient light condition. The biofilm was gently removed from the plastics using a wet paper tissue and the pieces were weighed after drying. The PVC pellets were dissolved in 5 mL tetrahydrofuran, followed by the precipitation of the polymer by adding 10 mL of hexane. An aliquot of the supernatant was diluted 1:100 and 980 μL of this dilution were transferred into a GC sample vial and 20 μL internal standard (DEHP D4, 50 ng/ μL) were added prior to GC-MS analysis. PE and PP plastics were extracted using 5 mL tetrahydrofuran in an ultrasonic bath for 12 h. After adding 10 mL of hexane, the samples were measured. Gas chromatography-mass spectrometry (GC-MS, Agilent 5975C inert GC/MSD) was used for the analysis of the plasticizers (column: HP5-MS, 60 m; oven program: 80°C held for 30 s, ramp to 300°C at a rate of 20°C/min, hold 10 min; inlet temperature: 300°C; transfer line: 280°C; carrier gas: He at 1 mL min⁻¹).

S2- After thawed the LDPE, HDPE and PP samples were cut into smaller pieces and put in 2mL eppendorfs. The glass and PVC spheres were also put into 2 mL eppendorfs. Samples were incubated in 500 μL of lysis solution (kit) and 10 μL lysozyme (1000 U mL⁻¹) at 37°C for 30 min. Afterwards, 5 μL proteinase k (kit) was added and mixed by inverting 25 times. About 0.325 g of beads were added per tube before bead beating two times for 45 s at a vertical speed of 4 m/s (FastPrep™, MP Biomedicals, USA). After incubating at 55°C for another 30 min, 4 μL RNase (kit) was added and mixed by inverting 50 times. Following a 30 min incubation at 37°C and 5 min on ice, 250 μL of protein precipitation solution (kit) was added to each tube and vortexed at high speed for 20 s. After centrifuging the tubes for 3 min at 14,000 *g*, the supernatant was transferred to a fresh tube containing 750 μL 100% isopropanol and inverted 50 times. Following another centrifuging step at 14,000 *g* for 5 min, the supernatant was discarded and tubes were drained from remaining isopropanol. As a washing step, 750 μL 70% ethanol was added and the tubes were inverted several times. After centrifugation for an additional 3 min, the supernatant was discarded again and tubes were drained and air-dried. The remaining DNA extract was re-suspended in 40 μL hydration solution (kit) and incubated at 65°C for 45 min to completely dissolve. DNA extracts were stored frozen at -80°C for later analyses.

Table S1 – Results of the ANOVA tests comparing diversity and richness indexes of the bacterial communities between the different sampling times (Month), different surfaces and water (Type) and the two exposure treatments (Exposure). * indicates significant differences ($p < 0.05$).

	OTU richness		Shannon diversity		Simpson diversity	
	F value	Pr(>F)	F value	Pr(>F)	F value	Pr(>F)
Type	24.7	$6.8 \times 10^{-11}*$	20.6	$6.9 \times 10^{-10}*$	18	$3.6 \times 10^{-9}*$
Month	110	$2.3 \times 10^{-15}*$	96.3	$2.6 \times 10^{-11}*$	130	$3.5 \times 10^{-13}*$
Exposure	30.4	$4.1 \times 10^{-06}*$	67.2	$2.3 \times 10^{-12}*$	55	$3.3 \times 10^{-11}*$
Type: Month	4.0	$7.0 \times 10^{-04}*$	8.6	$2.6 \times 10^{-05}*$	15	$1.4 \times 10^{-7}*$
Type: Exposure	5.6	$7.8 \times 10^{-04}*$	3.5	$2.3 \times 10^{-03}*$	4.9	$1.2 \times 10^{-4}*$
Month: Treatment	0.5	0.61	3.2	5.2×10^{-02}	16	$1.5 \times 10^{-5}*$
Type: Month: Exposure	2.5	0.025*	3.4	$3.9 \times 10^{-03}*$	4.4	$6.2 \times 10^{-4}*$

Table S2- Results of the post-hoc Tukey tests performed on the ANOVA comparing Shannon indexes (Table 1). * indicates significant differences ($p < 0.05$) between Shannon diversity indexes of the bacterial communities colonizing the different surfaces and the ambient water (A) after one week incubation, (B) after one month of incubation, (C) after two months of incubation. Diff – difference in means; lwr and upr – lower and upper confidence levels, respectively; p adj – adjusted p value for each pair.

(A)

	1 week incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	-0.05	-0.82	0.72	1.00	0.07	-0.69	0.84	1.00
LDPE-Glass	-0.29	-1.06	0.48	0.96	0.24	-0.53	1.00	1.00
PP-Glass	0.24	-0.53	1.00	1.00	0.00	-0.77	0.77	1.00
PVC DEHP-Glass	-0.70	-1.47	0.07	0.09	-0.13	-0.90	0.64	1.00
PVC DINP-Glass	-0.63	-1.40	0.14	0.16	-0.08	-0.84	0.69	1.00
SW-Glass	-0.29	-1.06	0.47	0.96	0.48	-0.29	1.24	0.51
LDPE-HDPE	-0.24	-1.01	0.53	0.99	0.16	-0.61	0.93	1.00
PP-HDPE	0.29	-0.48	1.06	0.97	-0.08	-0.85	0.69	1.00
PVC DEHP-HDPE	-0.65	-1.42	0.12	0.14	-0.20	-0.97	0.57	1.00
PVC DINP-HDPE	-0.58	-1.35	0.19	0.25	-0.15	-0.92	0.62	1.00
SW-HDPE	-0.24	-1.01	0.53	0.99	0.40	-0.37	1.17	0.74
PP-LDPE	0.53	-0.24	1.30	0.36	-0.24	-1.01	0.53	0.99
PVC DEHP-LDPE	-0.41	-1.18	0.36	0.71	-0.36	-1.13	0.40	0.84
PVC DINP-LDPE	-0.34	-1.11	0.43	0.90	-0.31	-1.08	0.46	0.94
SW-LDPE	0.00	-0.77	0.77	1.00	0.24	-0.53	1.01	0.99
PVC DEHP-PP	-0.94	-1.71	-0.17	0.01*	-0.13	-0.89	0.64	1.00
PVC DINP-PP	-0.87	-1.64	-0.10	0.02*	-0.07	-0.84	0.70	1.00
SW-PP	-0.53	-1.30	0.24	0.36	0.48	-0.29	1.25	0.50
PVC DINP-PVC DEHP	0.07	-0.70	0.84	1.00	0.05	-0.72	0.82	1.00
SW-PVC DEHP	0.41	-0.36	1.18	0.72	0.60	-0.16	1.37	0.20
SW-PVC DINP	0.34	-0.43	1.11	0.90	0.55	-0.22	1.32	0.31

(B)

	1 month incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	-0.37	-1.16	0.42	0.79	0.28	-0.51	1.07	0.96
LDPE-Glass	-0.09	-0.73	0.56	1.00	-0.14	-0.78	0.50	1.00
PP-Glass	0.43	-0.22	1.07	0.36	0.79	0.15	1.43	0.01*
PVC DEHP-Glass	-1.48	-2.12	-0.84	<0.01*	-0.08	-0.72	0.56	1.00
PVC DINP-Glass	-1.14	-1.92	-0.35	<0.01*	0.39	-0.25	1.03	0.46
SW-Glass	-1.40	-2.04	-0.76	<0.01*	-0.31	-0.95	0.33	0.75
LDPE-HDPE	0.28	-0.50	1.07	0.96	-0.42	-1.21	0.37	0.63
PP-HDPE	0.80	0.01	1.58	0.04*	0.51	-0.28	1.29	0.39
PVC DEHP-HDPE	-1.11	-1.90	-0.32	<0.01*	-0.36	-1.15	0.43	0.82
PVC DINP-HDPE	-0.77	-1.68	0.14	0.13	0.11	-0.68	0.90	1.00
SW-HDPE	-1.03	-1.82	-0.25	0.01*	-0.59	-1.38	0.20	0.22
PP-LDPE	0.51	-0.13	1.15	0.17	0.93	0.29	1.57	<0.01*
PVC DEHP-LDPE	-1.39	-2.04	-0.75	<0.01*	0.06	-0.58	0.71	1.00
PVC DINP-LDPE	-1.05	-1.84	-0.26	0.01*	0.53	-0.11	1.18	0.14
SW-LDPE	-1.32	-1.96	-0.67	<0.01*	-0.17	-0.81	0.47	1.00
PVC DEHP-PP	-1.91	-2.55	-1.26	<0.01*	-0.87	-1.51	-0.22	0.01*
PVC DINP-PP	-1.56	-2.35	-0.78	<0.01*	-0.40	-1.04	0.25	0.45
SW-PP	-1.83	-2.47	-1.19	<0.01*	-1.10	-1.74	-0.46	<0.01*
PVC DINP-PVC DEHP	0.34	-0.44	1.13	0.86	0.47	-0.17	1.11	0.25
SW-PVC DEHP	0.08	-0.56	0.72	1.00	-0.23	-0.88	0.41	0.96
SW-PVC DINP	-0.26	-1.05	0.52	0.98	-0.70	-1.35	-0.06	0.03

(C)

	2 months incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	0.74	-0.98	2.45	0.86	-0.52	-2.24	1.19	0.99
LDPE-Glass	0.66	-1.44	2.76	0.99	-0.40	-2.11	1.31	1.00
PP-Glass	-0.01	-1.72	1.71	1.00	-0.17	-1.88	1.54	1.00
PVC DEHP-Glass	-1.11	-2.82	0.61	0.39	-0.70	-2.42	1.01	0.90
PVC DINP-Glass	-0.60	-2.70	1.50	0.99	-0.65	-2.36	1.07	0.94
SW-Glass	-1.16	-3.26	0.94	0.59	-0.64	-2.74	1.46	0.99
LDPE-HDPE	-0.08	-2.18	2.02	1.00	0.12	-1.59	1.84	1.00
PP-HDPE	-0.74	-2.46	0.97	0.86	0.36	-1.36	2.07	1.00
PVC DEHP-HDPE	-1.84	-3.56	-0.13	0.03*	-0.18	-1.89	1.53	1.00
PVC DINP-HDPE	-1.34	-3.44	0.76	0.40	-0.12	-1.84	1.59	1.00
SW-HDPE	-1.90	-4.00	0.20	0.09	-0.12	-2.22	1.98	1.00
PP-LDPE	-0.66	-2.76	1.44	0.99	0.23	-1.48	1.95	1.00
PVC DEHP-LDPE	-1.76	-3.86	0.34	0.13	-0.30	-2.02	1.41	1.00
PVC DINP-LDPE	-1.26	-3.69	1.16	0.67	-0.25	-1.96	1.47	1.00
SW-LDPE	-1.82	-4.24	0.60	0.22	-0.24	-2.34	1.86	1.00
PVC DEHP-PP	-1.10	-2.81	0.61	0.40	-0.53	-2.25	1.18	0.99
PVC DINP-PP	-0.60	-2.70	1.50	0.99	-0.48	-2.19	1.24	1.00
SW-PP	-1.16	-3.25	0.94	0.60	-0.47	-2.57	1.63	1.00
PVC DINP-PVC DEHP	0.50	-1.60	2.60	1.00	0.06	-1.66	1.77	1.00
SW-PVC DEHP	-0.06	-2.15	2.04	1.00	0.06	-2.04	2.16	1.00
SW-PVC DINP	-0.56	-2.98	1.87	1.00	0.01	-2.09	2.11	1.00

Table S3- Results of the post-hoc Tukey tests performed on the ANOVA comparing Simpson indexes (Table 1). * indicates significant differences ($p < 0.05$) between Simpson diversity indexes of the bacterial communities colonizing the different surfaces and the ambient water (A) after one week incubation, (B) after one month of incubation, (C) after two months of incubation. Diff – difference in means; lwr and upr – lower and upper confidence levels, respectively; p adj – adjusted p value for each pair.

(A)

	1 week incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	-0.11	-0.24	0.03	0.17	0.04	-0.10	0.17	1.00
LDPE-Glass	-0.17	-0.30	-0.04	0.01*	0.08	-0.06	0.21	0.62
PP-Glass	0.07	-0.06	0.21	0.69	0.00	-0.13	0.14	1.00
PVC DEHP-Glass	-0.35	-0.48	-0.21	<0.01*	-0.01	-0.15	0.12	1.00
PVC DINP-Glass	-0.30	-0.44	-0.17	<0.01*	-0.01	-0.14	0.13	1.00
SW-Glass	-0.09	-0.22	0.04	0.40	0.29	0.15	0.42	<0.01*
LDPE-HDPE	-0.06	-0.20	0.07	0.87	0.04	-0.10	0.17	1.00
PP-HDPE	0.18	0.05	0.32	<0.01*	-0.04	-0.17	0.10	1.00
PVC DEHP-HDPE	-0.24	-0.37	-0.10	<0.01*	-0.05	-0.19	0.08	0.95
PVC DINP-HDPE	-0.20	-0.33	-0.06	<0.01*	-0.04	-0.18	0.09	0.99
SW-HDPE	0.02	-0.12	0.15	1.00	0.25	0.11	0.38	<0.01*
PP-LDPE	0.24	0.11	0.38	<0.01*	-0.08	-0.21	0.06	0.63
PVC DEHP-LDPE	-0.18	-0.31	-0.04	0.01*	-0.09	-0.23	0.04	0.38
PVC DINP-LDPE	-0.13	-0.27	0.00	0.05	-0.08	-0.22	0.05	0.53
SW-LDPE	0.08	-0.05	0.21	0.56	0.21	0.08	0.34	<0.01*
PVC DEHP-PP	-0.42	-0.55	-0.28	<0.01*	-0.02	-0.15	0.12	1.00
PVC DINP-PP	-0.38	-0.51	-0.24	<0.01*	-0.01	-0.14	0.13	1.00
SW-PP	-0.16	-0.30	-0.03	0.01	0.29	0.15	0.42	<0.01*
PVC DINP-PVC DEHP	0.04	-0.09	0.18	0.99	0.01	-0.13	0.14	1.00
SW-PVC DEHP	0.26	0.12	0.39	<0.01*	0.30	0.17	0.44	<0.01*
SW-PVC DINP	0.21	0.08	0.35	9.41	0.29	0.16	0.43	<0.01*

(B)

	1 month incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	-0.45	-1.31	0.41	0.66	0.18	-0.68	1.04	1.00
LDPE-Glass	-0.37	-1.07	0.34	0.67	-0.03	-0.73	0.67	1.00
PP-Glass	0.06	-0.64	0.76	1.00	0.43	-0.27	1.13	0.46
PVC DEHP-Glass	-1.04	-1.74	-0.34	<0.01*	-0.04	-0.74	0.66	1.00
PVC DINP-Glass	-0.99	-1.85	-0.13	0.02*	0.31	-0.40	1.01	0.85
SW-Glass	-0.94	-1.64	-0.24	0.01*	-0.02	-0.73	0.68	1.00
LDPE-HDPE	0.08	-0.78	0.94	1.00	-0.21	-1.07	0.65	1.00
PP-HDPE	0.51	-0.35	1.37	0.50	0.25	-0.61	1.11	0.99
PVC DEHP-HDPE	-0.59	-1.45	0.27	0.32	-0.22	-1.08	0.64	1.00
PVC DINP-HDPE	-0.54	-1.53	0.45	0.61	0.13	-0.73	0.99	1.00
SW-HDPE	-0.49	-1.35	0.37	0.55	-0.20	-1.06	0.66	1.00
PP-LDPE	0.43	-0.28	1.13	0.47	0.46	-0.24	1.16	0.37
PVC DEHP-LDPE	-0.67	-1.37	0.03	0.06	-0.01	-0.71	0.69	1.00
PVC DINP-LDPE	-0.63	-1.49	0.23	0.25	0.34	-0.36	1.04	0.76
SW-LDPE	-0.58	-1.28	0.13	0.15	0.01	-0.69	0.71	1.00
PVC DEHP-PP	-1.10	-1.80	-0.40	<0.01*	-0.47	-1.17	0.23	0.35
PVC DINP-PP	-1.05	-1.91	-0.19	0.01*	-0.12	-0.82	0.58	1.00
SW-PP	-1.00	-1.70	-0.30	<0.01*	-0.45	-1.15	0.25	0.39
PVC DINP-PVC DEHP	0.05	-0.81	0.91	1.00	0.35	-0.35	1.05	0.73
SW-PVC DEHP	0.10	-0.61	0.80	1.00	0.02	-0.68	0.72	1.00
SW-PVC DINP	0.05	-0.81	0.91	1.00	-0.33	-1.03	0.37	0.78

(C)

	2 months incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	0.45	-0.50	1.39	0.78	-0.20	-1.14	0.74	1.00
LDPE-Glass	0.43	-0.72	1.59	0.94	-0.10	-1.04	0.84	1.00
PP-Glass	-0.10	-1.04	0.84	1.00	-0.20	-1.14	0.75	1.00
PVC DEHP-Glass	-0.89	-1.84	0.05	0.07	-0.23	-1.17	0.72	1.00
PVC DINP-Glass	-0.72	-1.88	0.43	0.43	-0.19	-1.13	0.76	1.00
SW-Glass	-0.80	-1.96	0.36	0.31	-0.12	-1.27	1.04	1.00
LDPE-HDPE	-0.02	-1.17	1.14	1.00	0.10	-0.84	1.04	1.00
PP-HDPE	-0.55	-1.49	0.40	0.53	0.00	-0.94	0.95	1.00
PVC DEHP-HDPE	-1.34	-2.28	-0.40	<0.01*	-0.03	-0.97	0.92	1.00
PVC DINP-HDPE	-1.17	-2.33	-0.01	0.05*	0.01	-0.93	0.96	1.00
SW-HDPE	-1.25	-2.40	-0.09	0.03*	0.09	-1.07	1.24	1.00
PP-LDPE	-0.53	-1.69	0.62	0.81	-0.10	-1.04	0.85	1.00
PVC DEHP-LDPE	-1.32	-2.48	-0.17	0.02*	-0.13	-1.07	0.82	1.00
PVC DINP-LDPE	-1.15	-2.49	0.18	0.11	-0.09	-1.03	0.86	1.00
SW-LDPE	-1.23	-2.57	0.10	0.08	-0.01	-1.17	1.14	1.00
PVC DEHP-PP	-0.79	-1.74	0.15	0.13	-0.03	-0.97	0.92	1.00
PVC DINP-PP	-0.62	-1.78	0.53	0.63	0.01	-0.93	0.95	1.00
SW-PP	-0.70	-1.86	0.46	0.47	0.08	-1.07	1.24	1.00
PVC DINP-PVC DEHP	0.17	-0.99	1.33	1.00	0.04	-0.91	0.98	1.00
SW-PVC DEHP	0.09	-1.06	1.25	1.00	0.11	-1.04	1.27	1.00
SW-PVC DINP	-0.08	-1.41	1.26	1.00	0.07	-1.08	1.23	1.00

Table S4- Results of the post-hoc Tukey tests performed on the ANOVA comparing OTU richness (Table 1). * indicates significant differences ($p < 0.05$) between the OTU richness of the bacterial communities colonizing the different surfaces and the ambient water (A) after one week incubation, (B) after one month of incubation, (C) after two months of incubation. Diff – difference in means; lwr and upr – lower and upper confidence levels, respectively; p adj – adjusted p value for each pair.

(A)

	1 week incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	-32.5	-188	123	1.00	-31.8	-187	124	1.00
LDPE-Glass	-20.4	-17	135	1.00	-29.9	-185	125	1.00
PP-Glass	-24.3	-180	131	1.00	-25.9	-181	129	1.00
PVC DEHP-Glass	-120	-276	35.4	0.22	-107	-263	48.7	0.36
PVC DINP-Glass	-105	-261	50.7	0.39	-83.3	-239	72.5	0.71
SW-Glass	-40.2	-196	115	1.00	24.3	-131	180	1.00
LDPE-HDPE	12.1	-143	168	1.00	1.98	-153	157	1.00
PP-HDPE	8.21	-147	164	1.00	5.97	-149	161	1.00
PVC DEHP-HDPE	-87.8	-243	68	0.64	-75.2	-231	80.6	0.82
PVC DINP-HDPE	-72.6	-228	83.2	0.86	-51.4	-207	104	0.99
SW-HDPE	-7.69	-163	148	1.00	56.2	-99.6	212	0.98
PP-LDPE	-3.91	-159	151	1.00	3.99	-151	159	1.00
PVC DEHP-LDPE	-100	-255	55.8	0.46	-77.2	-233	78.6	0.80
PVC DINP-LDPE	-84.7	-240	71.1	0.69	-53.4	-209	102	0.99
SW-LDPE	-19.8	-175	136	1.00	54.2	-101	210	0.98
PVC DEHP-PP	-96.1	-251	59.7	0.52	-81.2	-237	74.6	0.74
PVC DINP-PP	-80.8	-236	75.0	0.75	-57.4	-213	98.4	0.97
SW-PP	-15.8	-171	140	1.00	50.2	-105	206	0.99
PVC DINP-PVC DEHP	15.2	-140	171	1.00	23.8	-132	179	1.00
SW-PVC DEHP	80.2	-75.6	236	0.76	131	-24.3	287	0.14
SW-PVC DINP	64.9	-90.9	220	0.93	107	-48.2	263	0.36

(B)

	1 month incubation							
	Dim light				Ambient light			
	diff	lwr	Upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	28.3	-194	251	1.00	-40.9	-263	181.68	1.00
LDPE-Glass	51.2	-130	233	1.00	-135	-317	46.18	0.23
PP-Glass	54.7	-127	236	0.99	44.5	-137	226.36	1.00
PVC DEHP-Glass	-318	-500	-136	<0.01*	-114	-296	67.34	0.42
PVC DINP-Glass	-191	-413	31.6	0.12	-75.4	-257	106.40	0.89
SW-Glass	-356	-538	-175	<0.01*	-264	-446	-82.52	<0.01*
LDPE-HDPE	22.8	-199	245	1.00	-94.6	-317	128.03	0.87
PP-HDPE	26.4	-196	249	1.00	85.5	-137	308.22	0.93
PVC DEHP-HDPE	-346	-569	-124	<0.01*	-73.4	-296	149.19	0.98
PVC DINP-HDPE	-219	-476	37.7	0.12	-34.4	-257	188.25	1.00
SW-HDPE	-385	-608	-162	<0.01*	-223	-446	-0.67	0.05
PP-LDPE	3.57	-178	185	1.00	180	-1.63	361.99	0.05
PVC DEHP-LDPE	-369	-551	-187	<0.01*	21.1	-160	202.97	1.00
PVC DINP-LDPE	-242	-464	-19.5	0.03	60.2	-121	242.03	0.98
SW-LDPE	-408	-590	-226	<0.01*	-128	-310	53.11	0.28
PVC DEHP-PP	-373	-555	-191	<0.01*	-159	-340	22.79	0.11
PVC DINP-PP	-245	-468	-23.1	0.03	-119	-301	61.85	0.36
SW-PP	-411	-593	-229	<0.01*	-308	-490	-127.0	<0.01*
PVC DINP-PVC DEHP	127	-95.2	350	0.55	39.0	-142	220.87	1.00
SW-PVC DEHP	-38.5	-220	143	1.00	-149	-331	31.96	0.14
SW-PVC DINP	-165	-388	56.6	0.23	-188	-370	-7.11	0.04

(C)

	2 months incubation							
	Dim light				Ambient light			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
HDPE-Glass	113	-77.7	304	0.23	-125	-481	230	0.75
LDPE-Glass	63.1	-170	296	0.81	-102	-458	253	0.87
PP-Glass	41.9	-148	232	0.90	0.84	-355	356	1.00
PVC DEHP-Glass	-157	-348	32.9	0.09	-175	-531	180	0.47
PVC DINP-Glass	-46.8	-280	186	0.93	-170	-526	185	0.50
SW-Glass	-226	-460	7.04	0.06	-258	-694	177	0.31
LDPE-HDPE	-50.0	-283	183	0.91	23.2	-332	379	1.00
PP-HDPE	-71.1	-262	119	0.58	126	-229	482	0.75
PVC DEHP-HDPE	-271	-462	-80.2	0.01*	-50.00	-405	305	0.99
PVC DINP-HDPE	-160	-393	73.7	0.16	-44.2	-400	311	1.00
SW-HDPE	-339	-573	-106	0.01*	-132	-568	303	0.84
PP-LDPE	-21.1	-254	212	1.00	103	-252	459	0.87
PVC DEHP-LDPE	-221	-454	12.7	0.06	-73.2	-429	282	0.97
PVC DINP-LDPE	-110	-379	159	0.51	-67.4	-423	288	0.98
SW-LDPE	-289	-559	-19.9	0.04*	-155	-591	280	0.74
PVC DEHP-PP	-199	-390	-9.02	0.04*	-176	-532	179	0.46
PVC DINP-PP	-88.8	-322	144	0.56	-171	-526	184	0.49
SW-PP	-268	-502	-34.9	0.03*	-259	-695	176	0.30
PVC DINP-PVC DEHP	111	-122	344	0.38	5.78	-350	361	1.00
SW-PVC DEHP	-68.7	-302	165	0.75	-82.7	-518	353	0.98
SW-PVC DINP	-179	-449	90.1	0.17	-88.5	-524	347	0.97

Table S5 – Results of the PERMANOVA comparing bacterial community composition between the different sampling times (Month), different surfaces (plastics + glass + water) (Type) and the two exposure treatments (Exposure), with and without autotrophs.

		Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
With autotrophs	Type	6	5.12	0.85	16.1	0.24	0.001*
	Exposure	1	2.08	2.08	39.3	0.09	0.001*
	Month	2	5.08	2.54	48.1	0.24	0.001*
	Type: Exposure	5	1.28	0.26	4.83	0.06	0.001*
	Type: Month	12	3.02	0.25	4.76	0.14	0.001*
	Exposure: Month	2	1.25	0.62	11.8	0.06	0.001*
	Type: Exposure: Month	10	1.68	0.17	3.18	0.08	0.001*
	Residuals	35	1.85	0.05		0.09	
	Total	73	21.4			1	
Without autotrophs	Type	6	5.34	0.89	17.6	0.25	0.001*
	Exposure	1	1.09	1.09	21.7	0.051	0.001*
	Month	2	5.75	2.88	56.8	0.27	0.001*
	Type: Exposure	5	1.09	0.22	4.34	0.05	0.001*
	Type: Month	12	3.36	0.28	5.54	0.16	0.001*
	Exposure: Month	2	1.15	0.57	11.3	0.05	0.001*
	Type: Exposure: Month	10	1.59	0.16	3.16	0.08	0.001*
	Residuals	35	1.77	0.05		0.08	
	Total	73	21.2			1	

* indicates significant differences ($p < 0.05$).

Table S6 – Results of the PERMANOVA comparing bacterial community composition between the different surfaces (plastics + glass) (Type) and the two exposure treatments (Exposure) for after one week, one month and two months of incubation. The Jaccard index was used as the distance measurement

		Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
After 1 week	Type	5	2.5575	0.51149	4.5796	0.34348	0.001*
	Exposure	1	1.5434	1.54342	13.819	0.20729	0.001*
	Type: Exposure	5	2.0046	0.40092	3.5896	0.26923	0.001*
	Residuals	12	1.3403	0.11169		0.18	
	Total	23	7.4457			1	
After 1 month	Type	5	1.7524	0.35047	3.023	0.32959	0.001*
	Exposure	1	0.9785	0.9785	8.4402	0.18404	0.001*
	Type: Exposure	5	1.3106	0.26212	2.261	0.24651	0.001*
	Residuals	11	1.2753	0.11593		0.23986	
	Total	22	5.3167			1	
After 2 months	Type	5	2.0168	0.40336	3.0467	0.33781	0.001*
	Exposure	1	1.3456	1.34555	10.1635	0.22538	0.001*
	Type: Exposure	5	1.284	0.2568	1.9397	0.21507	0.003*
	Residuals	10	1.3239	0.13239		0.22175	
	Total	21	5.9703			1	

* indicates significant differences ($p < 0.05$).

Table S7 – Results of the PERMANOVA comparing bacterial community composition between the different surfaces (plastics + glass) (Type) and the two exposure treatments (Exposure) for after one week, one month and two months of incubation. Bray-Curtis dissimilarity was used as the distance measurement

		Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
After 1 week	Type	5	2.193	0.43861	8.9118	0.38689	0.001*
	Exposure	1	1.4278	1.42779	29.0102	0.25189	0.001*
	Type: Exposure	5	1.4569	0.29139	5.9205	0.25703	0.001*
	Residuals	12	0.5906	0.04922		0.10419	
	Total	23	5.6684			1	
After 1 month	Type	5	1.2345	0.24689	4.613	0.37296	0.001*
	Exposure	1	0.712	0.71205	13.3043	0.21513	0.001*
	Type: Exposure	5	0.7747	0.15493	2.8949	0.23405	0.001*
	Residuals	11	0.5887	0.05352		0.17787	
	Total	22	3.3099			1	
After 2 months	Type	5	1.6556	0.33113	5.1858	0.39508	0.001*
	Exposure	1	1.1561	1.15607	18.1051	0.27587	0.001*
	Type: Exposure	5	0.7404	0.14809	2.3192	0.17669	0.007*
	Residuals	10	0.6385	0.06385		0.15237	
	Total	21	4.1907			1	

* indicates significant differences ($p < 0.05$).

Table S8 - Results of the LEfSe analysis identifying taxa (down to the family level) discriminating for either glass or either one of the plastics after one week of incubation.

Surfaces compared	Taxa		Surface	LDA score (log 10)	p value
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales	3.5	Glass	3.19	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SAR116clade	3.03	Glass	2.68	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae	3.23	Glass	2.80	0.02
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	2.64	Glass	2.51	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Granulosicoccaceae	2.16	Glass	2.04	0.14
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__KD4_96	2.01	Glass	2.95	0.02
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	2.42	Glass	2.15	0.25
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Nocardiaceae	1	Glass	2.44	0.13
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Porticoccaceae	1.77	Glass	2.77	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae	3.24	Glass	2.90	0.02
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria	3.21	Glass	2.81	0.04
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae2	1.06	DEHP	3.40	0.13
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae	2.61	Glass	2.29	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae	1.3	Glass	2.25	0.13
Glass vs DEHP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales	2.28	Glass	2.07	0.01
Glass vs DEHP	k__Bacteria; p__Proteobacteria	5.47	DEHP	4.94	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Moritellaceae	2.07	Glass	2.07	0.14
Glass vs DEHP	k__Bacteria; p__Chlamydiae	2.67	DEHP	2.29	0.25
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Caldilineae	2.61	Glass	2.23	0.19
Glass vs DEHP	k__Bacteria; p__Fusobacteria	2.27	Glass	2.04	0.14
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sandaracinaceae	2.54	Glass	2.23	0.02
Glass vs DEHP	k__Bacteria; p__Bacteroidetes	4.9	Glass	4.50	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Kiloniellaceae	2.01	Glass	2.45	0.02
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia	4.85	Glass	4.46	0.02
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	2.38	Glass	2.39	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	3.42	Glass	2.81	0.25
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales	2.09	Glass	2.19	0.13
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria	3.57	Glass	3.15	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales	3.3	Glass	2.89	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__ProteobacteriaIncertaeSedis	3.32	Glass	3.09	0.19
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__FFCH9454	0.79	DEHP	4.08	0.13
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae	2.11	Glass	2.04	0.14
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__BD7_8marinegroup	2.7	Glass	2.42	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__JTB255marinebenthicgroup	3.04	Glass	2.68	0.02
Glass vs DEHP	k__Bacteria	6	DEHP	4.56	0.01
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales	1.97	Glass	2.61	0.02
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Anaerolineae	2.39	Glass	2.00	0.39
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__OM182clade	2.62	Glass	2.29	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Spongiibacteraceae	3.33	Glass	2.99	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales	1.99	DEHP	2.52	0.04
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia	3.15	Glass	2.82	0.02
Glass vs DEHP	k__Archaea; p__Euryarchaeota; c__Thermoplasmata	2.49	Glass	2.24	0.01

Chapter I

Glass vs DEHP	k__Archaea; p__Euryarchaeota	2.49	Glass	2.26	0.01
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae	2.29	Glass	2.18	0.02
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Opitutae	3.52	Glass	3.22	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales	2.69	Glass	2.17	0.39
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.22	Glass	3.68	0.08
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Cytophagia	3.24	Glass	2.89	0.02
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae	2.75	Glass	2.36	0.15
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae	3.24	Glass	2.81	0.08
Glass vs DEHP	k__Bacteria; p__Gemmatimonadetes	2.17	Glass	2.42	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacterialIncertainSedis	3.51	Glass	3.05	0.04
Glass vs DEHP	k__Bacteria; p__Nitrospinae; c__Nitrospina; o__Nitrospinales; f__Nitrospinaeae	1.6	Glass	2.24	0.14
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Coriobacteriia	1.97	Glass	2.63	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae	2.83	Glass	2.48	0.04
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Bacteroidia	2.65	Glass	2.67	0.02
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales; f__Caldilineaceae	2.61	Glass	2.26	0.19
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Alcaligenaceae	2.56	Glass	2.27	0.08
Glass vs DEHP	k__Archaea; p__Euryarchaeota; c__Thermoplasmata; o__Thermoplasmatales	2.49	Glass	2.26	0.01
Glass vs DEHP	k__Bacteria; p__Spirochaetae; c__Spirochaetes	1.55	Glass	2.76	0.13
Glass vs DEHP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales; f__Lentisphaeraeae	2.28	Glass	2.07	0.01
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales; f__Desulfobacteraceae	2.73	Glass	2.42	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__SAR86clade	2.44	Glass	2.24	0.02
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales	2.61	Glass	2.32	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__K189Aclade	2.46	Glass	2.13	0.02
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionIII	2.24	Glass	2.17	0.14
Glass vs DEHP	k__Bacteria; p__Firmicutes	3.25	Glass	2.88	0.02
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionIII; f__FamilyI	2.24	Glass	2.17	0.14
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Actinobacteria	2.77	Glass	2.43	0.02
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Melainabacteria; o__Obscuribacteriales	2.08	Glass	2.09	0.13
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__Rickettsiaceae	2.46	Glass	2.37	0.15
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__RhizobialesIncertainSedis	1.93	Glass	2.15	0.32
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Phycisphaerae	3.25	Glass	2.87	0.02
Glass vs DEHP	k__Bacteria; p__Nitrospinae	1.91	Glass	2.42	0.14
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bacteriovoracaceae	2.93	Glass	2.59	0.08
Glass vs DEHP	k__Archaea; p__Euryarchaeota; c__Thermoplasmata; o__Thermoplasmatales; f__MarineGroupII	2.49	Glass	2.24	0.01
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales	2.7	Glass	2.42	0.04
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__unidentifiedmarinebacterioplankton	1.74	Glass	2.03	0.32
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Acidimicrobia; o__Acidimicrobiales; f__Sva0996marinegroup	2.73	Glass	2.42	0.02
Glass vs DEHP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Victivallales; f__PRD18C08	1.39	Glass	2.05	0.13
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales	3.24	Glass	2.92	0.02
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraeae	3.21	Glass	2.83	0.02
Glass vs DEHP	k__Bacteria; p__Planctomycetes	4.41	Glass	3.93	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae	3.29	Glass	2.93	0.02
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae1	2.52	Glass	2.45	0.02

Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales	5.13	DEHP	4.77	0.08
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__Acidimicrobiaceae	2.42	Glass	2.14	0.02
Glass vs DEHP	k__Bacteria; p__Acidobacteria	2.82	Glass	2.41	0.25
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis; o__UnknownOrder	3.32	Glass	3.08	0.19
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales	3.21	Glass	2.82	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales	3.11	Glass	2.74	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.52	Glass	3.10	0.15
Glass vs DEHP	k__Bacteria; p__Acidobacteria; c__Holophagae	2.46	Glass	2.15	0.19
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Marinilabiaceae	2.42	Glass	2.18	0.09
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Lithodendmiumundulatum	2.74	Glass	2.84	0.09
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae	2.24	Glass	2.01	0.02
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.22	Glass	3.67	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Halieaceae	3.35	Glass	2.98	0.02
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__DEV007	2.96	Glass	2.52	0.08
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae	4.78	Glass	4.44	0.02
Glass vs DEHP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria	2.37	Glass	2.12	0.01
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertainSedis	2.04	Glass	2.30	0.19
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales	2.17	Glass	2.04	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales	2.85	Glass	2.49	0.04
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Exanthemachrysisgayraliae	2.45	Glass	2.17	0.04
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__OM190	2.8	Glass	2.48	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae	3.37	Glass	2.86	0.08
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Stauroneisconstricta	2.93	Glass	2.98	0.24
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__P3OB_42	1.39	Glass	2.03	0.13
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales	2.39	Glass	2.00	0.39
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__SS1_B_06_26	4.14	Glass	3.76	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Ectothiorhodospiraceae	2.29	Glass	2.05	0.01
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__EC3	1.01	DEHP	3.54	0.32
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__R76_B128	2.32	Glass	2.06	0.09
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI	3.13	Glass	2.75	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__BD2_7	2.24	Glass	2.03	0.02
Glass vs DEHP	k__Bacteria; p__Nitrospinae; c__Nitrospina	1.6	Glass	2.25	0.14
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	1.97	Glass	2.72	0.02
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Pla4lineage	1.25	Glass	2.21	0.32
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Kazan_2B_17	1.32	Glass	2.66	0.32
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae	2.18	Glass	2.04	0.19
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae	2.59	Glass	2.27	0.02
Glass vs DEHP	k__Bacteria; p__Acidobacteria; c__Subgroup26	1.42	Glass	2.63	0.32
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	2.65	Glass	2.43	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae	5.12	DEHP	4.78	0.04
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae	3.21	Glass	2.88	0.02
Glass vs DEHP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae	2.09	Glass	2.21	0.13
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Minidiscustrioculatus	2.64	Glass	2.54	0.08

Chapter I

Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae	1.53	Glass	2.49	0.04
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SHWN_night2	1.75	Glass	3.16	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria	4.35	Glass	3.58	0.15
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales	3.02	Glass	2.67	0.02
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales	2.61	Glass	2.23	0.19
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	3.04	Glass	2.42	0.25
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales	1.93	Glass	2.01	0.09
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI	3.13	Glass	2.73	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bdellovibrionaceae	2.44	Glass	2.50	0.15
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__OCS116clade	1.98	Glass	2.34	0.25
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacterialIncertainSedis; f__UnknownFamily	3.51	Glass	3.04	0.04
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	4.04	Glass	3.66	0.02
Glass vs DEHP	k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales	2.67	DEHP	2.27	0.25
Glass vs DEHP	k__Bacteria; p__Fusobacteria; c__Fusobacteriia	2.27	Glass	2.02	0.14
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__AlphaproteobacterialIncertainSedis; f__UnknownFamily	2.77	DEHP	2.49	0.25
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	2.79	Glass	2.49	0.02
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Extubocellulisciriger	2.65	Glass	2.66	0.08
Glass vs DEHP	k__Bacteria; p__Cyanobacteria	5.35	Glass	5.03	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales; f__Desulfobulbaceae	2.87	Glass	2.51	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__ss1_B_07_44	2.21	Glass	2.04	0.09
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	2.62	Glass	2.37	0.04
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Clostridia	3.02	Glass	2.65	0.02
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae	2.4	Glass	2.13	0.04
Glass vs DEHP	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.22	Glass	3.66	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae	3.43	Glass	2.98	0.25
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__NS9marinegroup	2.57	Glass	2.31	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales	2.74	Glass	2.41	0.04
Glass vs DEHP	k__Bacteria; p__Nitrospinae; c__Nitrospina; o__Nitrospinales	1.6	Glass	2.26	0.14
Glass vs DEHP	k__Bacteria; p__Chlamydiae; c__Chlamydiae	2.67	DEHP	2.30	0.25
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales	3.05	Glass	2.67	0.04
Glass vs DEHP	k__Bacteria; p__Spirochaetae	1.55	Glass	2.75	0.13
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria	2.81	Glass	2.52	0.04
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	2.29	Glass	2.49	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales; f__Parvularculaceae	1.99	DEHP	2.52	0.04
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae	4.59	DEHP	4.25	0.25
Glass vs DEHP	k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales	2.27	Glass	2.09	0.14
Glass vs DEHP	k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae	2.26	Glass	2.11	0.14
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Musaitinerans	3.33	Glass	3.01	0.09
Glass vs DEHP	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales; f__Puniceococcaceae	3.5	Glass	3.16	0.02
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Bacilli	2.79	Glass	2.48	0.02
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Rhizosoleniaimbricata	2.19	Glass	2.02	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae	4.92	DEHP	4.57	0.08
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	2.53	Glass	2.25	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis; o__UnknownOrder; f__UnknownFamily	3.32	Glass	3.06	0.19

Chapter I

Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae	3.42	Glass	2.83	0.25
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__pltb_vmat_80	1.51	Glass	2.10	0.32
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae	2.69	Glass	2.18	0.39
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Helicobacteraceae	2.64	Glass	2.34	0.02
Glass vs DEHP	k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales; f__Simkaniaceae	2.66	DEHP	2.29	0.25
Glass vs DEHP	k__Archaea	3.12	Glass	2.83	0.01
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Ardenticatenia	1.46	Glass	2.08	0.13
Glass vs DEHP	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae	2.39	Glass	2.01	0.39
Glass vs DEHP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Carnobacteriaceae	1.98	Glass	2.06	0.32
Glass vs DEHP	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales	3.24	Glass	2.90	0.02
Glass vs DEHP	k__Bacteria; p__Actinobacteria	3.32	Glass	2.97	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae	2.18	Glass	2.75	0.02
Glass vs DEHP	k__Bacteria; p__Lentisphaerae	2.52	Glass	2.24	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__S25_593	2.23	Glass	2.04	0.08
Glass vs DEHP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Synedrahyperborea	3.85	Glass	3.57	0.02
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales	1.69	Glass	2.16	0.13
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales	3.43	Glass	2.94	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	2.7	Glass	2.45	0.04
Glass vs DEHP	k__Bacteria; p__Chloroflexi	2.93	Glass	2.57	0.08
Glass vs DEHP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	2.53	Glass	2.21	0.02
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales	3.5	Glass	3.23	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SAR116clade	3.03	Glass	2.67	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae	3.23	Glass	2.8	0.02
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	2.64	Glass	2.32	0.02
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	2.42	Glass	2.07	0.25
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Nocardiaceae	1	Glass	2.36	0.13
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Porticoccaceae	1.77	Glass	2.51	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae	3.24	Glass	2.9	0.02
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria	3.21	Glass	2.84	0.02
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae4	0.65	DINP	2.49	0.13
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae2	0.68	DINP	2.71	0.13
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae	2.61	Glass	2.3	0.04
Glass vs DINP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales	2.28	Glass	2.06	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria	5.46	DINP	4.88	0.02
Glass vs DINP	k__Bacteria; p__Chloroflexi; c__Caldilineae	2.61	Glass	2.2	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sandaracinaceae	2.54	Glass	2.13	0.02
Glass vs DINP	k__Bacteria; p__Acidobacteria; c__Subgroup17	0.65	DINP	2.57	0.13
Glass vs DINP	k__Bacteria; p__Bacteroidetes	4.9	Glass	4.42	0.02
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia	4.85	Glass	4.41	0.02
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	2.38	Glass	2.1	0.02
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia	3.86	DINP	2.89	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	3.42	Glass	2.78	0.39
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria	3.57	Glass	3.1	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales	3.3	Glass	2.85	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis	3.32	Glass	3.05	0.25

Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__BD7_8marinegroup	2.7	Glass	2.35	0.02
Glass vs DINP	k__Bacteria	6	DINP	4.08	0.01
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__OM182clade	2.62	Glass	2.24	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Spongiibacteraceae	3.33	Glass	2.94	0.02
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia	3.15	Glass	2.75	0.02
Glass vs DINP	k__Archaea; p__Euryarchaeota; c__Thermoplasmata	2.49	Glass	2.23	0.01
Glass vs DINP	k__Archaea; p__Euryarchaeota	2.49	Glass	2.22	0.01
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae	2.8	Glass	2.03	0.15
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__Opitutae	3.52	Glass	3.24	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales	2.69	Glass	2.12	0.39
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.22	Glass	3.79	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales	4.52	DINP	4.12	0.39
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Cytophagia	3.24	Glass	2.87	0.02
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae	2.75	Glass	2.27	0.08
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae	3.24	Glass	2.77	0.08
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacterialIncertaeSedis	3.51	Glass	3.01	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae	2.83	Glass	2.46	0.04
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Bacteroidia	2.65	Glass	2.34	0.02
Glass vs DINP	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales; f__Caldilineaceae	2.61	Glass	2.19	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Alcaligenaceae	2.56	Glass	2.22	0.25
Glass vs DINP	k__Archaea; p__Euryarchaeota; c__Thermoplasmata; o__Thermoplasmatales	2.49	Glass	2.2	0.01
Glass vs DINP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales; f__Lentisphaeraceae	2.28	Glass	2.04	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales; f__Desulfobacteraceae	2.73	Glass	2.32	0.02
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae	3.86	DINP	2.92	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__SAR86clade	2.44	Glass	2.19	0.02
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales	2.61	Glass	2.26	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__KI89Aclade	2.46	Glass	2.13	0.04
Glass vs DINP	k__Bacteria; p__Firmicutes	3.25	Glass	2.87	0.02
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Actinobacteria	2.77	Glass	2.41	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__Rickettsiaceae	2.46	Glass	2.13	0.02
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__Phycisphaerae	3.25	Glass	2.87	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kordiimonadales; f__Kordiimonadaceae	1.27	DINP	2.51	0.05
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bacteriovoracaceae	2.93	Glass	2.58	0.04
Glass vs DINP	k__Archaea; p__Euryarchaeota; c__Thermoplasmata; o__Thermoplasmatales; f__MarineGroupII	2.49	Glass	2.23	0.01
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales	2.7	Glass	2.34	0.02
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__Sva0996marinegroup	2.73	Glass	2.39	0.02
Glass vs DINP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Victivallales; f__PRD18C08	1.39	Glass	2.21	0.13
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales	3.24	Glass	2.92	0.02
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae	3.21	Glass	2.83	0.02
Glass vs DINP	k__Bacteria; p__Planctomycetes	4.41	Glass	4	0.02
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertaeSedis; o__OrderIII; f__UnknownFamily	1.49	Glass	2.37	0.13
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae	3.29	Glass	2.93	0.02

Chapter I

Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae1	2.52	Glass	2.19	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales	5.07	DINP	4.74	0.02
Glass vs DINP	k__Bacteria; p__Acidobacteria	2.82	Glass	2.44	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis; o__UnknownOrder	3.32	Glass	3.05	0.25
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales	3.21	Glass	2.81	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales	3.11	Glass	2.72	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.52	Glass	3	0.15
Glass vs DINP	k__Bacteria; p__Acidobacteria; c__Holophagae	2.46	Glass	2.09	0.25
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Marinilabiaceae	2.42	Glass	2.11	0.14
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Lithodendmiumundulatum	2.74	Glass	2.47	0.24
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.22	Glass	3.8	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Halieaceae	3.35	Glass	2.77	0.04
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__DEV007	2.96	Glass	2.54	0.15
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae	4.78	Glass	4.32	0.02
Glass vs DINP	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria	2.37	Glass	2.09	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales	2.85	Glass	2.48	0.04
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Exanthemachrysisgayraliae	2.45	Glass	2.17	0.02
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__OM190	2.8	Glass	2.48	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales	5.05	DINP	4.38	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae	3.37	Glass	2.64	0.39
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Stauroneisconstricta	2.93	Glass	2.63	0.24
Glass vs DINP	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales	2.39	Glass	2.02	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Ectothiorhodospiraceae	2.29	Glass	2.32	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__EC3	1.01	DINP	2.19	0.09
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__R76_B128	2.32	Glass	2.04	0.09
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI	3.13	Glass	2.77	0.02
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Halanaerobiales; f__ODP1230B8_23	0.92	DINP	2.75	0.13
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Caulobacteraceae	2.59	Glass	2.26	0.02
Glass vs DINP	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	2.65	Glass	2.22	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae	5.06	DINP	4.76	0.02
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae	3.21	Glass	2.88	0.02
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Minidiscutriculatus	2.64	Glass	2.35	0.15
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	1.69	Glass	2.27	0.13
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria	4.35	Glass	3.44	0.25
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales	3.02	Glass	2.66	0.02
Glass vs DINP	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales	2.61	Glass	2.19	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	3.04	Glass	2.37	0.39
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI	3.13	Glass	2.78	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacterialIncertainSedis; f__UnknownFamily	3.51	Glass	3.02	0.04
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	4.04	Glass	3.66	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	2.79	Glass	2.41	0.02
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Extubocellulusscribriger	2.65	Glass	2.32	0.25
Glass vs DINP	k__Bacteria; p__Cyanobacteria	5.35	Glass	5.07	0.04

Chapter I

Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobulbaceae	2.87	Glass	2.5	0.04
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	2.62	Glass	2.22	0.02
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Clostridia	3.02	Glass	2.64	0.02
Glass vs DINP	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.22	Glass	3.77	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae	3.43	Glass	2.79	0.39
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__NS9marinegroup	2.57	Glass	2.22	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales	2.74	Glass	2.36	0.08
Glass vs DINP	k__Bacteria; p__Gracilibacteria; c__marinemetagenome	3.53	DINP	3.32	0.08
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria	2.81	Glass	2.47	0.08
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	2.29	Glass	2.08	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae	4.51	DINP	4.13	0.08
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Musaitinerans	3.33	Glass	3.07	0.14
Glass vs DINP	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales; f__Puniceicoccaceae	3.5	Glass	3.22	0.02
Glass vs DINP	k__Bacteria; p__Firmicutes; c__Bacilli	2.79	Glass	2.43	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae	4.87	DINP	4.45	0.08
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	2.53	Glass	2.22	0.02
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__ProteobacterialncertaeSedis; o__UnknownOrder; f__UnknownFamily	3.32	Glass	3.05	0.25
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae	3.42	Glass	2.79	0.39
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae	2.69	Glass	2.11	0.39
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae	2.64	Glass	2.24	0.02
Glass vs DINP	k__Archaea	3.12	Glass	2.8	0.01
Glass vs DINP	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae	2.39	Glass	2.03	0.25
Glass vs DINP	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales	3.24	Glass	2.89	0.02
Glass vs DINP	k__Bacteria; p__Actinobacteria	3.32	Glass	2.92	0.02
Glass vs DINP	k__Bacteria; p__Lentisphaerae	2.52	Glass	2.24	0.02
Glass vs DINP	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Synedrahyperborea	3.85	Glass	3.56	0.04
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales	1.69	Glass	2.46	0.13
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales	3.43	Glass	2.74	0.15
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	2.7	Glass	2.35	0.02
Glass vs DINP	k__Bacteria; p__Chloroflexi	2.93	Glass	2.55	0.08
Glass vs DINP	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	2.53	Glass	2.17	0.04
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales	3.5	Glass	3.05	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae	3.23	Glass	2.42	0.15
HDPE vs Glass	k__Bacteria; p__Chloroflexi; c__KD4_96	2.01	Glass	2.05	0.15
HDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Nocardiaceae	1	Glass	2.92	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae	4.1	Glass	3.12	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae	3.24	Glass	2.61	0.04
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria	3.21	Glass	2.67	0.25
HDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales	2.28	Glass	2.28	0.02
HDPE vs Glass	k__Bacteria; p__Proteobacteria	5.22	HDPE	4.44	0.25
HDPE vs Glass	k__Bacteria; p__Chlamydiae	2.43	Glass	2.11	0.08
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia	4.93	HDPE	3.96	0.39
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	2.38	Glass	2.08	0.04
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia	3.77	Glass	2.77	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	3.68	HDPE	3.09	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria	3.57	Glass	2.59	0.25

HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales	3.3	Glass	2.5	0.15
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis	3.32	Glass	3.1	0.14
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Arctic97B_4marinegroup	2.12	HDPE	2.17	0.32
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales; f__Syntrophobacteraceae	2.33	HDPE	2.11	0.08
HDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales	1.97	Glass	2.51	0.08
HDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae	2.39	Glass	2.18	0.14
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Oligoflexales	1.39	HDPE	2.28	0.32
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae	3.52	Glass	3.04	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales	2.94	HDPE	2.26	0.39
HDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.22	Glass	3.74	0.15
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae	2.75	Glass	2.34	0.15
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae	3.24	Glass	2.69	0.15
HDPE vs Glass	k__Bacteria; p__Gemmatimonadetes	2.17	Glass	2.04	0.04
HDPE vs Glass	k__Bacteria; p__Nitrospinae; c__Nitrospina; o__Nitrospinales; f__Nitrospinaceae	1.6	Glass	2.18	0.17
HDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia	1.97	Glass	2.17	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae	2.83	Glass	2.46	0.04
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__ZD0405	2.18	HDPE	2.37	0.05
HDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Oligosphaeria; o__SS1_B_02_17	1.5	Glass	2.46	0.13
HDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales; f__Lentisphaeraceae	2.28	Glass	2.24	0.02
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobacteraceae	2.73	Glass	2.14	0.08
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae	3.73	Glass	2.66	0.39
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionIII	2.24	Glass	2.07	0.14
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionIII; f__FamilyI	2.24	Glass	2.06	0.14
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__RhizobialesIncertainSedis	1.93	Glass	2.38	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11clade; f__Surface2	2.4	HDPE	2.21	0.09
HDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae	3.25	Glass	2.65	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bacteriovoraceae	2.93	Glass	2.47	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales	2.7	Glass	2.31	0.08
HDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__Sva0996marinegroup	2.73	Glass	2.14	0.39
HDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Victivallales; f__PRD18C08	1.39	Glass	2.35	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales	3.24	Glass	2.62	0.04
HDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae	3.21	Glass	2.62	0.08
HDPE vs Glass	k__Bacteria; p__Planctomycetes	4.41	Glass	3.86	0.08
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXII	1.75	HDPE	2.07	0.17
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertainSedis; o__OrderIII; f__UnknownFamily	1.49	Glass	2.18	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae	3.65	HDPE	3.18	0.39
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae1	2.52	Glass	2.19	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__RhodospirillalesIncertainSedis	1.44	Glass	2.09	0.13
HDPE vs Glass	k__Bacteria; p__Acidobacteria	2.82	Glass	2.48	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis; o__UnknownOrder	3.32	Glass	3.06	0.14
HDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales	3.21	Glass	2.56	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.52	Glass	3.04	0.04
HDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae	2.46	Glass	2.18	0.19
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Lithodesmiumundulatum	2.74	Glass	2.43	0.37

Chapter I

HDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.22	Glass	3.74	0.15
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae	4.88	HDPE	4.04	0.39
HDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria	2.37	Glass	2.15	0.02
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertainSedis	2.04	Glass	2.18	0.19
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Sva0485	1.68	Glass	2.22	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales	2.85	Glass	2.47	0.04
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Exanthemachrysisgayraliae	2.45	Glass	2.21	0.02
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae	1.06	Glass	2.61	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales	5	HDPE	4.31	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__P3OB_42	1.39	Glass	2.3	0.13
HDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales	2.39	Glass	2.17	0.14
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__R76_B128	2.32	Glass	2	0.24
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI	3.13	Glass	2.59	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Hydrogenophilales; f__Hydrogenophilaceae	1.95	Glass	2.04	0.32
HDPE vs Glass	k__Bacteria; p__Nitrospinae; c__Nitrospina	1.6	Glass	2.16	0.17
HDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	1.97	Glass	2.68	0.08
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Kazan_2B_17	1.32	Glass	2.36	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Caulobacteraceae	2.59	Glass	2.16	0.15
HDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Subgroup26	1.42	Glass	2.23	0.13
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae	1.53	Glass	2.45	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	4.84	HDPE	4.27	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Oligoflexales; f__Oligoflexaceae	1.39	HDPE	2.28	0.32
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales	3.02	Glass	2.4	0.04
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales	1.93	Glass	2.02	0.14
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI	3.13	Glass	2.54	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Piscirickettsiaceae	2.68	HDPE	2.16	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacteriales	2.33	HDPE	2.12	0.08
HDPE vs Glass	k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales	2.43	Glass	2.07	0.08
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	2.79	Glass	2.01	0.39
HDPE vs Glass	k__Bacteria; p__Cyanobacteria	5.35	Glass	4.77	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__ss1_B_07_44	2.21	Glass	2.13	0.09
HDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia	3.02	Glass	2.48	0.08
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae	2.4	Glass	2.1	0.15
HDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.22	Glass	3.74	0.15
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__NS9marinegroup	2.57	Glass	2.13	0.04
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__M05_Pitesti	0.92	HDPE	2.54	0.13
HDPE vs Glass	k__Bacteria; p__Nitrospinae; c__Nitrospina; o__Nitrospinales	1.6	Glass	2.18	0.17
HDPE vs Glass	k__Bacteria; p__Chlamydiae; c__Chlamydiae	2.43	Glass	2.07	0.08
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Schleiferiaceae	1.39	Glass	2.51	0.13
HDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup10	2.29	Glass	2.07	0.24
HDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales; f__Puniceococcaceae	3.5	Glass	3.01	0.25
HDPE vs Glass	k__Bacteria; p__Marinimicrobia_SAR406clade; c__marinemetagenome	1.48	HDPE	2.27	0.13
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	2.53	Glass	2.19	0.02
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis; o__UnknownOrder; f__UnknownFamily	3.32	Glass	3.06	0.14

HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae	3.68	HDPE	3.12	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae	2.64	Glass	2.36	0.02
HDPE vs Glass	k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales; f__Simkaniaceae	2.38	Glass	2.02	0.25
HDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae	2.39	Glass	2.17	0.14
HDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Subgroup21	2.07	Glass	2.2	0.09
HDPE vs Glass	k__Bacteria; p__Actinobacteria	3.32	Glass	2.52	0.39
HDPE vs Glass	k__Bacteria; p__Lentisphaerae	2.52	Glass	2.13	0.25
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales	4.1	Glass	3.06	0.39
HDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup10; f__CA002	1.85	Glass	2.02	0.13
HDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Syndrahyperborea	3.85	Glass	3.43	0.15
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	2.7	Glass	2.31	0.08
HDPE vs Glass	k__Bacteria; p__Chloroflexi	2.93	Glass	2.42	0.39
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	2.53	Glass	2.06	0.39
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales	3.5	Glass	3.01	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SAR116clade	3.03	Glass	2.36	0.08
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae	3.57	LDPE	3	0.02
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	2.64	Glass	2.23	0.08
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Granulosicoccaceae	2.16	Glass	2.02	0.09
LDPE vs Glass	k__Bacteria; p__Chloroflexi; c__KD4_96	2.01	Glass	2.05	0.02
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Nocardaceae	1	Glass	3.01	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Porticoccaceae	1.77	Glass	2.67	0.02
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae	3.24	Glass	2.63	0.15
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae	2.61	Glass	2.23	0.25
LDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales	2.28	Glass	2.1	0.02
LDPE vs Glass	k__Bacteria; p__Proteobacteria	5.34	LDPE	4.7	0.08
LDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Caldilineae	2.61	Glass	2.32	0.19
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sandaracinaceae	2.54	Glass	2.26	0.02
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Pla3lineage	2.2	LDPE	2.41	0.32
LDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Subgroup17	1.63	LDPE	2.25	0.13
LDPE vs Glass	k__Bacteria; p__Bacteroidetes	4.9	Glass	4	0.39
LDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	2.38	Glass	2.22	0.02
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia	3.77	Glass	3	0.39
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	4.04	LDPE	3.58	0.15
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales	2.41	LDPE	2.15	0.37
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales	3.62	LDPE	3.05	0.02
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__ProteobacterialIncertainSedis	3.32	Glass	3.05	0.47
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__BD7_8marinegroup	2.7	Glass	2.36	0.02
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales	1.97	Glass	2.07	0.15
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Spongiibacteraceae	3.73	LDPE	3.14	0.39
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales	1.82	LDPE	2.04	0.17
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia	3.3	LDPE	2.51	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfurellales	2.36	LDPE	2.14	0.15
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae	3.52	Glass	3.03	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales	3.41	LDPE	3.1	0.15
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.22	Glass	3.74	0.08

Chapter I

LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Cytophagia	3.24	Glass	2.79	0.04
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae	3.24	Glass	2.47	0.39
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacteriaIncertaeSedis	3.51	Glass	2.67	0.39
LDPE vs Glass	k__Bacteria; p__Nitrospinae; c__Nitrospina; o__Nitrospinales; f__Nitrospinaceae	1.6	Glass	2	0.17
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia	1.97	Glass	2.11	0.15
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae	2.83	Glass	2.26	0.25
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Bacteroidia	2.65	Glass	2.08	0.15
LDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales; f__Caldilineaceae	2.61	Glass	2.3	0.19
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Alcaligenaceae	2.56	Glass	2.2	0.08
LDPE vs Glass	k__Bacteria; p__Fibrobacteres	1.93	Glass	2.03	0.13
LDPE vs Glass	k__Bacteria; p__Spirochaetae; c__Spirochaetes	1.55	Glass	2.2	0.13
LDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Oligosphaeria; o__SS1_B_02_17	1.5	Glass	2.32	0.13
LDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales; f__Lentisphaeraceae	2.28	Glass	2.1	0.02
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales; f__Desulfobacteraceae	2.73	Glass	2.1	0.25
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales	2.61	Glass	2.22	0.25
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae	3.25	Glass	2.6	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales	2.7	Glass	2.36	0.02
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__Sva0996marinegroup	2.73	Glass	2.36	0.08
LDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Victivallales; f__PRD18C08	1.39	Glass	2.32	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales	3.24	Glass	2.54	0.15
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__OPB35soilgroup	1.56	LDPE	2.4	0.14
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae	3.21	Glass	2.47	0.25
LDPE vs Glass	k__Bacteria; p__Planctomycetes	4.41	Glass	3.89	0.15
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertaeSedis; o__OrderIII; f__UnknownFamily	1.49	Glass	2.17	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__RhodospirillalesIncertaeSedis	1.44	Glass	2.02	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__ProteobacteriaIncertaeSedis; o__UnknownOrder	3.32	Glass	3.02	0.47
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales	3.21	Glass	2.58	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.52	Glass	3.13	0.02
LDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae	2.46	Glass	2.13	0.19
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Marinilabiaceae	2.42	Glass	2.07	0.47
LDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Lithodermiumundulatum	2.74	Glass	2.36	0.37
LDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	2.2	Glass	2.03	0.14
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.22	Glass	3.74	0.08
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Halieaceae	3.72	LDPE	3.11	0.25
LDPE vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria	2.37	Glass	2.04	0.15
LDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Exanthemachrysisgayraliae	2.45	Glass	2.02	0.14
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales	5.16	LDPE	4.58	0.02
LDPE vs Glass	k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales; f__Parachlamydiaceae	2.04	LDPE	2.2	0.32
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Ectothiorhodospiraceae	2.29	Glass	2.03	0.15
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__R76_B128	2.32	Glass	2.12	0.05
LDPE vs Glass	k__Bacteria; p__Nitrospinae; c__Nitrospina	1.6	Glass	2.02	0.17
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	1.97	Glass	2.06	0.15
LDPE vs Glass	k__Bacteria; p__Spirochaetae; c__Spirochaetes; o__Spirochaetales	1.55	Glass	2.2	0.13
LDPE vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Kazan_2B_17	1.32	Glass	2.36	0.13

Chapter I

LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Caulobacteraceae	2.59	Glass	2.03	0.08
LDPE vs Glass	k__Bacteria; p__Acidobacteria; c__Subgroup26	1.42	Glass	2.18	0.13
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	3.07	LDPE	2.67	0.39
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae	3.21	Glass	2.74	0.04
LDPE vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae	2.41	LDPE	2.1	0.37
LDPE vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae	1.92	LDPE	2.04	0.31
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SHWN_night2	1.75	Glass	2.49	0.02
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	1.69	Glass	2.65	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfurellales; f__Desulfurellaceae	2.36	LDPE	2.14	0.15
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	5.07	LDPE	4.66	0.02
LDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales	2.61	Glass	2.31	0.19
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacterialncertaeSedis; f__UnknownFamily	3.51	Glass	2.75	0.39
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	4.04	Glass	3.39	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	2.79	Glass	2.41	0.04
LDPE vs Glass	k__Bacteria; p__Cyanobacteria	5.35	Glass	4.89	0.39
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__ss1_B_07_44	2.21	Glass	2.11	0.09
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae	2.4	Glass	2.09	0.25
LDPE vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.22	Glass	3.75	0.08
LDPE vs Glass	k__Bacteria; p__Spirochaetae	1.55	Glass	2.18	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales; f__Parvularculaceae	1.82	LDPE	2	0.17
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae	3.48	Glass	2.81	0.39
LDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Musaitinerans	3.33	Glass	3.05	0.37
LDPE vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales; f__Puniceococcaceae	3.5	Glass	2.94	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__ProteobacterialncertaeSedis; o__UnknownOrder; f__UnknownFamily	3.32	Glass	3.06	0.47
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae	4.04	LDPE	3.56	0.15
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__pltb_vmat_80	1.51	Glass	2.33	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae	3.41	LDPE	3.05	0.15
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Helicobacteraceae	2.64	Glass	2.31	0.02
LDPE vs Glass	k__Bacteria; p__Chloroflexi; c__Ardenticatenia	1.46	Glass	2.27	0.13
LDPE vs Glass	k__Bacteria; p__Parcubacteria; c__CandidatusFalkowbacteria	2.03	Glass	2.14	0.13
LDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales	3.24	Glass	2.79	0.04
LDPE vs Glass	k__Bacteria; p__Lentisphaerae	2.52	Glass	2.16	0.15
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__S25_593	2.23	Glass	2.05	0.04
LDPE vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Synedrahyperborea	3.85	Glass	3.56	0.08
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales	1.69	Glass	2.52	0.13
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	2.7	Glass	2.33	0.02
LDPE vs Glass	k__Bacteria; p__Chloroflexi	2.93	Glass	2.45	0.25
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Legionellales	2.17	Glass	2.03	0.09
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	2.53	Glass	2.06	0.15
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SAR116clade	3.03	Glass	2.35	0.04
PP vs Glass	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o__Fibrobacteriales; f__Fibrobacteraceae	2.59	PP	2.26	0.04
PP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae	2.61	Glass	2.16	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria	5.16	PP	4.14	0.39

Chapter I

PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sandaracinaceae	2.54	Glass	2.04	0.39
PP vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	2.38	Glass	2	0.02
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	3.76	PP	3.21	0.15
PP vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Virgulinafragilis	3.4	PP	2.95	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__OM182clade	2.62	Glass	2.19	0.08
PP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia	3.15	Glass	2.49	0.25
PP vs Glass	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria	2.59	PP	2.25	0.04
PP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.22	Glass	3.52	0.25
PP vs Glass	k__Bacteria; p__Bacteroidetes; c__Cytophagia	3.5	PP	2.86	0.04
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae	2.83	Glass	2.28	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Alcaligenaceae	2.56	Glass	2.15	0.15
PP vs Glass	k__Bacteria; p__Fibrobacteres	2.59	PP	2.16	0.15
PP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales	2.61	Glass	2.12	0.25
PP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria	2.77	Glass	2.24	0.25
PP vs Glass	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o__Fibrobacterales	2.59	PP	2.26	0.04
PP vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae	3.25	Glass	2.51	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales	2.7	Glass	2.26	0.04
PP vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraeaceae	3.21	Glass	2.59	0.08
PP vs Glass	k__Bacteria; p__Planctomycetes	4.41	Glass	3.72	0.25
PP vs Glass	k__Bacteria; p__Acidobacteria	2.82	Glass	2.34	0.19
PP vs Glass	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales	3.21	Glass	2.56	0.08
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.52	Glass	3.02	0.15
PP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae	2.46	Glass	2.02	0.14
PP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.22	Glass	3.54	0.25
PP vs Glass	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria	2.37	Glass	2.05	0.04
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales	2.85	Glass	2.33	0.25
PP vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Exanthemachrysisgayraliae	2.45	Glass	2.18	0.02
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales	4.96	PP	4.14	0.39
PP vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales	2.39	Glass	2.01	0.47
PP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	2.65	Glass	2.04	0.08
PP vs Glass	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae	3.48	PP	2.85	0.02
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	4.81	PP	4.19	0.08
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	3.04	Glass	2.41	0.15
PP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	4.04	Glass	3.35	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	2.79	Glass	2.23	0.02
PP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.22	Glass	3.47	0.25
PP vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Musaitinerans	3.33	Glass	2.98	0.05
PP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	2.53	Glass	2.02	0.04
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae	3.76	PP	3.14	0.15
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae	2.64	Glass	2.21	0.04
PP vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae	2.39	Glass	2.02	0.47
PP vs Glass	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales	3.5	PP	2.88	0.04
PP vs Glass	k__Bacteria; p__Actinobacteria	3.32	Glass	2.71	0.15
PP vs Glass	k__Bacteria; p__Lentisphaerae	2.52	Glass	2.17	0.08
PP vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Synedrahyperborea	3.85	Glass	3.51	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	2.7	Glass	2.27	0.04

PP vs Glass	k__Bacteria; p__Chloroflexi	2.93	Glass	2.42	0.25
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	2.53	Glass	2.04	0.08

Table S9 - Results of the LEfSe analysis identifying taxa (down to the family level) discriminating for either glass or either one of the plastics after one month of incubation.

Surfaces compared	Taxa		Surface	LDA score (log 10)	p value
DEHP vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales	2.61	Glass	2.36	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup23	1.7	Glass	2.4	0.02
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__KD4_96	2.36	Glass	2.35	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Blastocatellia; o__Blastocatellales	2.35	Glass	2.2	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae	2.44	Glass	2.43	0.02
DEHP vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria	3.4	Glass	2.98	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae	3.18	Glass	2.75	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria	5.34	DEHP	4.6	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Moritellaceae	1.74	Glass	2.09	0.05
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__Caldilineae	3.31	Glass	2.88	0.04
DEHP vs Glass	k__Bacteria; p__Fusobacteria	1.78	Glass	2.61	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sanderacinaceae	2.96	Glass	2.46	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes	4.85	Glass	4.34	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales	1.81	Glass	2.07	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia	4.72	Glass	4.17	0.02
DEHP vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae	2.36	Glass	2.28	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__4_Org1_14	1.32	Glass	2.27	0.05
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia	4.09	Glass	3.76	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Solirubrobacterales	1.88	Glass	2.14	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__BD7_8marinegroup	2.89	Glass	2.58	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__S15_21	1.38	Glass	3.11	0.02
DEHP vs Glass	k__Bacteria; p__Deferribacteres; c__DeferribacteresIncertainSedis	1.59	Glass	2.38	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__JTB255marinebenthicgroup	3.63	Glass	3.22	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales; f__Syntrophobacteraceae	2.21	Glass	2.88	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales	1.74	Glass	2.24	0.04
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae	2.57	Glass	2.39	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__AT_s3_28	1.56	Glass	2.13	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__MBAE14	1.31	Glass	2.37	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae	3.5	DEHP	3.11	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfurellales	1.89	Glass	2.58	0.02
DEHP vs Glass	k__Bacteria; p__Deferribacteres; c__DeferribacteresIncertainSedis; o__UnknownOrder	1.59	Glass	2.27	0.05
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__KD4_96; o__Gram_positivebacteriumSOGA31	2.24	Glass	2.7	0.02
DEHP vs Glass	k__Bacteria; p__Gemmatimonadetes	2.53	Glass	2.94	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Thermoleophilia	2.23	Glass	2.13	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacteriaincertainSedis	3.84	Glass	3.33	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia	1.74	Glass	2.28	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae	2.77	Glass	2.47	0.02
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales; f__Caldilineaceae	3.31	Glass	2.86	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Alcaligenaceae	2.22	Glass	2.01	0.05
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Solirubrobacterales; f__TM146	1.74	Glass	2.36	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobacteraceae	2.67	Glass	2.49	0.02

DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae	4.03	Glass	3.73	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Nitrosomonadales	1.4	Glass	2.29	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__HOC36	2	Glass	3.04	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kordiimonadales; f__Kordiimonadaceae	2.52	DEHP	3.08	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales	2.35	Glass	2.16	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales	2.44	Glass	2.49	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales	3.52	DEHP	3.09	0.04
DEHP vs Glass	k__Bacteria; p__Aminicenantes	1.83	Glass	2.38	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria	3.25	Glass	2.87	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__PHOS_HE51	1.49	Glass	2.82	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae	1.3	Glass	2.36	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales	3.19	Glass	2.83	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.49	Glass	3.09	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae	2.94	Glass	2.64	0.02
DEHP vs Glass	k__Bacteria; p__Firmicutes; c__Erysipelotrichia	1.73	Glass	2.47	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae	3.4	DEHP	3.12	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Haliaceae	3.59	Glass	3.13	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertaeSedis; o__OrderII	2.53	Glass	2.21	0.04
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae	4.7	Glass	4.14	0.02
DEHP vs Glass	k__Bacteria; p__SBR1093	1.77	Glass	3.03	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertaeSedis	2.53	Glass	2.2	0.04
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales	2.85	Glass	2.43	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales	2.81	Glass	2.47	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae	4.76	DEHP	4.35	0.02
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales	2.57	Glass	2.43	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Ectothiorhodospiraceae	2.07	Glass	2.91	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Mycobacteriaceae	1.58	Glass	2.82	0.04
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	1.74	Glass	2.25	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae	2.14	Glass	2.14	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Blastocatellia; o__Blastocatellales; f__Blastocatellaceae_Subgroup4	2.35	Glass	2.18	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Subgroup26	1.8	Glass	3.09	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	2.84	Glass	2.6	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae	3.5	DEHP	3.09	0.02
DEHP vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Minidiscustrioculatus	2.64	Glass	2.35	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Nitrosomonadales; f__Nitrosomonadaceae	1.4	Glass	2.28	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kordiimonadales	2.52	DEHP	3.04	0.02
DEHP vs Glass	k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae	1.73	Glass	2.55	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfurellales; f__Desulfurellaceae	1.89	Glass	2.68	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__BacteroidetesIncertaeSedis; o__OrderII; f__Rhodothermaceae	2.53	Glass	2.21	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria	5.22	DEHP	4.49	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	3.49	DEHP	3.1	0.02
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__Caldilineae; o__Caldilineales	3.31	Glass	2.86	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	4.09	Glass	3.53	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales	1.56	Glass	2.62	0.01
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SM2D12	2.17	DEHP	2.62	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bdellovibrionaceae	3.24	Glass	2.78	0.02

Chapter I

DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__OCS116clade	3.02	Glass	2.59	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Birii41	1.04	Glass	2.6	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__GammaproteobacterialncertaeSedis; f__UnknownFamily	3.84	Glass	3.35	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	3.28	Glass	2.79	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales	2.21	Glass	2.65	0.02
DEHP vs Glass	k__Bacteria; p__Fusobacteria; c__Fusobacteriia	1.78	Glass	2.54	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Blastocatellia	2.35	Glass	2.25	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__AlphaproteobacterialncertaeSedis; f__UnknownFamily	3.98	DEHP	3.71	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobulbaceae	3.04	Glass	2.66	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__ss1_B_07_44	1.78	Glass	2.86	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__NS9marinegroup	2.89	Glass	2.56	0.02
DEHP vs Glass	k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales	1.73	Glass	2.5	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Schleiferiaceae	2.47	Glass	2.42	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales	3.26	Glass	2.81	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae	3.76	DEHP	3.44	0.02
DEHP vs Glass	k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales	1.78	Glass	2.62	0.04
DEHP vs Glass	k__Bacteria; p__Deferribacteres	1.59	Glass	2.24	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Sva0071	2.82	Glass	2.47	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup10	2.87	Glass	2.49	0.02
DEHP vs Glass	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales; f__Puniceococcaceae	2.61	Glass	2.31	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae	3.08	DEHP	2.68	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	3.16	Glass	2.74	0.02
DEHP vs Glass	k__Bacteria; p__Deferribacteres; c__DeferribacteresIncrtaeSedis; o__UnknownOrder; f__UnknownFamily	1.59	Glass	2.23	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae	2.31	Glass	2.21	0.02
DEHP vs Glass	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae	2.57	Glass	2.41	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Subgroup21	2.13	Glass	2.14	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae	1.96	Glass	3.01	0.04
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup10; f__Sva0725	2.36	Glass	2.46	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales	4.76	DEHP	4.35	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	2.35	Glass	2.18	0.02
DEHP vs Glass	k__Bacteria; p__Chloroflexi	3.47	Glass	3.02	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	2.52	Glass	2.46	0.02
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae	2.44	Glass	2.29	0.03
DINP vs Glass	k__Bacteria.p__Cyanobacteria.c__Cyanobacteria	3.4	Glass	2.94	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria	5.25	DINP	4.23	0.03
DINP vs Glass	k__Bacteria.p__Chloroflexi.c__Caldilineae	3.31	Glass	2.88	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Sphingomonadales.f__Kiloniellaceae	1.6	Glass	2.17	0.03
DINP vs Glass	k__Bacteria.p__Bacteroidetes.c__Sphingobacteriia	4.09	Glass	3.69	0.03
DINP vs Glass	k__Bacteria.p__Actinobacteria.c__Thermoleophilia.o__Solirubrobacterales	1.88	Glass	2.13	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__BD7_8marinegroup	2.89	Glass	2.52	0.03
DINP vs Glass	k__Bacteria.p__Bacteroidetes.c__Sphingobacteriia.o__Sphingobacteriales.f__S15_21	1.38	Glass	2.56	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales.f__JTB255marinebenthicgroup	3.63	Glass	3.23	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__OM182clade	2.06	Glass	2.03	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Oligoflexales	3.07	Glass	2.84	0.03
DINP vs Glass	k__Bacteria.p__Gemmatimonadetes	2.53	Glass	2.32	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__GammaproteobacterialncertaeSedis	3.84	Glass	3.41	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__Rhodospirillaceae	2.77	Glass	2.32	0.03

Chapter I

DINP vs Glass	k__Bacteria.p__Chloroflexi.c__Caldilineae.o__Caldilineales.f__Caldilineaceae	3.31	Glass	2.91	0.03
DINP vs Glass	k__Bacteria.p__Actinobacteria.c__Thermoleophilia.o__Solirubrobacterales.f__TM146	1.74	Glass	2.2	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfobacterales.f__Desulfobacteraceae	2.67	Glass	2.3	0.03
DINP vs Glass	k__Bacteria.p__Bacteroidetes.c__Sphingobacteriia.o__Sphingobacteriales.f__Saprospiraceae	4.03	Glass	3.66	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__HOC36	2	Glass	2.47	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__MD3_55	1.59	Glass	2.24	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales	2.44	Glass	2.24	0.03
DINP vs Glass	k__Bacteria.p__Actinobacteria.c__Acidimicrobiia.o__Acidimicrobiales.f__Acidimicrobiaceae	3.25	Glass	2.93	0.03
DINP vs Glass	k__Bacteria.p__Actinobacteria.c__Actinobacteria.o__Corynebacteriales	1.71	Glass	2.31	0.03
DINP vs Glass	k__Bacteria.p__Bacteroidetes.c__Sphingobacteriia.o__Sphingobacteriales.f__PHOS_HE51	1.49	Glass	2.57	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfobacterales	3.19	Glass	2.79	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Thiotrichales.f__Thiotrichaceae	3.49	Glass	3.15	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales	2.81	Glass	2.36	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales.f__Hyphomonadaceae	4.68	DINP	4.29	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Chromatiales.f__Ectothiorhodospiraceae	2.07	Glass	2.26	0.03
DINP vs Glass	k__Bacteria.p__Acidobacteria.c__Subgroup26	1.8	Glass	2.61	0.03
DINP vs Glass	k__Bacteria.p__Actinobacteria.c__Acidimicrobiia.o__Acidimicrobiales.f__OM1clade	2.84	Glass	2.4	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria	5.11	DINP	4.12	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Oleiphilaceae	3.7	DINP	3.35	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Oligoflexales.f__Oligoflexaceae	3.07	Glass	2.81	0.03
DINP vs Glass	k__Bacteria.p__Chloroflexi.c__Caldilineae.o__Caldilineales	3.31	Glass	2.92	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhizobiales.f__Phyllobacteriaceae	4.09	Glass	3.52	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales	1.56	Glass	2.3	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__GammaproteobacteriaIncertaeSedis.f__UnknownFamily	3.84	Glass	3.39	0.03
DINP vs Glass	k__Bacteria.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Cryomorphaceae	3.28	Glass	2.6	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__AlphaproteobacteriaIncertaeSedis.f__UnknownFamily	3.45	DINP	3.08	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfobacterales.f__Desulfobulbaceae	3.04	Glass	2.6	0.03
DINP vs Glass	k__Bacteria.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Schefferiaceae	2.47	Glass	2.16	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Cellvibrionales.f__Cellvibrionaceae	3.79	DINP	3.48	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Sva0071	2.82	Glass	2.41	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales	4.68	DINP	4.28	0.03
DINP vs Glass	k__Bacteria.p__Chloroflexi	3.47	Glass	3.01	0.03
DINP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionellales.f__Coxiellaceae	2.47	Glass	2.16	0.03
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodobacterales.f__Rhodobacteraceae	4.95	HDPE	4.22	0.04
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae	2.44	Glass	2.06	0.04
HDPE vs Glass	k__Bacteria.p__Proteobacteria	5.23	HDPE	3.91	0.02
HDPE vs Glass	k__Bacteria.p__Gemmatimonadetes	2.53	Glass	2.15	0.02
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__GammaproteobacteriaIncertaeSedis	3.84	Glass	3.17	0.04
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales	2.44	Glass	2.06	0.04
HDPE vs Glass	k__Bacteria.p__Aminicenantes	1.83	Glass	2	0.04
HDPE vs Glass	k__Bacteria.p__Acidobacteria	3.25	Glass	2.57	0.04
HDPE vs Glass	k__Bacteria.p__Acidobacteria.c__Subgroup26	1.8	Glass	2.32	0.02
HDPE vs Glass	k__Bacteria.p__Cyanobacteria.c__Chloroplast.o__Minidiscustrioculatus	2.64	Glass	2.22	0.02
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Myxococcales.f__Birri41	1.04	Glass	2.18	0.05
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__GammaproteobacteriaIncertaeSedis.f__UnknownFamily	3.84	Glass	3.16	0.04
HDPE vs Glass	k__Bacteria.p__Cyanobacteria	4.79	Glass	4.43	0.02

HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae	1.96	Glass	2.16	0.04
HDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodobacterales	4.95	HDPE	4.23	0.04
LDPE vs Glass	k__Bacteria.p__Bacteroidetes.c__Sphingobacteriia	4.09	Glass	3.52	0.04
LDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Sphingomonadales.f__Sphingomonadaceae	3.19	LDPE	2.63	0.02
LDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Pseudoalteromonadaceae	2.43	LDPE	2.06	0.04
LDPE vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales	2.36	Glass	2.14	0.02
LDPE vs Glass	k__Bacteria.p__Bacteroidetes.c__Sphingobacteriia.o__Sphingobacteriales.f__Saprospiraceae	4.03	Glass	3.45	0.04
LDPE vs Glass	k__Bacteria.p__Planctomycetes	4.57	Glass	3.7	0.04
LDPE vs Glass	k__Bacteria.p__Acidobacteria	3.26	Glass	2.72	0.04
LDPE vs Glass	k__Bacteria.p__Acidobacteria.c__Holophagae	2.94	Glass	2.42	0.04
LDPE vs Glass	k__Bacteria.p__Acidobacteria.c__Holophagae.o__Subgroup10	2.88	Glass	2.38	0.04
LDPE vs Glass	k__Bacteria.p__Acidobacteria.c__Holophagae.o__Subgroup10.f__CA002	2.52	Glass	2.19	0.04
PP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfuromonadales.f__Sva1033	1.86	PP	2.01	0.04
PP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__GammaproteobacterialIncertaeSedis	3.84	Glass	2.98	0.04
PP vs Glass	k__Bacteria.p__Proteobacteria.c__Milano_WF1B_44	1.11	PP	2.22	0.05
PP vs Glass	k__Bacteria.p__Chloroflexi.c__Thermomicrobia	0.87	PP	2.42	0.05
PP vs Glass	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfuromonadales	1.86	PP	2.11	0.04
PP vs Glass	k__Bacteria.p__Chloroflexi.c__Thermomicrobia.o__AKYG1722	0.87	PP	2.4	0.05
PP vs Glass	k__Bacteria.p__Acidobacteria.c__Subgroup26	1.8	Glass	2.06	0.02
PP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Oleiphilaceae	2.87	PP	2.18	0.04
PP vs Glass	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__GammaproteobacterialIncertaeSedis.f__UnknownFamily	3.84	Glass	2.94	0.04

Table S10 - Results of the LEfSe analysis identifying taxa (down to the family level) discriminating for either glass or either one of the plastics after two months incubation.

Surfaces compared	Taxa		Surface	LDA score (log 10)	p value
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales	1.94	Glass	2.32	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Granulosicoccaceae	2.89	Glass	2.85	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Blastocatellia; o__Blastocatellales	2.14	Glass	2.54	0.04
DEHP vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria	3.7	Glass	3.28	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae	3.41	Glass	3.05	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria	3.3	Glass	2.93	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales	1.64	Glass	2.95	0.01
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia	4.96	Glass	4.29	0.04
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia	4.72	Glass	4.34	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria	4.26	DEHP	3.72	0.04
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__FFCH9454	2.04	Glass	2.37	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__BD7_8marinegroup	3.39	Glass	3.07	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__JTB255marinebenthicgroup	3.54	Glass	3.11	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__OM182clade	2.5	Glass	2.59	0.04
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia	4.04	Glass	3.67	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__AT_s3_28	1.21	Glass	2.85	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kordiimonadales; f__Temperatibacteraceae	1.47	Glass	2.47	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__MBAE14	2.8	Glass	2.53	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales	4.93	DEHP	4.58	0.02

Chapter I

DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__1013_28.CG33	1.44	Glass	2.72	0.01
DEHP vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae	3.58	Glass	3.15	0.04
DEHP vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI	3.62	Glass	3.21	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteria; o__Sphingobacteriales; f__Saprospiraceae	4.6	Glass	4.22	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__K189Aclade	3.33	Glass	2.88	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__pltb_vmat_59	1.61	Glass	2.94	0.01
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__Rickettsiaceae	2.29	Glass	2.58	0.02
DEHP vs Glass	k__Bacteria; p__Parcubacteria; c__CandidatusCampbellbacteria; o__marinemetagenome	2.11	Glass	2.05	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__HOC36	1.72	Glass	3	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kordiimonadales; f__Kordiimonadaceae	2.41	DEHP	2.78	0.02
DEHP vs Glass	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__unidentifiedmarinebacterioplankton	1.76	Glass	3.19	0.04
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobia; o__Acidimicrobiales; f__Sva099marinegroup	3.88	Glass	3.52	0.04
DEHP vs Glass	k__Bacteria; p__Planctomycetes	4.63	Glass	4.14	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae	3.31	Glass	3.02	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobia; o__Acidimicrobiales; f__Acidimicrobiaceae	3.06	Glass	2.66	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae	1.33	Glass	2.71	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__EV818SWSAP88	2.6	Glass	2.43	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales	2.75	Glass	2.52	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.32	Glass	2.96	0.02
DEHP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.54	Glass	4.12	0.02
DEHP vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__DEV007	3.23	Glass	2.88	0.02
DEHP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.54	Glass	4.11	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__E6aD10	2.3	Glass	2.65	0.04
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae	4.92	Glass	4.29	0.04
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__SB_5	3.09	Glass	2.78	0.02
DEHP vs Glass	k__Bacteria; p__Parcubacteria; c__CandidatusCampbellbacteria	2.63	Glass	2.38	0.05
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Bifidobacteriales; f__Bifidobacteriaceae	1.63	Glass	2.34	0.01
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales	4.6	DEHP	4.23	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae	5.07	DEHP	4.76	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Ectothiorhodospiraceae	2.11	Glass	2.16	0.04
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Bifidobacteriales	1.63	Glass	2.31	0.01
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Blastocatellia; o__Blastocatellales; f__Blastocatellaceae_Subgroup4	2.14	Glass	2.55	0.04
DEHP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobia; o__Acidimicrobiales; f__OM1clade	2.72	Glass	2.43	0.02
DEHP vs Glass	k__Bacteria; p__Lentisphaerae; c__Oligosphaeria	1.33	Glass	2.72	0.05
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	4.53	DEHP	4.2	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	4.67	Glass	4.31	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales	1.88	Glass	3.18	0.04
DEHP vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI	3.62	Glass	3.19	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SM2D12	2.53	DEHP	2.74	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__OCS116clade	3.89	Glass	3.58	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Blastocatellia	2.14	Glass	2.55	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales; f__Desulfobulbaceae	2.56	Glass	2.49	0.02
DEHP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.54	Glass	4.09	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__NS9marinegroup	2.96	Glass	2.78	0.02
DEHP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup10; f__Sva0725	2.19	Glass	2.63	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Schleiferiaceae	2.85	Glass	2.56	0.02

Chapter I

DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales; f__Parvularculaceae	2.41	DEHP	2.74	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae	4.87	DEHP	4.55	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Sva0071	2.56	Glass	2.52	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae	3.61	DEHP	3.22	0.02
DEHP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	4.08	Glass	3.75	0.02
DEHP vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Carnobacteriaceae	1.86	Glass	2.68	0.02
DEHP vs Glass	k__Bacteria; p__Actinobacteria	4.05	Glass	3.67	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales	5.08	DEHP	4.75	0.02
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales	2.41	DEHP	2.71	0.04
DEHP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	3	Glass	2.8	0.02
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Granulosicoccaceae	2.89	Glass	2.81	0.03
DINP vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	2.24	Glass	3.05	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales	1.64	Glass	3.02	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia	4.96	Glass	4.27	0.03
DINP vs Glass	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	2.04	Glass	2.87	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__4_Org1_14	2.59	Glass	2.49	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia	4.72	Glass	4.44	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales	4.23	DINP	3.71	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__BD7_8marinegroup	3.39	Glass	3.13	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__JTB255marinebenthicgroup	3.54	Glass	3.06	0.03
DINP vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales	1.87	Glass	3.11	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__MBAE14	2.8	Glass	2.61	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales	4.38	DINP	3.91	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__1013_28_CG33	1.44	Glass	3.44	0.03
DINP vs Glass	k__Bacteria; p__Gemmatimonadetes	1.95	Glass	2.76	0.03
DINP vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia	1.87	Glass	2.98	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae	4.6	Glass	4.3	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__pltb_vmat_59	1.61	Glass	3.09	0.03
DINP vs Glass	k__Bacteria; p__Firmicutes	3.08	Glass	2.61	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__HOC36	1.72	Glass	3.3	0.03
DINP vs Glass	k__Bacteria; p__Planctomycetes	4.63	Glass	4.19	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae	3.31	Glass	2.87	0.03
DINP vs Glass	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__Acidimicrobiaceae	3.06	Glass	2.64	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Marinilabiaceae	1.6	Glass	3.53	0.03
DINP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae	4.54	Glass	4.08	0.03
DINP vs Glass	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__DEV007	3.23	Glass	2.78	0.03
DINP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	4.54	Glass	4.11	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__SB_5	3.09	Glass	2.86	0.03
DINP vs Glass	k__Bacteria; p__Planctomycetes; c__OM190	3.08	Glass	2.73	0.03
DINP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Bifidobacteriales; f__Bifidobacteriaceae	1.63	Glass	3.28	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales	4.78	DINP	4.44	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae	4.98	DINP	4.58	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__P3OB_42	2.71	DINP	2.7	0.03
DINP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Bifidobacteriales	1.63	Glass	3.31	0.03
DINP vs Glass	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	1.87	Glass	3.06	0.03
DINP vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae	2.36	Glass	2.97	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	4.69	DINP	4.38	0.03

DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	4.67	Glass	4.27	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales	1.88	Glass	3.4	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__OCS116clade	3.89	Glass	3.62	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	3.83	Glass	3.23	0.03
DINP vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	2.69	Glass	2.92	0.03
DINP vs Glass	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	4.54	Glass	4.08	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__NS9marinegroup	2.96	Glass	2.72	0.03
DINP vs Glass	k__Bacteria; p__Acidobacteria; c__Holophagae; o__Subgroup10; f__Sva0725	2.19	Glass	2.84	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Schleiferiaceae	2.85	Glass	2.62	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales; f__Parvularculaceae	2.53	DINP	2.67	0.03
DINP vs Glass	k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae	1.72	Glass	3.2	0.03
DINP vs Glass	k__Bacteria; p__Firmicutes; c__Bacilli	2.73	Glass	2.82	0.03
DINP vs Glass	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales	4.08	Glass	3.82	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales	4.98	DINP	4.63	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales	2.53	DINP	2.66	0.03
DINP vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	3	Glass	2.77	0.03
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	3.6	Glass	2.9	0.04
HDPE vs Glass	k__Bacteria; p__Acidobacteria; c__AT_s3_28	1.02	Glass	2.04	0.05
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__KI89Aclade	3.55	HDPE	3.06	0.04
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae	3.12	Glass	2.78	0.04
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae	3.11	Glass	2.55	0.04
HDPE vs Glass	k__Bacteria; p__Bacteroidetes; c__SB_5	2.89	Glass	2.63	0.04
HDPE vs Glass	k__Bacteria; p__Saccharibacteria	1.09	Glass	2.01	0.05
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	3.36	Glass	2.72	0.04
HDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae	3.6	Glass	2.91	0.04
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria	3.87	Glass	3.19	0.03
LDPE vs Glass	k__Bacteria; p__Spirochaetae; c__Spirochaetes	2.49	LDPE	2.08	0.03
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bacteriovoracaceae	2.81	Glass	2.37	0.03
LDPE vs Glass	k__Bacteria; p__Peregrinibacteria	2.85	Glass	2.43	0.03
LDPE vs Glass	k__Bacteria; p__Spirochaetae; c__Spirochaetes; o__Spirochaetales; f__Leptospiraceae	2.49	LDPE	2.07	0.03
LDPE vs Glass	k__Bacteria; p__Spirochaetae; c__Spirochaetes; o__Spirochaetales	2.49	LDPE	2.09	0.03
LDPE vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales	3.31	Glass	2.71	0.03
LDPE vs Glass	k__Bacteria; p__Spirochaetae	2.49	LDPE	2.03	0.03
PP vs Glass	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria	3.79	PP	3.17	0.04
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria	3.68	Glass	2.8	0.02
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bdellovibrionales; f__Bacteriovoracaceae	2.62	Glass	2.11	0.02
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae	3.11	Glass	2.48	0.02
PP vs Glass	k__Bacteria; p__Bacteroidetes; c__SB_5	2.89	Glass	2.53	0.04
PP vs Glass	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Mycobacteriaceae	1.22	PP	2.09	0.04
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Bradymonadales; f__DeltaproteobacteriabacteriumSMP_3	1.04	PP	2.12	0.05
PP vs Glass	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	3.36	Glass	2.69	0.04

Table S11 - Results of the LefSe analysis for each incubation time.

Incubation time	Taxa	Discriminating surface	log LDA score	p value
One week	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae	LDPE	3.24	0.00
One week	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o__Fibrobacteriales; f__Fibrobacteraceae	PP	2.41	0.02

Chapter I

One week	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	Glass	2.41	0.03
One week	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales	Glass	2.32	0.02
One week	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sandaracinaceae	Glass	2.39	0.02
One week	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__FamilyXI	Glass	2.63	0.04
One week	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales	LDPE	3.29	0.00
One week	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae	LDPE	2.41	0.03
One week	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales; f__Syntrophobacteraceae	HDPE	2.28	0.04
One week	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia	LDPE	3.01	0.02
One week	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria	PP	2.39	0.02
One week	k__Bacteria; p__Bacteroidetes; c__Cytophagia	PP	3.15	0.00
One week	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria; o__Lentisphaerales; f__Lentisphaeraceae	Glass	2.35	0.02
One week	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobacteraceae	Glass	2.49	0.02
One week	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o__Fibrobacterales	PP	2.40	0.02
One week	k__Bacteria; p__Planctomycetes; c__Phycisphaerae	Glass	2.89	0.04
One week	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae	Glass	2.82	0.04
One week	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales	Glass	2.83	0.04
One week	k__Bacteria; p__Lentisphaerae; c__Lentisphaeria	Glass	2.19	0.02
One week	k__Bacteria; p__Planctomycetes; c__OM190	LDPE	2.67	0.01
One week	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae	LDPE	2.48	0.01
One week	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	LDPE	2.80	0.02
One week	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae	PP	3.16	0.00
One week	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	LDPE	4.69	0.00
One week	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales	HDPE	2.36	0.04
One week	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	Glass	2.57	0.00
One week	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	LDPE	2.40	0.01
One week	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Rhizosoleniaimbricata	PP	2.40	0.05
One week	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae	Glass	2.52	0.04
One week	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales	PP	3.16	0.00
One week	k__Bacteria; p__Actinobacteria	LDPE	3.15	0.00
One week	k__Bacteria; p__Lentisphaerae	Glass	2.32	0.03
One week	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales	Glass	2.29	0.05
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Altererythrobacter	DEHP	3.12	0.03
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae	HDPE	2.74	0.04
One month	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacterales; f__env_OPS17	LDPE	3.95	0.01
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales	Glass	2.93	0.03
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquimarina; s__Aquimarina megateriumXH134	DEHP	2.92	0.01
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter	Glass	2.83	0.01
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sagittula; s__Sagittularina	DEHP	3.54	0.02
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae; g__Kangiella	PP	2.9	0.02
One month	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae; g__Ekhidna; s__Ekhidnasp_KYW635	Glass	3.25	0.02
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella	DEHP	4.77	0.02
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Lacinutrix; s__Lacinutrix algicola	LDPE	3.58	0.04
One month	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae	Glass	2.91	0.04
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae	Glass	2.93	0.03
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	DEHP	4.8	0.04
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavirhabdus	LDPE	3.96	0.04
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__Oleiphilus sp_HI0081	DINP	3.09	0.04
One month	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae; g__Rhodopirellula; s__Tigriopus californicus	LDPE	3.77	0.03
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Ectothiorhodospiraceae	HDPE	3.15	0.04

Chapter I

One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Muricauda; s__Flavobacteriaceae bacterium GUDS1159	DINP	3.71	0.02
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sagittula	DEHP	3.54	0.02
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Pseudahrensia	HDPE	4.01	0.01
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum adriaticum	PP	3.61	0.03
One month	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	HDPE	3.11	0.04
One month	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae; g__Roseivirga	HDPE	3.04	0.01
One month	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI; g__Synechococcus	Glass	3.51	0.05
One month	k__Bacteria; p__Proteobacteria	Glass	2.81	0.02
One month	k__Bacteria; p__Actinobacteria; c__Thermoleophila; o__Solirubrobacterales	Glass	2.67	0.05
One month	k__Bacteria; p__Actinobacteria; c__Thermoleophila; o__Solirubrobacterales; f__TM146	Glass	2.73	0.05
One month	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae; g__Phaeodactylibacter	Glass	3.05	0.03
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kordiimonadales; f__Kordiimonadaceae	DEHP	3.13	0.01
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavirhabdus; s__Flavobacteriaceae bacterium E4_2	LDPE	3.96	0.04
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aureitalea; s__Aureitalea marina	Glass	3.34	0.01
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	DINP	4.14	0.01
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Hyphomonas; s__Hyphomonas sp. L_53_1_40	DEHP	3.49	0.01
One month	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria	Glass	2.95	0.04
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Ferrimonadaceae	Glass	2.7	0.03
One month	k__Bacteria; p__Acidobacteria; c__Subgroup26	Glass	3.69	0.01
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__OM75clade	LDPE	4.38	0.03
One month	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales	Glass	2.96	0.04
One month	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	Glass	2.93	0.03
One month	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae	HDPE	2.97	0.03
One month	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Halieaceae; g__OM60_NOR5_clade	Glass	3.02	0.01
One month	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Helicobacteraceae; g__Sulfurovum	Glass	2.89	0.04
One month	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Planktomarina	Glass	3.25	0.03
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum sp. AB401d	LDPE	3.08	0.05
Two months	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Anaerostipes	Glass	3.75	0.02
Two months	k__Bacteria; p__SR1_Absconditabacteria	HDPE	3.25	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales	HDPE	2.72	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudooctadecabacter; s__Pseudooctadecabacter jejudonensis	HDPE	3.21	0.01
Two months	k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae; g__SM1A02; s__marinemetagenome	HDPE	3.02	0.01
Two months	k__Bacteria; p__Spirochaetae; c__Spirochaetes	PVC	3.35	0.02
Two months	k__Bacteria; p__Planctomycetes	Glass	4.23	0.01
Two months	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__Acidimicrobiaceae	Glass	3.19	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Meridianimaribacter	PP	3.85	0.02
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquibacter	PP	4.44	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter	PP	3.1	0.04
Two months	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae; g__Portibacter	Glass	3.17	0
Two months	k__Bacteria; p__Deinococcus_Thermus; c__Deinococci; o__Deinococcales; f__Trueperaceae	HDPE	3.02	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Nitrincola; s__Nitrincolalacisaponensis	PVC	3.17	0
Two months	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae; g__Enhygromyx sp. SIS_1	Glass	2.84	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae; g__Kangiella	PP	2.97	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter; s__Maribacter sp. KCTC42508	PP	3.07	0.03

Chapter I

Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella	PVC	4.41	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Lacinutrix; s__Lacinutrixalgalicola	LDPE	3.55	0.03
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Porphyrobacter	PVC	3.45	0.01
Two months	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae; g__Olsenella	PP	3.03	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Saccharophagus	PVC	4.24	0
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales	PVC	4.5	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavirhabdus	LDPE	3.94	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Pseudahrensia; s__Pseudahrensiatodarodis	Glass	4.38	0
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Aestuariicella; s__Proteobacteria	PVC	4.11	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae	PP	3.05	0.02
Two months	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales	Glass	4.08	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales	PVC	4.63	0
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Teredinibacter; s__Teredinibacterturnerae	PVC	2.78	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__K189Aclade	HDPE	3.97	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Pseudahrensia	Glass	4.46	0
Two months	k__Bacteria; p__Deinococcus_Thermus; c__Deinococci; o__Deinococcales; f__Trueperaceae; g__Truepera	HDPE	2.98	0.01
Two months	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade	PP	2.77	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__Filomicrobium	HDPE	3.56	0.04
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculumadriaticum	PP	3.57	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Schleiferiaceae; g__Schleiferia	Glass	2.88	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Robiginitalea; s__bacteriumAMSU	PP	2.84	0.01
Two months	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Catellicoccus	PP	3.61	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Teredinibacter	PVC	2.79	0.02
Two months	k__Bacteria; p__Deinococcus_Thermus	HDPE	3.02	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanelia	PP	3.67	0
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanelia; s__alphaproteobacteriumVS_101	HDPE	3.05	0.02
Two months	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae	PP	2.85	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudophaeobacter	PVC	3.75	0.01
Two months	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales	PP	2.82	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__MBAE14	LDPE	3.68	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__FlavobacterialesbacteriumALC_1	Glass	3.56	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Gilvibacter; s__Gilvibactersediminis	Glass	2.92	0.02
Two months	k__Bacteria; p__Actinobacteria; c__Coriobacteriia	PP	2.79	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Nitrincola	PVC	3.24	0
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__pltb_vmat_59	Glass	3.21	0
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Aestuariicella	PVC	4.11	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius	PP	4.05	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Litoreibacter	PP	4.03	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavirhabdus; s__FlavobacteriaceabacteriumE4_2	LDPE	3.92	0.02
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter; s__Maribactersp_HME8202	PP	3.14	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae	LDPE	3.55	0.01
Two months	k__Bacteria; p__Deinococcus_Thermus; c__Deinococci; o__Deinococcales	HDPE	3.03	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae	HDPE	3.19	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Hyphomonas	HDPE	3.17	0.04
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maritimimonas; s__Maritimimonasrapanae	PP	2.88	0.01

Chapter I

Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae	PVC	4.65	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae	HDPE	4.21	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Muricauda; s__Bacteroidetesbacteriumb1b3	HDPE	3.05	0
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__Hyphomonas; s__Hyphomonassp_L_53_1_40	PVC	4.09	0.01
Two months	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Peptostreptococcus	PP	2.86	0.01
Two months	k__Bacteria; p__Planctomycetes; c__Planctomycetacia; o__Planctomycetales; f__Planctomycetaceae; g__Blastopirellula	Glass	4.1	0
Two months	k__Bacteria; p__Planctomycetes; c__Planctomycetacia	Glass	4.08	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvularculales; f__Parvularculaceae	HDPE	2.92	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudophaeobacter; s__Phaeobactersp_11ANDIMAR09	PVC	3.76	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae; g__Leucothrix; s__LeucothrixmucorDSM2157	PP	2.95	0.02
Two months	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Saprospiraceae; g__Lewinella; s__LewinellacoherensDSM23179	Glass	3.46	0.03
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquimarina; s__Aquimarinasp_RZW4_3_2	PVC	2.91	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus	PVC	4.65	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Schleiferiaceae	Glass	2.86	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudooctadecabacter	HDPE	3.19	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Sandaracinaceae	PVC	3.01	0.04
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales	Glass	3.13	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Croceitalea; s__Croceitaleasp_CBA3205	LDPE	3.83	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__Cycloclasticus	PVC	3.19	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Saccharophagus; s__Saccharophagussp_MM1_2b	PVC	4.24	0
Two months	k__Bacteria; p__Spirochaetae; c__Spirochaetes; o__Spirochaetales	PVC	3.35	0.02
Two months	k__Bacteria; p__Spirochaetae	PVC	3.35	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingorhabdus; s__Sphingopyxisp_MEBiC05060	PVC	3.66	0.01
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Dokdonia; s__Dokdoniasp_HMF2319	LDPE	3.06	0.01
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Simidiua	PVC	4.05	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aureisphaera	PP	3.22	0.01
Two months	k__Bacteria; p__Deinococcus_Thermus; c__Deinococci	HDPE	2.97	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__OCS116clade	HDPE	4.34	0
Two months	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__BD2_7	Glass	3.14	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales	PVC	4.24	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maritimimonas	PP	4.19	0.01
Two months	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__Puniceococcales; f__Puniceococcaceae	PP	3.53	0
Two months	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Meridianimaribacter; s__Meridianimaribactersp_xn12	PP	3.84	0.02
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingorhabdus; s__Sphingorhabdusarenillitoris	HDPE	2.84	0.03
Two months	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__Ruegeriasp_MME_070	Glass	2.77	0.03
Two months	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae; g__Olsenella; s__OlsenellaprofusaF0195	PP	3.02	0.02

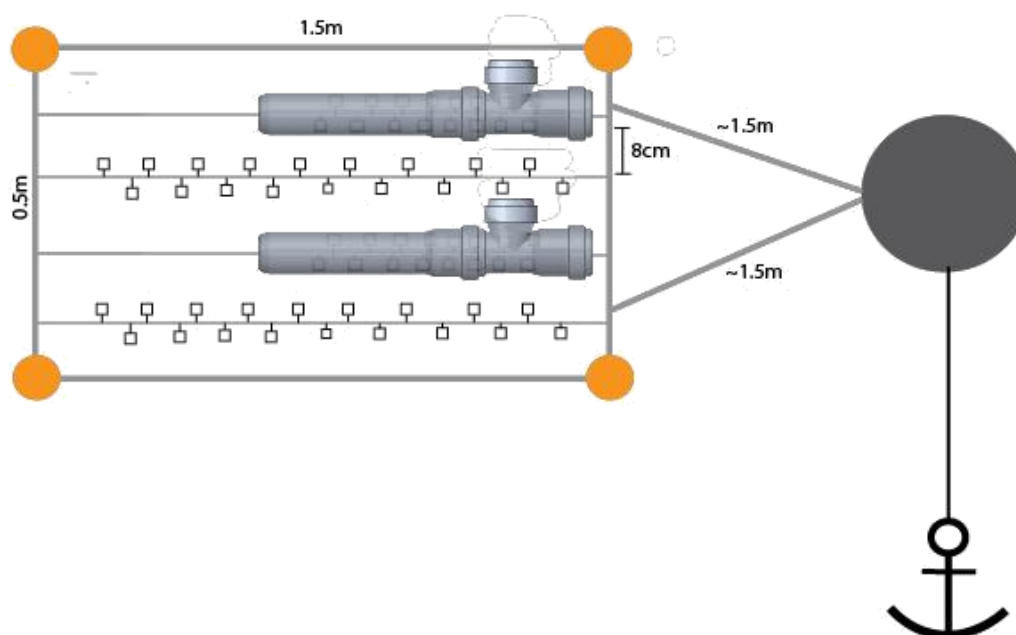


Figure S1 – Scheme of the structure used to incubate the plastics and glass. Orange dots = buoys, big grey dot = main float with anchor. Dim light conditions were established by placing the plastics and glass slides in grey tubes (10 cm inner diameter) open on both sides to ensure water exchange. The rectangular frame was constructed from plumbing tubes connected to four floats to ensure positive buoyancy. The frame was linked to a main float and anchored at the seafloor. The floating frame oriented itself to the direction of the currents allowing water flowing through the tubes in the dim light treatment. All the samples in the dim light treatment were placed in the center of the tube to avoid direct sunlight entering from the sides.

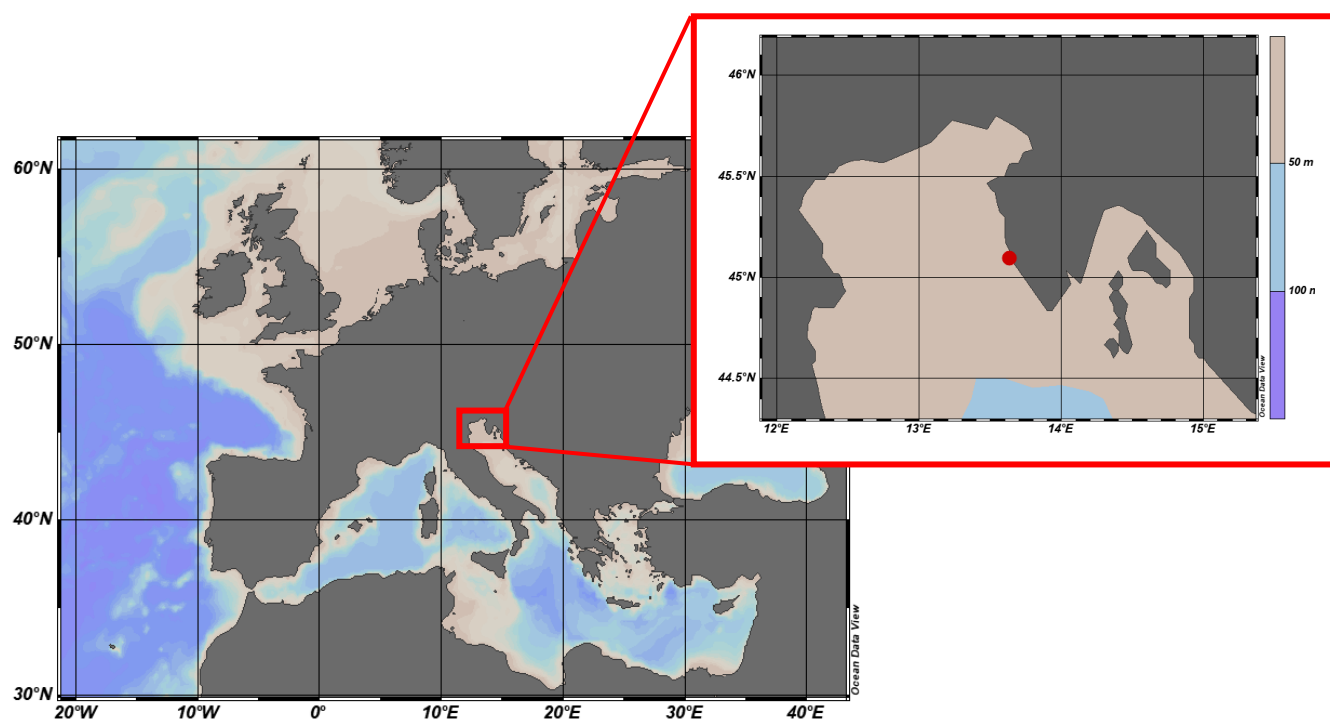
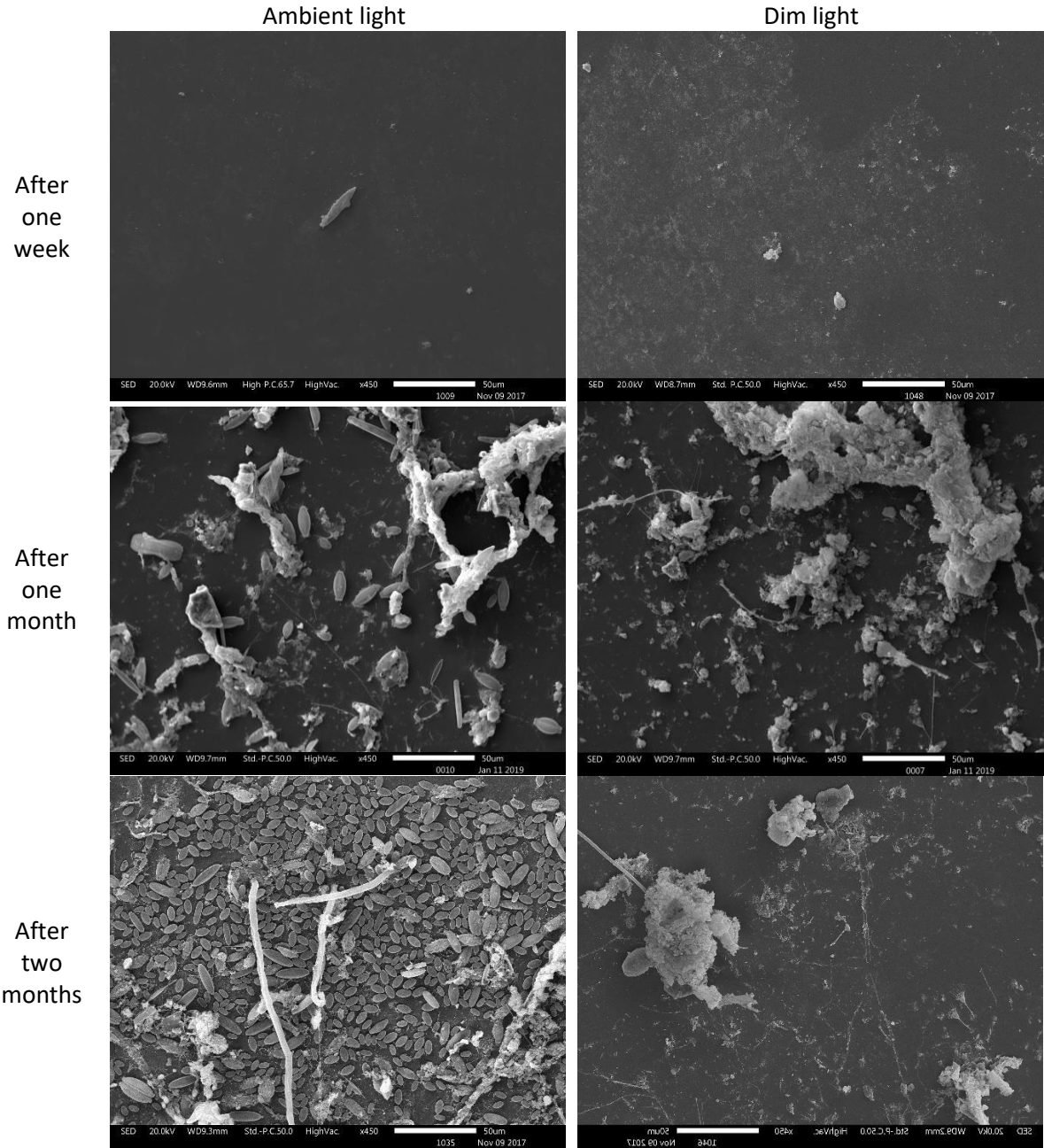
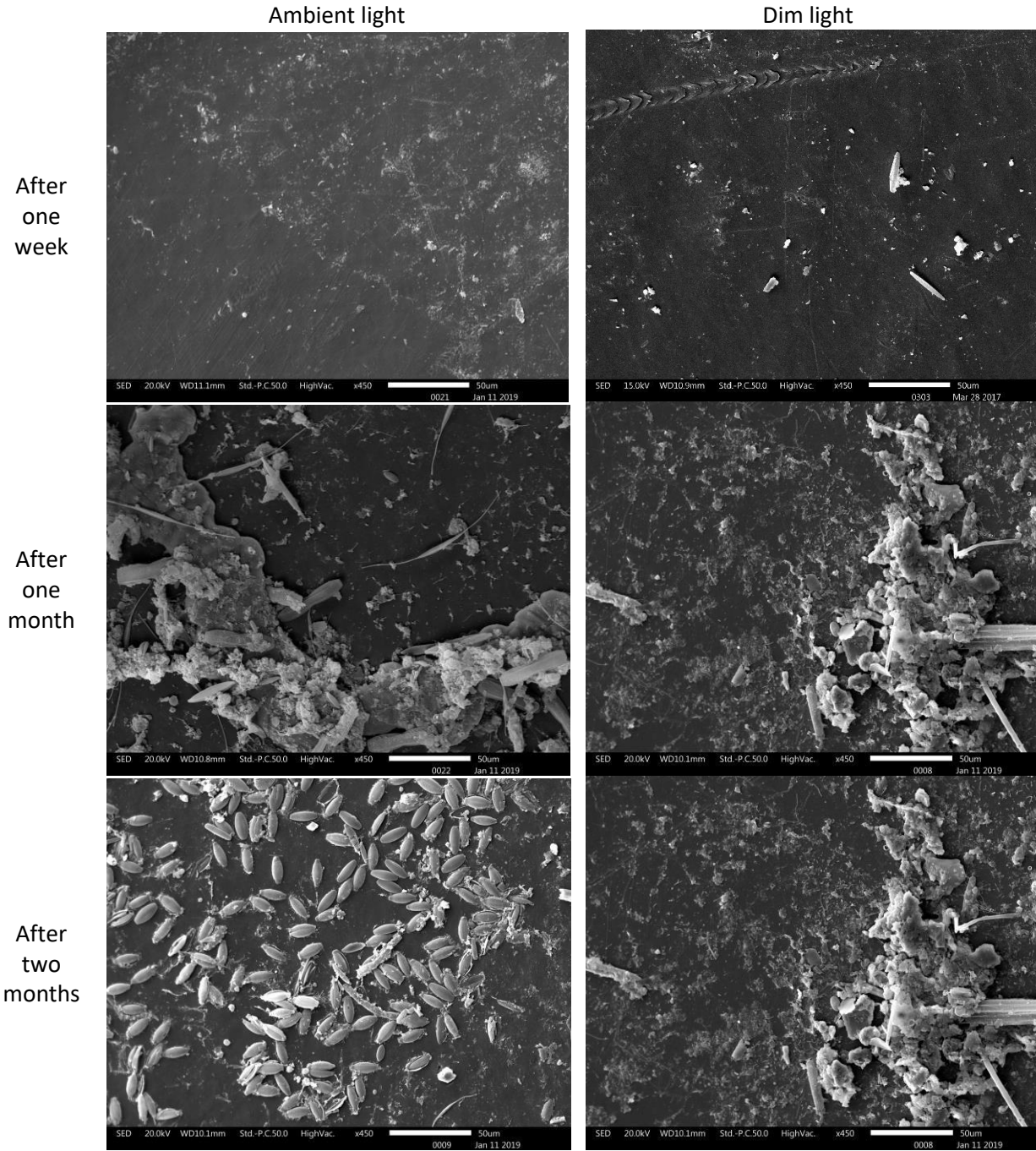


Figure S2 – Map of the location where the experiment was deployed in the Northern Adriatic Sea, 1 km off the coast of Rovinj, Croatia. Location is marked with a red dot.

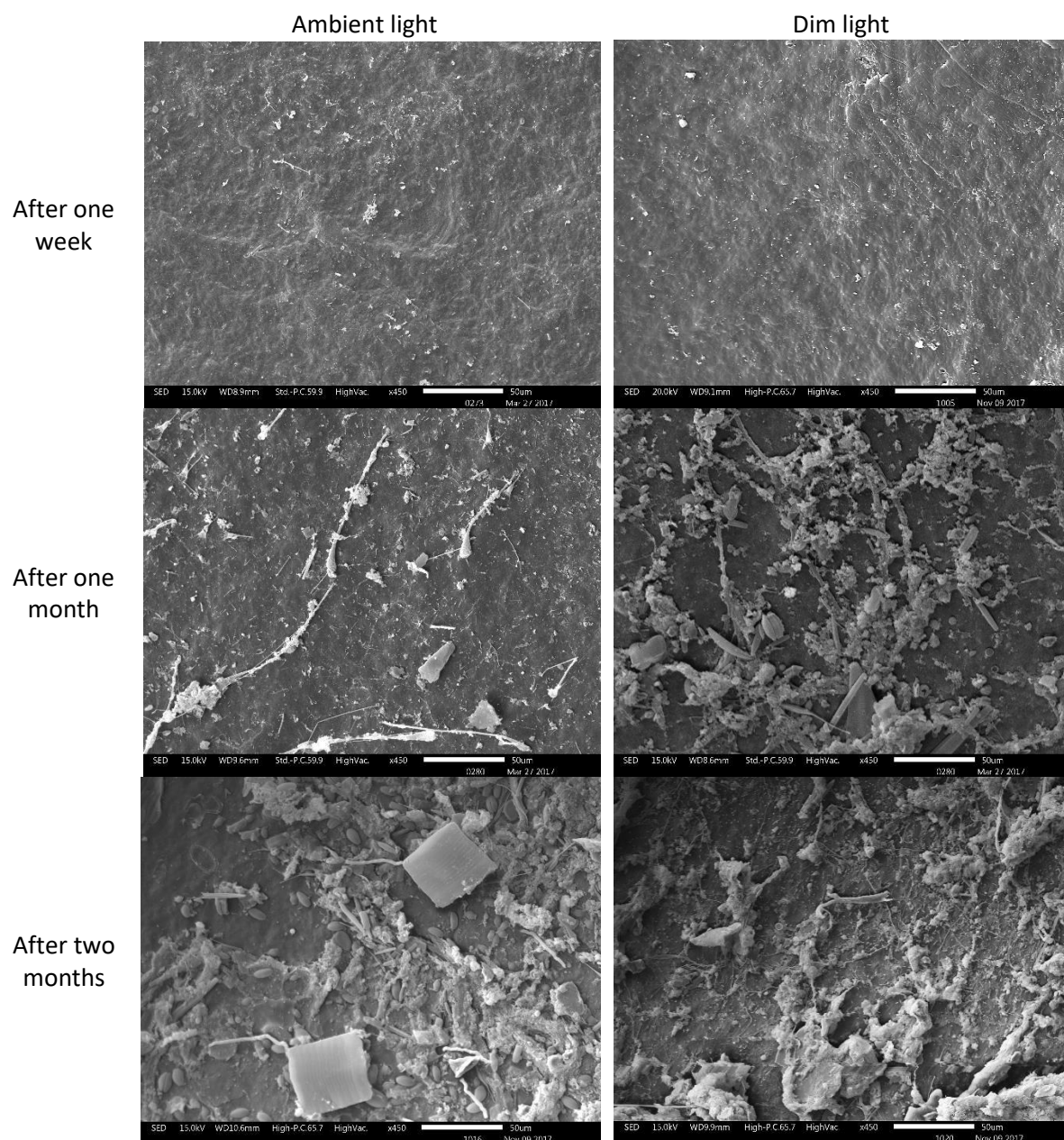
(A) Glass



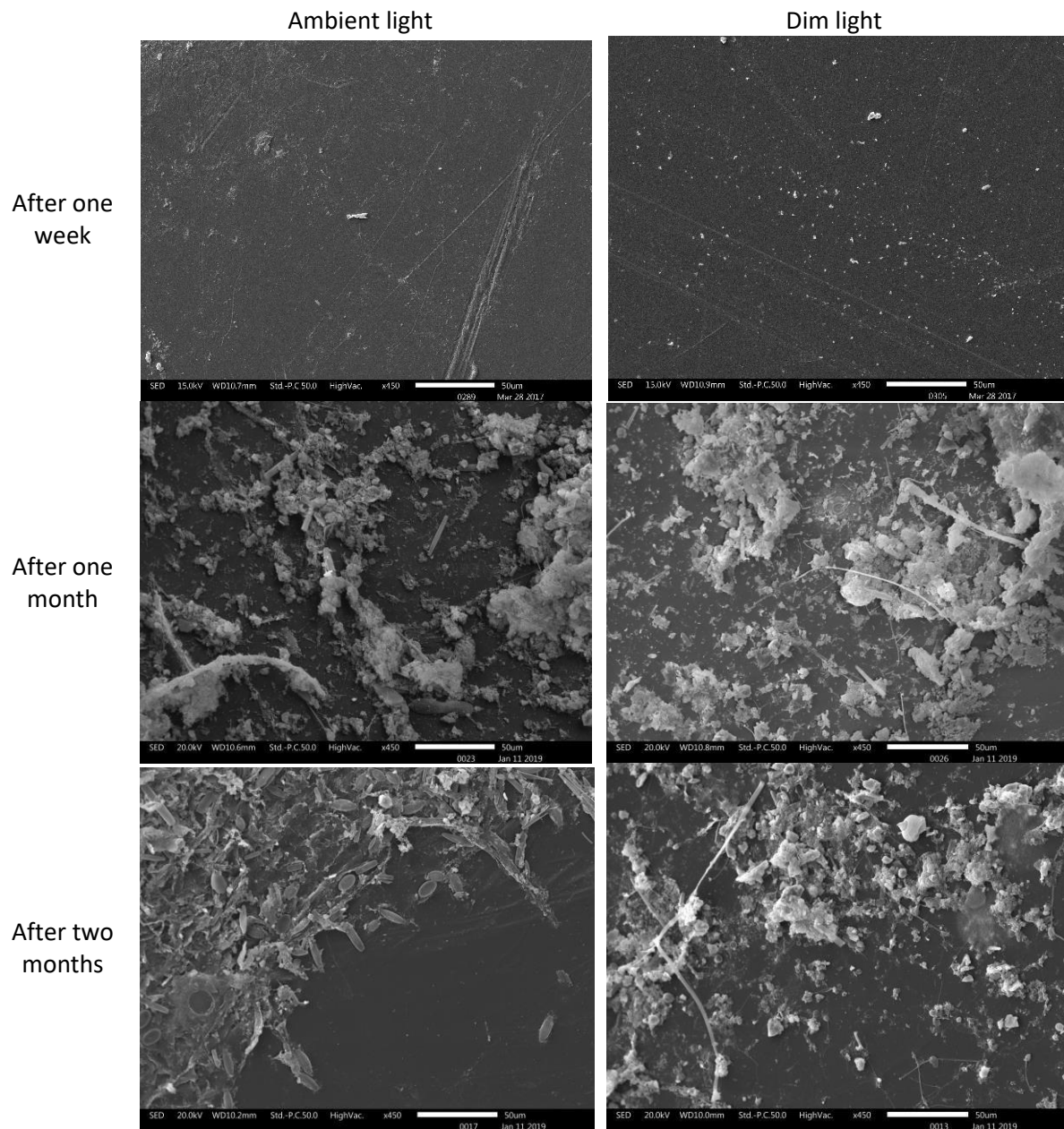
(B) LDPE



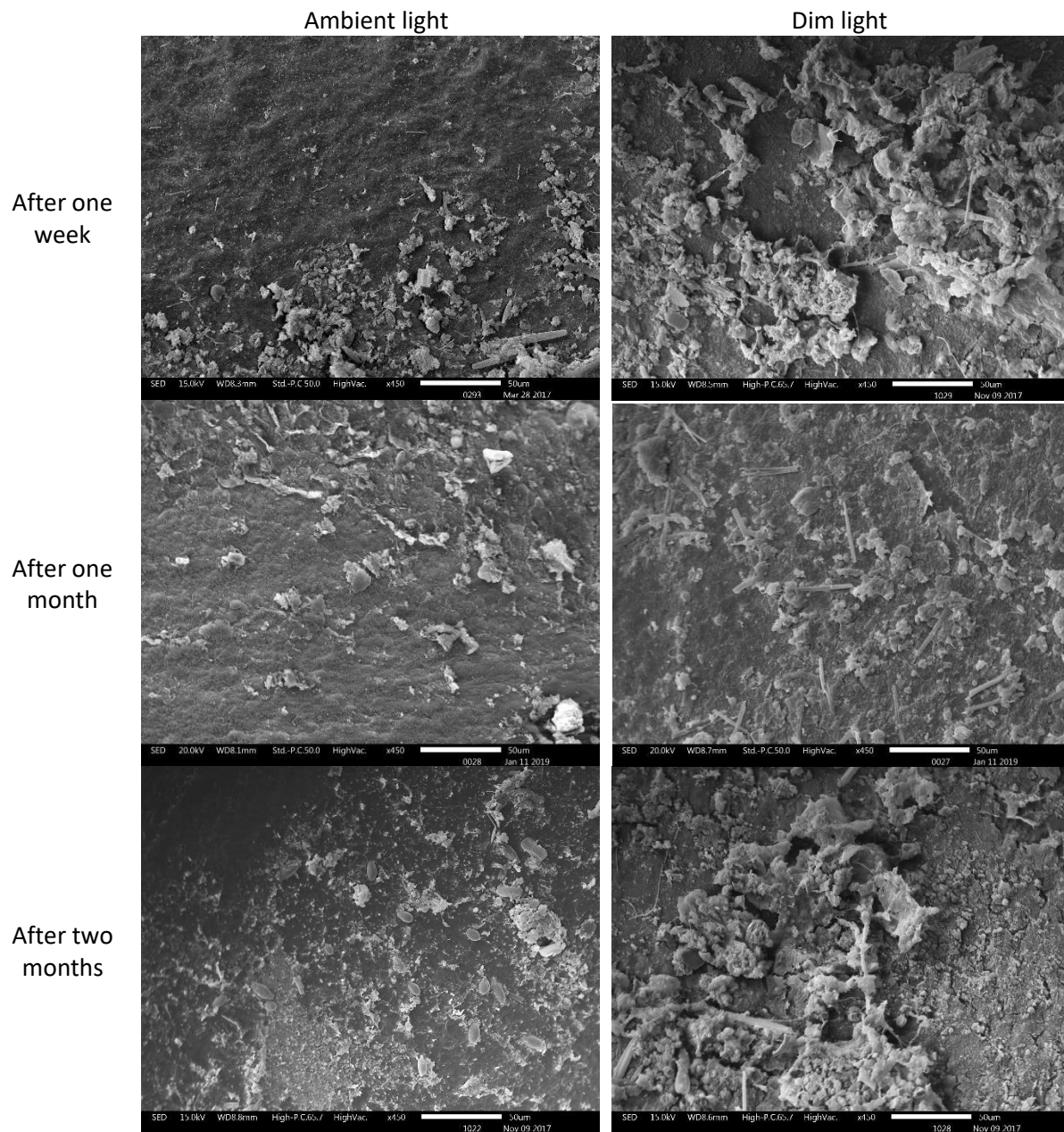
(C) HDPE



(D) PP



(E) PVC DINP



(F) PVC DEHP

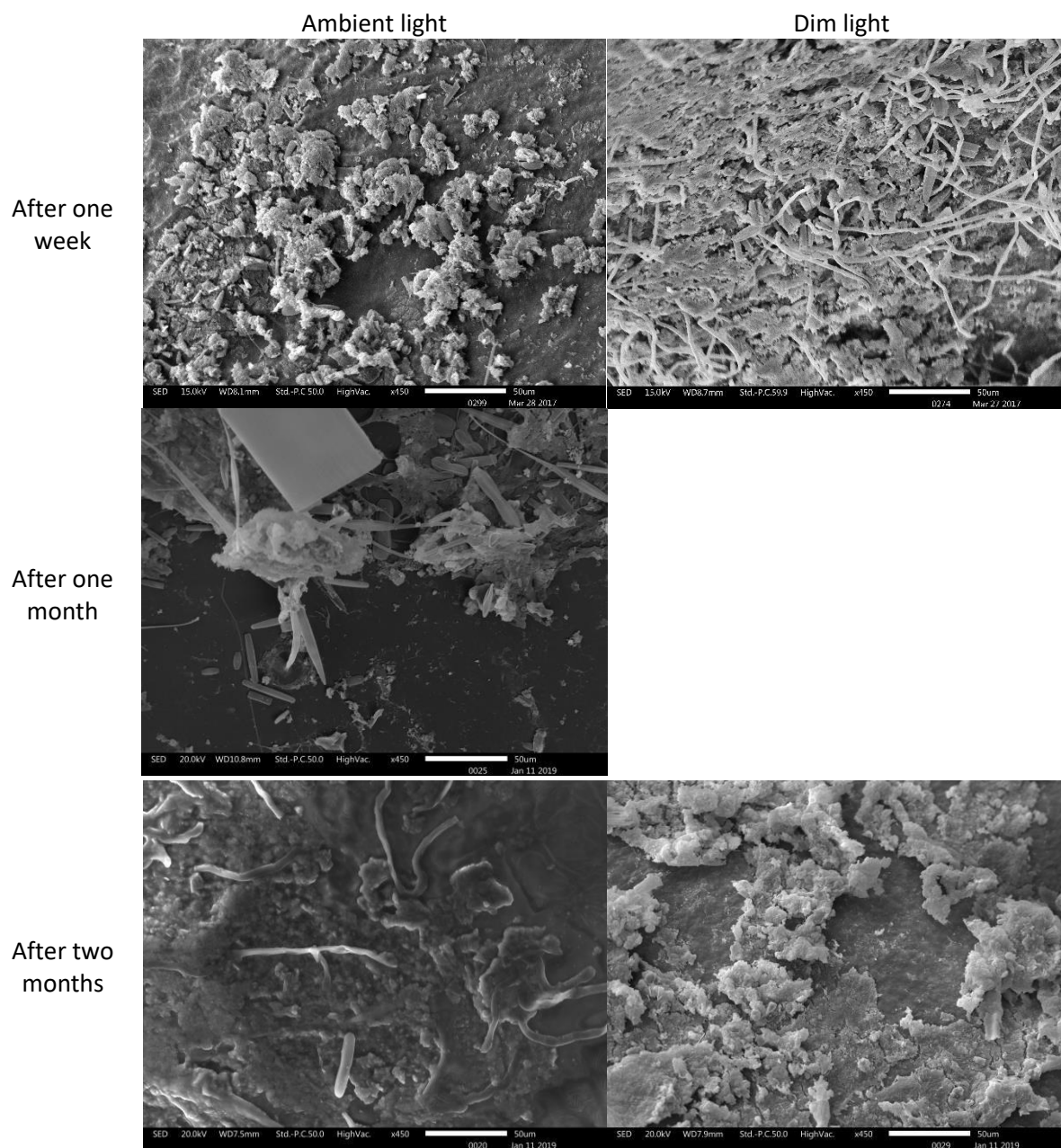


Figure S3 – SEM images of: (A) glass, (B) PP, (C) HDPE, (D) LDPE, (E) PVC DINP and (F) PVC DEHP, incubated for one week, one month and two months, under both ambient and dim light conditions.

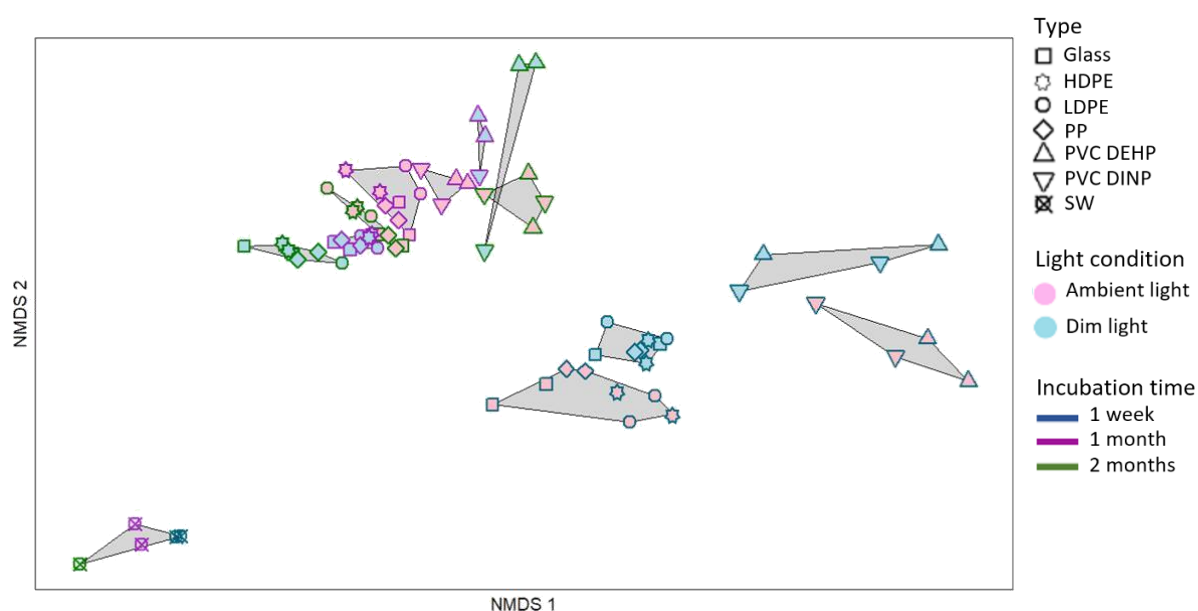
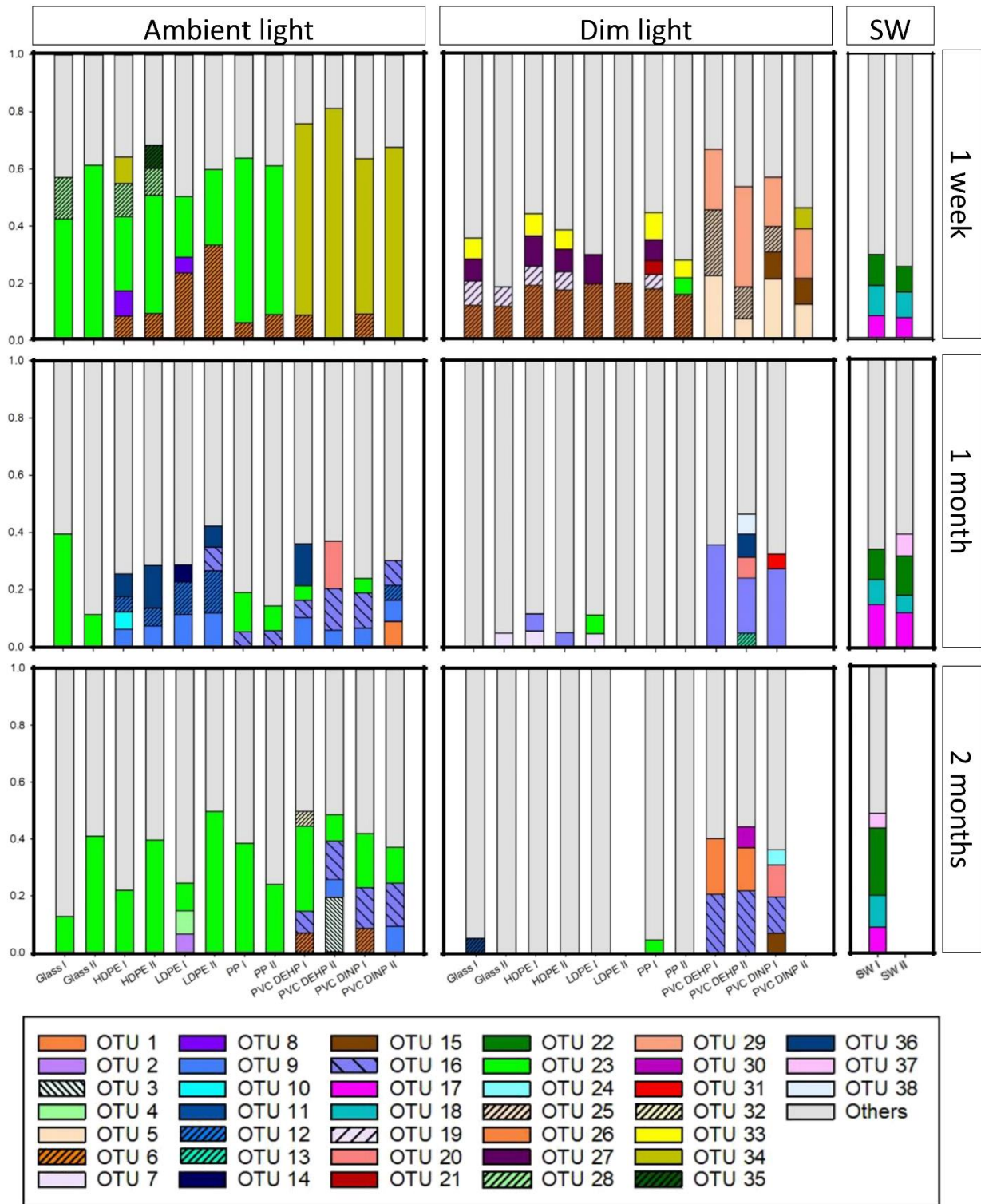


Figure S4– NMDS representation of the similarity between the bacterial community composition of the biofilm on different surfaces and seawater, when excluding the autotrophic component, i.e., Cyanobacteria. Each point represents one sample. The grey polygons connect samples from each time point subjected to the same light conditions from substrates that presented relatively similar bacterial community compositions throughout the experiment.



OUT 1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter radioresistens DSM 6976 = NBRC 102413 = CIP 103788
OTU 2	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flaviramulus; s__marinebacterium J20-17
OTU 3	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__Robiginitomaculum; s__uncultured alpha proteobacterium
OTU 4	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionIII; f__FamilyI; g__Phormidium; s__uncultured bacterium
OTU 5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__uncultured; s__uncultured bacterium
OTU 6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured bacterium AD12-E7
OTU 7	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquibacter; s__uncultured bacterium
OTU 8	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Mesoflavibacter; s__Mesoflavibacter sp. NBRC 110217
OTU 9	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanella; s__uncultured alpha proteobacterium

OTU 10	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter; s__uncultured bacterium
OTU 11	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Pseudahrensia; s__uncultured marine bacterium
OTU 12	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Ruegeria; s__uncultured Ruegeria sp.
OTU 13	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__AlphaproteobacterialIncertaeSedis; f__Unknown Family; g__uncultured; s__uncultured bacterium
OTU 14	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Hoeftia; s__uncultured bacterium
OTU 15	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Aestuariicella; s__Proteobacteria
OTU 16	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__uncultured; s__uncultured bacterium
OTU 17	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1clade; g__CandidatusActinomarina; s__uncultured bacterium
OTU 18	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Surface 1; g__uncultured bacterium
OTU 19	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Pseudofulvibacter; s__Pseudofulvibacter geojedonensis
OTU 20	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella; s__uncultured proteobacterium
OTU 21	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__Oleiphilus sp. HI0081
OTU 22	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI; g__Synechococcus; s__uncultured bacterium
OTU 23	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__uncultured cyanobacterium
OTU 24	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhodobiaceae; g__uncultured; s__uncultured bacterium
OTU 25	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Simidiua; s__uncultured bacterium
OTU 26	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__uncultured; s__uncultured bacterium
OTU 27	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum aiptasiae
OTU 28	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__uncultured bacterium
OTU 29	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Spongiispira; s__Spongiispira norvegica
OTU 30	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Leptobacterium; s__uncultured bacterium
OTU 31	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae; g__uncultured; s__uncultured proteobacterium
OTU 32	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured Oleiphilus sp.
OTU 33	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__SS1-B-06-26; g__uncultured bacterium
OTU 34	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Alteromonas; s__uncultured bacterium
OTU 35	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Virgulinema fragilis
OTU 36	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudophaeobacter; s__Phaeobacter sp. 11ANDIMAR09
OTU 37	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter 4; s__uncultured bacterium
OTU 38	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphin

Figure S5 – Stack plot representing the relative abundances of the OTUs representing > 5% of the total bacterial community in each sample. OTUs representing < 5 % of the total bacterial community were grouped into the category “Others”. The taxonomic classification of OTUs was obtained using a 97% similarity of the partial 16S rRNA gene and the SILVA database.

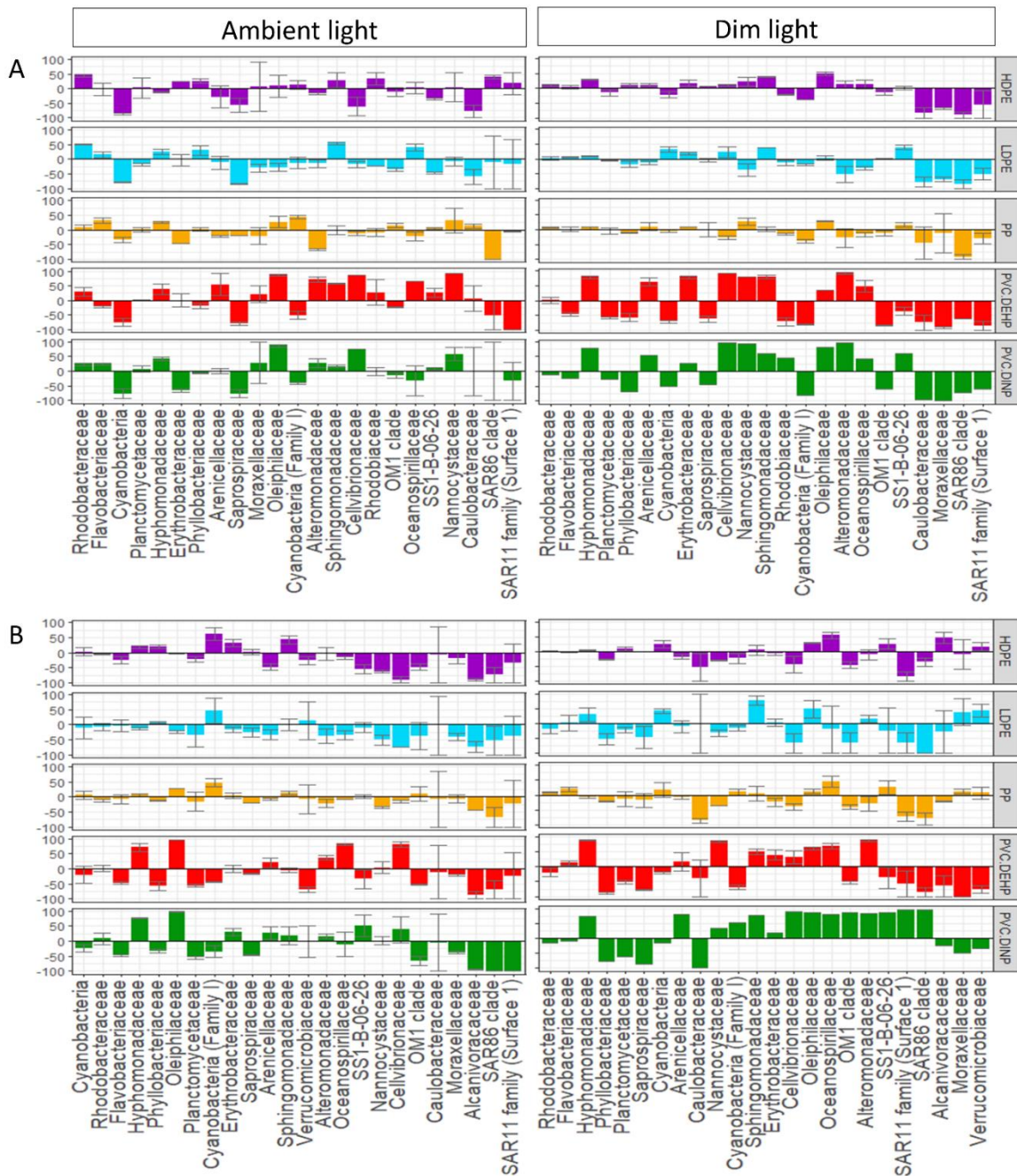


Figure S6 -Values of i_F representing the preference of the most abundant bacterial families (with 5% or more relative abundance in at least one of the samples) for either one of the plastics or glass after one month (A) and two months incubation (B) and under the two different light conditions. The bars hit the middle value between the two duplicates and the grey lines connect the two duplicate values. Families with bars below the zero line showed a higher preference for glass and the ones with bars above the zero line showed preference for the plastic in question over glass. The families are ordered from the left to right from the most to the least relative abundant when considering all samples of that treatment and time point.

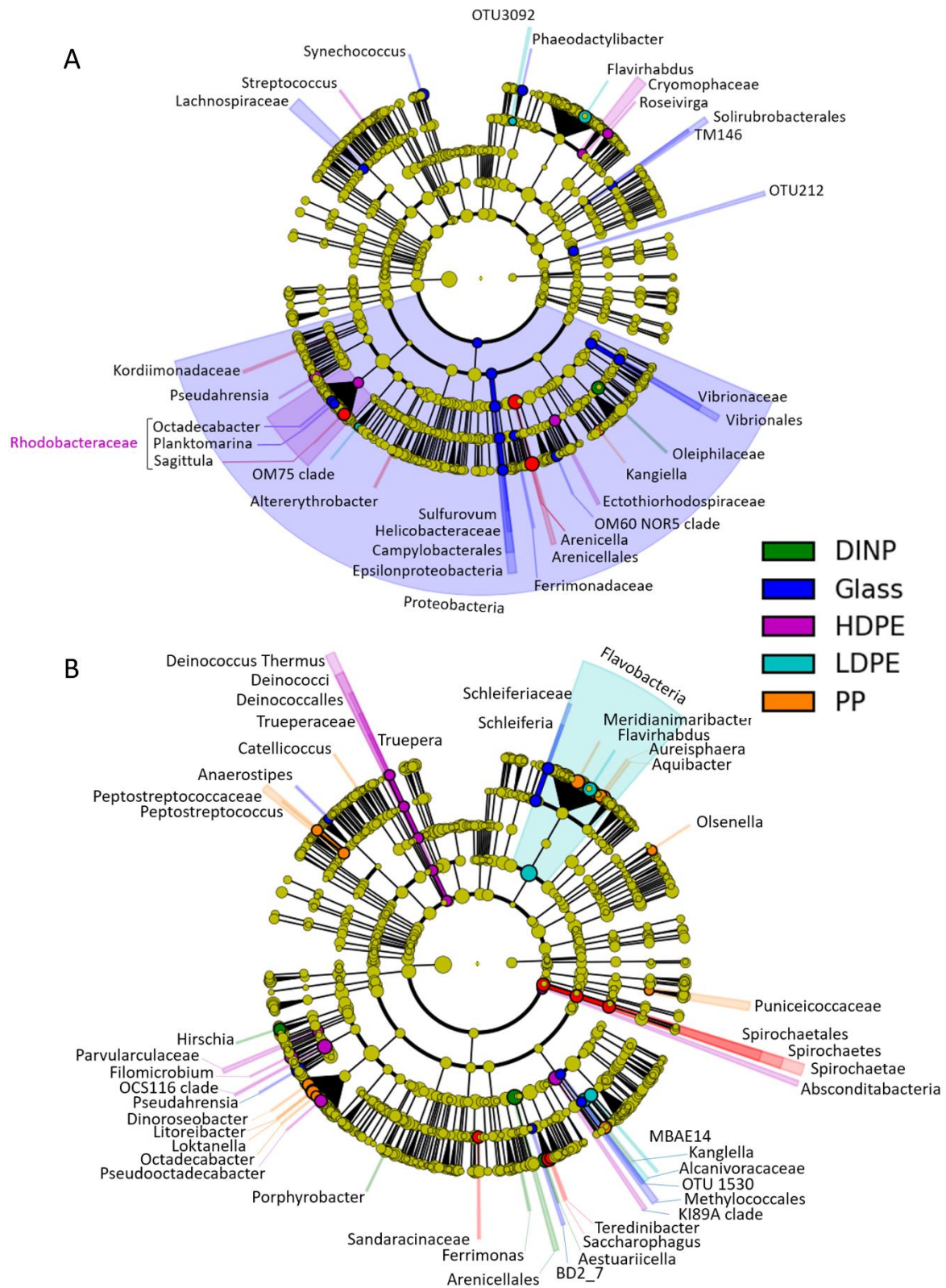


Figure S7- Representation of the taxa that discriminated for one of the surfaces over all the others considering both treatments, determined by the discriminant linear analysis (LEfSe) after one month (A) and two months (B) incubation. The LEfSe analysis results can be found in Table S7.

CHAPTER II

Putative degraders of low-density polyethylene-derived compounds in the ocean

Maria Pinto^{1, 2*}, Zihao Zhao¹, Katja Klun³, Eugen Libowitzky⁴, Gerhard J Herndl^{1, 2, 5 *}

¹ Department of Functional and Evolutionary Ecology, University of Vienna, Vienna, Austria

² Research Platform 'Plastics in the Environment and Society', University of Vienna, Vienna, Austria

³ Marine Biology Station, National Institute of Biology, Piran, Slovenia

⁴ Department for Mineralogy and Crystallography, University of Vienna, Austria

⁵ NIOZ, Department of Marine Microbiology and Biogeochemistry, Royal Netherlands Institute for Sea Research, Utrecht University, Den Burg, The Netherlands

*Corresponding authors: maria.pinto@univie.ac.at and gerhard.herndl@univie.ac.at

In review in Scientific Reports

Abstract

Polyethylene (PE) is one of the most found plastics in the ocean. The development of a biofilm on PE in the ocean has been reported, yet whether some of the biofilm-forming organisms can biodegrade this plastic and/or associated chemicals in the environment remains unknown. We taxonomically and functionally analysed three biofilm communities using low-density polyethylene (LDPE) as their sole carbon source for up to two years. Several of the taxa that increased in relative abundance over time were closely related to known degraders of alkane and other hydrocarbons. Alkane degradation has been proposed to be involved in PE degradation, and the majority of the organisms that increased in relative abundance over time harboured genes encoding for proteins essential in alkane degradation, such as the genes *alkB* and *CYP153*, encoding for an alkane monooxygenase and a cytochrome P450 alkane hydroxylase. Weight loss of PE sheets when incubated with these communities and chemical and electron microscopic analyses provided evidence for alteration of the PE surface over time. Taken together, these results provide evidence for the utilization of LDPE-originating compounds by the incubated prokaryotic communities. This study identifies a group of genes potentially involved in the degradation of LDPE in the ocean and describes a phylogenetic diverse community of plastic biofilm-dwelling microbes with the potential of utilizing LDPE-originating compounds as carbon and energy source.

Introduction

Over the last decades plastic production and consequently plastic pollution in the ocean have drastically increased, with 4.8 to 12.7 million tons of plastic estimated to enter the ocean each year (Jambeck *et al.*, 2015). Despite the urgent need for understanding the impact of plastics on marine ecosystems and the growing body of literature on this subject, the fate of plastics in the oceans remains largely enigmatic.

Once in the sea, plastics are rapidly colonized by a diverse microbial community (Amaral-Zettler *et al.*, 2020). Several studies have focused on describing the taxonomic composition of these communities and the factors that might be responsible for their succession and development (Zettler *et al.*, 2013; Amaral-Zettler *et al.*, 2015; Oberbeckmann *et al.*, 2015, 2016, 2018; Kirstein *et al.*, 2016; Dussud *et al.*, 2018a; Dussud *et al.*, 2018b; Pinto *et al.*, 2019; Dudek *et al.*, 2020). It has been suggested that some of these microorganisms are

able to degrade plastics (Roager and Sonnenschein, 2019). This idea mostly stems from the fact that the amount of plastic that has thus far been detected in marine environments is less than what would be expected (Krueger *et al.*, 2015). Also, microorganisms related to hydrocarbon-degraders have been found to be relatively more abundant on specific plastic types than on other plastics and non-plastic surfaces (Harrison *et al.*, 2014; Ogonowski *et al.*, 2018; Dudek *et al.*, 2020), especially at the early stages of biofilm formation (Pinto *et al.*, 2019). However, the reasons provoking these differences in the colonization pattern of different plastic types remain enigmatic. The physical and chemical properties of the plastics and the presence of additives are likely playing a major role in the initial colonization of plastics by microbes and the subsequent microbial biofilm development (Oberbeckmann *et al.*, 2015). Despite these uncertainties, however, there is growing evidence that some organisms forming biofilms on plastic in the ocean do have the ability of degrading plastics (Syranidou *et al.*, 2019).

Polyethylene (PE) is the most used plastic, mainly for packaging. In the year 2018, polyethylene resin demand was estimated to make up 36% of the total non-fiber plastic production (Geyer *et al.*, 2017). At sea, together with polypropylene, PE is usually the most abundant plastic at the sea surface (Cózar *et al.*, 2014; Jambeck *et al.*, 2015).

PE is considered to be highly resistant to biodegradation, especially in the absence of previous weathering by, for instance, photo-degradation. However, studies have reported weight loss and changes in the physical and chemical structure of PE when incubated with specific microorganisms. For instance, bacteria of the genera *Bacillus* and *Pseudomonas* have been associated with PE degradation both in the marine environment (Sudhakar *et al.*, 2007; Harshvardhan and Jha, 2013; Devi *et al.*, 2019; Kumari *et al.*, 2019) and in soil (Yoon *et al.*, 2012; Das and Kumar, 2014; Muhonja *et al.*, 2018). Some studies have also suggested the implication of the *alkB* gene and alkane degradation pathways in PE biodegradation (Yoon *et al.*, 2012; Syranidou *et al.*, 2017).

This *alkB* gene encodes an alkane-monooxygenase that oxidizes the initial terminal end of n-alkanes. Because the main molecular structure of PE polymers is similar to alkanes, it has been suggested that the metabolism responsible for PE bio-degradation is similar to that of hydrocarbons, specifically to alkanes (Restrepo-Flórez *et al.*, 2014). Alkanes are degraded through a succession of oxidation steps leading to beta-oxidation and consequently, to the entering of acetyl-CoA into the citric acid cycle. The first oxidation step is the initial terminal hydroxylation of the alkane chains, which can be carried out by enzymes belonging to different

families, usually depending on the alkane chain length (Wang and Shao, 2013). In organisms degrading short-chained alkanes, it is usually carried out by methane monooxygenase. The initial hydroxylation of medium-chained alkanes (C5-C17) is mediated by organisms that frequently contain soluble cytochromes P450, typically the cytochrome P450 CYP153 alkane hydroxylase, and integral membrane non-heme iron monooxygenases, typically alkB. *Alcanivorax borkumensis*, for example, has genes encoding for both types of medium-chained alkane monooxygenases in its genome (Schneiker *et al.*, 2006). Organisms capable of hydroxylating long-chained alkanes (>C18), such as *Alcanivorax dieselolei* and *Geobacillus thermoleovorans*, have been shown to have the hydroxylases AlmA and LadA, respectively (Boonmak *et al.*, 2014; Wang and Shao, 2014). Except for the alkB encoded monooxygenase, any other potential enzyme or pathway that might be involved in PE biodegradation is only poorly studied, particularly in the marine environment.

In this study we investigated the potential of three PE biofilm communities (hereafter called communities A, B and C), initially attached to three different plastics collected from the Northern Adriatic Sea, to metabolize LDPE and/or associated compounds. The communities were incubated in artificial seawater (ASW) amended with inorganic nutrients and with LDPE as their sole carbon source for two years. To identify which taxa and metabolic pathways became enriched during the incubation, metagenomes were analyzed after one and two years. Oxygen consumption measurements were performed as a metabolic activity parameter to determine whether the microbial communities incubated with LDPE are more active than communities on inert surfaces such as glass. Weighing of the plastic, scanning electron microscopy (SEM) and attenuated total reflection Fourier-transform infrared (ATR-FTIR) spectroscopy were performed on different types of PE sheets to determine whether any physical and/or chemical changes to the surface of the plastic occurred due to the presence of the microbial communities (see Fig. S1 for experimental setup).

Results

Microbial community composition

In total, we obtained six metagenomes, one from the original community A (community A0), one for each of the communities after one year of incubation (communities A1, B1 and C1) and one for each of the communities A and C after two years of incubation (communities A2 and C2, respectively). mOTU (operational taxonomic unit obtained with the mOTUs software) diversity and richness of communities A and C decreased from the original community (A0) to after one year of incubation in the case of community A (A1), and after two years of incubation in the communities A and C (A2 and C2) (Fig. S2).

Analysis of the 16S rRNA gene assembled from the metagenomes revealed that, after two years of incubation, both community A2 and C2 exhibited a similar taxonomic composition at the family level (Fig. S3) with *Phycisphaeraceae*, *Planctomycetaceae*, *Rhodobacteraceae*, *Rhodospirillaceae* and *Saprospiraceae* representing similar relative abundances and constituting a major fraction of the classified families (Fig. S3). The *Rhodobacteraceae* was the most abundant of all the identified families in both communities, A2 and C2, with relative abundances of 16% and 20% in community A2 and C2, respectively. *Rhodobacteraceae* were also abundant in community B1 with a relative abundance of 7%. It is nevertheless important to note that 55%, 64%, 68%, 73% and 70% of the families classified with matam from communities A1, A2, B1, C1, C2, respectively, remained unclassified.

Phylogenetic classification of metagenome assembled genomes (MAGs)

From the 733,317 co-assembled contigs, a total of 61 MAGs with >50% completeness and <10% contamination was recovered (Table S1). The % of bps from the total reads of each sample assigned to the identified MAGs varied greatly between samples, with 3.3%, 58.9%, 78.5%, 24.6%, 73.2% and 81.9% of the total bps of the metagenomes from communities A0, A1, A2, B1, C1 and C2, respectively, assigned to the bps of all 61 MAGs. Sixty of the MAGs were classified as bacterial and one as archaeal (MAG 53) (Fig.1). The archaeal bin was classified as *Crenarchaeota* and was most abundant in community C1, but was not found anymore in C2, and was also present in very low relative abundances in communities B1 and A2 (Fig. 1, Table S1).

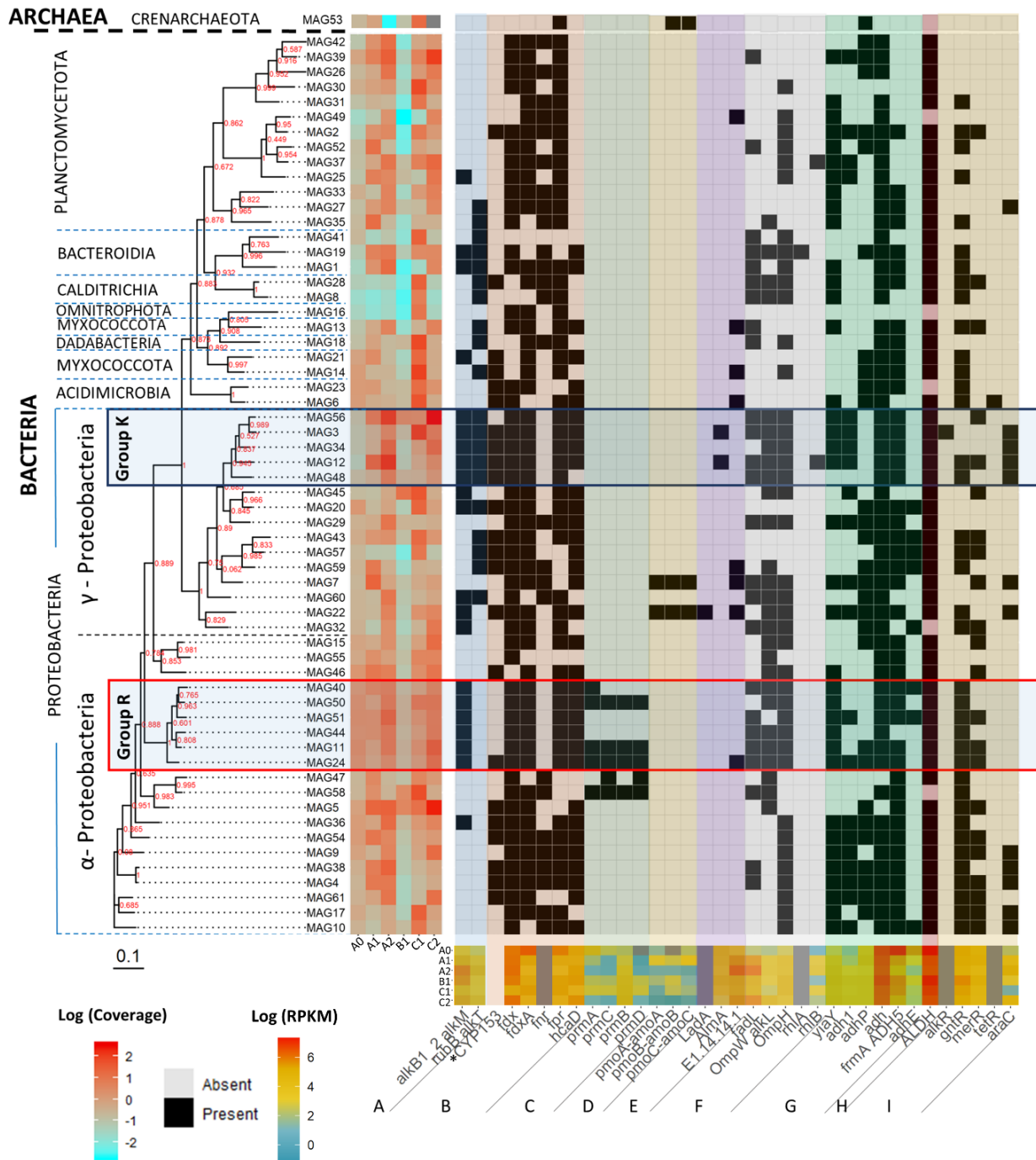


Fig.1 – Phylogenetic tree of the identified MAGs, their coverage in the six metagenomes plus the presence or absence of selected alkane and/or fatty acid degradation related genes (Table S2) in each of the MAGs and their RPKM in the different samples. The tree was built with Fasttree using the multiple sequence alignment obtained with gtdb-tk. Bootstrap values of each tree branch are given in red. The different gene groups refer to: (A) genes related to the alkane 1-monooxygenase-encoding gene *alkB*; (B) genes related to the cytochrome P450 alkane hydroxylase *CYP153*; (C) a propane oxygenase encoding genes; (D) a methane monooxygenase encoding genes; (E) genes encoding long-chain alkane related monooxygenases and fatty acid oxygenases; (F) transporters and biosurfactant synthesis genes; (G) alcohol dehydrogenase genes; (H) aldehyde dehydrogenase genes; and (I) genes encoding for proteins thought to be involved in transcription regulation of alkane degradation. Group K is a taxonomic clade, classified as *Pseudomonadales* that includes the MAGs that had a high number of the selected genes and were closely related to *Ketobacter sp.* and *Alcanivorax sp.* Group R includes all MAGs classified as *Rhodobacteraceae*, which all have the *alkB* gene encoding the alkane monooxygenase most typically associated with alkane degradation. KEGG annotations were used to determine RPKM values of genes in different samples. *The *CYP153* gene does not have an assigned KO identifier, its presence/absence in MAGs was identified using hmm models.

MAGs 5 and 56, belonging to the family *Parvibaculaceae* and genus *Ketobacter*, respectively, increased in coverage in both community A and C from the first to the second year, and were among the MAGs with the highest coverage in the communities A2, B1 and C2 (Fig. 1, Table S1). We compared the obtained MAGs with the genomes of potential hydrocarbon, alkane or plastic degraders (Table S3) retrieved from NCBI (Fig. 2A). MAGs 5 and 56 clustered together with alkane degrading species of the genus *Parvibaculum* and alkane degrader *Ketobacter alkanivorans*, respectively (Fig. 2A). MAG 56 was grouped in a larger cluster (Group K in Figs. 1 and 2) composed of MAGs classified as *Alcanivoraceae* and *Ketobacteraceae* and the genomes of known *Alcanivorax* species and *Ketobacter alkanivorans* (Fig. 2). Generally, MAGs from Group K increased over time (Fig. 1). Other MAGs also increased in coverage over time in the communities A and C (MAGs 1, 13, 15, 26, 27, 37, 39, 42, 44, 49, 51, 60, 61) (Fig. 1). Most MAGs exhibited a very low coverage in community B1, with the exception of some classified as *Proteobacteria*, which is also supported by the analysis of the 16S rRNA gene recovered from the metagenomes (Fig. S3). MAGs 5, 58, 45 and 56 were the only ones with coverage values higher than 1 in community B1, with values of 3.93, 2.95, 12.57 and 5.11, respectively.

Functional gene dominance in the metagenome over time

To determine which metabolic pathways increased in the incubations over time, we investigated the predicted genes with RPKM (reads per kilobase million) values that increased from the original community to after one year of incubation in the case of community A, and from one to two years of incubation in both, communities A and C. Predicted genes annotated as GST (glutathione S-transferases) homologues were overall the most abundant genes increasing in RPKM over time (Table S4), even though they were already present in fairly high relative abundance in the original sample A0 (Table S4).

GST homologue genes are involved in PAH (polycyclic aromatic hydrocarbons) degradation in prokaryotes, as well as in the biodegradation of other xenobiotics (Allocati *et al.*, 2009). Other enriched genes in the LDPE treatments, like *atzF* and *mlhB*, are also involved in xenobiotics degradation.

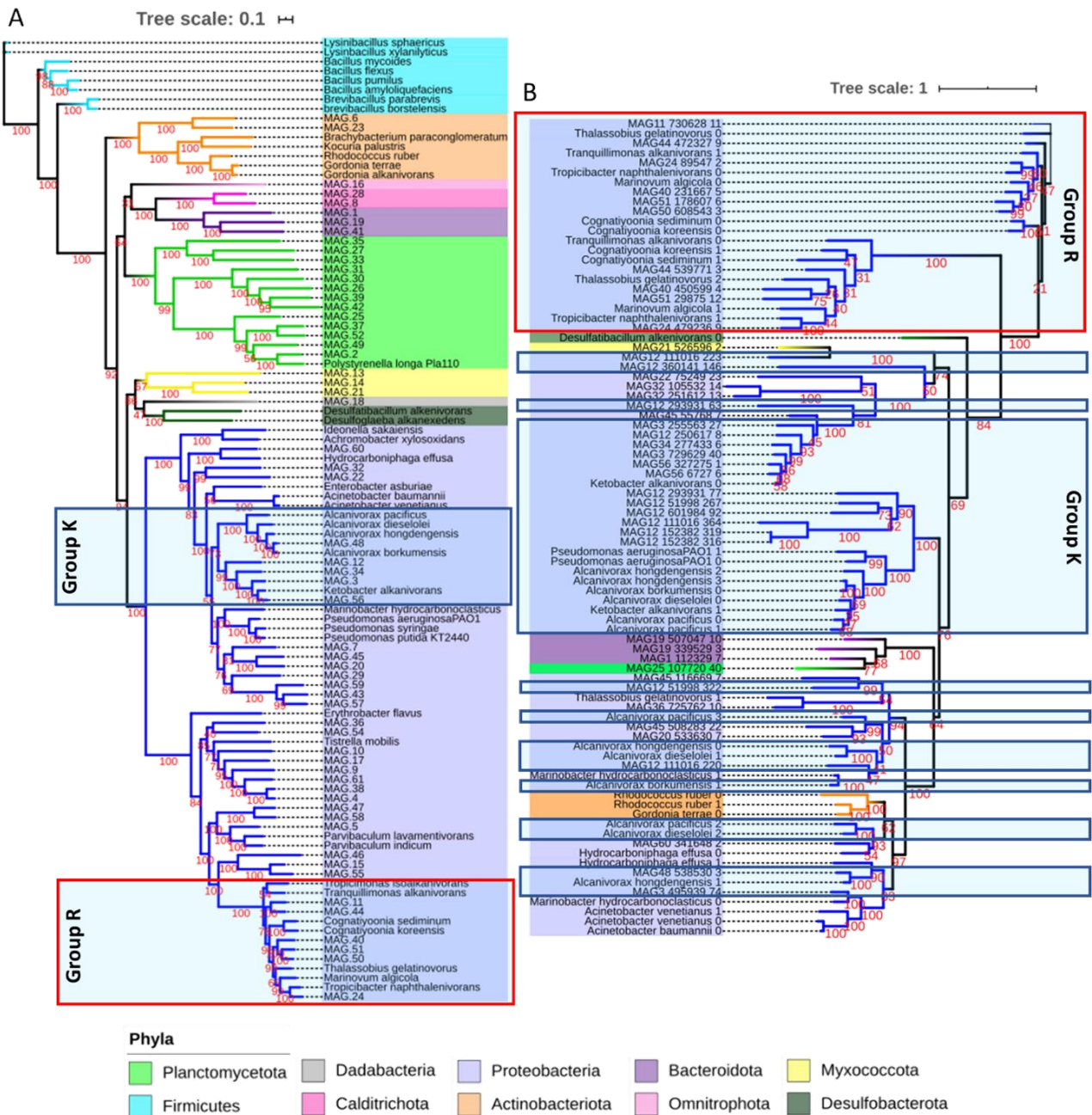


Fig.2 – Phylogenetic placement of (A) the MAGs and selected genomes (Table S3) and (B) putative alkB sequences identified in MAGs and genomes. Bootstrap values are indicated in red. Group K (blue boxes) and Group R (red boxes) refer to the same groups as described in Fig.1.

A large part of the oxidoreductase-encoding genes increasing in RPKM in the communities A2 and C2 were annotated as genes related to lipid metabolism, especially fatty acid and steroid metabolism (Table S5). Furthermore, all the identified complete KEGG pathway modules with increasing RPKM values were related to lipid metabolism, particularly fatty acid biosynthesis, fatty acid beta-oxidation with the synthesis of acyl-CoA, and acylglycerol and sphingosine degradation. The CYP51 gene (annotated by KEGG) was the gene

of the oxidoreductases category that increased most pronouncedly in RPKM in community A2 and C2 over time (Fig. S4). It encodes sterol 14 alpha-demethylase, a cytochrome P450 enzyme which plays an important role in sterol synthesis and also in fatty acid metabolism (Van Bogaert *et al.*, 2011). Another oxidoreductase, *cypD_E*, also significantly increased in RPKM over time, especially in community C2 (Fig. S4). *CypD_E* encodes for cytochrome P450/NADPH-cytochrome P450 reductase linked to fatty acid oxidation. It catalyzes the hydroxylation of a range of long-chain fatty acids, oxidises reduced nicotinamide adenine dinucleotide phosphate (NADPH) by electron transfer to the heme iron of the cytochrome P450 N-terminal domain (Gustafsson *et al.*, 2004).

Two predicted genes, annotated as monooxygenases involved in fatty acid degradation, also significantly increased in RPKM over time in the communities A2 and C2. While one of the predicted genes was classified encoding an unspecific monooxygenase (EC:1.14.14.1, KO identification K00493), the other gene was annotated as gene *alkB1_2*, encoding an alkane 1-monooxygenase involved in alkane degradation (Fig. 1 and Fig. S4). Alkane 1-monooxygenases catalyse the hydroxylation of n-alkanes and fatty acids in the presence of NADH-rubredoxin reductase and rubredoxin. A gene annotated as *rub*, encoding the rubredoxin-NAD(+) reductase, was also among the most enriched genes over time (Fig. 1, Tables S4 and S5). The rubredoxin-NAD(+) reductase transfers electrons from NADH to rubredoxin reductase and further through rubredoxin to alkane 1-monooxygenase.

There were several other genes increasing over time encoding enzymes related to fatty acid metabolism. Some of these genes, i.e., genes encoding lipid and fatty acid transporters (genes *lip*, *fadL* and *OmpW*) and alcohol (genes *yiaY*, *adh1*) and aldehyde (gene *ALDH7A1*) dehydrogenases (Tables S4 and S5)(Wang and Shao, 2013) are the key genes in the alkane degradation pathway.

Putative hydrocarbon degradation genes in MAGs

Overall, most MAGs that increased in coverage over time either showed the potential to degrade alkanes or had genes encoding for alkane and hydrocarbon transporters. MAGs 3, 12 and 22 had at least one medium-length alkane oxidation related gene and either the *AlmA* or the *LadA* gene, encoding enzymes potentially degrading both long- and medium-length chain alkanes (Fig. 1). MAG 22 also had all three genes encoding a methane/ammonia monooxygenase, suggesting that this organism is also capable of degrading short-chain alkanes. Furthermore, these MAGs also had at least one gene encoding a surfactant and

alkane membrane transporters. Group K MAGs (shown in Fig. 1) all had genes encoding aldehyde and alcohol dehydrogenases, at least two alkane related transporters and proteins associated with surfactant production. They also harboured the *alkB1_2* and *alkT* gene that encode for alkane monooxygenase and rubredoxin---NAD⁺ reductase, respectively, which together form a complex capable of oxidizing medium-chained alkanes (Fig. 1). The Group K MAGs also harboured genes encoding a cytochrome P450 alkane monooxygenase (CYP153), the associated transcription regulator gene *araC* and the genes encoding for a ferredoxin and ferredoxin reductase, which are required for the transfer of electrons from NAD(P)H to the cytochrome (Funhoff *et al.*, 2006).

MAG 5 also increased in relative abundance over time and harboured a gene encoding a protein associated with surfactant production and alkane transport into the cell (*OmpW*, *alkL*). MAGs 24, 11, 44, 51, 50 and 40, which together formed the *Rhodobactereaceae* clade (Group R in Fig. 1) all had genes annotated as *alkB1_2*, *hcaD* and the surfactant producing membrane protein encoding gene *OmpH*. These genes all increased in relative abundance over time and were present, even if apparently not in high abundances, in community B1. No rubredoxin reductase encoding gene was annotated in the Group R MAGs. However, they all had genes encoding for ferredoxin and ferredoxin reductase. It has been suggested that ferredoxin and ferredoxin reductase might replace rubredoxin and rubredoxin reductase, usually associated with *alkB* (Nie *et al.*, 2014). Together with MAG 58, three of the Group R MAGs also had the four genes encoding for the different subunits (Fig. 1, *prmABCD*) of an oxidoreductase that oxidises propane (propane 2-monooxygenase), a three-carbon alkane that is a gas at standard temperature and pressure.

Furthermore, group R MAGs, except MAG 51, harboured the gene *OmpW/alkL* encoding an outer membrane protein, involved in 1-alkanes transport into the cell and surfactant production. MAG 24 also had a gene annotated as an unspecific monooxygenase (E1.14.14.1). With the exception of MAG 50, all other Group R MAGs harboured the gene *fadL*. Almost all MAGs harboured at least one aldehyde dehydrogenase and one transcriptional regulator encoding gene, both involved in several metabolic processes within the cell.

Distribution of the *alkB* and CYP153 gene in the MAGs

HMM models were used to identify putative *alkB* and CYP153 genes in the MAGs and the genomes of potential hydrocarbon and plastic degraders (Table S3). A total of 21 and 23 MAGs had at least one copy of genes classified as *alkB* and CYP153, respectively (Fig. 1). *AlkB*

was found in one *Myxococcota* and one *Planctomycetota* MAG, in two *Bacteroidota* and in seventeen *Proteobacteria* MAGs. Multiple copies of the *alkB* gene were found in some of the MAGs, especially in MAGs from Group K. The highest number of *alkB* genes in one MAG was 12, found in MAG 12 (Fig. 2B). *AlkB* genes belonging to Group R MAGs clustered together in one single group. The *alkB* genes from Group R MAGs clustered with the *alkB* genes from known marine *Rhodobacteraceae* alkane degraders (Fig. 2B). In contrast, *alkB* genes from Group K clustered together in several groups, with some of them grouping with sequences from other *Proteobacteria* MAGs (Fig. 2B).

CYP153 was detected in one MAG of *Calditrichota* and of *Planctomycetota*, in two MAGS of *Actinobacteriota* and of *Myxococcota* and in seventeen MAGs classified as *Proteobacteria*. There were several clusters composed only of *Proteobacteria* CYP153, however, there were also CYP153 genes from MAGs of different phyla clustering together (Fig. S5). There were several MAGs with more than one copy of a gene classified as CYP153 (Fig. S5).

Cell abundance and respiration measurements

To determine respiration rates of the biofilms on plastic in comparison to glass, oxygen consumption measurements were performed after the surfaces were incubated for three months with communities A2, B2 and C2 (Fig. S1). Just before starting the respiration measurements, the abundance of all three microbial communities was significantly higher in the incubations with plastics than with glass ($F=955.18$, $p<0.001$) (Fig. 3B and Fig. S6). The cell abundance of the three communities growing on LDPE also differed between each other ($F=96.41$, $p<0.001$, Table S6), with community C exhibiting a significantly higher number of cells than the communities A and B (Fig. 3). No cells were found on the surface of both LDPE controls (Control I and Control II).

Oxygen consumption rates per cm^2 surface area were significantly higher in the microbial communities associated with LDPE than on glass ($F=48.84$, $p<0.001$) and in the controls (Fig. 3A, Table S7). However, cell-specific oxygen consumption rates were higher in microbial communities in the glass than in the plastic treatment (Fig. 3C). Incubations with community B2 showed the least difference in bulk oxygen consumption rates between the glass and plastic treatment. Additionally, from all the treatments with LDPE, community B2 exhibited the highest cell-specific oxygen consumption rate. The communities A2 and C2 showed similar cell-specific oxygen consumption rates (Fig. 3C, $p=0.99$). However, when incubated with glass,

community A2 showed a higher oxygen consumption rate than community C2 (Fig. 3C, $p < 0.001$).

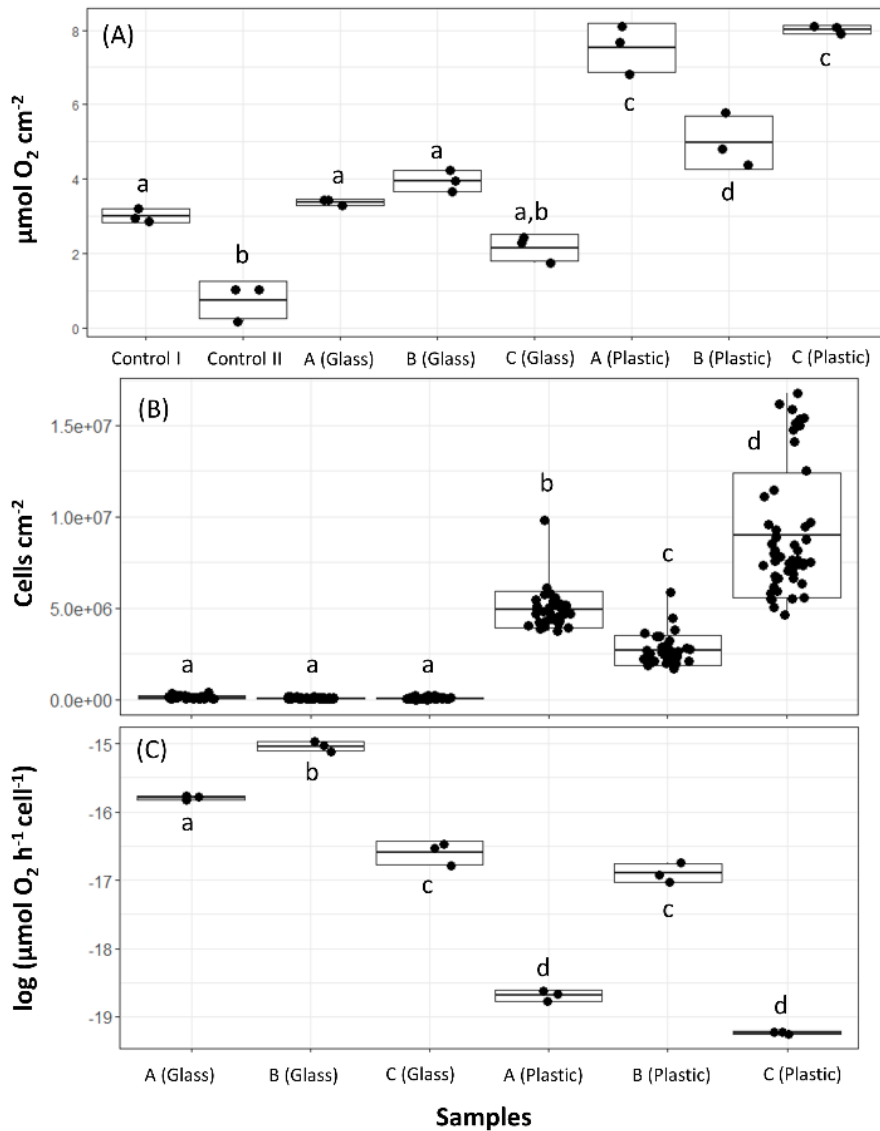


Fig.3 – Oxygen consumption rates of microbes in the plastic and glass treatments. The boxplots represent the mean $\pm$ SD. (A) Total oxygen consumption in each sample in μmol per cm^2 of plastic or glass. Each black dot represents one replicate. (B) Number of cells per cm^2 of plastic or glass. The boxplot lines in A, B and C (Plastic) represent the maximum number of cells cm^{-2} counted in a photo of that sample. Each black dot corresponds to the number of cells per cm^2 of one photo. The controls were excluded from this and the next plot because no cells in those samples were detected. (C) Oxygen consumption $\text{cell}^{-1} \text{ h}^{-1}$. Samples with different letters on each plot were significantly different from each other (p -value < 0.05 , Tukey test results in Tables S2-4).

Alteration of plastic surfaces determined by ATR-FTIR, SEM and weight

The ATR-FTIR spectra of the untreated LDPE sheets, packaging LDPE and UV-treated LDPE sheets (prior to microbial incubations) after six months of exposure to microbial communities growing previously on PE as sole carbon and energy source for two years are

depicted in Fig. 4. All plastics shared the typical LDPE bands for CH_3 and $-\text{CH}_2-$ groups at 2916, 2849, 1469, 1375 and 718 cm^{-1} .

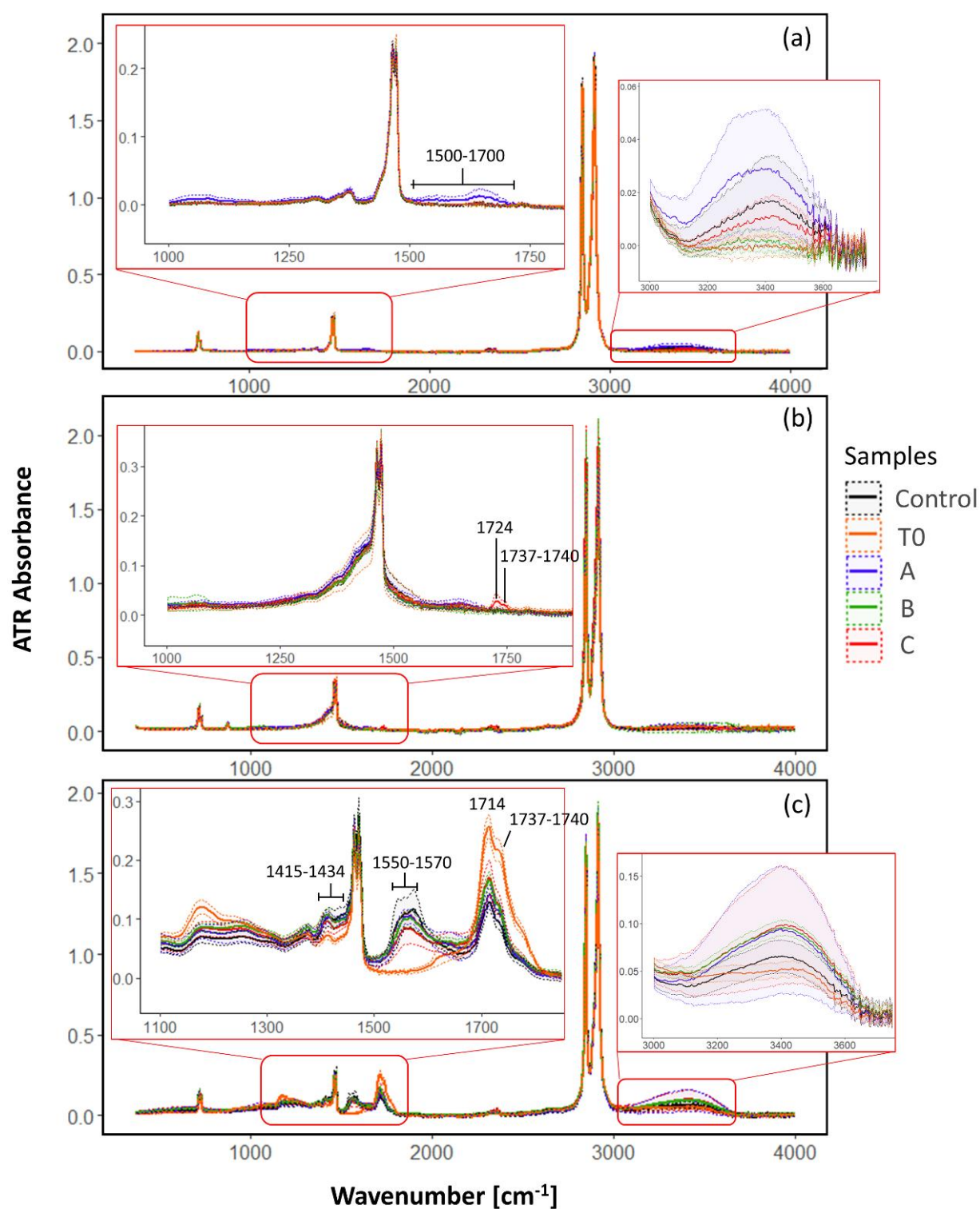


Fig. 4 – ATR-FTIR spectra of (a) non-weathered LDPE sheets; (b) packaging PE sheets; and (c) UV-weathered LDPE sheets prior to the incubation and after six months incubated with the three microbial communities. The lines correspond to the mean value of the replicates and the same-coloured dashed lines represent the corresponding standard deviation.

In non-weathered LDPE plastics incubated with community A, a band spreading from 1500 to 1700 cm^{-1} appeared indicating the presence of carbonyl ($>\text{C}=\text{O}$) and vinyl groups ($-\text{CH}=\text{CH}-$). Also, a small peak at 3400 cm^{-1} was detected which might indicate the appearance of hydroxyl groups. Bands at around 1640 and 3400 cm^{-1} , however, might also indicate the presence of water. The spectra from packaging PE pieces incubated with community C revealed peaks at 1724 and at 1737-1740 cm^{-1} , corresponding to the appearance of carbonyl groups, carboxylic groups and aldehydes, respectively. At the beginning of the incubations, UV-weathered plastics exhibited an additional band at 1714 cm^{-1} , corresponding to the appearance of carbonyl groups resulting from photo-oxidation of polyethylene. After six months of incubation, peaks indicating carboxylates appeared at 1550-1570 cm^{-1} and 1415-1434 cm^{-1} in all incubations. The peak at 1714 cm^{-1} had higher intensity in UV-weathered plastics incubated with microbes than in the control samples without microbes, but of lower intensity than prior to the incubation experiment. A small peak at about 3400 cm^{-1} also appeared, especially in the plastics incubated with bacteria. There were also signs of degradation in the control treatment without microbes of the UV-weathered LDPE. This degradation might be the result of the presence of inorganic ions working as oxidizing catalysts of the carbonyl compounds to carboxylic compounds (Da Costa *et al.*, 2018).

After three months of incubation a visible biofilm developed on all PE samples, except in the controls (Fig. 5 A-F). In some samples, after removal of the biofilm, there were some visible holes and apparent changes in the plastic surface, especially in the previously UV-weathered LDPE and packaging PE (Fig. 5 G-I) when incubated with the community A and C.

Significant weight losses were found between different treatments and/or time points in the packaging PE and non-weathered LDPE ($F=6.847$, $p<0.001$ and $F=9.34$, $p<0.001$ respectively). Non-weathered LDPE plastics significantly decreased in weight over a period of eight months of incubation compared to the controls without bacteria, (Fig. 6, Table S8). The loss in weight over the eight months amounted to 7.5%, 5% and 8.5% in plastics incubated with communities A, B and C, respectively. All PE packaging plastics, including the control samples, significantly decreased in weight after eight months of incubation (Fig. 6).

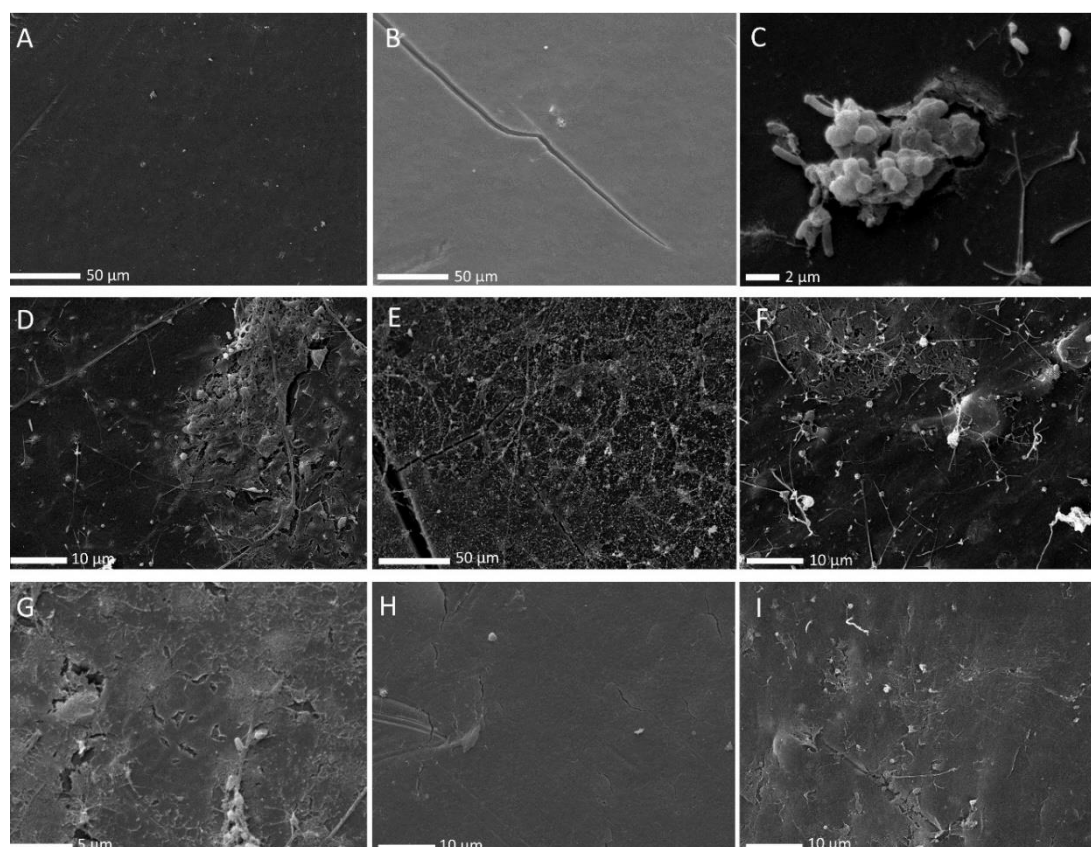


Fig. 5- SEM images of samples collected after three months incubated with the three different communities. (A) LDPE control sheet; (B) UV-weathered LDPE control; (C) LDPE sheet incubated with community C2; (D) LDPE sheet incubated with community A2; (E) UV-weathered LDPE incubated with community C2; (F) Packaging PE incubated with community C2; (G) LDPE sheet incubated with C2, after biofilm removal; (H) UV-weathered LDPE sheet incubated with B1 after biofilm removal; (I) Packaging PE incubated with C2 after biofilm removal. The white bars represent the scale of the image.

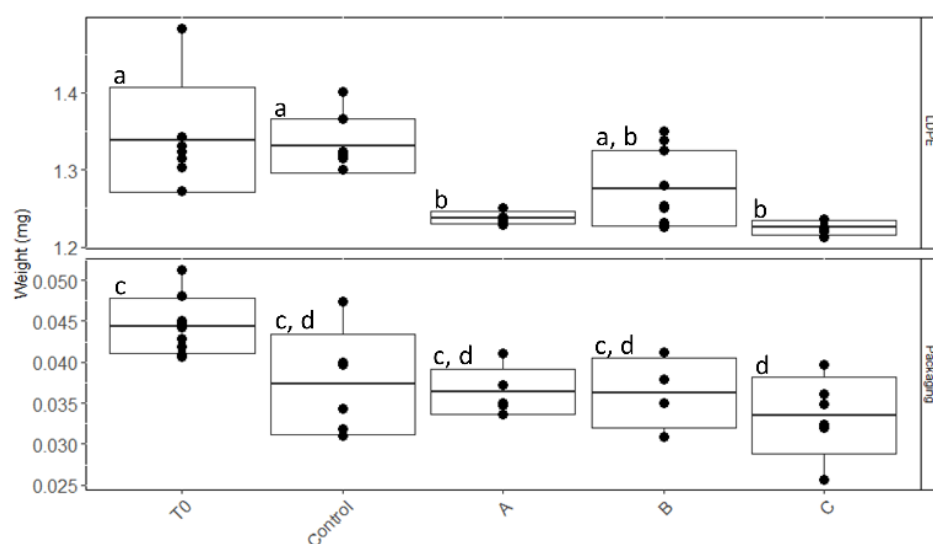


Fig. 6- Weight of non-weathered LDPE and packaging PE pieces incubated with the three different communities A, B and C for eight months. The boxplot represents the mean $\pm$ SD with the whiskers representing the minimum and maximum weight values. Each dot represents the weight of an individual plastic piece. Different letters within each panel refer to samples with statistically significant differences (p-value < 0.05, Table S8).

Discussion

Our results suggest that LDPE can serve as a carbon and energy source for at least a part of the plastic biofilm community. Furthermore, the fact that most of the enriched genes in our experiments encode enzymes involved in alkane and fatty acid metabolism suggests that alkane degradation-related pathways are the main mechanisms responsible for the degradation of LDPE-originating compounds.

Even though the three communities were derived from three different plastics and even a different season in the case of community C, there were several similarities in taxonomy and functional diversity between the communities A and C after two years of incubation. The original community A0 was dominated by families typically found in plastic biofilms, such as *Flavobacteriaceae*, *Pseudoalteromonaceae*, *Alteromonadaceae* and *Rhodobacteraceae* (Fig. S3) (De Tender *et al.*, 2017). Over time, the families *Flavobacteriaceae*, *Pseudoalteromonaceae*, *Alteromonadaceae* decreased in relative abundance, while the family *Rhodobacteraceae* dominated the classified families in the communities A2 and C2 (Fig. S3).

The two MAGs with the highest coverage in the A2 and C2 communities, classified as *Parvibaculaceae* and *Ketobacter* sp. (bins 5 and 56, respectively), are closely related to species known to be involved in alkane degradation (Fig. 2A). *Ketobacter alkanivorans* is a recently characterized marine n-alkane degrading bacterium and, until now, the only classified species of the *Ketobacter* genus (Kim *et al.*, 2018). Even though in the recently proposed rank-normalised GTDB taxonomy (Parks *et al.*, 2018) *Ketobacter* belongs to the *Ketobacteraceae* family, it was previously grouped together with the genus *Alcanivorax* in the *Alcanivoraceae* family. *Alcanivorax* and closely-related bacteria have been shown to thrive after oil spills (Kostka *et al.*, 2011) and dominate petroleum-contaminated waters when adequate amounts of nitrogen and phosphorus are available (Kasai *et al.*, 2002). This is mainly attributed to their high ability in degrading alkanes. In our incubations, *Ketobacteraceae* and *Alcanivorax* were among the MAGs with the highest increase in relative abundance over time and they have the genetic potential for alkane degradation. While the role of alkane degradation in LDPE degradation is unclear, our results further suggest that if the LDPE polymer can in fact be degraded, alkane-related metabolism is likely involved.

The family *Parvibaculaceae* (previously *Rhodobiaceae*) to which MAG 5 belongs to, comprises species from the genus *Parvibaculum* known for their ability to degrade polycyclic aromatic hydrocarbons and laundry detergents (Wang *et al.*, 2010; Lai *et al.*, 2011; Schleheck

et al., 2011). Additionally, some of the other relatively abundant MAGs in the communities A and C after one and two years of incubation, like the ones classified as *Acidimicrobia* (previously *Actinobacteria*) and *Myxococcota* (previously order *Myxococcales*), have also been found in hydrocarbon polluted areas and associated with alkane degradation (Abbasian *et al.*, 2016). These MAGs also harboured essential genes encoding enzymes for alkane degradation. The fact that several of the most abundant MAGs in communities A2, B1 and C2 were identified as close relatives to hydrocarbon degraders and harboured genes encoding all essential enzymes for alkane degradation is additional evidence that hydrocarbon degrading organisms were positively selected in our incubations. This supports the hypothesis that alkane degradation pathways might be used in the degradation of LDPE. While *Actinobacteriota* and several alkane degrading *Proteobacteria*, like those belonging to the *Alcanivorax* genus or the *Rhodobacteraceae* family, have already been identified and characterized (Yakimov *et al.*, 1998; Kummer *et al.*, 1999; Liu and Shao, 2005; Harwati *et al.*, 2008; Nicdao and Rivera, 2012), alkane degraders belonging to the *Myxococcota* and *Planctomycetota* phyla are poorly studied. Our phylogenetic analysis coupled with the identification of alkane oxygenase genes in taxonomically distant MAGs indicates that there might be a relatively high diversity of unidentified alkane degraders in the biofilm of PE in the sea. The few studies that looked into the genetic potential for PE degradation in the ocean mainly focused on the *alkB* gene (Syranidou *et al.*, 2017). After two years of incubation, the enrichment of MAGs with other non-*alkB* alkane monooxygenase genes indicates that pathways other than those associated to *alkB*, might also be relevant for the utilization of PE-originating compounds and should be considered in future research. Even after two years of incubation, some of the MAGs do apparently not have the genes required for alkane oxidation or transport into the cell. This suggests that there might be other non-identified pathways involved in the utilization of LDPE derived carbon. This could, for example, explain the increase in relative abundance of several *Planctomycetota* MAGs in which no alkane oxidase gene was found. While two of the *Planctomycetota* MAGs had genes classified as alkane oxygenases, the majority did not. Albeit in low relative abundances, members of this phylum have been previously found in oil-degrading consortia (Gao *et al.*, 2015) and in fact, some have been reported to have alkane monooxygenase genes (Guibert *et al.*, 2016). As common elements of plastic biofilms (Pinto *et al.*, 2019; Gerritse *et al.*, 2020), the potential for members of this phylum to utilize PE originating compounds should be considered.

The lack of genes in some MAGs related to alkane degradation, however, can also be a result of the low completeness of some of these genomes, not allowing the detection of the specific genes. It might also simply reflect the fact that some of these MAGs do indeed not have the ability to degrade hydrocarbons derived from LDPE and are sustained by by-products of the hydrocarbon-degrading component of the community or other compounds potentially leaching from the plastic or generated by the biofilm associated microbes. Community B1 appears to also have been dominated by bacteria from Groups R and K and MAG 5 (Fig. 1), giving the community the necessary repertoire of genes for surfactant production and alkane degradation. However, this community showed slower biofilm development than the other two communities despite exhibiting similar diversity (Fig. S2, Fig. 3). Furthermore, non-weathered LDPE sheets lost less weight when incubated with community B than with any of the other two communities (Fig. 6). This might be a result of differences in LDPE degradation efficiency between the different organisms in each of the incubations but might also suggest that community B might have been limited in specific compounds that communities A and C were able to produce. This implies that, if the degradation of LDPE-originating hydrocarbons is in fact taking place, the degraders, while capable of sustaining growth of a diverse bacterial community, might be relatively slow growing and require metabolic diversity to efficiently degrade LDPE-derived compounds. This is in accordance with laboratory experiments on the degradation of untreated PE by bacterial monocultures, exhibiting low biodegradation rates (Sudhakar *et al.*, 2008; Harshvardhan and Jha, 2013).

Generally, the FTIR spectra revealed that changes in the surface of the PE incubated with the three communities were relatively small after six months. However, bacterially mediated modifications of the surface of the plastics, especially on non-weathered LDPE by community A and on packaging PE when incubated with community C, caused an apparent weight loss of these plastics after eight months of incubation (Fig. 6). Furthermore, holes and cracks appeared in some of the plastics incubated with bacteria (Fig. 5C, G-H). This might indicate that the communities are degrading the surface of the plastic at very slow rates, taking up the oxidation products at the same rate as they are set free from the LDPE. Thus, most changes in the surface structure were small or undetectable by our ATR-FTIR analysis (Fig. 4). It might also indicate that the communities are mainly utilizing compounds passively released by the plastics into the surrounding seawater, rather than actively degrading the polymer. Previously, it has been reported that the same LDPE sheets as used in this study release dissolved organic carbon (DOC) into the surrounding seawater, even when kept in the

dark. This released DOC can subsequently be taken up by the marine microbial community (Romera-Castillo *et al.*, 2018). Additionally, plastic additives can also leach into the environment (Suhrhoff and Scholz-Böttcher, 2016). Recent evidence shows that certain bacteria can degrade specific additives, some through pathways that also lead to fatty acid β -oxidation (Wright *et al.*, 2020). The degradation of these compounds in the marine environment is only poorly studied and to date there is no evidence that alkane-degraders like the ones enriched in our incubations can also degrade additives. However, due to the lack of knowledge of pathways involved in the biodegradation of most additives and the high variety of additive compounds, it is possible that certain organisms in our communities can utilize leaching LDPE-additives as energy and carbon source.

There was also evidence of abiotic oxidation of plastics, as shown by low oxygen consumption in the controls (where microbes were absent) and in the ATR-FTIR spectra of the previously UV-weathered plastics. In our experiments abiotic oxidation of plastics was most obvious in the incubations with UV-weathered LDPE sheets (Fig. 4), where chemical compound classes were not detected in non-weathered LDPE and carbonyl groups decreased after six months of incubation even in the abiotic control (Weiland *et al.*, 1995). Usually, plastic biodegradation by microorganisms is more efficient when the polymer has previously undergone partial photo-oxidation (Montazer *et al.*, 2018). In our incubations this could not be detected, possibly due to the masking effect of the abiotic oxidation. This reinforces the fact that, if LDPE biodegradation occurs, it takes place at relatively slow rates, even when the plastic was previously UV-exposed.

Several heterotrophic bacteria like the organisms from Group R (Fig. 1) (*Rhodobactereaceae*) might have the ability to use alkanes as carbon and energy source. Whether they actually utilize plastics in the presence of other carbon sources, however, remains unknown. *Rhodobactereaceae* are typically among the most abundant families found in marine biofilms and are commonly enriched in plastic biofilms (Bryant *et al.*, 2016; Debroas *et al.*, 2017; Kesý *et al.*, 2019; Oberbeckmann and Labrenz, 2019). Although the Group R MAGs were slightly enriched over time, they were already relatively abundant in the original community A0. They all harboured a gene encoding for at least one alkane monooxygenase and the gene *fadL*, encoding a fatty acid transporter, was detected in all except one. In natural marine biofilms these organisms might have access to more easily accessible and metabolizable carbon and energy sources and therefore, might not participate in the uptake of LDPE-derived hydrocarbons albeit, this is unknown. In contrast, obligatory

hydrocarbonoclastic organisms, like *Alcanivorax borkumensis*, are specialized and dependent on degrading hydrocarbons (Schneiker *et al.*, 2006). Group K organisms (Fig. 1) did exhibit several metabolic similarities and were closely related to *Alcanivorax borkumensis*, potentially occupying the same or a similar metabolic niche in the environment. For example, MAG 56, one of the most enriched MAGs, appears to lack proteins involved in the transport of sugars and aminoacids into the cell. This might be an indication that, similar to *Alcanivorax borkumensis*, this bacterium relies exclusively on alkanes as a carbon source. However, we did not obtain completely closed genomes for any of the organisms in our incubations, which makes it impossible to determine with certainty whether they really lack these functions. Interestingly, even if present in relatively low abundances, the family *Alcanivoraceae* has been associated with plastics including PE in the marine environment (Oberbeckmann *et al.*, 2014, 2016; Delacuvellerie *et al.*, 2019). This might be an indication that these bacteria utilize PE as a carbon and energy source in the environment, consequently playing a role in the fate of plastics in the sea.

Taken together, we have identified the potential importance of genes other than the gene *alkB* and pathways in the utilization of LDPE-originating compounds in the marine environment. We identified a taxonomically diverse set of plastic biofilm-dwelling microorganisms, some of them abundant in plastic biofilms, with the potential for alkane and potentially LDPE degradation.

Material and Methods

Experimental setup

We collected three plastic pieces from the sea surface of the Northern Adriatic Sea, approximately 500 m off the coast of Rovinj, Croatia. Two were collected in November 2016 (plastics A and B) and one in August 2016 (plastic C). The plastics were immediately taken to the laboratory submerged in seawater (Fig. S7). A piece from each plastic was cut and frozen at -80°C for DNA analysis and another piece was taken for Raman spectroscopy to determine the plastic type. The three plastics were classified as polyethylene (PE). The remaining plastics were transferred to separate 1 L borosilicate bottles filled with artificial seawater (ASW) and amended with 2 µM of NaPO₄ and 10 µM of NH₄Cl. The bottles were kept at room temperature (21°C- 22.5°C) (Table S9).

After three weeks, the plastics were transferred to fresh 1 L bottles with ASW. This process was repeated seven times for plastic C and four times for plastics A and B. One small piece of each plastic type was then cut and incubated in a new bottle with ASW amended with inorganic nutrients (as described above) together with sterile low-density polyethylene (LDPE) pieces. The LDPE sheets were purchased from Goodfellow. Each bottle contained 10 LDPE squares (1x1 cm). After three weeks, one of these LDPE pieces was transferred to a new bottle with ASW, again together with new sterile LDPE pieces. This process was repeated for two years. After one and two years, a plastic sample from each of the incubations was taken and frozen at -80°C for metagenomic analyses. After two years, samples were also taken for respiration measurements.

All tools and bottles used were made of materials other than plastic and muffled or sterilized.

DNA extraction and sequencing

DNA from plastics was extracted using a modified bead-beating approach combined with the Puregene Tissue DNA extraction kit (Qiagen, Valencia, CA) as previously described (Debeljak *et al.*, 2017). Samples with sufficient amount of DNA were single-end sequenced (1 x 150bp) with Illumina NextSeq technology at Microsynth AG, Switzerland. These were plastic A right after collection (A0), after one year of incubation (A1), and after two years of incubation (A2), plastic C after one year and two years incubation (C1 and C2, respectively) and plastic B after one year of incubation (B1). All raw sequences files are available from the NCBI Sequence Read Archive (SRA) database (BioProject: PRJNA599974). Due to low DNA concentrations, samples from plastics B and C right after collection (samples B0 and C0) and sample B2 were not sequenced.

Oxygen consumption measurements

At the end of the incubations after two years, one plastic piece from each of the incubations was transferred to a new bottle with ASW together with 16 sterile LDPE pieces. A second plastic piece from each of the incubations was incubated in a separate bottle with ASW with 16 glass pieces of 1 cm x 2.25 cm. As a control, 16 sterile LDPE pieces of dimensions 1.5 cm x 1.5 cm were incubated in a separate bottle with ASW (Control I). In order to let the biofilm develop on both glass and plastic without the influence of the old LDPE pieces, after one

month, the plastics and glass were transferred to new ASW bottles and incubated for two additional months.

After two months, 15 pieces from each of the incubations were distributed among three BOD bottles of approximately 120 mL filled with ASW, resulting in triplicate bottles with five plastic pieces each. The same was done for the glass samples. One piece was also taken for bacterial abundance determination by adding it to 4% formaldehyde for 10 min and storing it at -80°C. Before transferring the glass and plastic to the BOD bottles for oxygen consumption measurements, one piece of glass and one of LDPE from each of the incubations were taken to determine cell abundance. The protocol for the oxygen and cell abundance measurements can be found in the Supplementary Information.

Assessing the physical and chemical properties of the PE surface

To determine changes of the surface of PE sheets when incubated with the three communities after two years, we incubated one plastic colonized with one of the three communities in sterile ASW with three different types of PE pieces: (1) the same LDPE sheets as mentioned above; (2) the same LDPE sheets but previously UV-weathered (irradiated with UV radiation, wavelength 300-400 nm) under artificial conditions in a SUNSET CPS+ (Atlas-MTS) for two weeks, and (3) PE sheets from a pear packaging bag bought in a supermarket. Twenty pieces of each of the different types of PE sheets were incubated in 500 mL bottles, filled up to 300 mL with ASW and with one plastic already colonized with one of the three communities. A control bottle for each of the PE sheet types was prepared without the addition of an already colonized plastic. The bottles were kept at 21.5°C. After three months of incubation, one plastic sample from each bottle was collected for scanning electron microscopy (SEM) and at least quadruplicate samples were collected after six months for attenuated total reflection Fourier-transform infrared (ATR-FTIR) analysis. After eight months of incubation, at least five plastics were weighed from each incubation. Protocols for SEM and ATR-FTIR analysis can be found in the Supplementary Information.

Statistical analysis and bioinformatics

ANOVA was performed to compare differences in total oxygen consumption and cell-specific oxygen consumption rates between samples with different communities and substrate. To assess differences between specific pairs of samples, post-hoc Tukey tests were performed. An ANOVA and post-hoc Tukey tests were also performed to compare the weight

of plastics incubated with different communities after eight months of incubation. All statistical analyses and plots were done with the program R, unless otherwise stated.

Genomic assembly and annotation

Read quality was assessed with fastqc. Overrepresented sequences were removed and reads were shortened to 149 bp in all samples using the adapterremoval program. After filtering and trimming, a total of 35,326,547, 15,541,923, 38,372,532, 3,180,678, 35,388,001 and 37,988,480 reads from samples A0, A1, A2, B1, C1 and C2, respectively, were co-assembled using the program Megahit (Li *et al.*, 2015) with default settings. Since we were aiming at identifying organisms and pathways enriched in the cultures, sample A0 was excluded from the co-assembly to decrease complexity.

Predicted genes were identified from the co-assembly using the Prodigal (Hyatt *et al.*, 2010) software with default settings. Functional annotation of the predicted genes was performed with the online EggNOG-mapper v1 using Diamond as the sequence aligner with a maximum E-value cut-off of 10^{-5} . A total of 2,500,984 predicted genes were recovered from the co-assembly, from which 736,382 were annotated with the eggNOG mapper and from which 9,532 unique KO orthologies were identified. A total of 958 genes were enriched, i.e., increased in RPKM (reads per kilobase million) value over time (Table S5), from which 154 were classified as oxidoreductases (Table S6).

rRNA genes from each individual sample were assembled and further annotated through matam (Pericard *et al.*, 2017) using Silva_132_SSURef_Nr99 as the reference database. The identification of taxonomic units with matam is directly dependent on the correct assembly of one single gene (16S rRNA gene). Hence, it is likely to underestimate diversity in samples with a low number of reads by failing to assemble the gene of rare species. Metagenomes A1 and B1 had a significantly lower number of reads than the other samples. Therefore, to compare taxonomic diversity among all samples, the relative abundance and counts of mOTUs were determined by the software mOTUs (Milanese *et al.*, 2019). This software classifies taxa based on a group of 40 universal marker genes and hence, it is likely to be less biased towards identifying only relatively abundant taxa than matam.

mOTU diversity indexes Shannon and Simpson and mOTU richness were calculated using the iNext R package (Hsieh *et al.*, 2016). Coverage-based rarefaction was used to normalize all samples to a coverage of 84%, corresponding to the calculated coverage of the B1 metagenome which was the lowest of all samples.

Read mapping

To obtain coverage information for assembled contigs and bins in all samples, the reads were mapped to the assembled contigs using the Burrows-Wheeler Aligner (BWA) (Li and Durbin, 2009). The mapped read counts, coverage and rpkms were extracted using `bbmap/pileup`.

Binning

To recover individual genomes of the organisms enriched in the incubations, contigs from the co-assembly with a minimum of 1500 bp were binned using `metabat` (Kang *et al.*, 2015) and `maxbin` (Wu *et al.*, 2014). In both cases, both tetra-nucleotide frequency and contig coverage in every individual sample were used for binning.

To obtain high-quality draft genomes, the resulting bins from each program were refined using `metaWRAP` (Uritskiy *et al.*, 2018). The resulting refined bins with completeness > 50% and contamination < 10% were used for further analysis. Hereafter, bins are called MAGs (metagenome assembled genomes).

Taxonomic classification of the MAGs was conducted via phylogenetic inference through marker genes using the software GTDB-Tk which uses the taxonomy as suggested by the Genome Taxonomy Database (Parks *et al.*, 2018). We used `Fasttree` to build a phylogenetic tree with the multiple sequence alignment output by GTDB-Tk (Chaumeil *et al.*, 2019). MAG coverage in each sample was calculated by dividing the total number of bp of reads mapped to the MAG by the total length of all contigs, and multiplying it by 10^6 divided by the total number of bp of the sample. The count of mapped reads to the contigs of each MAG was obtained as described above. Gene calling of each MAG was predicted using `Prodigal` (Hyatt *et al.*, 2010), sequences encoding `alkB` and `P450` were retrieved by HMMER search (`hmmsearch`) against a curated model downloaded from FunGene (<http://fungene.cme.msu.edu/>) with the threshold of domain coverage > 30%. The gene encoding `CYP153` was further refined from the `P450` gene with a customized hmm model with domain coverage > 75%. `MAFFT` (Katoh and Standley, 2013) was used to build alignment for both, the `alkB` gene and `CYP153` gene. The phylogenetic tree was generated using `RAxML` (Stamatakis, 2014) under `PROTGAMMALG` model with 100 bootstraps. Tree visualization was carried using the Interactive Tree Of Life (iTOL) webtool (Letunic and Bork, 2016).

Enriched genes and metabolic pathways

Because oxidoreductase profiles have been found to be best suited to functionally characterize a microbial community (Ramírez-Flandes *et al.*, 2019), in addition to determining genes that increased in RPKM value over time, we specifically looked at the enriched oxidoreductases over time. Oxidoreductases were obtained by selecting KEGG orthology (KO) annotations obtained with EggNOG and classified as oxidoreductases (EC1). The EC numbers were obtained using KO to EC information provided by the ko2ec tool. The KO numbers of enriched genes were used as an input into the online KEGG Mapper reconstruction option and the complete enriched pathway modules were identified. We also analysed the relative abundance of selected genes (Table S2), encoding for enzymes previously suggested in the literature as being related to alkane degradation, in all our metagenomes and also determined their presence in the individual MAGs.

Acknowledgments

We thank the Center for Marine Research of the Ruder Boskovic Institute, Croatia, for accommodating us during sampling, especially Dario, Mirjana, Ingrid, Paolo and Marino for all the support provided. We acknowledge Daniela Gruber for all the help provided during processing and analysis of the SEM samples. We also thank Miguel Guerreiro and Zihao Zhao for the assisting in bioinformatics issues. Financial support was provided by a Doctoral Fellowship (DOC scholarship) from the Austrian Academy of Sciences (ÖAW) awarded to MP, the ARTEMIS project of the Austrian Science Fund (P 28781-B21) to GJH and the research platform PLENTY financially supported by the University of Vienna, Austria.

References

- Abbasian, F., Palanisami, T., Megharaj, M., Naidu, R., Lockington, R., and Ramadass, K. (2016) Microbial diversity and hydrocarbon degrading gene capacity of a crude oil field soil as determined by metagenomics analysis. *Biotechnol Prog* **32**: 638–648.
- Allocati, N., Federici, L., Masulli, M., and Di Ilio, C. (2009) Glutathione transferases in bacteria. *FEBS J* **276**: 58–75.
- Amaral-Zettler, L.A., Zettler, E.R., and Mincer, T.J. (2020) Ecology of the plastisphere. *Nat Rev Microbiol.* 1-13
- Amaral-Zettler, L.A., Zettler, E.R., Slikas, B., Boyd, G.D., Melvin, D.W., Morrall, C.E., et al. (2015) The biogeography of the Plastisphere: implications for policy. *Front Ecol Environ* **13**: 541–546.
- Van Bogaert, I.N.A., Groeneboer, S., Saerens, K., and Soetaert, W. (2011) The role of cytochrome P450 monooxygenases in microbial fatty acid metabolism. *FEBS J* **278**: 206–221.
- Boonmak, C., Takahashi, Y., and Morikawa, M. (2014) Cloning and expression of three ladA-type alkane monooxygenase genes from an extremely thermophilic alkane-degrading bacterium *Geobacillus thermoleovorans* B23. *Extremophiles* **18**: 515–523.
- Bryant, J.A., Clemente, T.M., Viviani, D.A., Fong, A.A., Thomas, K.A., Kemp, P., et al. (2016) Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. *mSystems* **1**: e00024-16.
- Chaumeil, P.-A., Mussig, A.J., Hugenholtz, P., and Parks, D.H. (2019) GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. *Bioinformatics*.
- Da Costa, J.P., Nunes, A.R., Santos, P.S.M., Girão, A. V, Duarte, A.C., and Rocha-Santos, T. (2018) Degradation of polyethylene microplastics in seawater: Insights into the environmental degradation of polymers. *J Environ Sci Heal Part A* **53**: 866–875.
- Cózar, A., Echevarría, F., González-Gordillo, J.I., Irigoien, X., Úbeda, B., Hernández-León, S., et al. (2014) Plastic debris in the open ocean. *Proc Natl Acad Sci* **111**: 10239–10244.
- Das, M. and Kumar, S. (2014) An approach to low-density polyethylene biodegradation by *Bacillus amyloliquefaciens*. *3 Biotech* 1–6.
- Debeljak, P., Pinto, M., Proietti, M., Reisser, J., Ferrari, F.F., Abbas, B., et al. (2017) Extracting DNA from ocean microplastics: a method comparison study. *Anal Methods* **9**: 1521–1526.
- Debroas, D., Mone, A., and Ter Halle, A. (2017) Plastics in the North Atlantic garbage patch: A boat-microbe for hitchhikers and plastic degraders. *Sci Total Environ* **599–600**: 1222–1232.
- Delacuvellerie, A., Cyriaque, V., Gobert, S., Benali, S., and Wattiez, R. (2019) The plastisphere in marine ecosystem hosts potential specific microbial degraders including *Alcanivorax borkumensis* as a key player for the low-density polyethylene degradation. *J Hazard Mater* **380**: 120899.
- Devi, R.S., Ramya, R., Kannan, K., Antony, A.R., and Kannan, V.R. (2019) Investigation of biodegradation potentials of high density polyethylene degrading marine bacteria isolated from the coastal regions of Tamil Nadu, India. *Mar Pollut Bull* **138**: 549–560.
- Dudek, K.L., Cruz, B.N., Polidoro, B., and Neuer, S. (2020) Microbial colonization of microplastics in the Caribbean Sea. *Limnol Oceanogr Lett* 5–17.
- Dussud, C., Hudec, C., George, M., Fabre, P., Higgs, P., Bruzard, S., et al. (2018) Colonization of Non-biodegradable and Biodegradable Plastics by Marine Microorganisms. *Front Microbiol* **9**: 1571.
- Dussud, C., Meistertzheim, A.L., Conan, P., Pujo-Pay, M., George, M., Fabre, P., et al. (2018) Evidence of niche partitioning among bacteria living on plastics, organic particles and surrounding seawaters. *Environ Pollut* **236**: 807–816.
- Funhoff, E.G., Bauer, U., García-Rubio, I., Witholt, B., and van Beilen, J.B. (2006) CYP153A6, a Soluble P450 Oxygenase Catalyzing Terminal-Alkane Hydroxylation. *J Bacteriol* **188**: 5220–5227.
- Gao, X., Gao, W., Cui, Z., Han, B., Yang, P., Sun, C., and Zheng, L. (2015) Biodiversity and degradation potential of oil-degrading bacteria isolated from deep-sea sediments of South Mid-Atlantic Ridge. *Mar Pollut Bull* **97**: 373–380.

- Gerritse, J., Leslie, H.A., de Tender, C.A., Devriese, L.I., and Vethaak, A.D. (2020) Fragmentation of plastic objects in a laboratory seawater microcosm. *Sci Rep* **10**: 10945.
- Geyer, R., Jambeck, J.R., and Law, K.L. (2017) Production, use, and fate of all plastics ever made. *Sci Adv* **3**: e1700782.
- Guibert, L.M., Loviso, C.L., Borglin, S., Jansson, J.K., Dionisi, H.M., and Lozada, M. (2016) Diverse Bacterial Groups Contribute to the Alkane Degradation Potential of Chronically Polluted Subantarctic Coastal Sediments. *Microb Ecol* **71**: 100–112.
- Gustafsson, M.C.U., Roitel, O., Marshall, K.R., Noble, M.A., Chapman, S.K., Pessegueiro, A., et al. (2004) Expression, Purification, and Characterization of *Bacillus subtilis* Cytochromes P450 CYP102A2 and CYP102A3: Flavocytochrome Homologues of P450 BM3 from *Bacillus megaterium*. *Biochemistry* **43**: 5474–5487.
- Harrison, J.P., Schratzberger, M., Sapp, M., and Osborn, a (2014) Rapid bacterial colonization of low-density polyethylene microplastics in coastal sediment microcosms. *BMC Microbiol* **14**: 232.
- Harshvardhan, K. and Jha, B. (2013) Biodegradation of low-density polyethylene by marine bacteria from pelagic waters, Arabian Sea, India. *Mar Pollut Bull* **77**: 100–106.
- Harwati, T.U., Kasai, Y., Kodama, Y., Susilaningih, D., and Watanabe, K. (2008) *Tranquillimonas alkanivorans* gen. nov., sp. nov., an alkane-degrading bacterium isolated from Semarang Port in Indonesia. *Int J Syst Evol Microbiol* **58**: 2118–2121.
- Hsieh, T.C., Ma, K.H., and Chao, A. (2016) iNEXT : an R package for rarefaction and extrapolation of species diversity (Hill numbers). 1451–1456.
- Hyatt, D., Chen, G.-L., LoCascio, P.F., Land, M.L., Larimer, F.W., and Hauser, L.J. (2010) Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* **11**: 119.
- Jambeck, J.R., Geyer, R., Wilcox, C., Siegler, T.R., Perryman, M., Andrady, A., et al. (2015) Plastic waste inputs from land into the ocean. *Science* **347**: 768–771.
- Kang, D.D., Froula, J., Egan, R., and Wang, Z. (2015) MetaBAT, an efficient tool for accurately reconstructing single genomes from complex microbial communities. *PeerJ* **3**: e1165–e1165.
- Kasai, Y., Kishira, H., Sasaki, T., Syutsubo, K., Watanabe, K., and Harayama, S. (2002) Predominant growth of *Alcanivorax* strains in oil-contaminated and nutrient-supplemented sea water. *Environ Microbiol* **4**: 141–147.
- Katoh, K. and Standley, D.M. (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol* **30**: 772–780.
- Kesy, K., Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2019) Spatial Environmental Heterogeneity Determines Young Biofilm Assemblages on Microplastics in Baltic Sea Mesocosms. *Front Microbiol* **10**: 1665.
- Kim, S.-H., Kim, J.-G., Jung, M.-Y., Kim, S.-J., Gwak, J.-H., Yu, W.-J., et al. (2018) *Ketobacter alkanivorans* gen. nov., sp. nov., an n-alkane-degrading bacterium isolated from seawater. *Int J Syst Evol Microbiol* **68**: 2258–2264.
- Kirstein, I. V., Kirmizi, S., Wichels, A., Garin-Fernandez, A., Erler, R., Löder, M., and Gerdt, G. (2016) Dangerous hitchhikers? Evidence for potentially pathogenic *Vibrio* spp. on microplastic particles. *Mar Environ Res* **120**: 1–8.
- Kostka, J.E., Prakash, O., Overholt, W.A., Green, S.J., Freyer, G., Canion, A., et al. (2011) Hydrocarbon-Degrading Bacteria and the Bacterial Community Response in Gulf of Mexico Beach Sands Impacted by the Deepwater Horizon Oil Spill. *Appl Environ Microbiol* **77**: 7962–7974.
- Krueger, M.C., Harms, H., and Schlosser, D. (2015) Prospects for microbiological solutions to environmental pollution with plastics. *Appl Microbiol Biotechnol* **99**: 8857–8874.
- Kumari, A., Chaudhary, D.R., and Jha, B. (2019) Destabilization of polyethylene and polyvinylchloride structure by marine bacterial strain. *Environ Sci Pollut Res* **26**: 1507–1516.
- Kummer, C., Schumann, P., and Stackebrandt, E. (1999) *Gordonia alkanivorans* sp. nov., isolated from tar-contaminated soil. *Int J Syst Evol Microbiol* **49**: 1513–1522.
- Lai, Q., Wang, L., Liu, Y., Yuan, J., Sun, F., and Shao, Z. (2011) *Parvibaculum indicum* sp. nov., isolated

- from deep-sea water. *Int J Syst Evol Microbiol* **61**: 271–274.
- Letunic, I. and Bork, P. (2016) Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. *Nucleic Acids Res* **44**: 242–245.
- Li, D., Liu, C.-M., Luo, R., Sadakane, K., and Lam, T.-W. (2015) MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. *Bioinformatics* **31**: 1674–1676.
- Li, H. and Durbin, R. (2009) Fast and accurate short read alignment with Burrows–Wheeler transform. *Bioinformatics* **25**: 1754–1760.
- Liu, C. and Shao, Z. (2005) *Alcanivorax dieselolei* sp. nov., a novel alkane-degrading bacterium isolated from sea water and deep-sea sediment. *Int J Syst Evol Microbiol* **55**: 1181–1186.
- Milanese, A., Mende, D.R., Paoli, L., Salazar, G., Ruscheweyh, H.-J., Cuenca, M., et al. (2019) Microbial abundance, activity and population genomic profiling with mOTUs2. *Nat Commun* **10**: 1–11.
- Montazer, Z., Habibi-Najafi, M.B., Mohebbi, M., and Oromiehei, A. (2018) Microbial Degradation of UV-Pretreated Low-Density Polyethylene Films by Novel Polyethylene-Degrading Bacteria Isolated from Plastic-Dump Soil. *J Polym Environ* **26**: 3613–3625.
- Muhonja, C.N., Makonde, H., Magoma, G., and Imbuga, M. (2018) Biodegradability of polyethylene by bacteria and fungi from Dandora dumpsite Nairobi-Kenya. *PLoS One* **13**: e0198446.
- Nicdao, M.A.C. and Rivera, W.L. (2012) Two strains of *Gordonia terrae* isolated from used engine oil-contaminated soil utilize short-to long-chain n-alkanes. *Philipp Sci Lett* **5**: 1–10.
- Nie, Y., Chi, C.-Q., Fang, H., Liang, J.-L., Lu, S.-L., Lai, G.-L., et al. (2014) Diverse alkane hydroxylase genes in microorganisms and environments. *Sci Rep* **4**: 4968.
- Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2018) Environmental Factors Support the Formation of Specific Bacterial Assemblages on Microplastics. *Front Microbiol* **8**: 2709.
- Oberbeckmann, S. and Labrenz, M. (2019) Marine Microbial Assemblages on Microplastics: Diversity, Adaptation, and Role in Degradation. *Ann Rev Mar Sci*.
- Oberbeckmann, S., Löder, M.G.J., and Labrenz, M. (2015) Marine microplastic-associated biofilms—a review. *Environ Chem* **12**: 551–562.
- Oberbeckmann, S., Loeder, M.G.J., Gerdts, G., and Osborn, A.M. (2014) Spatial and seasonal variation in diversity and structure of microbial biofilms on marine plastics in Northern European waters. *FEMS Microbiol Ecol* **90**: 478–492.
- Oberbeckmann, S., Osborn, A.M., and Duhaime, M.B. (2016) Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. *PLoS One* **11**: e0159289.
- Ogonowski, M., Motiei, A., Ininbergs, K., Hell, E., Gerdes, Z., Udekwu, K.I., et al. (2018) Evidence for selective bacterial community structuring on microplastics. *Environ Microbiol* **20**: 2796–2808.
- Parks, D.H., Chuvochina, M., Waite, D.W., Rinke, C., Skarshewski, A., Chaumeil, P.-A., and Hugenholtz, P. (2018) A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. *Nat Biotechnol* **36**: 996–1004.
- Pericard, P., Dufresne, Y., Couderc, L., Blanquart, S., and Touzet, H. (2017) MATAM: reconstruction of phylogenetic marker genes from short sequencing reads in metagenomes. *Bioinformatics* **34**: 585–591.
- Pinto, M., Langer, T.M., Hüffer, T., Hofmann, T., and Herndl, G.J. (2019) The composition of bacterial communities associated with plastic biofilms differs between different polymers and stages of biofilm succession. *PLoS One* **14**: e0217165.
- Ramírez-Flandes, S., González, B., and Ulloa, O. (2019) Redox traits characterize the organization of global microbial communities. *Proc Natl Acad Sci* **116**: 3630–3635.
- Restrepo-Flórez, J.-M., Bassi, A., and Thompson, M.R. (2014) Microbial degradation and deterioration of polyethylene – A review. *Int Biodeterior Biodegradation* **88**: 83–90.
- Roager, L. and Sonnenschein, E.C. (2019) Bacterial Candidates for Colonization and Degradation of Marine Plastic Debris. *Environ Sci Technol* **53**: 11636–11643.

- Romera-Castillo, C., Pinto, M., Langer, T.M., Álvarez-Salgado, X.A., and Herndl, G.J. (2018) Dissolved organic carbon leaching from plastics stimulates microbial activity in the ocean. *Nat Commun* **9**: 1–7.
- Schleheck, D., Weiss, M., Pitluck, S., Bruce, D., Land, M.L., Han, S., et al. (2011) Complete genome sequence of *Parvibaculum lavamentivorans* type strain (DS-1 T). *Stand Genomic Sci* **5**: 298.
- Schneiker, S., dos Santos, V.A.P.M., Bartels, D., Bekel, T., Brecht, M., Buhrmester, J., et al. (2006) Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium *Alcanivorax borkumensis*. *Nat Biotechnol* **24**: 997–1004.
- Stamatakis, A. (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**: 1312–1313.
- Sudhakar, M., Doble, M., Murthy, P.S., and Venkatesan, R. (2008) Marine microbe-mediated biodegradation of low- and high-density polyethylenes. *Int Biodeterior Biodegradation* **61**: 203–213.
- Sudhakar, M., Trishul, A., Doble, M., Suresh Kumar, K., Syed Jahan, S., Inbakandan, D., et al. (2007) Biofouling and biodegradation of polyolefins in ocean waters. *Polym Degrad Stab* **92**: 1743–1752.
- Suhrhoff, T.J. and Scholz-Böttcher, B.M. (2016) Qualitative impact of salinity, UV radiation and turbulence on leaching of organic plastic additives from four common plastics — A lab experiment. *Mar Pollut Bull* **102**: 84–94.
- Syranidou, E., Karkanorachaki, K., Amorotti, F., Avgeropoulos, A., Kolvenbach, B., Zhou, N.-Y., et al. (2019) Biodegradation of mixture of plastic films by tailored marine consortia. *J Hazard Mater* **375**: 33–42.
- Syranidou, E., Karkanorachaki, K., Amorotti, F., Repouskou, E., Kroll, K., Kolvenbach, B., et al. (2017) Development of tailored indigenous marine consortia for the degradation of naturally weathered polyethylene films. *PLoS One* **12**: e0183984.
- De Tender, C., Schlundt, C., Devriese, L.I., Mincer, T.J., Zettler, E.R., and Amaral-Zettler, L.A. (2017) A review of microscopy and comparative molecular-based methods to characterize “Plastisphere” communities. *Anal Methods* **9**: 2132–2143.
- Uritskiy, G. V., DiRuggiero, J., and Taylor, J. (2018) MetaWRAP—a flexible pipeline for genome-resolved metagenomic data analysis. *Microbiome* **6**: 1–13.
- Wang, L., Wang, W., Lai, Q., and Shao, Z. (2010) Gene diversity of CYP153A and AlkB alkane hydroxylases in oil-degrading bacteria isolated from the Atlantic Ocean. *Environ Microbiol* **12**: 1230–1242.
- Wang, W. and Shao, Z. (2013) Enzymes and genes involved in aerobic alkane degradation. *Front Microbiol* **4**: 116.
- Wang, W. and Shao, Z. (2014) The long-chain alkane metabolism network of *Alcanivorax dieselolei*. *Nat Commun* **5**: 5755.
- Weiland, M., Daro, A., and David, C. (1995) Biodegradation of thermally oxidized polyethylene. *Polym Degrad Stab* **48**: 275–289.
- Wright, R.J., Bosch, R., Gibson, M.I., and Christie-Oleza, J.A. (2020) Plasticizer Degradation by Marine Bacterial Isolates: A Proteogenomic and Metabolomic Characterization. *Environ Sci Technol* **54**: 2244–2256.
- Wu, Y.-W., Tang, Y.-H., Tringe, S.G., Simmons, B.A., and Singer, S.W. (2014) MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm. *Microbiome* **2**: 26.
- Yakimov, M.M., Golyshin, P.N., Lang, S., Moore, E.R.B., Abraham, W.-R., Lünsdorf, H., and Timmis, K.N. (1998) *Alcanivorax borkumensis* gen. nov., sp. nov., a new, hydrocarbon-degrading and surfactant-producing marine bacterium. *Int J Syst Evol Microbiol* **48**: 339–348.
- Yoon, M., Jeon, H., and Kim, M. (2012) Biodegradation of polyethylene by a soil bacterium and AlkB cloned recombinant cell. *J Bioremed Biodegrad* **3**: 1–8.
- Zettler, E.R., Mincer, T.J., and Amaral-Zettler, L. (2013) Life in the “plastisphere”: Microbial communities on plastic marine debris. *Environ Sci Technol* **47**: 7137–7146.

Supporting information

S1- Supplementary Methods

Table S1 –Information on obtained MAGs, their taxonomic classification and coverage in each sample.

Table S2 – Selected genes encoding for enzymes previously suggested to be involved in alkane and fatty acid biodegradation.

Table S3 – List of bacterial strains associated with hydrocarbon and plastic degradation.

Table S4 – RPKM values for all genes that increase in RPKM over time in both A and C samples. The genes are ordered by their mean RPKM values, from most abundant on top to least abundant

Table S5 – RPKM values for enriched genes encoding for oxidoreductases. The genes are ordered by their mean RPKM values, from most abundant on top to least abundant.

Table S6 –Tukey test results comparing the cell abundance (cells cm⁻¹) between different pairs of samples.

Table S7 –Tukey test results comparing the total oxygen consumption (μmol O₂ cm⁻²) and the oxygen consumption rates (μmol O₂ h⁻¹ cell⁻¹) between different pairs of samples.

Table S8 –Tukey test results comparing the weight (in mg) of the packaging PE and non-weathered LDPE incubated with the three different microbial communities.

Table S9 – Artificial seawater (ASW) recipe.

Fig. S1 – Scheme of the experimental setup.

Fig. S2 - mOTU diversity indexes and richness of the six metagenomes.

Fig. S3 - Relative abundance of the abundant classified classes and families.

Fig. S4 - Plot showing the RPKM values (in log) of genes encoding for KEGG-annotated oxidoreductases and in all six metagenomes.

Fig. S5 – Phylogenetic placement of (A) the MAGs and selected genomes and (B) putative CYP153 sequences identified in MAGs and genomes.

Fig. S6 - Fluorescence microscope photos of DAPI stained cells on plastic and glass.

Fig. S7 – Plastics A, B and C.

S1- Supplementary Methods

Oxygen measurements

All the BOD flasks were kept at 21°C for 24h prior to the experiment. Additionally, before adding the plastic to the BOD bottles, they were put in petri dishes filled with the same ASW and slightly bent to fit them through the narrow end into the BOD bottles. The bottles were filled up to half with ASW, then the plastics were carefully placed inside and the rest of the bottle was gently filled up with ASW. Care was taken to avoid any air bubbles enclosed in the BOD flasks. Additionally, three control bottles were added by incubating sterile LDPE pieces that had not been previously incubated in ASW (Control II). The bottles were immediately submerged in a water bath kept at 21°C and incubated for approximately 40 h. For determining the initial oxygen concentration in the ASW (T_0), three BOD bottles only filled with ASW were fixed immediately and thoroughly shaken.

The respiration measurements followed the protocol described by Labasque et al. (2004) for spectrophotometric Winkler determination of dissolved oxygen. After fixation and addition of sulphuric acid, absorbance was measured using a Shimadzu UV-VIS 1800 PC spectrophotometer with a flow-through cell connected to a Masterflex L/S peristaltic pump within 5 min. Flow was maintained at around 10 mL min⁻¹.

Measurements were done in a temperature-controlled room (set to 21°C). The amount of total iodine and tri-iodide in the samples was determined at a wavelength of 466 nm. The spectrophotometer was calibrated using standard additions of potassium iodate to BOD bottles filled with ASW to which the Winkler chemicals were added in reverse order.

Cell abundance

The samples were washed in sterile ASW, immersed in 2% formaldehyde and after 10 min stored at -80°C. A DAPI mix (4', 6-diamidino-2-phenylindole, 2 µg mL⁻¹ final concentration) was used to stain the cells attached to the surface of one of the sides of the glass and plastic pieces. Each sample was placed on a drop of Milli-Q water on a glass slide, a drop of DAPI mix was pipetted onto the entire exposed surface of the sample and a cover slip was placed on top of the sample. After 10 min incubation in the dark, the samples were analyzed under an epifluorescence microscope (Axio Imager M2, Carl Zeiss, 1,250x magnification). Between 35 and 50 photos were taken from different randomly selected locations of each of the samples, corresponding to, an average of $1.95 \times 10^7 \pm 6.17 \times 10^6$, $1.22 \times 10^7 \pm 3.67 \times 10^6$ and $4.05 \times 10^7 \pm$

1.52×10^7 cells on plastics incubated with communities A, B and C, respectively, and an average of $5.68 \times 10^6 \pm 3.02 \times 10^5$, $3.14 \times 10^5 \pm 1.63 \times 10^5$ and $2.88 \times 10^5 \pm 2.03 \times 10^5$ cells on the glass pieces incubated with communities A, B and C, respectively (Supplementary Figure 2).

The number of DAPI-stained cells per photo was counted with the program ImageJ2 (Rueden *et al.*, 2017). To determine the number of cells cm^{-2} on each surface, the number of cells on each photo was divided by the area of one photo ($1.4 \times 10^{-4} \text{ cm}^2$). Subsequently, the total number of cells in each of the incubations was estimated by multiplying the cells cm^{-2} on each photo by the total area of the plastics and glass (4.5 cm^2) and averaging the result from all photos per treatment.

ATR-FTIR analysis

To characterize changes of the surface of the plastic material and avoid interference of the biofilm itself in the ATR-FTIR analysis and plastic weight, the biofilm was removed prior to the ATR-FTIR analysis and the weighing of the plastic. To remove the biofilm, the plastic pieces were immersed in 2% SDS in a Greiner tube, the tube was briefly vortexed and then left at room temperature for 4 h. Thereafter, the plastics were immersed in Milli-Q water in a new Greiner tube, the tube vortexed again and then, the plastics were carefully dried wrapped in clean paper and kept at 4°C until analysis. Prior to ATR-FTIR analysis, the plastics were again dried with a clean paper.

ATR-FTIR was used to detect the functional chemical groups of the PE sheets. A Bruker Tensor 27 FTIR spectrometer (glowbar MIR light source, KBr beam splitter, DLaTGS detector) equipped with a Harrick MVP2 diamond ATR unit was used and the spectra were obtained and processed with the Bruker program OPUS 5.5. Spectra were acquired from 4000 to 370 cm^{-1} with 4 cm^{-1} resolution. To obtain a good signal-to-noise ratio, spectra were averaged from each 32 scans. Background scans from the empty ATR unit were performed prior to sample analysis. At least three separate plastic pieces of each of the incubations were analysed.

To determine whether the bacterial communities influenced plastic weight, the pieces were weighed on a Mettler MT5 balance. A hole puncher was used to obtain pieces of the exact same size (0.5 cm diameter) of the non-weathered LDPE. For the packaging PE, the originally incubated 1 cm^2 pieces were weighed. Due to extreme irregular shapes of the UV-weathered pieces and their brittleness, which did not allow for further manipulation, they were not considered for this part of the experiment.

SEM analysis

SEM analyses was performed on plastics after removing the biofilm and without removing the biofilm. Samples for SEM were incubated in 2% glutaraldehyde for 10 min and then stored at -80°C until further processing. SEM samples were dehydrated with an ethanol dilution series of 30%, 50%, 70%, 80%, 90%, 95% each for 10 min and three times in 100% absolute ethanol for 10 min. The dehydrated samples were CO₂ critical-point dried with a CPD 300 auto critical-point dryer (Leica Microsystems). The dried pieces were gold-coated using a JFC-2300HR sputter coater (JEOL Ltd.) for 80s. Pictures were taken using a secondary electron detector with a JEOL JSM-IT300 scanning electron microscope with 15kV acceleration voltage in ultra-high vacuum.

Table S1 –Information on obtained MAGs, their taxonomic classification and coverage in each sample.

MAG	Comp	Cont	N50	Size	Taxonomic classification (GTDB)	A0	A1	A2	B1	C1	C2
MAG 5	100	0.14	745361	3895291	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvibaculales; f__Parvibaculaceae; g__Mf105b01; s__	0.87	22.37	26.36	3.93	12.61	242.06
MAG 41	100	0.27	87431	3084926	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__koll-22; g__; s__	0.23	0.04	0.10	0.01	27.97	0.12
MAG 1	99.45	2.46	28314	11123943	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__; f__; g__; s__	0.04	2.08	17.03	0.00	0.03	4.00
MAG 12	99.07	7.61	234482	9471037	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__; g__; s__	0.09	33.00	188.90	0.11	0.81	5.04
MAG 53	99.02	0.00	24034	1664407	d__Archaea; p__Crenarchaeota; c__Nitrososphaeria; o__Nitrososphaerales; f__Nitrosopumilaceae; g__Nitrosopumilus; s__	0.23	0.83	0.00	0.12	18.20	0.00
MAG 19	98.73	4.00	15304	12080241	d__Bacteria ; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__; s__	0.07	5.09	7.92	0.07	3.33	3.53
MAG 17	98.61	1.34	47395	5060925	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__TMED26; f__TMED26; g__; s__	0.55	0.21	0.51	0.06	29.46	0.85
MAG 58	98.54	2.70	41302	3459658	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methyloligellaceae; g__; s__	0.26	2.42	0.29	2.95	65.00	0.48
MAG 7	98.42	1.06	21386	3081040	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Porticoccaceae; g__HB2-32-21; s__	0.24	24.99	0.72	0.12	0.51	1.01
MAG 2	98.33	1.89	42250	6448840	d__Bacteria ; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Planctomycetaceae; g__Planctomyces_B; s__	0.06	1.91	3.54	0.01	8.19	1.38

MAG 9	98.2	2.39	42693	5107237	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__UBA8366; f__GCA- 2696645; g__ ; s__	0.80	0.33	4.67	0.08	0.70	17.67
MAG 25	97.75	3.37	59869	6972596	d__Bacteria ; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Planctomycetaceae; g__Fuerstia; s__	0.11	6.02	3.71	0.20	0.10	9.99
MAG 45	97.63	0.85	15447	2824614	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__UBA7434; g__UBA7434; s__	0.18	0.15	0.55	12.57	46.69	0.43
MAG 37	97.63	1.15	19887	8632239	d__Bacteria ; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Planctomycetaceae; g__ ; s__	0.15	0.65	10.66	0.15	5.91	20.28
MAG 51	97.53	1.33	23076	4309013	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudooceanicola_B; s__	3.57	3.25	33.85	0.46	2.89	9.78
MAG 11	97.46	2.32	34011	4094806	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Actibacterium; s__	4.02	1.31	12.22	0.42	3.27	48.43
MAG 6	97.24	1.71	85959	4418656	d__Bacteria ; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__UBA11606; g__UBA11606; s__	1.15	0.47	0.35	0.19	49.18	0.45
MAG 18	97.05	5.04	14646	2444598	d__Bacteria ; p__Dadabacteria; c__UBA1144; o__ ; f__ ; g__ ; s__	0.14	0.79	0.20	0.25	76.13	0.44
MAG 38	97.01	1.74	40177	5199004	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__UBA8366; f__GCA- 2717185; g__ ; s__	0.38	6.65	25.89	0.08	0.28	0.74
MAG 14	95.8	0.97	198859	5518563	d__Bacteria ; p__Myxococcota; c__UBA9160; o__UBA9160; f__UBA9160; g__ ; s__	1.18	0.28	0.30	0.06	102.64	0.45
MAG 28	95.53	1.10	68475	8507862	d__Bacteria ; p__Calditrichota; c__Calditrichia; o__RBG- 13-44-9; f__ ; g__ ; s__	0.06	0.04	0.06	0.01	28.94	0.06

Chapter II

MAG 50	94.55	3.85	17978	5407104	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudooceanicola_B; s__Pseudooceanicola_B lipolyticus	3.05	1.26	10.92	0.43	11.99	13.77
MAG 3	94.33	2.82	184566	5398687	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Ketobacteraceae; g__; s__	0.15	0.51	5.65	0.28	148.34	10.76
MAG 39	94.31	1.70	124924	3792665	d__Bacteria ; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__SM1A02; g__UBA1926; s__	0.71	5.89	31.65	0.05	5.21	114.75
MAG 4	94.27	2.36	12093	5200958	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__UBA8366; f__GCA- 2717185; g__; s__	0.28	8.57	8.63	0.04	0.19	0.50
MAG 35	94.11	0.07	14530	8036327	d__Bacteria ; p__Planctomycetota; c__UBA1135; o__UBA1135; f__GCA- 002686595; g__; s__	0.20	16.01	0.21	0.02	0.33	0.34
MAG 36	93.27	3.26	9949	4195412	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__NRL2; f__NRL2; g__NRL2; s__	1.16	0.74	17.15	0.21	1.48	4.69
MAG 30	92.87	1.37	16356	2981322	d__Bacteria ; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__SM1A02; g__; s__	0.41	0.87	1.53	0.04	73.19	3.15
MAG 56	92.32	3.69	10007	4829534	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Ketobacteraceae; g__Ketobacter; s__Ketobacter sp002471665	0.21	11.67	154.18	5.11	4.63	337.63
MAG 15	91.99	4.55	10449	3153575	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Maricaulaceae; g__Maricaulis; s__	0.70	0.49	2.29	0.10	0.87	16.61
MAG 52	91.88	4.87	9896	12069388	d__Bacteria ; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Planctomycetaceae; g__; s__	0.16	13.55	0.22	0.01	0.82	0.38

Chapter II

MAG 46	89.03	1.92	11796	3320277	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__Henriciella; s__	1.65	8.92	5.95	0.09	2.42	10.28
MAG 32	87.75	2.81	13119	2831065	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__UBA4575; f__UBA4575; g__UBA1858; s__	0.33	0.09	2.36	0.04	0.29	8.71
MAG 43	87.62	4.84	7614	4757787	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__HTCC2089; g__UBA4421; s__	0.47	1.60	2.29	0.14	18.06	1.65
MAG 23	87.13	7.26	6873	5157944	d__Bacteria ; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__UBA8592; g__ ; s__	1.24	1.38	0.23	0.20	15.68	1.98
MAG 13	85.53	4.41	6959	7775395	d__Bacteria ; p__Myxococcota; c__Polyangia; o__Polyangiales; f__SG8- 38; g__GCA-2699025; s__	0.11	0.53	4.79	0.02	0.32	5.16
MAG 24	85.34	4.89	9297	4719056	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sagittula; s__	3.02	0.91	4.11	0.33	1.73	21.02
MAG 34	85.05	4.63	5192	4936592	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Ketobacteraceae; g__GCA-2748575; s__	0.16	0.57	33.08	0.09	1.49	26.68
MAG 16	83.77	1.08	18496	3184617	d__Bacteria ; p__Omnitrophota; c__koll11; o__UBA10015; f__kpj58rc; g__UBA12451; s__	0.04	0.01	0.03	0.00	10.59	0.04
MAG 29	83.09	5.65	5557	3747874	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudohongiellaceae; g__UBA9145; s__	0.34	0.47	10.61	0.28	0.29	0.42
MAG 44	80.87	4.55	6277	3348750	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Confluentimicrobium; s__	2.95	3.37	11.92	0.32	1.65	10.45
MAG 22	79.97	3.04	7020	3873558	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Ga0077536; f__Ga0077536; g__ ; s__	0.29	0.23	4.80	0.07	2.08	4.09

Chapter II

MAG 20	79.91	0.94	4891	2424194	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__UBA7434; g__UBA7434; s__	1.54	0.20	0.69	0.06	23.05	0.90
MAG 21	79.1	3.76	4122	5100900	d__Bacteria ; p__Myxococcota; c__UBA9160; o__UBA9160; f__UBA4427; g__ ; s__	0.77	2.97	0.20	0.04	20.21	0.49
MAG 57	79.01	8.49	6796	5095117	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__HTCC2089; g__UBA4421; s__	0.23	0.10	0.10	0.01	9.41	0.11
MAG 60	76.35	4.64	5084	3282305	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Nevskiales; f__ ; g__ ; s__	0.28	0.21	9.82	0.09	0.29	0.62
MAG 31	73.41	2.91	4802	4082548	d__Bacteria ; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__SM1A02; g__ ; s__	0.13	0.31	0.25	0.01	10.40	0.37
MAG 26	70.92	0.38	6484	3105361	d__Bacteria ; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__SM1A02; g__ ; s__	0.23	0.54	11.39	0.02	1.34	8.14
MAG 54	70.39	1.67	3935	4010313	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__GCA-2731375; f__GCA- 2731375; g__ ; s__	1.19	10.04	3.90	0.11	0.80	1.41
MAG 48	70.08	1.24	4363	2955247	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Alcanivoracaceae; g__Alcanivorax; s__Alcanivorax sp000155615	0.24	0.51	10.03	0.42	0.49	2.34
MAG 42	69.96	1.14	8469	2968090	d__Bacteria ; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__SM1A02; g__UBA1924; s__UBA1924 sp002337545	0.10	2.10	14.42	0.01	0.58	1.60
MAG 49	68.03	1.55	4045	5020956	d__Bacteria ; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Planctomycetaceae; g__ ; s__	0.03	0.08	1.94	0.00	0.03	4.42
MAG 40	67.5	1.38	4612	3034243	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__ ; s__	2.01	5.29	7.50	0.26	1.11	6.20

Chapter II

MAG 10	66.69	0.00	8668	3045626	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales_A; f__UBA4479; g__UBA4479; s__	0.31	0.13	0.58	0.18	10.18	0.52
MAG 27	65.4	3.41	5117	6138770	d__Bacteria ; p__Planctomycetota; c__UBA1135; o__UBA2386; f__GCA- 002748355; g__ ; s__	0.15	1.32	4.69	0.14	0.19	3.82
MAG 33	64.98	3.41	5809	6231867	d__Bacteria ; p__Planctomycetota; c__UBA1135; o__UBA2386; f__UBA2386; g__GCA-2684655; s__	0.38	0.15	4.78	0.03	1.27	5.72
MAG 47	60.97	0.00	3414	1738336	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methylogellaceae; g__ ; s__	0.25	3.65	0.24	0.13	3.97	1.35
MAG 8	60.83	1.10	3064	3208169	d__Bacteria ; p__Calditrichota; c__Calditrichia; o__RBG- 13-44-9; f__RBG-13-44-9; g__ ; s__	0.02	0.01	0.03	0.00	6.28	0.02
MAG 61	60.5	6.09	4468	5557013	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__UBA8366; f__GCA- 2717185; g__GCA- 2717185; s__	0.33	0.75	10.53	0.04	0.21	13.77
MAG 59	57.52	1.77	2687	3279497	d__Bacteria ; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__HTCC2089; g__UBA4421; s__	0.30	8.55	0.36	0.02	0.39	0.30
MAG 55	51.88	0.86	2954	1884709	d__Bacteria ; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Maricaulaceae; g__ ; s__	0.54	2.37	0.90	0.14	4.19	4.48

Table S2 – Selected genes encoding for enzymes previously suggested to be involved in alkane and fatty acid biodegradation. Genes in grey were not found in any of MAGs. *This gene has not been attributed a KO identification.

KEGG number	Gene name	Function	Cluster
K00496	alkB1_2, alkM	Alkane 1-monooxygenase	(A) AlkB cluster
K05297	rubB, alkT	Rubredoxin---NAD ⁺ reductase	
K21738	alkT	Rubredoxin---NAD ⁺ reductase	
K22567	nroR	Rubredoxin---NAD ⁺ reductase	
NA*	CYP153	Cytochrome P450 alkane hydroxylase	(B) CYP153 cluster
K04755	fdx	ferredoxin, 2Fe-2S	
K05524	fdxA	ferredoxin	
K21567	fnr	ferredoxin/flavodoxin---NADP ⁺ reductase	
K00528	fpr	ferredoxin/flavodoxin---NADP ⁺ reductase	
K18914	fdxR	adrenodoxin-NADP ⁺ reductase	
K00529	hcaD	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin reductase component	(C) Propane oxygenase cluster
K18223	prmA	propane 2-monooxygenase large subunit	
K18224	prmC	propane 2-monooxygenase small subunit	
K18225	prmB	propane monooxygenase reductase component	
K18226	prmD	propane monooxygenase coupling protein	(D) Methane oxygenase cluster
K10944	pmoA-amoA	Methane/ammonia monooxygenase subunit A	
K10945	pmoB-amoB	Methane/ammonia monooxygenase subunit B	
K10946	pmoC-amoC	Methane/ammonia monooxygenase subunit C	
K20938	LadA	Long-chain alkane monooxygenase	(E) Long-chain alkane related monooxygenases and fatty acid oxygenases
K00485	AlmA	Dimethylaniline monooxygenase/flavin containing monooxygenase	
K07425	CYP4_A	long-chain fatty acid omega-monooxygenase	
K15401	CYP86A1	long-chain fatty acid omega-monooxygenase	
K20495	CYP704B1	long-chain fatty acid omega-monooxygenase	
K22887	CYP52M1	long-chain fatty acid omega-monooxygenase	
K00493	E1.14.14.1	Unspecific monooxygenase [EC:1.14.14.1]	(F) Transporters and biosurfactant synthesis
K06076	fadL	Long-chain fatty acid transport protein	
K10940	OmpT	Outer membrane protein/ long-chain fatty acid transport protein involved in the alkane assimilation	
K07275	OmpW, alkL	Outer membrane protein (surfactant and transports 1-alkanes into the cell)	
K06142	OmpH	Outer membrane protein (surfactant)	
K18100	rhIA	Rhamnosyltransferase subunit A (rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis)	
K18101	rhIB	Rhamnosyltransferase subunit B (rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis)	

K13954	yiaY	Alcohol dehydrogenase	(G) Alcohol dehydrogenases
K19954	adh1	Alcohol dehydrogenase	
K13951	ADH1_7	Alcohol dehydrogenase 1/7	
K13980	ADH4	Alcohol dehydrogenase 4	
K13952	ADH6	Alcohol dehydrogenase 6	
K13953	adhP	alcohol dehydrogenase, propanol-preferring	
K00001	adh	Alcohol dehydrogenase	
K00121	frmA, ADH5, adhC	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	
K04072	adhE	Acetaldehyde dehydrogenase / alcohol dehydrogenase	
K18857	ADH1	alcohol dehydrogenase class-P	
K00128	ALDH	Aldehyde dehydrogenase (NAD ⁺)	(H) Aldehyde dehydrogenases
K14085	ALDH7A1	Aldehyde dehydrogenase family 7 member A1	
K00149	ALDH9A1	Aldehyde dehydrogenase family 9 member A1	
K21747	alkR	AraC family transcriptional regulator, alkane utilization regulator	(I) Transcriptional regulators
K21748	alkS	LuxR family transcriptional regulator, alkane degradation pathway regulator	
K00375	gntR	GntR family transcriptional regulator / MocR family aminotransferase	
K08365	merR	MerR family transcriptional regulator, mercuric resistance operon regulatory protein	
K18476	tetR	TetR/AcrR family transcriptional regulator, tetracycline repressor protein	
K02099	araC	AraC family transcriptional regulator, arabinose operon regulatory protein	

Table S3- List of bacterial strains associated with hydrocarbons or plastics degradation.

Strain	Type of substrate	Additional information	Environment	Reference
<i>Rhodococcus ruber</i>	PE and PS		Culture	(Sivan <i>et al.</i> , 2006)
<i>Brevibacillus borstelensis</i>	PE		Soil	(Hadad <i>et al.</i> , 2005)
<i>Bacillus mycoides</i>	PE	Same as <i>Bacillus weihenstephanensis</i>	Soil	(Ingavale and Raut, 2018)
<i>Bacillus amyloliquefaciens</i>	PE		Guts of waxworms	(Yang <i>et al.</i> , 2014)
<i>Bacillus pumilus</i>	PE		Seawater	(Harshvardhan and Jha, 2013)
<i>Bacillus subtilis</i>	PE		Seawater	(Harshvardhan and Jha, 2013; Ibiene <i>et al.</i> , 2013)
<i>Achromobacter xylosoxidans</i>	PE		Soil	(Kowalczyk <i>et al.</i> , 2016)
<i>Enterobacter asburiae</i>	PE		Guts of waxworms	(Yang <i>et al.</i> , 2014)
<i>Kocuria palustris</i>	PE		Seawater	(Harshvardhan and Jha, 2013)
<i>Lysinibacillus xylanilyticus</i>	PE		Soil	(Esmaeili <i>et al.</i> , 2013)
<i>Pseudomonas aeruginosa</i> PAO1	PE		Culture	(Kyaw <i>et al.</i> , 2012)
<i>Pseudomonas putida</i> KT2440	PE		Culture	(Kyaw <i>et al.</i> , 2012)
<i>Pseudomonas syringae</i>	PE		Culture	(Kyaw <i>et al.</i> , 2012)
<i>Brevibacillus parabrevis</i>	PE		Landfill	(Pramila <i>et al.</i> , 2012)
<i>Acinetobacter baumannii</i>	PE		Landfill	(Pramila <i>et al.</i> , 2012)
<i>Lysinibacillus sphaericus</i>	PE	Same as <i>Bacillus sphaericus</i>	Seawater	(Artham <i>et al.</i> , 2009)
<i>Ideonella sakaiensis</i>	PET		Sediments	(Yoshida <i>et al.</i> , 2016)
<i>Desulfatibacillum alkenivorans</i>	Alkanes		Oil-polluted sediments	(Cravo-Laureau <i>et al.</i> , 2004)
<i>Alcanivorax pacificus</i>	Alkanes		Deep sea sediments	(Lai, Wang, Liu, Fu, <i>et al.</i> , 2011)
<i>Acinetobacter venetianus</i>	Alkanes		Venice Lagoon	(Di Cello <i>et al.</i> , 1997)
<i>Tistrella mobilis</i>	Alkanes		Seawater	(W. Wang <i>et al.</i> , 2010)
<i>Gordonia terrae</i>	Alkanes		Oil-contaminated soil	(Nicdao and Rivera, 2012)
<i>Brachybacterium paraconglomeratum</i>	Alkanes	Surfactant-producing bacteria	Corn steep liquor	(L. Wang <i>et al.</i> , 2010; Kiran <i>et al.</i> , 2014)

<i>Erythrobacter flavus</i>	Alkanes		Seawater	(Harwati <i>et al.</i> , 2007; L. Wang <i>et al.</i> , 2010)
<i>Bacillus flexus</i>	Alkanes		Seawater	(L. Wang <i>et al.</i> , 2010; Wang and Shao, 2012)
<i>Parvibaculum indicum</i>	Alkanes		Seawater	(Lai, Wang, Liu, Yuan, <i>et al.</i> , 2011)
<i>Tropicimonas isoalkanivorans</i>	Alkanes		Seawater from port	(Harwati <i>et al.</i> , 2009b)
<i>Tranquillimonas alkanivorans</i>	Alkanes		Seawater from port	(Harwati <i>et al.</i> , 2008)
<i>Desulfoglaeba alkanexedens</i>	Alkanes		Naval wastewater-storage facility	(Davidova <i>et al.</i> , 2006)
<i>Gordonia alkanivorans</i>	Alkanes		Tar-contaminated soil	(Kummer <i>et al.</i> , 1999)
<i>Ketobacter alkanivorans</i>	Alkanes		Seawater	(Kim <i>et al.</i> , 2018)
<i>Alcanivorax dieselolei</i>	Alkanes		Seawater and deep-sea sediments	(Liu and Shao, 2005)
<i>Alcanivorax hongdengensis</i>	Alkanes		Seawater	(Wu <i>et al.</i> , 2009)
<i>Alcanivorax borkumensis</i>	Alkanes	Surfactant-producing bacteria	Seawater	(Yakimov <i>et al.</i> , 1998)
<i>Hydrocarboniphaga effusa</i>	Alkane and aromatic hydrocarbon		Oil-contaminated soil	(Palleroni <i>et al.</i> , 2004)
<i>Parvibaculum lavamentivorans</i>	Initiates catabolism of linear alkylbenzenesulfonate (surfactants)		Activated sludge	(Schleheck <i>et al.</i> , 2004)
<i>Tropicibacter naphthalenivorans</i>	PAH		Seawater from a port	(Harwati <i>et al.</i> , 2009a)
<i>Thalassobius gelatinovorans</i>	PAH		Seawater	(Rodrigo-Torres <i>et al.</i> , 2017)
<i>Marinobacter hydrocarbonoclasticus</i>	Hydrocarbons		Seawater	(Gauthier <i>et al.</i> , 1992)
<i>Polystyrenella longa Pla110</i>	PS	Isolated from PS particles, but no indication that it can degrade PS	Seawater	(Peeters <i>et al.</i> , 2020)
<i>Marinovum algicola</i>	Oil	Previously <i>Ruegeria algicola</i>	Seawater	(Katayama <i>et al.</i> , 2003)
<i>Cognatiyoonia koreensis</i> *	PE	Previously <i>Loktanella koreensis</i>	Sea sand	(Wirth and Whitman, 2018), unpublished data
<i>Cognatiyoonia sediminum</i> *	PE	Previously <i>Loktanella sediminum</i>	Marine sediments	(Wirth and Whitman, 2018), unpublished data

* Members from the *Cognatiyoonia* genus are associated with PE biofilms across different oceanic regions (unpublished data)

Table S4 – RPKM values for all genes that increase in RPKM over time in both A and C samples. The genes are ordered by their mean RPKM values, from most abundant on top to least abundant

Gene	Enzyme	A0	A1	A2	B1	C1	C2	KEGG KOs
GST, gst	glutathione S-transferase	1089.4	1387.2	1391.2	1703.7	1195.7	1342.2	K00799
dgcB	diguanylate cyclase	63.8	295.9	607	492.5	395.7	841.3	K13590
CYP51	sterol 14alpha-demethylase	21.6	479.2	810	168.8	197.1	266.3	K05917
cypD_E, CYP102A2_3	cytochrome P450 / NADPH-cytochrome P450 reductase	122.9	465.4	812.6	128.8	179.6	277.8	K14338
lip, TGL2	triacylglycerol lipase	29	368.7	472.6	396	173.4	416	K01046
KAE1, tsaD, QRI7	N6-L-threonylcarbamoyladenine synthase	259.9	269.1	271.7	460.5	302.8	359.8	K01409
gph	phosphoglycolate phosphatase	113.1	256.4	329.2	368	306.8	378.9	K01091
mutT, NUDT15, MTH2	8-oxo-dGTP diphosphatase	231.1	300	335	341.2	279.3	374.7	K03574
2phoD	alkaline phosphatase D	66	285.9	351.5	401	188.3	340.7	K01113
mlhB, chnC	epsilon-lactone hydrolase	36.1	302.6	315.5	389.4	152.6	405.5	K14731
phoR	two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR	113.7	226.1	274.4	431.9	209.1	344.7	K07636
K02484	two-component system, OmpR family, sensor kinase	32.5	207.1	307.1	432.9	135.2	357.8	K02484
atzF	allophanate hydrolase	124.2	186.4	233.1	391.7	180.1	381	K01457
hsdR	type I restriction enzyme, R subunit	130.1	133.4	159.7	568.5	112.2	234.6	K01153
alkB1_2, alkM	alkane 1-monoxygenase	48.1	185	371.8	285.9	114.7	218.2	K00496
apbE	FAD:protein FMN transferase	22.8	153.7	240.1	274.2	186.4	295.8	K03734
E1.14.14.1	unspecific monooxygenase	52.5	238.7	430.3	137	112.7	224	K00493
pnbA	para-nitrobenzyl esterase	61.8	224	279.2	120.3	187.7	315.3	K03929
slt	soluble lytic murein transglycosylase	96.1	139.7	190.4	277.6	168.9	283	K08309
folK	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine diphosphokinase	52.8	153.2	201.1	216.6	217.1	268.3	K00950
cheBR	two-component system, chemotaxis family, CheB/CheR fusion protein	107.8	227.1	235.2	160.2	146	245.6	K13924
ubiG	2-polyprenyl-6-hydroxyphenyl methylase / 3- demethylubiquinone-9 3-methyltransferase	129.6	164.7	215.7	238.7	184.7	193.2	K00568
tatD	TatD DNase family protein	130.4	132.6	206.8	236.8	173.5	233.8	K03424
E2.7.1.4, scrK	fructokinase	132.7	135.3	152.7	367.8	147.6	166.2	K00847
cobC, phpB	alpha-ribazole phosphatase	26.6	166.3	174.3	194.9	42.4	386.3	K02226
cheB	two-component system, chemotaxis family, protein-glutamate methylesterase/glutaminase	19.8	154	188.6	246.2	117	252.8	K03412
clsA_B	cardiolipin synthase A/B	16.7	114.2	146.8	242.6	118.9	305.5	K06131
xlyAB	N-acetylmuramoyl-L-alanine amidase	24.6	154	228.7	181.7	92.8	251.2	K01447
amgK	N-acetylmuramate 1-kinase	29.5	120.6	192.8	236.9	139.7	202.3	K07102
fabZ	3-hydroxyacyl-[acyl-carrier-protein] dehydratase	90.8	164	178.3	233.2	151.9	161.4	K02372
ubiH	2-octaprenyl-6-methoxyphenol hydroxylase	102.6	113.8	156.1	255.6	131.5	223.8	K03185
pldB	lysophospholipase	26	139.3	176.7	164.5	160.9	238.3	K01048
nifV	homocitrate synthase NifV	160	217.5	273.5	148.8	93.3	126.2	K02594
entF	enterobactin synthetase component F	72.1	111.1	190.9	226.1	35.8	275.5	K02364
ectB, dat	diaminobutyrate-2-oxoglutarate transaminase	20	151.4	249.3	159.1	70.5	207.1	K00836
proC	pyrroline-5-carboxylate reductase	63.8	108.1	145.3	215.4	178	187.9	K00286
rpfC	two-component system, sensor histidine kinase RpfC	125	151.5	175.5	120.6	91.5	294.3	K10715
E4.1.3.4, HMGCL, hmgL	hydroxymethylglutaryl-CoA lyase	139.4	191.7	263.9	157.7	88.6	107.2	K01640
nadC, QPRT	nicotinate-nucleotide pyrophosphorylase (carboxylating)	72.9	111.1	129.6	257.7	142.9	150.2	K00767
hsdM	type I restriction enzyme M protein	107.2	143.5	150.2	211.7	120	164.8	K03427
mnmE, trmE, MSS1	tRNA modification GTPase	33.9	127	139.2	215.6	118.3	171.7	K03650
alr	alanine racemase	110.3	139.1	146.8	178	134.4	172.9	K01775
GMPP	mannose-1-phosphate guanylyltransferase	16.9	107.9	141.6	191.3	142.6	183.8	K00966
gpsA	glycerol-3-phosphate dehydrogenase (NAD(P)+)	112.6	113.4	140.1	229.5	108.5	174.3	K00057
mhpA	3-(3-hydroxy-phenyl)propionate hydroxylase	71.5	93.4	155.3	201.5	110.7	195.4	K05712
choD	cholesterol oxidase	14.4	34.2	153.9	181.9	180.5	204.1	K03333
acpD, azoR	FMN-dependent NADH-azoreductase	90.3	108.2	146.8	146.1	116.9	224.8	K01118
aroK, qutE	3-dehydroquininate dehydratase II	75.4	82.6	98.9	254	97.2	206.5	K03786
holB	DNA polymerase III subunit delta'	41	101.4	125.2	126.8	120.2	253.7	K02341
barA, gacS, varS	two-component system, NarL family, sensor histidine kinase BarA	57.6	108.7	234.1	95.8	70.3	203.3	K07678
folKP	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine diphosphokinase/ dihydropteroate synthase	48.1	112.5	116.6	179.5	141.5	150.6	K13941
kstD	3-oxosteroid 1-dehydrogenase	77.2	121.2	242	51.5	83.8	201.2	K05898
sul2	dihydropteroate synthase type 2	48.1	111.4	113.8	179.5	142.8	146.9	K18824

phzF	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	45.3	82.5	121.6	154.5	73.2	247.5	K06998
sixA	phosphohistidine phosphatase	26.8	112.4	134.3	168.8	92.9	164.2	K08296
rimI	[ribosomal protein S18]-alanine N-acetyltransferase	12.1	57.6	100.3	180.8	93.5	230.1	K03789
per, rfbE	perosamine synthetase	44.3	104.8	120.4	109.8	89.4	237.6	K13010
ribD	diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	34.3	135.7	148.5	146.9	74	146.1	K11752
kdtA, waaA	3-deoxy-D-manno-octulosonic-acid transferase	55.2	83.8	148	144.8	126.6	145.9	K02527
E3.5.1.28D, amiD	N-acetylmuramoyl-L-alanine amidase	13	111.5	165.8	160.1	47.6	162.9	K11066
pbpG	serine-type D-Ala-D-Ala endopeptidase (penicillin-binding protein 7)	88.5	92.3	105.3	164.4	79.8	204.9	K07262
rfbF	glucose-1-phosphate cytidylyltransferase	60.3	96.9	125.4	123.8	99	194.9	K00978
sulD	dihydroneopterin aldolase / 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase	36.9	86.8	93.2	177.7	96.4	174.2	K13940
E3.2.1.123	endoglycosylceramidase	0	82.6	112.8	206.5	46.5	171.1	K05991
ribD1	diaminohydroxyphosphoribosylaminopyrimidine deaminase	31.8	122.8	141.1	146.9	61.6	142.8	K01498
atuE	isohexenylglutaconyl-CoA hydratase	19.8	85.8	112.6	240.7	40.3	133.8	K13779
E2.7.13.3	histidine kinase	11.2	80.7	169.1	188.5	49.8	124	K10819
E2.5.1.56, neuB	N-acetylneuraminate synthase	11.1	99.4	113.3	168.2	77.9	141.2	K01654
MTHFS	5-formyltetrahydrofolate cyclo-ligase	27.2	92	127.6	125.4	90.4	163.8	K01934
PTR1	pteridine reductase	59.1	71.4	112.1	131.5	95.5	187.1	K03793
E2.4.2.21, cobU, cobT	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	58.2	79.1	107.5	227.3	66.7	99.5	K00768
envZ	two-component system, OmpR family, osmolarity sensor histidine kinase EnvZ	38.1	69.2	74.2	161.9	79.9	193.1	K07638
purT	phosphoribosylglycinamide formyltransferase 2	42.2	61.6	66.4	254.5	57.9	133	K08289
SCD, desC	stearoyl-CoA desaturase (Delta-9 desaturase)	84.4	109.8	131.6	106.5	109.7	114.8	K00507
mobA	molybdenum cofactor guanylyltransferase	36.4	96.9	103	94	114.8	143.7	K03752
atuH	citronellyl-CoA synthetase	47.2	95.8	145.8	61.3	43.6	201.4	K13776
yfeX	porphyrinogen peroxidase	5	94.8	166.8	82.9	46.8	156.2	K07223
gidB, rsmG	16S rRNA (guanine527-N7)-methyltransferase	48.9	88.4	116.2	83.3	109.4	149.7	K03501
hmp, YHB1	nitric oxide dioxygenase	24.4	89.3	101.9	126.9	86.3	126.7	K05916
maa	maltose O-acetyltransferase	16	54.8	82.7	86.5	93.6	208.8	K00661
dadA	D-amino-acid dehydrogenase	42.9	71.2	88.7	146	49.1	170.5	K00285
thnR	CoA pyrophosphatase	50.9	69.1	69.2	181.9	48.7	153.3	K18568
budC	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	70.6	97.3	124.8	99	55.2	144.3	K18009
crtR	beta-carotene hydroxylase	19.1	72.4	95.7	185.4	48.8	114	K02294
murU	N-acetyl-alpha-D-muramate 1-phosphate uridylyltransferase	12.4	81.5	125.1	87.3	86.7	131.1	K00992
tusA, sirA	tRNA 2-thiouridine synthesizing protein A	25.8	70.6	82.9	80.2	124.9	143.8	K04085
mltF	membrane-bound lytic murein transglycosylase F	11	71.2	71.6	118.2	61	169.8	K18691
cbiB, cobD	adenosylcobinamide-phosphate synthase	29.5	63.9	121.6	81.8	53.4	170.3	K02227
mobAB	molybdopterin-guanine dinucleotide biosynthesis protein	34.6	68.7	93.9	86	106.4	135.2	K13818
gluQ	glutamyl-Q tRNA(Asp) synthetase	43	65	72.8	178.6	73.6	100	K01894
hddC	D-glycero-alpha-D-manno-heptose 1-phosphate guanylyltransferase	13.5	64.6	112.1	77.2	89	142.1	K15669
yiaY	alcohol dehydrogenase	14.4	62.6	94.5	123.4	91	105.8	K13954
trmL, cspR	tRNA (cytidine/uridine-2'-O-)-methyltransferase	52.1	99.3	113.4	37	98.7	126.5	K03216
bsdC	4-hydroxybenzoate decarboxylase subunit C	40.5	85.3	105.5	186.8	40.2	57	K16239
E1.3.99.16	isoquinoline 1-oxidoreductase	68.4	96.2	129	121	33.5	90.9	K00256
E2.1.1.95	tocopherol O-methyltransferase	78.2	104.4	144.1	80	45.1	91.7	K05928
UNG, UDG	uracil-DNA glycosylase	30.4	81.7	97.7	135.7	43.7	98	K03648
pcpC	tetrachlorohydroquinone reductive dehalogenase	40.4	100.7	106.9	39.9	49.5	157.7	K15241
E2.7.8.26, cobS, cobV	adenosylcobinamide-GDP ribazoletransferase	22.4	72.3	105.7	78.4	53.1	142.9	K02233
clsC	cardiolipin synthase C	0	51.6	87	97.1	42.1	172.9	K06132
piID, pppA	leader peptidase (prepilin peptidase) / N-methyltransferase	29.6	74	105.7	111.6	60.7	97.2	K02654
dbpA	ATP-independent RNA helicase DbpA	41.8	55.2	93.9	111.8	23.1	152.8	K05591
hepA	ATP-dependent helicase HepA	17.6	46.1	76	88.9	98.1	124.2	K03580
PGLS, pgl, devB	6-phosphogluconolactonase	22.8	40.1	76.8	105.9	77.5	126.7	K01057
mfnA, adc	tyrosine decarboxylase / aspartate 1-decarboxylase	40.1	90.5	101.1	149.8	24.1	56.6	K18933
K11527	two-component system, sensor histidine kinase and response regulator	50	79.7	88.1	62.7	49.1	141.6	K11527
argA	amino-acid N-acetyltransferase	5.5	56.5	100.6	107.5	69.3	83.2	K00619
ydfG	3-hydroxy acid dehydrogenase / malonic semialdehyde reductase	9.1	50.9	85.2	166.8	33.3	79.3	K16066
BCHE	cholinesterase	23.6	59.7	108	37.6	69.7	139.7	K01050
TYDC	tyrosine decarboxylase	40.1	82.7	101.4	149.8	24.1	55.9	K01592
sdh	serine 3-dehydrogenase (NADP+)	5.8	50.3	90.4	142.1	30.8	98.6	K05886
regB, regS, acts	two-component system, sensor histidine kinase RegB	70	85.2	96	124.4	23.1	81.4	K15011

Chapter II

gspO	general secretion pathway protein O	24.7	66.4	101.5	108.3	37.4	93.1	K02464
hofD, hopD	leader peptidase HopD	24.7	66.4	101.5	108.3	37.4	93.1	K02506
comC	leader peptidase (prepilin peptidase) / N-methyltransferase	24.7	66.2	101.5	108.3	37.4	91.6	K02236
mhpE	4-hydroxy 2-oxovalerate aldolase	19.1	51.2	87.5	141.3	45.3	74.9	K01666
nqrA	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit A	32.2	51.6	80.7	119.5	73.9	74.4	K00346
speA	arginine decarboxylase	52.7	60.5	67.4	97.9	57.2	111.6	K01585
stp1, pppA	serine/threonine protein phosphatase Stp1	6.7	64.5	126.9	73.3	32.5	94.3	K11915
ampD	N-acetyl-anhydromuramoyl-L-alanine amidase	5.2	64.4	104.6	97	19.3	95.5	K03806
egtD	L-histidine Nalpha-methyltransferase	29.3	67.7	76.9	94.3	68.7	69.4	K18911
isfD	sulfoacetaldehyde reductase	8.5	49.7	78.1	142.1	27.5	77.5	K15373
epd	D-erythrose 4-phosphate dehydrogenase	15.5	31.9	58.3	93.6	60.7	129.4	K03472
thrB2	homoserine kinase type II	11.7	74.6	95.2	76.2	36	91.1	K02204
mhpD	2-keto-4-pentenolate hydratase	26.9	57.7	97.6	66.7	55.3	92.3	K02554
wbpP	UDP-N-acetylglucosamine 4-epimerase	23.2	29.8	54.1	59	88	134.2	K02473
ahpF	alkyl hydroperoxide reductase subunit F	25.4	36.3	94.9	99.6	52.6	79.7	K03387
rep	ATP-dependent DNA helicase Rep	31.1	69.8	90	65.3	59.8	75.1	K03656
rubB, alkT	rubredoxin---NAD ⁺ reductase	14	56.1	130	47.9	40	84	K05297
fre, ubiB	aquacobalamin reductase / NAD(P)H-flavin reductase	9.6	51.8	87	64.8	69	84.7	K05368
lytF, cwIE	peptidoglycan DL-endopeptidase LytF	10.4	40.3	46	110.1	79.9	80.4	K19223
E3.2.1.14	chitinase	42.3	73.1	116.6	36.7	20.4	109.3	K01183
tcpJ	toxin coregulated pilus biosynthesis protein J	22.2	51.3	98.7	84.2	24.1	88.7	K10966
E2.4.1.7	sucrose phosphorylase	24.5	38.5	69.7	49.5	60.6	128.3	K00690
speD, AMD1	S-adenosylmethionine decarboxylase	12.9	69.8	98.2	64.5	39.4	74.2	K01611
nicE, maiA	maleate isomerase	48.5	82.4	122.7	49.3	40.2	51	K01799
rbtD	ribitol 2-dehydrogenase	46.6	47	84.7	80.7	30.7	100	K00039
rlmJ	23S rRNA (adenine2030-N6)-methyltransferase	15.5	20.5	54.7	119.3	43.2	104.2	K07115
mcrB	5-methylcytosine-specific restriction enzyme B	5.1	32.2	75.2	55.1	32	140.6	K07452
rsmJ	16S rRNA (guanine1516-N2)-methyltransferase	0.8	30.8	95	73.7	53.7	81.7	K15984
SRD5A1	3-oxo-5-alpha-steroid 4-dehydrogenase 1	24.3	44.7	102.1	75.1	31.7	81	K12343
FBP, fbp	fructose-1,6-bisphosphatase I	43.4	51.6	88.1	60.6	39.5	92.1	K03841
norW	nitric oxide reductase FIRd-NAD(+) reductase	0.5	55.6	128.4	58.3	3.5	84.2	K12265
rnfB	Na ⁺ -translocating ferredoxin:NAD ⁺ oxidoreductase subunit B	20.7	34.6	48.8	139.6	17.4	86.2	K03616
E3.2.1.96	mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase	4.4	39.3	44.7	87.3	72.9	79.6	K01227
mhpC	2-hydroxy-6-oxonona-2,4-dienedioate hydrolase	21.3	56.5	90.4	46	44.1	84.2	K05714
E1.1.1.65	pyridoxine 4-dehydrogenase	7.7	33.4	80	80.9	15.3	111	K05275
cmoB	tRNA (mo5U34)-methyltransferase	15.2	36.5	44.8	90	62.5	86	K15257
E4.1.1.17, ODC1, speC, speF	ornithine decarboxylase	56.5	58.2	66.7	120	34.3	40.1	K01581
bphH, xylJ, tesE	2-oxopent-4-enoate/cis-2-oxohex-4-enoate hydratase	11.8	55.6	99.7	60.4	19.6	83.4	K18364
PRDX3	peroxiredoxin 3	6.7	39.2	39.8	73.6	44.5	119.7	K20011
cmpC	bicarbonate transport system ATP-binding protein	22.4	26.5	79.8	102.7	33.4	73.6	K11952
cmpD	bicarbonate transport system ATP-binding protein	22.4	26.5	79.8	102.7	33.4	73.6	K11953
hsaA	3-hydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione monooxygenase	18.6	61.6	128.7	29.6	13.5	79.4	K16047
dge1	diguanylate cyclase	8.8	31.5	60.5	61.7	15.5	143.3	K18967
nhoA	N-hydroxyarylamine O-acetyltransferase	7.4	27.3	43.9	72.6	39.4	125.4	K00675
wcaF	putative colanic acid biosynthesis acetyltransferase WcaF	9.8	21.7	77.3	25.8	29.6	148.7	K03818
E2.3.1.8, pta	phosphate acetyltransferase	30.3	31.6	53.6	28.8	77.2	111.1	K00625
eda	2-dehydro-3-deoxyphosphogluconate aldolase / (4S)-4-hydroxy-2-oxoglutarate aldolase	47.4	48.1	54.8	65.2	42.7	90.6	K01625
maiA, GSTZ1	maleylacetoacetate isomerase	25.1	54.2	70.6	112.6	26.9	33.6	K01800
hoxU	[NiFe] hydrogenase diaphorase moiety small subunit	2.4	27.1	109.3	32.3	3.6	123.9	K18006
dprE2	decaprenylphospho-beta-D-erythro-pentofuranosid-2-ulose 2-reductase	5.6	50.8	87.3	21.9	49	85.1	K16652
K16881	mannose-1-phosphate guanylyltransferase / phosphomannomutase	6.5	20.7	34	121.2	26.7	88.3	K16881
nagL	maleylpyruvate isomerase	24.4	53.5	68.3	112.6	23.8	32	K01801
yihU	4-hydroxybutyrate dehydrogenase / sulfolactaldehyde 3-reductase	7.7	48	95	54	10	81.7	K08318
cpdA	3',5'-cyclic-AMP phosphodiesterase	8.1	63.2	92.3	18.1	26	87.2	K03651
exoM	succinoglycan biosynthesis protein ExoM	5.3	14.9	70.8	35.6	7.8	154.5	K16556
E2.7.7.65	diguanylate cyclase	3.3	11.7	52	68.9	64.6	85	K13069
mgtA	phosphatidylinositol alpha 1,6-mannosyltransferase	22.4	54.6	59.5	59.2	53.9	55	K12583
SDR16C5	all-trans-retinol dehydrogenase (NAD ⁺)	0	36.4	72.8	80.1	13.9	76.5	K15734
malQ	4-alpha-glucanotransferase	35.6	47.5	58.3	46.6	29.6	95.6	K00705
hsaD	4,5,9,10-diseco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate hydrolase	7.6	59.5	98.7	22.2	12.5	84.7	K16050
dmpP, poxF, tomA5	phenol/toluene 2-monooxygenase (NADH) P5/A5	10.1	22.2	40.8	59.1	70.3	84	K16246

Chapter II

ubiC	chorismate--pyruvate lyase	0	42.1	89	20.4	32.4	92.1	K03181
nifD	nitrogenase molybdenum-iron protein alpha chain	3.7	12.6	66.1	48.4	5.7	141.6	K02586
por	protochlorophyllide reductase	8.1	36.6	41.5	77.4	41.2	73.9	K00218
rstB	two-component system, OmpR family, sensor histidine kinase RstB	6.7	48.8	78.1	42.4	9.4	90.5	K07639
prmB	propane monooxygenase reductase component	10.1	17.9	38.6	59.1	68.9	84	K18225
tpx	thiol peroxidase, atypical 2-Cys peroxiredoxin	6	28.1	43.1	39.8	71.3	84.8	K11065
cymAb	p-cymene methyl-monoxygenase electron transfer component	9.6	17.9	37.7	59.1	68	83	K18293
ubiX, bsdB, PAD1	flavin prenyltransferase	12.3	25.6	45.1	51.3	68.5	73.5	K03186
por, nifJ	pyruvate-ferredoxin/ flavodoxin oxidoreductase	28.7	33.3	56.8	65.3	19.8	87.4	K03737
E3.3.2.8	limonene-1,2-epoxide hydrolase	3.3	36.9	52.9	37.3	63.5	71.6	K10533
nat	arylamine N-acetyltransferase	0	17.4	38.3	48.5	34.2	122.6	K00622
tpH1	terephthalate 1,2-dioxygenase reductase component	9.6	15	37.7	59.1	66.2	83	K18077
E1.1.1.387	L-serine 3-dehydrogenase (NAD+)	4.1	37.3	88.6	49	6.5	78.7	K19711
bphI, xylK, nahM, tesG	4-hydroxy-2-oxovalerate/4-hydroxy-2-oxohexanoatealdolase	9.2	27.3	83.1	74.9	0.8	72	K18365
bphJ, xylQ, nahO, tesF	acetaldehyde/propanal dehydrogenase	20.4	42.2	82.5	50.6	8.5	72.5	K18366
hsaC	3,4-dihydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione 4,5-dioxygenase	6.6	42	73.4	59.6	15.2	59.5	K16049
nifK	nitrogenase molybdenum-iron protein beta chain	0.3	11.4	62.4	35.3	4.7	133.7	K02591
adh1	alcohol dehydrogenase	5.2	9.7	32.5	73.8	57.3	73.1	K19954
RETSAT	all-trans-retinol 13,14-reductase	8.6	44.6	47	33.7	44	76.3	K09516
hyaB, hybC	hydrogenase large subunit	0.5	14.8	32.2	78.5	49.3	70.5	K06281
hoxF	[NiFe] hydrogenase diaphorase moiety large subunit	11.9	41.7	81.7	36.7	8.9	75.4	K18005
ptb	phosphate butyryltransferase	4.1	14.5	47.3	28.2	55.5	98.8	K00634
PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase-like protein 1	0	13.8	74.4	17.8	0.1	136	K13712
pgIC	undecaprenyl phosphate N,N'-diacetyl bacillosamine 1-phosphate transferase	9.6	23.2	45.1	44.3	9.9	116.2	K15915
PTGS2, COX2	prostaglandin-endoperoxide synthase 2	4.5	60.1	91.4	46.2	2.5	37.6	K11987
K08303	putative protease	2.8	30.9	43.4	65	16.1	82.3	K08303
K16153	glycogen phosphorylase/synthase	25.4	27.8	31.4	97.3	15.1	65.3	K16153
narX	two-component system, NarL family, nitrate/nitrite sensor histidine kinase NarX	0	10.9	63.9	31.4	5.7	123.9	K07673
hoxY	NAD-reducing hydrogenase small subunit	2.8	24.4	98	26.7	1.8	84.5	K18007
acdH	short/branched chain acyl-CoA dehydrogenase	9.6	44.1	61.4	72.8	14.7	42.2	K11410
K14136	decaprenyl-phosphate phosphoribosyltransferase	28.7	29.3	40.4	29.1	49.8	86.1	K14136
E3.1.21.7, nfi	deoxyribonuclease V	0	32.2	37.7	39.6	51.2	73.9	K05982
iucD	lysine N6-hydroxylase	0	7.8	36.3	76.5	46.5	64.3	K03897
ybaK, ebsC	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase	6.5	23.2	44.1	46.5	53.4	63.5	K03976
spnN, oleW	dTDP-3,4-didehydro-2,6-dideoxy-alpha-D-glucose 3-reductase	51.5	66.8	79.1	19.3	15.7	48.3	K13327
yiaC	putative acetyltransferase	0	25.5	42.2	27.6	43.6	89.5	K03826
tupC, vupC	tungstate transport system ATP-binding protein	49.7	59.7	67.2	53.1	18.3	25.3	K06857
E3.1.3.41	4-nitrophenyl phosphatase	9.6	12.2	37.6	57.6	45.9	69.1	K01101
treC	trehalose-6-phosphate hydrolase	19.4	32.8	39	33.3	56	60.1	K01226
actVA5	two-component flavin-dependent monooxygenase	10.9	31.2	77.2	26.5	7.6	73.8	K14630
iucC	aerobactin synthase	0	5.7	34.7	53.7	48.5	72.2	K03895
sad	succinate-semialdehyde dehydrogenase	15.3	37.9	78	16.9	5.3	75.8	K08324
NEK1_4_5	NIMA (never in mitosis gene a)-related kinase 1/4/5	16.6	26.8	29	83.5	35.9	37.4	K08857
bphC	biphenyl-2,3-diol 1,2-dioxygenase	6.6	40.1	72.8	24.7	15.2	59.5	K00462
PXDN, VPO1	peroxidase	7.1	15.1	34.7	47.3	50.3	60	K19511
mnmc	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein	19.5	26.4	26.9	88.6	27.9	37.1	K15461
arnB, pmrH	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase	6.7	16.3	43.2	64.6	27.1	53.9	K07806
entD	enterobactin synthetase component D	7.4	9.4	43.4	30	41.7	77.1	K02362
tsdA	thiosulfate dehydrogenase	23.1	26.1	42.4	49.5	10.2	72.4	K19713
pseG	UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranose hydrolase	0.5	21.5	40.2	60	15.5	62.3	K15897
nudE	ADP-ribose diphosphatase	2	24.7	39.4	18.2	36.1	79.6	K08312
yfbR	5'-deoxynucleotidase	12.2	21.8	34.8	22.3	43.5	73.6	K08722
fas	fatty acid synthase, bacteria type	18.7	23.3	28.5	34.1	45.3	63.9	K11533
fabY	acetoacetyl-[acyl-carrier protein] synthase	18.7	23.3	28.5	34.1	45.3	63.9	K18473
epmC	elongation factor P hydroxylase	0	7.9	41.9	58.9	8.7	77.2	K09906
astE	succinylglutamate desuccinylase	0	14.5	40.4	17.8	48	73.5	K05526
etk-wzc	tyrosine-protein kinase Etk/Wzc	6.5	38.5	48.8	12.5	24.2	66.3	K16692
todE	3-methylcatechol 2,3-dioxygenase	2.8	30	72	22.8	3.8	59	K16270
phoQ	two-component system, OmpR family, sensor histidine kinase PhoQ	0.6	25.3	42.9	29.7	13.4	76.3	K07637
dfx	superoxide reductase	0	7.3	38	16.5	39	82.3	K05919

K14330	fatty aldehyde-generating acyl-ACP reductase	1.1	6.8	45.4	20.7	34.9	74.8	K14330
E2.4.1.213	glucosylglycerol-phosphate synthase	2.1	6.1	30.9	76	2.7	66.1	K03692
rutF	flavin reductase	0	58.9	65.8	14.7	9	32.8	K09024
E1.12.7.25	ferredoxin hydrogenase small subunit	0	18.9	29.8	33.5	16.4	79.9	K00534
cdgJ	c-di-GMP phosphodiesterase	3.6	30.2	41.2	29	4.8	72.5	K07181
gfo	glucose-fructose oxidoreductase	6.8	50.5	68	32.5	9.8	16	K00118
iucB	acetyl CoA:N6-hydroxylysine acetyl transferase	0	7.9	35.7	31.4	33.4	67.1	K03896
DVR	divinyl chlorophyllide a 8-vinyl-reductase	0	24.7	76.3	22.7	0.1	51.6	K19073
rlmG	23S rRNA (guanine1835-N2)-methyltransferase	5.1	9	32	20.3	44.4	66.3	K11391
PLD1_2	phospholipase D1/2	5.2	16.8	47	22.1	6.1	78.3	K01115
psel, neuB3	pseudaminic acid synthase	4.6	25.4	43	25.4	17.2	58.1	K15898
ERCC2, XPD	DNA excision repair protein ERCC-2	4.5	18.9	35.5	31.3	12.5	69.3	K10844
cmtE	HOMODA hydrolase	16.6	20.6	39.6	21.1	5.1	77.7	K10623
iucA	N2-citryl-N6-acetyl-N6-hydroxylysine synthase	0	8.2	33.5	20	32.8	68.1	K03894
mvpA, vapC	tRNA(fMet)-specific endonuclease VapC	0	44.5	45.2	3.5	13	54.9	K18828
oxa	beta-lactamase class D	2	18.1	30.1	26.2	20.4	61.9	K17838
ICMT, STE14	protein-S-isoprenylcysteine O-methyltransferase	0	15	44.1	16.5	2.3	75.3	K00587
pseC	UDP-4-amino-4,6-dideoxy-L-N-acetyl-beta-L-altrosamine transaminase	4.4	29.6	32.5	16	22.6	50.2	K15895
astB	succinylarginine dihydrolase	4.2	12.4	33.7	13.7	10.9	76.1	K01484
E3.5.5.7	aliphatic nitrilase	10.5	30.9	49.2	43.4	5.4	16	K01502
mdoC	glucans biosynthesis protein C	0	12	31.9	16.4	18	66.1	K11941
waaH	heptose III glucuronosyltransferase	0	12.5	35.2	22.3	0	74.1	K19354
HIS4	phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP cyclohydrolase / histidinol dehydrogenase	8.6	25.2	31.5	14.7	17.3	52.1	K14152
MAN2C1	alpha-mannosidase	1.7	16.4	17.8	66.2	18.2	20.1	K01191
capD	UDP-glucose 4-epimerase	16.8	19.2	29.1	36	13.6	39.1	K17716
caiA	crotonobetainyl-CoA dehydrogenase	0	29.6	52.8	14.9	0.3	38.2	K08297
MGLL	acylglycerol lipase	0	9.7	33.7	15.3	2.4	68.1	K01054
ich-P	itaconyl-CoA hydratase / mesaconyl-C4 CoA hydratase	33.9	35	38.5	8.5	8.7	35.9	K18291
sqhC	sporulenol synthase	6.5	36.7	51.9	19.7	8	10.1	K18115
stpA	glucosylglycerol 3-phosphatase	0	7.9	32.9	15.3	0	69.2	K05978
RDH11	retinol dehydrogenase 11	0	8.2	30.6	23.1	0.9	61.4	K11152
draT	NAD+---dinitrogen-reductase ADP-D-ribosyltransferase	0	9.2	32.8	9	0	69.2	K05951
dusC	tRNA-dihydrouridine synthase C	5.2	42.9	58.4	6.1	5.6	6.7	K05541
PIP5K	1-phosphatidylinositol-4-phosphate 5-kinase	0	8.8	43.1	0	0	65	K00889
plc	phospholipase C	5.3	21.5	24.2	49.9	4.6	14.7	K01114
nudJ	phosphatase NudJ	1.2	31.2	67.9	3.1	1.4	10.4	K12152
FDF1	farnesyl-diphosphate farnesyltransferase	1.5	17.7	18.1	28.8	14.2	34	K00801
pglD	UDP-N-acetylglucosamine N-acetyltransferase	0	19.5	35.5	0	0	55.5	K15913
L2HGDH	2-hydroxyglutarate dehydrogenase	9.1	15.3	15.7	30.8	16.3	31.9	K00109
wbpB	UDP-N-acetyl-2-amino-2-deoxyglucuronate dehydrogenase	0.5	26.7	51.6	13.2	7	9.6	K13016
pdxB	erythronate-4-phosphate dehydrogenase	3.1	28.9	53.4	4	10.2	11.4	K03473
narQ	two-component system, NarL family, nitrate/nitrite sensor histidine kinase NarQ	0	5.7	30.3	13.6	1.5	56.6	K07674
ABCC1	ATP-binding cassette, subfamily C (CFTR/MRP), member 1	2.5	29.6	63.6	1.4	0.3	10.9	K05665
crtP	diapolycopene oxygenase	1.8	4.7	12.2	43.8	16.6	25.7	K10210
soxG	sarcosine oxidase, subunit gamma	8.5	11.7	21.1	44	11.2	12.7	K00305
E2.7.11.-	protein-serine/threonine kinase	20.6	25.6	45	4.8	3.1	18	K08286
lpxM, msbB	lauroyl-Kdo2-lipid IVA myristoyltransferase	0.8	10.3	21.8	7.5	7.7	49.1	K02560
dgkA, DGK	diacylglycerol kinase (ATP)	0	15.6	22	47.1	5.2	6.5	K00901
APA1_2	sulfate adenyltransferase (ADP) / ATP adenyltransferase	9.3	28.2	55.4	4.9	1.5	5.7	K00988
tauX	taurine dehydrogenase small subunit	8.4	20.2	56	0	1.4	11.3	K07255
eryG	erythromycin 3"-O-methyltransferase	0	25.9	42.5	17.4	0.8	1.8	K14369
PCYT1	choline-phosphate cytidyltransferase	0	25.7	42.9	17.3	0.2	1.6	K00968
NVD, DAF36	cholesterol 7-desaturase	0	30.7	48	3.1	1.4	2.2	K14938
mvhA, vhuA, vhcA	F420-non-reducing hydrogenase large subunit	0.4	17.4	44.9	16.6	1.2	4.2	K14126
tmcA	tRNA(Met) cytidine acetyltransferase	0.6	18.3	52.5	0	5.2	8	K06957
cobD	threonine-phosphate decarboxylase	3.1	6.3	7.4	25	20.8	22.9	K04720
mqnB	futalosine hydrolase	0	11.4	20.7	1.4	10.7	33.5	K11783
andAd	anthranilate 1,2-dioxygenase small subunit	1.1	21.2	22.7	18.5	2.6	11.8	K16320
wecG, rffM	UDP-N-acetyl-D-mannosaminouronate:lipid I N-acetyl-D-mannosaminouronosyltransferase	1.3	15.8	17.3	3.4	9.7	29.4	K02852
mcsB	protein arginine kinase	1.5	10.6	14.1	1.1	23	25.6	K19405
EPHX2	soluble epoxide hydrolase / lipid-phosphate phosphatase	0	19.3	47.7	1.1	0.2	1.7	K08726
aac3-I	aminoglycoside 3-N-acetyltransferase I	9.8	23.1	43.3	0	0.1	2.9	K03395
PHO	acid phosphatase	1.5	6.6	19.6	3.2	13	25.3	K01078
TPP1, CLN2	tripeptidyl-peptidase I	1.1	16.6	32.4	4.3	0	14.1	K01279
iaaM	tryptophan 2-monoxygenase	4.4	18.3	42	3.3	0.4	2	K00466
nocJ	nocardicin-A epimerase	0	17.6	42	0	0	0.7	K19105
K10253	DOPA 4,5-dioxygenase	10.1	18.3	25.7	1.5	5.6	7.1	K10253
PMA1, PMA2	H+-transporting ATPase	1.5	11.7	21.5	0	3.3	21.6	K01535

Chapter II

gspK	glucosamine kinase	0	6.6	11.9	34.9	0	3.6	K18676
mtnC, ENOPH1	enolase-phosphatase E1	0	2	11.2	36.8	3.2	3.6	K09880
TGL4	TAG lipase / steryl ester hydrolase / phospholipase A2 / LPA acyltransferase	0.8	2.2	3.7	34.4	0	16.1	K14674
TGL3	TAG lipase / lysophosphatidylethanolamine acyltransferase	0.8	2.2	3.5	34.4	0	15.6	K14675
E3.2.1.89	arabinogalactan endo-1,4-beta-galactosidase	0	6.6	8.1	34.7	2.2	2.7	K01224
saeS	two-component system, OmpR family, sensor histidine kinase SaeS	0	4	7.4	0	16.2	25.5	K10681
ABCB1, CD243	ATP-binding cassette, subfamily B (MDR/TAP), member 1	0	12.4	12.7	17.9	3.7	5.7	K05658
wcaB	putative colanic acid biosynthesis acetyltransferase WcaB	0	2.7	11.2	0	13.6	24.4	K03819
trcS	two-component system, OmpR family, sensor histidine kinase TrcS	0	3.1	6.5	0	15.4	24.9	K07656
dkgA	2,5-diketo-D-gluconate reductase A	1.3	1.9	6	35.8	1.5	4.4	K06221
PDC, pdc	pyruvate decarboxylase	0	0.8	1.4	46	0.5	0.6	K01568
STK38, NDR	serine/threonine kinase 38	12.5	15.5	23.5	1.6	0.1	8.4	K08790
HERC2	E3 ubiquitin-protein ligase HERC2	0	13.1	15.7	5.5	2.9	7.4	K10595
RPB1, POLR2A	DNA-directed RNA polymerase II subunit RPB1	8.4	15	17.3	1.6	2.7	6.7	K03006
RRM1	ribonucleoside-diphosphate reductase subunit M1	7.4	15.9	16.9	0	0	10	K10807
SGK2	serum/glucocorticoid-regulated kinase 2	7.2	12.9	18.4	1.9	0.6	8	K13303
rlmM	23S rRNA (cytidine2498-2'-O)-methyltransferase	1.9	2.1	7.4	22.9	1.7	6.2	K06968
rhaD	rhamnulose-1-phosphate aldolase	6.8	9	9.5	0	8.4	11.2	K01629
CPK	calcium-dependent protein kinase	0	10.8	15.8	1.4	0	10	K13412
AKT	RAC serine/threonine-protein kinase	7.2	12.6	16.1	1.9	0.4	6.5	K04456
CMPK1, UMPK	UMP-CMP kinase	8.2	11	18.9	0	0.1	7.2	K13800
CAMK1	calcium/calmodulin-dependent protein kinase I	0.7	7.9	17.2	1.4	0	9.8	K08794
MCM3	DNA replication licensing factor MCM3	2.1	7.7	13.7	2.2	0	12.6	K02541
UBE1, UBA1	ubiquitin-activating enzyme E1	0	6.9	17.8	0	0.7	10.4	K03178
TOP3	DNA topoisomerase III	1.7	12.2	15.3	0.7	0.1	7.3	K03165
CHD7	chromodomain-helicase-DNA-binding protein 7	3.1	9.1	14.2	4.6	0	7.3	K14437
pht5	4,5-dihydroxyphthalate decarboxylase	0.6	3.5	8.7	7.4	1.9	13.7	K04102
araB	L-ribulokinase	3	9.6	12.5	1	3.7	8.4	K00853
cpmB, carB	carboxymethylproline synthase	2.6	7.8	15.8	0.7	0.8	9.4	K18317
thnE	carboxymethylproline synthase	2.6	7.8	15.8	0.7	0.8	9.4	K18583
E7.6.2.1	phospholipid-translocating ATPase	0	6	16.8	0	0	11.4	K01530
RPC1, POLR3A	DNA-directed RNA polymerase III subunit RPC1	6.8	8.7	17.6	0	0	7.4	K03018
DDX56, DBP9	ATP-dependent RNA helicase DDX56/DBP9	0	10.8	11.3	4.6	0.2	6.7	K14810
NXN	nucleoredoxin	3.6	10.7	16.2	1	0	5.4	K17609
ADAM33	disintegrin and metalloproteinase domain-containing protein 33	0	1.1	6.9	0	0	24.5	K08616
PDIA6, TXNDC7	protein disulfide-isomerase A6	0	4.2	6.3	18.8	0	2.7	K09584
xynC	glucuronoarabinosyl endo-1,4-beta-xylanase	0	1.4	6.4	0	1.2	22.9	K15924
GME	GDP-D-mannose 3', 5'-epimerase	0	10.5	15.5	0	0	6	K10046
CDC2L	cell division cycle 2-like	0	1.7	3.7	24.8	0.1	0.5	K08818
6GAL	galactan endo-1,6-beta-galactosidase	0	1.4	6.4	0	0	22.9	K18579
HECTD1	E3 ubiquitin-protein ligase HECTD1	9.6	11.9	13.5	0	0	5.2	K12231
ATP2B	P-type Ca2+ transporter type 2B	2.1	6	12.4	1.9	0	9.7	K05850
nagH	salicylate 5-hydroxylase small subunit	0	4	4.2	18.5	0	3.2	K18243
ATP1A	sodium/potassium-transporting ATPase subunit alpha	0.3	8.2	13.9	0	1.1	6.6	K01539
dgkA	undecaprenol kinase	0	0.2	2.4	20	2	4.1	K00887
irp5, ybtE	yersiniabactin salicyl-AMP ligase	0	1.1	5.1	18	1.5	2.8	K04783
RPS6KB	ribosomal protein S6 kinase beta	0.6	8.7	14	0	0.3	5.3	K04688
XR	D-xylose reductase	2.9	5.7	5.8	4.6	2.8	8.9	K17743
STK24_25_MST4	serine/threonine-protein kinase 24/25/MST4	6.4	7	13.1	1.4	0	5.4	K08838
UPF1, RENT1	regulator of nonsense transcripts 1	1.8	7.9	13.7	0	0	5.2	K14326
SNRNP200, BRR2	pre-mRNA-splicing helicase BRR2	3.4	5	12.2	1.3	0.2	7.4	K12854
CMAH	CMP-N-acetylneuraminate monooxygenase	0	2.3	3.2	18.8	0.7	1.1	K08080
wbbl	N-acetylglucosaminyl-diphospho-decaprenol L-rhamnosyltransferase	2	5.9	7.6	2.9	2.6	6.3	K16870
pvdA, SIDA	L-ornithine N5-monooxygenase	0	0.6	2.1	22.5	0	0.1	K10531
CTSB	cathepsin B	0	7.5	9	0	3.1	4.9	K01363
SMS	spermine synthase	0	0.3	13.8	0	0	10.3	K00802
PPP4C	serine/threonine-protein phosphatase 4 catalytic subunit	0	8.2	10	0	0	6	K15423
USP34	ubiquitin carboxyl-terminal hydrolase 34	2.6	3.3	11.4	2.4	0	6.6	K11853
NAA20, NAT3	N-terminal acetyltransferase B complex catalytic subunit	2.1	3.9	5.5	8.4	0.2	5.4	K17972
PRKAA, AMPK	5'-AMP-activated protein kinase, catalytic alpha subunit	3.2	5.7	9.9	2.3	0	5.5	K07198
ACLY	ATP citrate (pro-S)-lyase	0	7.4	11.2	0	1	3.4	K01648
MOGAT2, MGAT2	2-acylglycerol O-acyltransferase 2	3.8	6.8	11.7	0	0.1	4.5	K14457
tphA3	terephthalate 1,2-dioxygenase oxygenase component beta subunit	0	8.4	10.2	0	0	4.1	K18075
DRS2, ATP8A	phospholipid-transporting ATPase	0	3.8	9.9	0	0	8.9	K14802

MAN2B1, LAMAN	lysosomal alpha-mannosidase	0	7	10.6	1.5	0.1	3.4	K12311
dsdA	D-serine dehydratase	0	0.9	1.3	19.5	0	0.7	K01753
CTSA, CPY	cathepsin A (carboxypeptidase C)	0	8	9.3	0	0	5	K13289
MIOX	inositol oxygenase	0.6	5.9	7.9	1.1	2.6	4.7	K00469
CSNK2A	casein kinase II subunit alpha	0	6.8	9.8	1.6	0	3.8	K03097
wbdA, wbpX, mtfA	alpha-1,2-mannosyltransferase/rhamnosyltransferase	0.4	2.3	4.6	0	4.8	10.2	K12993
CDKL	cyclin-dependent kinase-like	2.3	7	9.7	0	0	5.1	K08824
UBE2D, UBC4, UBC5	ubiquitin-conjugating enzyme E2 D	2.6	6.5	8.8	0.6	0	5.7	K06689
SMARCA5, SNF2H, ISWI	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	0	5.9	10	0	0.3	5	K11654
AASS	alpha-aminoadipic semialdehyde synthase	0	5	6.3	6.8	0.2	2.9	K14157
TER, TSC13, CER10	very-long-chain enoyl-CoA reductase	0	0.4	0.9	19.4	0	0.2	K10258
SCPL-II	serine carboxypeptidase-like clade II	0	6.4	8.8	0	0	5.6	K16297
BRSK	BR serine/threonine kinase	0	8.7	9	0	0	3	K08796
HDAC1_2	histone deacetylase 1/2	2.4	6.1	7.7	2.9	0.4	3.4	K06067
HACD, PHS1, PAS2	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase	4.9	5.7	10	0	1.5	3.3	K10703
CSNK1, CKI	casein kinase 1	0	5.4	9.9	0	0	5.1	K02218
POLE	DNA polymerase epsilon subunit 1	2.7	5.6	11.2	0	0	3.5	K02324
SGK1	serum/glucocorticoid-regulated kinase 1	0.6	5.7	11	0	0.3	3.3	K13302
DHFR-TS	dihydrofolate reductase / thymidylate synthase	0	3.3	10.9	1.8	0.8	3.6	K13998
dmpD, xylF	2-hydroxymuconate-semialdehyde hydrolase	0	4	9.2	0.7	1.9	4.3	K10216
carC	2-hydroxy-6-oxo-6-(2'-aminophenyl)hexa-2,4-dienoate hydrolase	0	4	9.2	0.7	1.9	4.3	K15756
USP9_24	ubiquitin carboxyl-terminal hydrolase 9/24	2.6	2.9	8.8	2.4	0	5.5	K11840
PPM1L, PP2CE	protein phosphatase 1L	0	4.9	6.6	1.3	0.1	6.4	K17506
adaA	AraC family transcriptional regulator, regulatory protein of adaptative response / methylphosphotriester-DNA alkyltransferase methyltransferase	0	0.4	4.7	10.5	0.1	3.7	K13530
padB	phenylacetyl-CoA:acceptor oxidoreductase	3.7	4.3	5.5	7	0.1	2.2	K18361
bls	(carboxyethyl)arginine beta-lactam-synthase	0	0.3	11.2	0	0	7.5	K12674
cpmA, carA	carbapenam-3-carboxylate synthase	0	0.3	11.2	0	0	7.5	K18316
thnM	carbapenam-3-carboxylate synthase	0	0.3	11.2	0	0	7.5	K18582
mfnE	5-(aminomethyl)-3-furanmethanol phosphate kinase	0	3.1	3.3	3.8	3.1	5.5	K07144
SMARCA2_4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 2/4	0	4.1	10.5	0	0	4.2	K11647
todF	2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	0	2.3	9.2	0.7	1.9	4.3	K10702
etbD	2-hydroxy-6-oxo-octa-2,4-dienoate hydrolase	0	2.3	9.2	0.7	1.9	4.3	K18092
CPVL	vitellogenic carboxypeptidase-like protein	0	6.3	7.6	0	0.8	3.6	K09645
HECTD4	E3 ubiquitin-protein ligase HECTD4	0.6	3.8	9.7	0	0.7	4.1	K17849
DDX3X, bel	ATP-dependent RNA helicase DDX3X	0	5.6	9.1	0	0.2	3.2	K11594
PMPCB, MAS1	mitochondrial-processing peptidase subunit beta	0.9	5.6	9	0	0	3.4	K17732
POLD1	DNA polymerase delta subunit 1	0	5.8	8.5	0	0	3.5	K02327
phoN	acid phosphatase (class A)	0	2.5	3.3	0	2.3	9.6	K09474
BLM, RECQL3, SGS1	bloom syndrome protein	0.7	3.6	8.9	1.5	0	3.7	K10901
HECT	other hect domain ubiquitin protein ligase E3	0	3.8	9.7	0	0	4.1	K03874
K01954	carbamoyl-phosphate synthase	4.7	6.1	8.3	0	0.1	2.9	K01954
MTR4, SKIV2L2	ATP-dependent RNA helicase DOB1	3.4	3.9	8.5	0.9	0	4	K12598
CAS1	cycloartenol synthase	0	0.9	1.4	13.5	0	1.3	K01853
MBTPS1	membrane-bound transcription factor site-1 protease	0	5.5	7.2	1	0	3.3	K08653
COASY	phosphopantetheine adenyllyltransferase / dephospho-CoA kinase	0	4.7	9.1	0	0	3.2	K02318
ARSI_J	arylsulfatase I/J	0	5.3	7.1	0	0	4.6	K12375
URA2	carbamoyl-phosphate synthase / aspartate carbamoyltransferase	4.7	6.1	8.2	0	0	2.5	K11541
STE11	mitogen-activated protein kinase kinase kinase	0	5.9	7.3	0	0.2	3.3	K11228
MESO1, ERG25	methylsterol monooxygenase	0	6	6.3	0	1.4	2.9	K07750
bioJ	pimeloyl-[acyl-carrier protein] methyl ester esterase	0	1	10.8	0.7	0	4.1	K19561
entE, dhbE, vibE, mxcE	2,3-dihydroxybenzoate-AMP ligase	0	0.1	3.9	0	0	12.5	K02363
BRIP1, BACH1, FANCI	fanconi anemia group J protein	1.2	5.6	6.3	1.1	0.5	2.8	K15362
ZDHHC	palmitoyltransferase	2	3.6	5.5	4.3	0	2.9	K18932
ped	(S)-1-phenylethanol dehydrogenase	0	3.5	9.8	0	0.1	2.8	K14746
PPP3C, CNA	serine/threonine-protein phosphatase 2B catalytic subunit	0	5	7.9	0	0.1	3.2	K04348
ACACA	acetyl-CoA carboxylase / biotin carboxylase 1	1.3	2.4	6.8	2.2	0	4.7	K11262
ZDHHC13_17, HIP14	palmitoyltransferase ZDHHC13/17	0	2.4	8.8	0	0	4.5	K20032
PDE4	cAMP-specific phosphodiesterase 4	1.4	2.4	6.2	3	0	4	K13293

Chapter II

DHX8, PRP22	ATP-dependent RNA helicase DHX8/PRP22	1.3	3.8	6.7	0	0	5	K12818
DHX38, PRP16	pre-mRNA-splicing factor ATP-dependent RNA helicase DHX38/PRP16	0	4.1	6.9	0	0	4.2	K12815
WAXY	granule-bound starch synthase	0	4.5	8	1.6	0	1.1	K13679
LSC1	succinyl-CoA synthetase alpha subunit	2.4	2.9	3.4	6.4	0.7	1.9	K01899
FPGS	folypolyglutamate synthase	0	6.1	6.3	0	0	2.7	K01930
REV3L, POLZ	DNA polymerase zeta	0	4.5	7.7	0	0	2.9	K02350
PIKFYVE, FAB1	1-phosphatidylinositol-3-phosphate 5-kinase	0	4.8	6.7	0	0	3.4	K00921
CPA2	carboxypeptidase A2	3.2	3.8	8.9	0	0.1	2	K01298
DDX47, RRP3	ATP-dependent RNA helicase DDX47/RRP3	0	3.9	5.1	0	0.8	4.8	K14777
JOSD	josephin	0	0.8	4.6	6.9	1	1.3	K15235
ENTPD2	adenosinetriphosphatase	0	4.6	6.6	0	0	3.3	K01509
DDX5, DBP2	ATP-dependent RNA helicase DDX5/DBP2	0	2.9	4.4	3	1.4	2.8	K12823
TOP2	DNA topoisomerase II	0	2.1	4.4	5.3	0	2.6	K03164
UBR4, ZUBR1	E3 ubiquitin-protein ligase UBR4	0	3.3	6.8	1.6	0.1	2.5	K10691
IL4I1	L-amino-acid oxidase	0	1.2	1.6	11.1	0	0.4	K03334
SNF1	carbon catabolite-derepressing protein kinase	0	5.1	6.1	0	0	3.1	K12761
TNNI3K	serine/threonine-protein kinase TNNI3K	0	0.3	1.4	12.1	0	0.3	K17535
mgfA, mgfB	P-type Mg2+ transporter	0	0.1	6	0	3.3	4.3	K01531
XRN2, RAT1	5'-3' exoribonuclease 2	0	2.8	5.2	2.9	0	2.7	K12619
CDC15	cell division control protein CDC15	0.9	4.5	5.9	0.8	0	2.3	K06683
MAP2K1, MEK1	mitogen-activated protein kinase kinase 1	0	0.9	5.8	0	0	6.8	K04368
folM	dihydromonapterin reductase / dihydrofolate reductase	0	0.4	5.9	2.5	0	4.6	K13938
LTA4H	leukotriene-A4 hydrolase	0	4.6	6.5	0	0	2.3	K01254
HUWE1, MULE, ARF-BP1	E3 ubiquitin-protein ligase HUWE1	0	3.4	5.9	0	0	4	K10592
LIG3	DNA ligase 3	1	4.3	5	1.2	0.8	2.1	K10776
ATM, TEL1	serine-protein kinase ATM	0	0.3	5.9	0	0	7.1	K04728
SMO2	plant 4alpha-monomethylsterol monooxygenase	0	0.2	7.3	0	0	5.8	K14424
GOT1	aspartate aminotransferase, cytoplasmic	0	4.4	4.6	0	0	4.2	K14454
POLQ	DNA polymerase theta	0	4.6	6.5	0	0	2.1	K02349
RIOX1, NO66	bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	0	3.9	6.8	0	0	2.5	K16914
PPIL4	peptidyl-prolyl cis-trans isomerase-like 4	0	4.3	6.3	0	0	2.2	K12735
ATP2A	P-type Ca2+ transporter type 2A	1.5	3.4	6.5	0	0.1	2.9	K05853
MDH1	malate dehydrogenase	2.8	3.7	5.8	1.2	0	2	K00025
dddL	dimethylpropiothetin dethiomethylase	0	0.3	4.6	1.2	3.1	3.5	K16953
ACSBG	long-chain-fatty-acid--CoA ligase ACSBG	0	1.5	4	3.8	0	3.3	K15013
SUR2	sphinganine C4-monooxygenase	0	0.2	7.2	0	0	5.2	K04713
WRN, RECQL2	werner syndrome ATP-dependent helicase	0	4.1	5.9	0	0	2.6	K10900
UGCG	ceramide glucosyltransferase	0	0.6	3.7	0	1.8	6.4	K00720
USP6_32	ubiquitin carboxyl-terminal hydrolase 6/32	0	1.5	5.1	1	0	4.9	K11837
NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	0	4.7	5	0	0	2.8	K03942
SMT1, ERG6	sterol 24-C-methyltransferase	0	2.1	4.9	0	2	3.5	K00559
SPAST	spastin	0	3.2	7.2	0	0	2	K13254
NMNAT	nicotinamide mononucleotide adenyltransferase	0	4	5.5	0	0	2.9	K06210
JMJD7	peptidyl-lysine (3S)-dioxygenase / protease	0	2.6	6.9	0	0	2.6	K19219
TRMT10, TRM10, RG9MTD	tRNA (guanine9-N1)-methyltransferase	0	2.7	6.9	0	0	2.5	K15445
PIGO	GPI ethanolamine phosphate transferase 3 subunit O	0	2.8	6.5	0	0	2.6	K05288
INPP5B_F	inositol polyphosphate 5-phosphatase INPP5B/F	0	3.2	5.7	0	0	2.9	K01099
DHX35	ATP-dependent RNA helicase DDX35	0.8	4.2	5.7	0	0	1.9	K13117
pqsC	2-heptyl-4(1H)-quinolone synthase subunit PqsC	0	0.3	7.3	0	0	4.1	K18002
SIRT6, SIR2L6	NAD+-dependent protein deacetylase sirtuin 6	0	3.1	5.3	0	0	3.2	K11416
ATP12A	non-gastric H+/K+-exchanging ATPase	0	3.1	5.8	0	0	2.7	K01544
ILVBL	acetolactate synthase-like protein	0	1.3	3.6	5.1	0	1.6	K11259
ATRX	transcriptional regulator ATRX	0.6	3.1	5.9	0	0	2.6	K10779
PSMB6	20S proteasome subunit beta 1	0	4.7	5.5	0	0	1.3	K02738
SHPK	sedoheptulokinase	0	1.8	3	0.7	1.3	4.7	K11214
ALG12	alpha-1,6-mannosyltransferase	0	4.2	5.1	0	0	2.1	K03847
E2.1.1.143	24-methylenesterol C-methyltransferase	0	1.4	6.2	0	0.7	3.1	K08242
PDE1	calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase	1.4	1.6	3.5	3	0	3.3	K13755
ZDHHC9_14_18	palmitoyltransferase ZDHHC9/14/18	0	2.6	6	0.9	0	1.7	K16675
PMPCA, MAS2	mitochondrial-processing peptidase subunit alpha	0	2.8	5.7	0	0	2.7	K01412
DDX17	ATP-dependent RNA helicase DDX17	0	2.9	3.9	3	0	1.4	K13178
ACHE	acetylcholinesterase	0	4	5	0	0	2.2	K01049
EIF4A3, FAL1	ATP-dependent RNA helicase	0	2	6	0	0	3.2	K13025
DHX36, RHAU	ATP-dependent RNA helicase DHX36	0	1.3	4.4	2.7	0	2.8	K14442
PIK3CA_B_D	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha/beta/delta	0	1.3	6.4	0	0.7	2.7	K00922
DGAT1	diacylglycerol O-acyltransferase 1	0	4.4	4.7	0	0	1.9	K11155
ALG11	alpha-1,2-mannosyltransferase	0	4.1	4.4	0	0	2.4	K03844
PKA	protein kinase A	0	1.2	5.1	0	0	4.6	K04345

PIIP5K, VIP	inositol-hexakisphosphate/diphosphoinositol-pentakisphosphate 1-kinase	0	0.3	2.9	2.8	0	4.9	K13024
ATP4A	H ⁺ /K ⁺ -exchanging ATPase subunit alpha	0	3.1	5.4	0	0.1	2.3	K01542
PDE8	high affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8	0	2.5	5.2	0.4	0.1	2.5	K18437
XYL4	xylan 1,4-beta-xylosidase	0	3.1	4.9	0	0	2.7	K15920
DET2	steroid 5-alpha-reductase	0	0.3	4.5	0	2.6	3.3	K09591
CNOT6, CCR4	CCR4-NOT transcription complex subunit 6	0	2.1	5.4	0	0	3.2	K12603
wcaH	colanic acid biosynthesis protein WcaH	0	4.6	5.4	0	0	0.6	K03207
RECQL	ATP-dependent DNA helicase Q1	0	3.8	5.2	0	0	1.7	K10899
MCM6	DNA replication licensing factor MCM6	0	2.7	5.8	0	0	2.1	K02542
SOAT	sterol O-acyltransferase	0	3.6	5	0	0	2	K00637
CAPN15	calpain-15	0	2.4	3.6	1.4	0	3.1	K08582
INO80, INOC1	DNA helicase INO80	0	3.4	5	0	0	2.2	K11665
UBE1L, UBA7	ubiquitin-activating enzyme E1-like	0	2.1	5	0	0.4	3.1	K10698
PRPF19, PRP19	pre-mRNA-processing factor 19	0	3	5.8	0	0	1.7	K10599
SHPRH	E3 ubiquitin-protein ligase SHPRH	0	2.3	2.7	4.4	0	1.2	K15710
PSMA7	20S proteasome subunit alpha 4	0	2.9	5.4	0	0.2	2	K02731
RAD54L, RAD54	DNA repair and recombination protein RAD54 and RAD54-likeprotein	0.6	1.9	5.7	0	0	2.8	K10875
UHMK1, KIS	serine/threonine-protein kinase Kist	0	3.4	4.7	0	0	2.3	K08877
PRCP	lysosomal Pro-X carboxypeptidase	0	3.1	4.6	0	0	2.6	K01285
SGPL1, DPL1	sphinganine-1-phosphate aldolase	0	3.2	5	0	0	2	K01634
UBE2A, UBC2, RAD6A	ubiquitin-conjugating enzyme E2 A	0	3.5	4.5	0	0	2.2	K10573
MOV10	helicase MOV-10	0	3.7	4.3	0	0	2.2	K18422
CPB1	carboxypeptidase B	1.4	2.3	6.4	0	0	1.5	K01291
CPA3	carboxypeptidase A3	1.4	2.3	6.4	0	0	1.5	K08780
CPA6	carboxypeptidase A6	1.4	2.3	6.4	0	0	1.5	K08782
NAA30, MAK3	N-alpha-acetyltransferase 30	0	0.7	6.1	0	0	3.4	K00670
CCRK	cell cycle related kinase	0	2.9	4.6	0	0	2.6	K08817
kdgD	5-dehydro-4-deoxyglucarate dehydratase	0	1.6	7	0	0.1	1.3	K01707
PRKX	protein kinase X	0	1.2	3.9	0	0	4.9	K19584
CDK2	cyclin-dependent kinase 2	1.6	2.3	5.5	0	0	2.2	K02206
ACACB	acetyl-CoA carboxylase / biotin carboxylase 2	1.3	1.4	3.3	2.2	0	3.1	K01946
ASCC3	activating signal cointegrator complex subunit 3	0	2	5.6	0	0.2	2.1	K18663
GSK3B	glycogen synthase kinase 3 beta	0	1.8	4.7	0	0	3.5	K03083
PDIA3, GRP58	protein disulfide-isomerase A3	0	3.2	4.1	0	0	2.7	K08056
RDR, RDRP	RNA-dependent RNA polymerase	0	3.2	4.5	0	0	2.2	K11699
E2.7.1.-	kinase	0	2.2	4.2	0	0	3.5	K00924
CAMK4	calcium/calmodulin-dependent protein kinase IV	0	3.3	4	0	0	2.5	K05869
ALDH7A1	aldehyde dehydrogenase family 7 member A1	1.5	3	3.7	0	0.8	2.4	K14085
LYS4	homoaconitate hydratase	0	3.1	4	0	1.1	1.5	K01705
KEX1	carboxypeptidase D	0	3.3	4.2	0	0	2.1	K01288
E6.5.1.3	RNA ligase	0	0.2	1.4	6.3	0	1.8	K14680
araA	L-arabinose isomerase	0.7	2.8	4.9	0	0	1.9	K01804
HERC4	E3 ubiquitin-protein ligase HERC4	0	1.7	4.5	1	0	2.4	K10615
CPA4	carboxypeptidase A4	1.4	2.6	5.6	0	0	1.4	K08637
WNK, PRKWNK	WNK lysine deficient protein kinase	0	2.8	4.4	0	0	2.3	K08867
POLB	DNA polymerase beta	0	1.5	3	1.6	0.9	2.4	K02330
DDX55, SPB4	ATP-dependent RNA helicase DDX55/SPB4	0	3.1	4.7	0	0	1.6	K14809
IRG1	aconitate decarboxylase	0	1.1	3.8	0	0.1	4.5	K17724
mapP	maltose 6'-phosphate phosphatase	0	0.8	1.3	4.6	0.8	1.8	K06896
PIF1	ATP-dependent DNA helicase PIF1	0	3.5	3.9	0	0	1.9	K15255
DHX37, DHR1	ATP-dependent RNA helicase DHX37/DHR1	0	1.7	2.6	3.2	0	1.8	K14780
agaA	N-acetylglucosamine-6-phosphate deacetylase	0	2.6	4	0.4	0	2.2	K02079
POLRMT, RPO41	DNA-directed RNA polymerase, mitochondrial	0	2.8	3.9	0	0	2.6	K10908
PARG	poly(ADP-ribose) glycohydrolase	0	3.4	4.2	0	0	1.7	K07759
MOGAT1, MGAT1	2-acylglycerol O-acyltransferase 1	0	3.3	4.3	0	0	1.2	K14458
USP4_11, UBP12	ubiquitin carboxyl-terminal hydrolase 4/11	0	2.1	4	0	0	2.8	K11835
NAGLU	alpha-N-acetylglucosaminidase	0	2.2	3.9	0	0.1	2.7	K01205
OXSR1, STK39	serine/threonine-protein kinase OSR1/STK39	0	2.8	4.1	0	0	1.9	K08835
dhaK	phosphoenolpyruvate--glycerone phosphotransferase subunit DhaK	1.6	2	2.9	0	1.1	2.8	K05878
ARIH1	ariadne-1	0	2.2	3.9	0	0	2.6	K11968
TDH	threonine 3-dehydrogenase	0	2.7	4	0	0	2	K15789
SIRT2, SIR2L2	NAD ⁺ -dependent protein deacetylase sirtuin 2	0	2.9	3.2	0	0	2.6	K11412
KCS	3-ketoacyl-CoA synthase	0	2.5	3.6	0	0	2.6	K15397
E3.5.1.52, NGLY1, PNG1	peptide-N4-(N-acetyl-beta-glucosaminyl)asparagineamidase	0	1.3	4	2.4	0	0.9	K01456
RIPK2	receptor-interacting serine/threonine-protein kinase 2	0	1.8	3.9	0	0	2.8	K08846
kdhL	6-hydroxypseudoxynicotine dehydrogenase subunit gamma	0	0.7	2.9	0	0	5	K19187
PSMA1	20S proteasome subunit alpha 6	0	2.2	4.1	0	0	2.2	K02725
HAO	(S)-2-hydroxy-acid oxidase	0	0.5	2.8	2.6	0	2.5	K11517
RBOH	respiratory burst oxidase	0	2	2.5	2.1	0	1.8	K13447
GPD1	glycerol-3-phosphate dehydrogenase (NAD ⁺)	0	2.7	3.7	0	0	1.9	K00006

Chapter II

STK32, YANK	serine/threonine kinase 32	0	2.5	4	0	0	1.9	K08793
LSS, ERG7	lanosterol synthase	0.9	0.9	2.7	3.3	0.1	1.3	K01852
ASP5	aspartate aminotransferase, chloroplastic	0	2.8	4.5	0	0	1	K00811
GOT2	aspartate aminotransferase, mitochondrial	0	3.5	4.4	0	0	0.4	K14455
EXO1	exonuclease 1	0	2.3	3.6	0	0	2.4	K10746
CPB2	carboxypeptidase B2	1.4	1.5	5.6	0	0	1.1	K01300
CPA1	carboxypeptidase A1	1.4	1.5	5.6	0	0	1.1	K08779
PSMB9, LMP2	20S proteasome subunit beta 9	0	3.3	4.1	0	0	0.8	K02741
RPA1, POLR1A	DNA-directed RNA polymerase I subunit RPA1	0	1	2.5	1.9	0	2.7	K02999
dhaL	phosphoenolpyruvate---glycerone phosphotransferase subunit DhaL	0	3.4	3.4	0	0.4	0.9	K05879
TRIP12	E3 ubiquitin-protein ligase TRIP12	0	2.5	4.3	0	0	1.3	K10590
CLA4	serine/threonine-protein kinase CLA4	0	2.3	4.2	0	0.1	1.6	K19833
citF	citrate lyase subunit alpha / citrate CoA-transferase	0	1.2	6.4	0	0	0.5	K01643
lucI	renilla-luciferin 2-monoxygenase	0	0.2	5.4	0	0	2.6	K18053
ALKB8, TRM9	alkylated DNA repair protein alkB homolog 8	0	1.5	2.7	2.5	0	1.4	K10770
PLMT	phosphatidyl-N-methylethanolamine N-methyltransferase	0	2.5	4.5	0	0	1.1	K00550
HERC3	E3 ubiquitin-protein ligase HERC3	0	0.4	3.8	1	0.1	2.7	K10614
NAAA	N-acyl ethanolamine-hydrolysing acid amidase	0	2.5	3.4	0	0	2.2	K13720
MARK	MAP/microtubule affinity-regulating kinase	0	1	5.4	0	0.1	1.5	K08798
PIGA, GPI3	phosphatidylinositol N-acetylglucosaminyltransferase subunitA	0	1.8	4.1	0	0	2	K03857
RPC2, POLR3B	DNA-directed RNA polymerase III subunit RPC2	0	2.1	3.3	0	0	2.6	K03021
SEN8, NEDP1, DEN1	sentrin-specific protease 8	0	2.5	4	0	0	1.4	K08597
RIA1	ribosome assembly protein 1	0	1.4	3.5	0	0	2.9	K14536
POLL	DNA polymerase lambda	0	1.5	2.7	1.6	0	1.9	K03512
SIRT7, SIRT2L7	NAD+-dependent protein deacetylase sirtuin 7	0	1.8	3.4	0	0	2.6	K11417
LYPLA2	lysophospholipase II	0	3	3.4	0	0	1.3	K06130
MAP3K7, TAK1	mitogen-activated protein kinase kinase kinase 7	0	1.3	4.9	0	0	1.5	K04427
SRCAP	helicase SRCAP	2.4	2.7	3.6	0	0	1.3	K11661
ZAK, MLTK	sterile alpha motif and leucine zipper containing kinase AZK	0	1.6	4.1	0	0	1.9	K04424
PIGM	GPI mannosyltransferase 1 subunit M	0	1.7	2.7	1.2	0	2	K05284
PFKFB3	6-phosphofructo-2-kinase / fructose-2,6-biphosphatase 3	0	2.5	3.7	0	0	1.5	K01103
UCHL3, YUH1	ubiquitin carboxyl-terminal hydrolase L3	1.5	2.2	2.9	0	0	2.4	K05609
RAD54L2	RAD54-like protein 2	0.6	1.2	4.3	0	0	2	K10876
PAK1	p21-activated kinase 1	0	2.1	4.1	0	0.1	1.2	K04409
APEX2	AP endonuclease 2	0	3.1	3.6	0	0	0.8	K10772
PDE11	dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11	0	2.8	3.2	0	0	1.5	K13298
PDE5	cGMP-specific 3',5'-cyclic phosphodiesterase	0	2.8	3.2	0	0	1.5	K13762
MAN2	alpha-mannosidase II	0	2.7	3.5	0	0	1.3	K01231
DDX11, CHL1, CTF1	chromosome transmission fidelity protein 1	0	1.6	2.8	0	0	3.1	K11273
TTL1	tubulin polyglutamylase TTL1	0	1.3	4.2	0	0	1.9	K16599
UBE3A, E6AP	ubiquitin-protein ligase E3 A	0	2.1	2.9	0	0	2.3	K10587
CTSS	cathepsin S	0	1.9	3	0	0	2.5	K01368
PNKP	bifunctional polynucleotide phosphatase/kinase	0	1.8	3.2	0	1.1	1.2	K08073
LRRK2	leucine-rich repeat kinase 2	0	0.2	5.6	0	0.7	0.8	K08844
PP1G	peptidyl-prolyl isomerase G (cyclophilin G)	0	0.6	2.8	2.4	0	1.5	K09566
PSMB1	20S proteasome subunit beta 6	0	2.6	3.9	0	0	0.7	K02732
MAN1	mannosyl-oligosaccharide alpha-1,2-mannosidase	0	1.8	3	0	0.1	2.3	K01230
CAPN10	calpain-10	0	0.5	2	4.3	0	0.4	K08579
kdul	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	0	1.6	2.4	0.5	1	1.6	K01815
HERC1	E3 ubiquitin-protein ligase HERC1	0	0.6	3.8	0	0	2.6	K10594
PAK2	p21-activated kinase 2	0	2.1	3.6	0	0.1	1.2	K04410
PAK3, MRX30	p21-activated kinase 3	0	2.1	3.6	0	0.1	1.2	K05733
PAK4	p21-activated kinase 4	0	2.1	3.6	0	0.1	1.2	K05734
PAK6	p21-activated kinase 6	0	2.1	3.6	0	0.1	1.2	K05735
PAK5, PAK7	p21-activated kinase 5	0	2.1	3.6	0	0.1	1.2	K05736
PAP	poly(A) polymerase	0	2.3	3.2	0	0	1.5	K14376
SDHB, SDH2	succinate dehydrogenase (ubiquinone) iron-sulfur subunit	0.6	1.2	2.1	0	0.6	3.1	K00235
KATNA1	katanin p60 ATPase-containing subunit A1	0	1.6	2.3	1.8	0	1.3	K07767
DDX54, DBP10	ATP-dependent RNA helicase DDX54/DBP10	0	1.5	2.8	0	0	2.6	K14808
OCH1	alpha 1,6-mannosyltransferase	0	2.6	3.4	0	0	0.9	K05528
HACE1	E3 ubiquitin-protein ligase HACE1	0	1.5	2.9	0	0	2.5	K12166
DDX51, DBP6	ATP-dependent RNA helicase DDX51/DBP6	0	1.5	2.9	0	0	2.4	K14807
DHX15, PRP43	pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15/PRP43	0	1.7	3.1	0	0	2	K12820
PTDSS2	phosphatidylserine synthase 2	0	1.4	4.1	0	0	1.2	K08730
E1.12.7.2	ferredoxin hydrogenase	1.7	1.9	2.7	0	0.2	2	K00532
GANAB	mannosyl-oligosaccharide alpha-1,3-glucosidase	1.8	2.2	3.4	0	0.2	0.9	K05546
UBE3C	ubiquitin-protein ligase E3 C	0	0.9	2.2	0	0	3.5	K10589

Chapter II

SIK3	serine/threonine-protein kinase SIK3	0	1	4.1	0	0	1.5	K19009
GCLC	glutamate-cysteine ligase catalytic subunit	0	1.1	4.9	0	0	0.5	K11204
PDIA5	protein disulfide-isomerase A5	0	1.6	3.8	0	0	1.1	K09583
MCM5, CDC46	DNA replication licensing factor MCM5	0	1.6	2.7	0	0	2.2	K02209
PI4KA	phosphatidylinositol 4-kinase A	0	2.4	2.4	0	0	1.6	K00888
USP5_13, UBP14	ubiquitin carboxyl-terminal hydrolase 5/13	0	1.3	3.5	0	0	1.6	K11836
DOHH	deoxyhypusine monooxygenase	0	1.8	2.1	0	0.8	1.6	K06072
bdhAB	butanol dehydrogenase	0	0.7	4.5	0	0	1.1	K00100
PIGN	GPI ethanolamine phosphate transferase 1	0	0.1	3.4	0.7	0	2.1	K05285
prfB	two-component system, OmpR family, sensor histidine kinase PrrB	0.7	1	2.2	1.5	0.8	0.9	K07655
TTL4	tubulin polyglutamylase TTL4	0	1.9	3.2	0	0	1.2	K16601
plc	1-phosphatidylinositol phosphodiesterase	0	1.4	3.8	0	0	1.1	K01771
CDK12_13	cyclin-dependent kinase 12/13	0	2.5	2.9	0	0	0.9	K08819
AK9	adenylate/nucleoside-diphosphate kinase	0	0.5	4.5	0	0	1.3	K18533
DUSP, MKP	dual specificity MAP kinase phosphatase	0	1.2	3.6	0	0	1.5	K04459
PRMT3	type I protein arginine methyltransferase	0	1.9	3.5	0	0	0.9	K11436
ADO	cysteamine dioxygenase	0.7	2.5	3	0	0	0.8	K10712
NOP2	25S rRNA (cytosine2870-C5)-methyltransferase	0	0.9	3.4	0	0	2	K14835
HRAD1, RAD17	cell cycle checkpoint protein	0	2.3	2.9	0	0	1	K02830
hphCD	3-benzylmalate isomerase	0.7	0.7	2.7	0	0	2.8	K17749
EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	0	2	3.4	0	0	0.8	K16194
DDX24, MAK5	ATP-dependent RNA helicase DDX24/MAK5	0	2.7	2.7	0	0	1	K14805
GLDH	L-galactono-1,4-lactone dehydrogenase	0	2	2.8	0	0	1.5	K00225
PCSK5	proprotein convertase subtilisin/kexin type 5	0	2.5	2.8	0	0	0.8	K08654
LYPLA1	lysophospholipase I	0	1.6	3.2	0	0	1.3	K06128
CERS	ceramide synthetase	0	1.9	2.7	0	0	1.5	K04710
USP48	ubiquitin carboxyl-terminal hydrolase 48	0	0.2	2.8	0	0	3.1	K11858
GANC	neutral alpha-glucosidase C	1.8	2.2	2.9	0	0.2	0.9	K12317
GP63	leishmanolysin	0	1.1	3.7	0	0	1.4	K01404
ACAD8	isobutyryl-CoA dehydrogenase	0	1.3	3.9	0	0	0.9	K11538
ALG10	alpha-1,2-glucosyltransferase	0	1.8	2.9	0	0	1.3	K03850
RRP8	ribosomal RNA-processing protein 8	0	1.7	2.4	0	0	1.9	K14850
WHSC1, MMSSET, NSD2	histone-lysine N-methyltransferase NSD2	0	2.1	2.6	0	0	1.3	K11424
WHSC1L1, NSD3	histone-lysine N-methyltransferase NSD3	0	2.1	2.6	0	0	1.3	K11425
DDX18, HAS1	ATP-dependent RNA helicase DDX18/HAS1	0	1.8	3.2	0	0	0.9	K13179
CDO1	cysteine dioxygenase	0	1.3	3.8	0	0	0.8	K00456
ACP5	tartrate-resistant acid phosphatase type 5	0	1.7	2.7	0	0	1.5	K14379
CSNK1D	casein kinase 1, delta	0	1.7	1.9	0	0	2.3	K08959
CSNK1E	casein kinase 1, epsilon	0	1.7	1.9	0	0	2.3	K08960
RABGGTA	geranylgeranyl transferase type-2 subunit alpha	0	1.8	2.8	0	0	1.3	K14050
POLA1	DNA polymerase alpha subunit A	0	0.9	3.6	0	0	1.4	K02320
PPP5C	serine/threonine-protein phosphatase 5	0	0.4	3.4	0	0	1.9	K04460
CDK4	cyclin-dependent kinase 4	0	1.9	3	0	0	0.9	K02089
CDK6	cyclin-dependent kinase 6	0	1.9	3	0	0	0.9	K02091
EP300, CREBBP, KAT3	E1A/CREB-binding protein	0	0.8	2.4	0	0	2.6	K04498
XRN1, SEP1, KEM1	5'-3' exoribonuclease 1	0	0.3	2.4	1.2	0.1	1.7	K12618
MYLK	myosin-light-chain kinase	1	1.6	2.4	0	0.1	1.6	K00907
RBBP6	E3 ubiquitin-protein ligase RBBP6	0	1	2.9	0	0	1.7	K10624
PPIL6	peptidyl-prolyl cis-trans isomerase-like 6	0	1.7	2	0	0	1.9	K12739
HIP2, UBC1	ubiquitin-conjugating enzyme (huntingtin interacting protein2)	0	2.3	2.4	0	0	0.8	K04649
PPWD1	peptidylprolyl isomerase domain and WD repeat-containing protein 1	0	2.2	2.9	0	0	0.4	K12736
GALC	galactosylceramidase	0	0.5	2.9	0	0	2.1	K01202
FAHD1	acylpyruvate hydrolase	0	1.8	2.3	0	0	1.4	K01557
RNF144	E3 ubiquitin-protein ligase RNF144	0	1.6	2.3	0	0	1.7	K11975
PGM3	phosphoacetylglucosamine mutase	0	0.1	1.1	2.7	0	1.5	K01836
NOP1, FBL	rRNA 2'-O-methyltransferase fibrillarin	0	1.1	3.5	0	0	0.9	K14563
DUS2	tRNA-dihydrouridine synthase 2	0	0.9	2.8	0	0	1.8	K05543
pehX	exo-poly-alpha-galacturonosidase	0	2.2	2.5	0	0	0.7	K18650
QTRTD1	queuine tRNA-ribosyltransferase subunit QTRTD1	0	1.7	2.6	0	0	1.1	K15407
cmtD, dhhB	HCOMODA/2-hydroxy-3-carboxy-muconic semialdehyde decarboxylase	0	1.6	2	0	0	1.8	K10622
CTS2	cathepsin X	0	1.7	2	0	0	1.7	K08568
RANBP2, NUP358	E3 SUMO-protein ligase RanBP2	0	1.7	2.5	0	0	1.2	K12172
MYCBP2, PAM	E3 ubiquitin-protein ligase MYCBP2	0	1.9	2.6	0	0	0.8	K10693
TRAF2	TNF receptor-associated factor 2	0	1.4	2.6	0	0	1.4	K03173
SIRT4, SIRT4L4	NAD+-dependent protein deacetylase sirtuin 4	0	1	1.7	0	0.8	1.8	K11414
CPS1	carbamoyl-phosphate synthase (ammonia)	0	2.2	2.3	0	0	0.8	K01948
KEX2	kexin	0	1.4	3	0.2	0	0.7	K01341
DDX27, DRS1	ATP-dependent RNA helicase DDX27	0	0.9	2	0	0	2.3	K13181
POR	NADPH-ferrihemoprotein reductase	0	1.2	2.8	0	0	1.3	K00327
TGS1	trimethylguanosine synthase	0	0.8	2.4	1.1	0	0.9	K14292

Chapter II

RNF38_44	E3 ubiquitin-protein ligase RNF38/44	0	2	2.1	0	0	1.2	K19041
EP400	E1A-binding protein p400	1.6	1.6	2.3	0	0	1.3	K11320
MYST1, MOF, KAT8	histone acetyltransferase MYST1	0	1.6	2.4	0	0	1.2	K11308
mal	methylaspartate ammonia-lyase	0	1.2	2.2	0	0	1.7	K04835
UBE1L2, UBA6	ubiquitin-activating enzyme E1-like protein 2	0	1	3	0	0.5	0.6	K10699
cobR	cob(II)yrinic acid a,c-diamide reductase	0	0.8	3.3	0	0	1	K13786
RET	proto-oncogene tyrosine-protein kinase Ret	0	1.5	2.7	0	0	0.9	K05126
TOR	tyrosine-protein kinase receptor torso	0	1.5	2.7	0	0	0.9	K12378
AAK	AP2-associated kinase	0	0.9	2.7	0	0	1.4	K08853
COQ2	4-hydroxybenzoate polyprenyltransferase	0	0.2	2.9	1	0	0.9	K06125
COQ5	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	0	1.3	3	0	0	0.6	K06127
SGMS	shingomyelin synthase	0	1.4	3	0	0	0.6	K04714
AURKX	aurora kinase, other	0	1	2.8	0	0.1	1	K08850
TTL5, TTL10	tubulin polyglutamylase TTL5	0	0.4	3.2	0	0	1.3	K16602
F13A1	coagulation factor XIII A1 polypeptide	0	1.8	2.4	0	0	0.8	K03917
hndD	NADP-reducing hydrogenase subunit HndD	0	1.9	2.3	0	0.1	0.6	K18332
PPIH, CYPH	peptidyl-prolyl isomerase H (cyclophilin H)	0	1.3	3	0	0	0.6	K09567
ISN1	IMP and pyridine-specific 5'-nucleotidase	0	0.5	1.2	1.2	0.6	1.4	K18550
USP36_42	ubiquitin carboxyl-terminal hydrolase 36/42	0	1	2.7	0	0	1.2	K11855
hexPS, COQ1	hexaprenyl-diphosphate synthase	0	1.3	2.5	0	0	1	K05355
PDSS1	decaprenyl-diphosphate synthase subunit 1	0	1.3	2.5	0	0	1	K12504
PDSS2	decaprenyl-diphosphate synthase subunit 2	0	1.3	2.5	0	0	1	K12505
CHEK1	serine/threonine-protein kinase CHEK1	0	1.2	2.7	0	0	1	K02216
sucD	succinate-semialdehyde dehydrogenase	0	1.1	1.2	0	0	2.5	K18119
DDX60	ATP-dependent RNA helicase DDX60	0	0.5	2.3	0.6	0	1.4	K20103
PFKFB4	6-phosphofructo-2-kinase / fructose-2,6-biphosphatase 4	0	0.1	2.9	0	0	1.8	K19030
HDAC6	histone deacetylase 6	0	0.9	1.5	1.6	0	0.9	K11407
BNA3	kynurenine aminotransferase	0	0.9	3.3	0	0	0.6	K14264
OTUD5, DUBA	OTU domain-containing protein 5	0	1.7	2.3	0	0	0.8	K12655
LPIN	phosphatidate phosphatase LPIN	0	1.6	2	0	0	1.2	K15728
CAPN7	calpain-7	0	1.8	2.3	0	0	0.6	K08576
NR	nitrate reductase (NAD(P)H)	0.5	1.8	1.8	0	0	1.1	K10534
ERG4	Delta24(24(1))-sterol reductase	0	0.2	0.3	3.7	0	0.5	K00223
KLK4, PRSS17	kallikrein 4	0	0.4	0.5	3.6	0	0.2	K08666
rbtK	D-ribulokinase	0	0.1	1.4	1	0	2.2	K00875
CDC25B	M-phase inducer phosphatase 2	0	2.1	2.3	0	0	0.3	K05866
CDC25C	M-phase inducer phosphatase 3	0	2.1	2.3	0	0	0.3	K05867
CDC25A	M-phase inducer phosphatase 1	0	2.1	2.3	0	0	0.3	K06645
STG	M-phase inducer phosphatase	0	2.1	2.3	0	0	0.3	K16723
CTSL	cathepsin L	0	0.9	1.9	0	0	1.8	K01365
K18613	3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-decarboxylase	0	1.6	1.7	0	0	1.4	K18613
ZDHHC2_15_20	palmitoyltransferase ZDHHC2/15/20	0	1.6	2.3	0	0	0.7	K20028
USP10, UBP3	ubiquitin carboxyl-terminal hydrolase 10	0	1.3	2.8	0	0	0.5	K11841
IMP1	mitochondrial inner membrane protease subunit 1	0	1.1	2.4	0	0	1.2	K09647
SPS1	sporulation-specific protein 1	0	1.7	2	0	0	0.9	K12771
PPIL2, CYC4, CHP60	peptidyl-prolyl cis-trans isomerase-like 2	0	1.2	1.9	0	0	1.5	K10598
RNF31, HOIP	E3 ubiquitin-protein ligase RNF31	0	1.8	2	0	0	0.7	K11974
USP7, UBP15	ubiquitin carboxyl-terminal hydrolase 7	0	0.7	2.9	0	0	1	K11838
DHRX	dehydrogenase/reductase SDR family member X	0	1.9	2	0	0	0.6	K11170
DDX46, PRP5	ATP-dependent RNA helicase DDX46/PRP5	0	1.3	2.3	0	0	0.9	K12811
TUT	terminal uridylyltransferase	0	1.1	2.3	0	0	1.1	K13291
MTR2, MT48	cap2 methyltransferase	0	0.9	2.7	0	0	0.8	K18776
GAK	cyclin G-associated kinase	0	0.9	2.3	0	0	1.2	K08855
BRAP	BRCA1-associated protein	0	1.4	1.9	0	0	1	K10632
NSUN2, TRM4	tRNA (cytosine34-C5)-methyltransferase	0	0.4	1.9	0	0	2.1	K15335
AOAH	acyloxyacyl hydrolase	0	1.2	2	0	0	1.2	K01065
csxA	exo-1,4-beta-D-glucosaminidase	0	1.2	2.2	0	0	0.9	K15855
DOLPP1	dolichyldiphosphatase	0	1.6	2.1	0	0	0.7	K07252
EZH2	histone-lysine N-methyltransferase EZH2	0	1.4	2.2	0	0	0.7	K11430
RHBDL1_2_3	rhomboid-related protein 1/2/3	0	1.2	1.9	0	0	1.2	K02857
APE3	aminopeptidase Y	0	0.1	1.8	0	0.7	1.6	K01264
STH1_SNF2	ATP-dependent helicase STH1/SNF2	0	0.2	2.2	0	0	1.8	K11786
RIMKLB, NAAGS-I	beta-citrylglutamate/N-acetylaspartylglutamate synthase	0	0.9	2.3	0	0	1.1	K18310
RIMKLA, NAAGS-II	N-acetylaspartylglutamate/N-acetylaspartylglutamylglutamate synthase	0	0.9	2.3	0	0	1.1	K18311
RIB2, PUS8	tRNA pseudouridine32 synthase / 2,5-diamino-6-(5-phospho-D-ribitylamino)-pyrimidin-4(3H)-one deaminase	0	1.3	2.2	0	0	0.8	K14655
PRUNE, PPX1	exopolyphosphatase	0	1.5	2.2	0	0	0.5	K01514
METTL3_14	mRNA m6A methyltransferase	0	1.5	2	0	0	0.7	K05925
CCBL	kynurenine---oxoglutarate transaminase / cysteine-S-conjugate beta-lyase / glutamine---phenylpyruvate transaminase	0	0.4	3.2	0	0.1	0.5	K00816

ATPeV1A, ATP6A	V-type H ⁺ -transporting ATPase subunit A	0	1.4	1.6	0	0	1.1	K02145
RPP1, RPP30	ribonuclease P/MRP protein subunit RPP1	0	1	2	0	0	1.1	K03539
ADRBK, GRK	beta-adrenergic-receptor kinase	0	1	1.7	0	0	1.3	K00910
algG	mannuronan 5-epimerase	0	0.7	2.1	0	0	1.2	K01795
LPCAT1_2	lysophosphatidylcholine acyltransferase / lyso-PAF acetyltransferase	0	1	1.9	0	0	1.1	K13510
THEX1, ERI1	3'-5' exoribonuclease 1	0	0.6	1.2	0	0.2	2	K18416
TAF1	transcription initiation factor TFIID subunit 1	0	0.8	2	0	0	1.3	K03125
ETNK, EKI	ethanolamine kinase	0	0.7	1.9	0	0	1.5	K00894
FHIT	bis(5'-adenosyl)-triphosphatase	0	1.4	1.6	0	0	1	K01522
DDX31, DBP7	ATP-dependent RNA helicase DDX31/DBP7	0	0.9	1.9	0	0	1.1	K14806
PIG2, SMP3	GPI mannosyltransferase 4	0	1.1	1.7	0	0	1.2	K08098
PCBC	isopenicillin-N synthase	0	1.4	1.7	0	0	0.8	K04126
PRMT7	type III protein arginine methyltransferase	0	0.8	1.9	0	0	1.2	K11438
act12, oxyB, tcmL, snoa2, aknC, mtmK	minimal PKS chain-length factor (CLF/KS beta)	0	0.3	2.7	0	0	0.9	K05552
whiEIV	minimal PKS chain-length factor (CLF/KS beta)	0	0.3	2.7	0	0	0.9	K14668
FTSJ1, TRM7	tRNA (cytidine32/guanosine34-2'-O)-methyltransferase	0	1.3	2.3	0	0	0.3	K14864
MCM9	DNA helicase MCM9	0	0.9	2	0	0	1	K10738
IsrG	(4S)-4-hydroxy-5-phosphonoxy-pentane-2,3-dione isomerase	0	0.3	1.9	0	0	1.7	K11530
PUS9	tRNA pseudouridine32 synthase	0	1.1	1.7	0	0	1	K15454
ENPP1_3, CD203	pyrophosphatase/phosphodiesterase family member 1/3	0	0.2	1.6	0	0	2.1	K01513
PTDSS1	phosphatidylserine synthase 1	0	0.6	2.5	0	0	0.8	K08729
MIB	E3 ubiquitin-protein ligase mind-bomb	0	0.2	1.5	1.1	0	1.1	K10645
PIK3C3, VPS34	phosphatidylinositol 3-kinase	0	0.2	1	0	0	2.6	K00914
SMG1	serine/threonine-protein kinase SMG1	0.1	1.4	1.8	0	0	0.6	K08873
IGHMBP2	ATP-dependent RNA/DNA helicase IGHMBP2	0	0.4	0.8	0.6	0	2	K19036
PIGB	GPI mannosyltransferase 3	0	0.4	2.4	0	0	1	K05286
CTU1, NCS6	cytoplasmic tRNA 2-thiolation protein 1	0	0.8	2.3	0	0	0.7	K14168
SCH9	serine/threonine protein kinase SCH9	0	0.6	2.2	0	0	1	K19800
PSMB2	20S proteasome subunit beta 4	0	1.1	2.5	0	0	0.3	K02734
STK10, LOK	serine/threonine kinase 10	0	0.7	2.5	0	0	0.6	K08837
UBE4B, UFD2	ubiquitin conjugation factor E4 B	0	1.3	1.7	0	0	0.7	K10597
TAD1, ADAT1	tRNA-specific adenosine deaminase 1	0	1.1	1.9	0	0	0.7	K15440
SPHK	sphingosine kinase	0	1.2	1.8	0	0	0.8	K04718
phdI	1-hydroxy-2-naphthoate dioxygenase	0	0.3	1.5	0	0	2	K11948
DPH7, RRT2	diphthine methyl ester acylhydrolase	0	1	1.8	0	0	0.9	K17868
E2.7.12.1	dual-specificity kinase	0	0.5	2.9	0	0	0.3	K08287
PTGS1, COX1	prostaglandin-endoperoxide synthase 1	0	1.1	2.1	0	0	0.5	K00509
DPH6	diphthine-ammonia ligase	0	1.1	1.9	0	0	0.7	K06927
PAPD5_7, TRF4	non-canonical poly(A) RNA polymerase PAPD5/7	0	0.5	0.9	0.9	0	1.4	K03514
BMT5	25S rRNA (uracil2634-N3)-methyltransferase	0	1.5	1.6	0	0	0.5	K19307
MTMR14	myotubularin-related protein 14	0	1.1	1.7	0	0	0.8	K18086
epsL	sugar transferase EpsL	0	0.8	1.8	0	0.1	0.9	K19428
ACS	1-aminocyclopropane-1-carboxylate synthase	0	0.9	1.8	0	0	0.9	K01762
ATL41	E3 ubiquitin-protein ligase ATL41	0	1.4	1.8	0	0	0.4	K19038
GSK3A	glycogen synthase kinase 3 alpha	0	0.6	1.8	0	0	1.2	K08822
MDS1, RIM11	serine/threonine-protein kinase MDS1/RIM11	0	0.6	1.8	0	0	1.2	K12766
EBM	mannosylglycoprotein endo-beta-mannosidase	0	1.2	1.8	0	0	0.6	K18577
RAD9A	cell cycle checkpoint control protein RAD9A	0	0.8	2.3	0	0	0.4	K10994
CHD1	chromodomain-helicase-DNA-binding protein 1	0	0.4	2.1	0	0	1.1	K11367
hydA	iron-hydrogenase subunit alpha	0	1.5	1.6	0	0.1	0.3	K17997
USP43	ubiquitin carboxyl-terminal hydrolase 43	0	1	1.7	0	0	0.8	K11856
TRM11, TRMT11	tRNA (guanine10-N2)-methyltransferase	0	0.6	1.9	0	0	1	K15430
NIM1	serine/threonine-protein kinase NIM1	0	1.3	1.7	0	0	0.5	K16310
GCS1	mannosyl-oligosaccharide glucosidase	0	0.9	1.8	0	0	0.7	K01228
RNF115_126	E3 ubiquitin-protein ligase RNF115/126	0	1.5	1.5	0	0	0.4	K11982
GLB1, ELNR1	beta-galactosidase	0	1	1.5	0	0	1	K12309
HECTD3	E3 ubiquitin-protein ligase HECTD3	0	1.2	1.7	0	0	0.6	K12233
RIPK4	receptor-interacting serine/threonine-protein kinase 4	0	1.5	1.5	0	0	0.5	K08848
SPPL3	signal peptide peptidase-like 3	0	0.4	2.3	0	0	0.7	K09598
MEKK1	mitogen-activated protein kinase kinase 1	0	0.9	2	0	0	0.5	K13414
HOC1	mannan polymerase II complex HOC1 subunit	0	1.1	1.9	0	0	0.5	K05534
PLA2G4, CPLA2	cytosolic phospholipase A2	0	1.1	1.6	0	0	0.7	K16342
mbtA	mycobactin salicyl-AMP ligase	0	0.1	1.4	0	0	1.9	K04787
PIK3R4, VPS15	phosphoinositide-3-kinase, regulatory subunit 4	0	0.8	1.8	0	0	0.8	K08333
PRKCQ	novel protein kinase C theta type	0	0.2	1.7	0	0	1.4	K18052
SGK3	serum/glucocorticoid-regulated kinase 3	0	0.5	2.4	0	0	0.4	K13304
CBR4	carbonyl reductase 4 / 3-oxoacyl-[acyl-carrier protein] reductase beta subunit	0	1.1	1.6	0	0	0.7	K11539
CHFR	E3 ubiquitin-protein ligase CHFR	0	1.3	1.7	0	0	0.3	K10644
DDX20, GEMIN3	ATP-dependent RNA helicase DDX20	0	0.9	1.7	0	0	0.7	K13131
ARIH2	ariadne-2	0	0.7	1.5	0	0	1.1	K11969

ADAM12	disintegrin and metalloproteinase domain-containing protein 12	0	0.8	1.8	0	0	0.8	K06835
KPC1, RNF123	Kip1 ubiquitination-promoting complex protein 1	0	1.4	1.4	0	0	0.5	K12169
PTC4	protein phosphatase PTC4	0	0.8	1.6	0	0	0.8	K19705
BUD23	18S rRNA (guanine1575-N7)-methyltransferase	0	0.9	1.8	0	0	0.5	K19306
P38	p38 MAP kinase	0	0.7	1.5	0	0	1	K04441
PSMB10, MECL1	20S proteasome subunit beta 10	0	0.6	1.8	0	0	0.9	K02733
PSMB7	20S proteasome subunit beta 2	0	0.6	1.8	0	0	0.9	K02739
PNCK	pregnancy upregulated non-ubiquitously expressed CaM kinase	0	0.6	1.9	0	0	0.7	K08795
TGM3	transglutaminase 3	0	1.1	1.4	0	0	0.7	K05620
DDX52, ROK1	ATP-dependent RNA helicase DDX52/ROK1	0	0.6	2.1	0	0	0.5	K14779
IYD, DEHAL1	iodotyrosine deiodinase	0	0.2	2.3	0	0	0.7	K17231
SAR1	GTP-binding protein SAR1	0	0.9	1.1	0	0	1.2	K07953
PTP4A	protein tyrosine phosphatase type IVA	0	0.5	1.6	0	0	1.1	K18041
SMPD1, ASM	sphingomyelin phosphodiesterase	0	1.3	1.6	0	0	0.3	K12350
DNM1_3	dynamins 1/3	0	1.1	1.2	0	0.3	0.6	K01528
DNM1L	dynamins 1-like protein	0	1.1	1.2	0	0.3	0.6	K17065
PTC7, PPTC7	protein phosphatase PTC7	0	1.3	1.3	0	0	0.6	K17508
IRAK1	interleukin-1 receptor-associated kinase 1	0	1.2	1.4	0	0	0.5	K04730
SIRT1, SIR2L1	NAD ⁺ -dependent protein deacetylase sirtuin 1	0	1.3	1.4	0	0	0.5	K11411
SMARCA3, HLTf	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A3	0	1	1.5	0	0	0.5	K15711
CYP6	cytochrome P450 family 6	0	0.8	1.3	0	0	1	K14999
MOV10L1	putative helicase MOV10L1	0	1.3	1.3	0	0	0.5	K13983
ARM1	RNA helicase arm1	0	1.3	1.3	0	0	0.5	K18432
STUB1, CHIP	STIP1 homology and U-box containing protein 1	0	1.1	1.3	0	0	0.7	K09561
NSD1	histone-lysine N-methyltransferase NSD1	0	0.9	1.5	0	0	0.7	K15588
UBE2N, BLU, UBC13	ubiquitin-conjugating enzyme E2 N	0	0.6	1.8	0	0	0.6	K10580
CDK7	cyclin-dependent kinase 7	0	0.3	2	0	0	0.8	K02202
DHX16	pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	0	0.4	1.1	0	0	1.6	K12813
CYP734A1, BAS1	PHYB activation tagged suppressor 1	0	0.9	1.3	0	0	0.8	K15639
DCXR	L-xylulose reductase	0	1	1.4	0	0	0.6	K03331
bpsA	N4-bis(aminopropyl)spermidine synthase	0	0.2	1.1	0	0.8	0.9	K07057
TTLL3_8	tubulin monoglycylase TTLL3/8	0	0.2	1.4	0	0	1.4	K16608
E3.1.1.14	chlorophyllase	0	0.8	1.2	0	0	0.9	K08099
XGD1	xylogalacturonan beta-1,3-xylosyltransferase	0	1.2	1.2	0	0	0.6	K18789
ACAA1	acetyl-CoA acyltransferase 1	0	1.2	1.6	0	0	0.1	K07513
PCYT2	ethanolamine-phosphate cytidylyltransferase	0	1.2	1.5	0	0	0.1	K00967
RPS6KA4, MSK2	ribosomal protein S6 kinase alpha-4	0	0.7	1.7	0	0	0.5	K16510
HIF1AN	hypoxia-inducible factor 1-alpha inhibitor (HIF hydroxylase)	0	0.4	1.7	0	0	0.8	K18055
DHRS13	dehydrogenase/reductase SDR family member 13	0	0.2	1.8	0	0	0.8	K11169
ABHD10	abhydrolase domain-containing protein 10	0	0.5	0.8	0	0	1.6	K13702
SMG6, EST1A	protein SMG6	0	0.5	1.5	0	0	0.9	K11124
EST1	telomere elongation protein	0	0.5	1.5	0	0	0.9	K11132
ADAM9	disintegrin and metalloproteinase domain-containing protein 9	0	0.8	1.5	0	0	0.5	K06834
REV1	DNA repair protein REV1	0	1	1.2	0	0	0.7	K03515
rcsD	two-component system, NarL family, sensor histidine kinase RcsD	0	0.6	1	0	0	1.2	K07676
TYRAAT	arogenate dehydrogenase (NADP ⁺), plant	0	0.7	1.6	0	0	0.5	K15227
C1GALT1	glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase	0	1.1	1.2	0	0	0.5	K00731
SRPK3, STK23	serine/threonine-protein kinase SRPK3	0	0.1	1.6	0	0	1	K08832
LOX1_5	linoleate 9S-lipoxygenase	0	0.2	0.6	1.2	0	0.8	K15718
LRRK1	leucine-rich repeat kinase 1	0	0.2	1.7	0	0	0.8	K08843
KTR6	mannosylphosphate transferase	0	1.1	1.4	0	0	0.2	K05537
KTR1_3	alpha 1,2-mannosyltransferase	0	1.1	1.4	0	0	0.2	K10967
SSH	protein phosphatase slingshot	0	0.6	1.7	0	0	0.5	K05766
SLK	STE20-like kinase	0	0.7	1.5	0	0	0.6	K08836
CHD2	chromodomain-helicase-DNA-binding protein 2	0	0.4	1.3	0	0	1	K20091
MAP3K3, MEKK3	mitogen-activated protein kinase kinase kinase 3	0	1.2	1.4	0	0	0.1	K04421
CRYM	thiomorpholine-carboxylate dehydrogenase	0	0.2	1.3	0	0	1.2	K18258
CNOT4, NOT4, MOT2	CCR4-NOT transcription complex subunit 4	0	0.7	1.3	0	0	0.8	K10643
MECR, NRBF1	mitochondrial enoyl-[acyl-carrier protein] reductase / trans-2-enoyl-CoA reductase	0	1	1.1	0	0	0.6	K07512
PHF8, JHDM1F	lysine-specific demethylase PHF8	0	0.9	1.4	0	0	0.4	K19415
PSMA5	20S proteasome subunit alpha 5	0	0.8	1.4	0	0	0.5	K02729
SKI2, SKIV2L	antiviral helicase SKI2	0	0.4	2	0	0	0.3	K12599
ZDHHC4, SWF1	palmitoyltransferase ZDHHC4	0	0.2	1	0	0	1.4	K20003
ABA3	molybdenum cofactor sulfurtransferase	0	0.4	0.7	0	0	1.5	K15631
DPC2	mRNA-decapping enzyme subunit 2	0	0.7	1.4	0	0	0.4	K12613
PPEF, PPP7C	serine/threonine-protein phosphatase with EF-hands	0	0.1	1.4	0	0	1.1	K13807

CDK10	cyclin-dependent kinase 10	0	0.9	1.3	0	0	0.4	K02449
MASTL, GW	serine/threonine-protein kinase greatwall	0	1.1	1.2	0	0	0.3	K16309
ANPRB, NPR2	atrial natriuretic peptide receptor B	0	0.2	0.7	0	0	1.6	K12324
HDAC3	histone deacetylase 3	0	0.3	1	0.9	0	0.4	K11404
HOS2	histone deacetylase HOS2	0	0.3	1	0.9	0	0.4	K11483
E2.7.1.105, PFK	6-phosphofructo-2-kinase	0	0.1	1.2	0	0	1.2	K00900
ADAM23	disintegrin and metalloproteinase domain-containing protein 23	0	0.9	1.3	0	0	0.3	K06837
PSMA6	20S proteasome subunit alpha 1	0	0.2	2	0	0	0.3	K02730
APLF	apataxin and PNK-like factor	0	0.4	1.4	0	0	0.6	K13295
ADPRHL2	poly(ADP-ribose) glycohydrolase ARH3	0	0.8	1.2	0	0	0.4	K11687
PSEN1, PS1	presenilin 1	0	0.3	1.2	0	0	0.9	K04505
CHD6	chromodomain-helicase-DNA-binding protein 6	0	0.3	1.5	0	0	0.5	K14436
CKX	cytokinin dehydrogenase	0	0.4	0.7	0	0	1.2	K00279
E2.1.3.1-1.35	methylmalonyl-CoA carboxyltransferase 1.35 subunit	0	0.5	1.7	0	0	0.2	K17490
DDX28	ATP-dependent RNA helicase DDX28	0	0.6	0.9	0	0	0.8	K20096
RECQL4	ATP-dependent DNA helicase Q4	0	0.8	0.9	0	0	0.6	K10730
STAMBP, AMSH	STAM-binding protein	0	0.6	1.3	0	0	0.4	K11866
POLH	DNA polymerase eta	0	0.1	1.8	0	0	0.3	K03509
CANT1	soluble calcium-activated nucleotidase 1	0	0.2	0.9	0	0	1	K12304
POL5, MYBBP1A	DNA polymerase phi	0	0.4	1.3	0	0	0.4	K02331
LPCAT4, AGPAT7	lysophospholipid acyltransferase	0	0.6	1	0	0	0.4	K13512
kdnB	3-deoxy-alpha-D-manno-octulosonate 8-oxidase	0	0.8	1.1	0	0	0.3	K19714
ENPEP, CD249	glutamyl aminopeptidase	0	0.4	0.9	0	0	0.8	K11141
SLH1	antiviral helicase SLH1	0	0.4	1.1	0	0	0.5	K18664
MDP1	magnesium-dependent phosphatase 1	0	0.1	1.4	0	0	0.5	K17619
cmcH	hydroxymethyl cephem carbamoyltransferase	0	0.1	0.9	0	0	0.9	K04128
E3.1.3.56	inositol-1,4,5-trisphosphate 5-phosphatase	0	0.6	1	0	0	0.4	K01106
SHIP1, INPP5D	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1	0	0.6	1	0	0	0.4	K03084
RRM2	ribonucleoside-diphosphate reductase subunit M2	0	0.2	1.1	0	0	0.6	K10808
DUSP12, YVH1	dual specificity phosphatase 12	0	0.6	0.9	0	0	0.3	K14819
NTAN1	protein N-terminal asparagine amidohydrolase	0	0.6	1	0	0	0.2	K14662
PDXP	pyridoxal phosphatase	0	0.4	0.6	0	0	0.8	K07758
MAN2B2	epididymis-specific alpha-mannosidase	0	0.4	0.6	0	0	0.8	K12312
AGL	glycogen debranching enzyme	0	0.1	1.5	0	0	0.2	K01196
DDX42, SF3B125	ATP-dependent RNA helicase DDX42	0	0.3	0.8	0	0	0.7	K12835
PPM1E, POPX1	protein phosphatase 1E	0	0.4	0.7	0	0	0.6	K17501
CPSF3L, INTS11	integrator complex subunit 11	0	0.3	1	0	0	0.4	K13148
USP2	ubiquitin carboxyl-terminal hydrolase 2	0	0.3	0.3	0	0	1	K11833
USP8, UBP5	ubiquitin carboxyl-terminal hydrolase 8	0	0.3	0.3	0	0	1	K11839
MLK4, KIAA1804	mitogen-activated protein kinase kinase kinase MLK4	0	0.3	0.6	0	0	0.7	K17534
epsF	glycosyltransferase EpsF	0	0.2	0.4	0	0	0.9	K19424
CTSE	cathepsin E	0	0.2	1	0	0	0.3	K01382
DBR1	lariat debranching enzyme	0	0.2	1	0	0	0.3	K18328
GPS	geranyl diphosphate synthase	0	0.2	0.7	0	0	0.5	K14066
PFAM1	M1-family aminopeptidase	0	0.4	0.5	0	0	0.5	K13725
MAPK7	mitogen-activated protein kinase 7	0	0.4	0.4	0	0	0.4	K04464
ZEP, ABA1	zeaxanthin epoxidase	0	0.2	0.6	0	0	0.4	K09838
PAXM, ATMM, LTMM	FAD dependent monooxygenase	0	0.2	0.6	0	0	0.4	K18386
RNF19A	E3 ubiquitin-protein ligase RNF19A	0	0.2	0.4	0	0	0.6	K11972
RNF19B	E3 ubiquitin-protein ligase RNF19B	0	0.2	0.4	0	0	0.6	K11973
ART1, CD296	ADP-ribosyltransferase 1	0	0.1	0.6	0	0	0.4	K06716
ART5	ADP-ribosyltransferase 5	0	0.1	0.6	0	0	0.4	K19977
E3.4.14.-	dipeptidyl aminopeptidase	0	0.1	0.6	0	0	0.4	K01282
CROT	carnitine O-octanoyltransferase	0	0.3	0.3	0	0	0.2	K05940
SRPK2	serine/threonine-protein kinase SRPK2	0	0.1	0.4	0	0	0.3	K08831
HPSE2	heparanase 2	0	0.2	0.4	0	0	0.1	K07965

Table S5 – RPKM values for enriched genes encoding for oxidoreductases. The genes are ordered by their mean RPKM values, from most abundant on top to least abundant.

Gene	Enzyme	A0	A1	A2	B1	C1	C2	KEGG KOs
CYP51	sterol 14alpha-demethylase	21.6	479.2	810	168.8	197.1	266.3	K05917
cypD_E, CYP102A2_3	cytochrome P450 / NADPH-cytochrome P450 reductase	122.9	465.4	812.6	128.8	179.6	277.8	K14338
alkB1_2, alkM	alkane 1-monooxygenase	48.1	185	371.8	285.9	114.7	218.2	K00496
E1.14.14.1	unspecific monooxygenase	52.5	238.7	430.3	137	112.7	224	K00493
ubiH	2-octaprenyl-6-methoxyphenol hydroxylase	102.6	113.8	156.1	255.6	131.5	223.8	K03185
proC	pyrroline-5-carboxylate reductase	63.8	108.1	145.3	215.4	178	187.9	K00286
gpsA	glycerol-3-phosphate dehydrogenase (NAD(P)+)	112.6	113.4	140.1	229.5	108.5	174.3	K00057
mhpA	3-(3-hydroxy-phenyl)propionate hydroxylase	71.5	93.4	155.3	201.5	110.7	195.4	K05712
choD	cholesterol oxidase	14.4	34.2	153.9	181.9	180.5	204.1	K03333
acpD, azoR	FMN-dependent NADH-azoreductase	90.3	108.2	146.8	146.1	116.9	224.8	K01118
kstD	3-oxosteroid 1-dehydrogenase	77.2	121.2	242	51.5	83.8	201.2	K05898
PTR1	pteridine reductase	59.1	71.4	112.1	131.5	95.5	187.1	K03793
SCD, desC	stearoyl-CoA desaturase (Delta-9 desaturase)	84.4	109.8	131.6	106.5	109.7	114.8	K00507
yfeX	porphyrinogen peroxidase	5	94.8	166.8	82.9	46.8	156.2	K07223
hmp, YHB1	nitric oxide dioxygenase	24.4	89.3	101.9	126.9	86.3	126.7	K05916
dadA	D-amino-acid dehydrogenase	42.9	71.2	88.7	146	49.1	170.5	K00285
budC	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	70.6	97.3	124.8	99	55.2	144.3	K18009
crtR	beta-carotene hydroxylase	19.1	72.4	95.7	185.4	48.8	114	K02294
yiaY	alcohol dehydrogenase	14.4	62.6	94.5	123.4	91	105.8	K13954
E1.3.99.16	isoquinoline 1-oxidoreductase	68.4	96.2	129	121	33.5	90.9	K00256
pcpC	tetrachlorohydroquinone reductive dehalogenase	40.4	100.7	106.9	39.9	49.5	157.7	K15241
ydfG	3-hydroxy acid dehydrogenase / malonic semialdehyde reductase	9.1	50.9	85.2	166.8	33.3	79.3	K16066
sdh	serine 3-dehydrogenase (NADP+)	5.8	50.3	90.4	142.1	30.8	98.6	K05886
isfD	sulfoacetaldehyde reductase	8.5	49.7	78.1	142.1	27.5	77.5	K15373
epd	D-erythrose 4-phosphate dehydrogenase	15.5	31.9	58.3	93.6	60.7	129.4	K03472
ahpF	alkyl hydroperoxide reductase subunit F	25.4	36.3	94.9	99.6	52.6	79.7	K03387
rubB, alkT	rubredoxin---NAD+ reductase	14	56.1	130	47.9	40	84	K05297
fre, ubiB	aquacobalamin reductase / NAD(P)H-flavin reductase	9.6	51.8	87	64.8	69	84.7	K05368
rbdD	ribitol 2-dehydrogenase	46.6	47	84.7	80.7	30.7	100	K00039
SRD5A1	3-oxo-5-alpha-steroid 4-dehydrogenase 1	24.3	44.7	102.1	75.1	31.7	81	K12343
norW	nitric oxide reductase FIRD-NAD(+) reductase	0.5	55.6	128.4	58.3	3.5	84.2	K12265
E1.1.1.65	pyridoxine 4-dehydrogenase	7.7	33.4	80	80.9	15.3	111	K05275
PRDX3	peroxiredoxin 3	6.7	39.2	39.8	73.6	44.5	119.7	K20011
hsaA	3-hydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione monooxygenase	18.6	61.6	128.7	29.6	13.5	79.4	K16047
hoxU	[NiFe] hydrogenase diaphorase moiety small subunit	2.4	27.1	109.3	32.3	3.6	123.9	K18006
dprE2	decaprenylphospho-beta-D-erythro-pentofuranosid-2-ulose 2-reductase	5.6	50.8	87.3	21.9	49	85.1	K16652
yihU	4-hydroxybutyrate dehydrogenase / sulfolactaldehyde 3-reductase	7.7	48	95	54	10	81.7	K08318
SDR16C5	all-trans-retinol dehydrogenase (NAD+)	0	36.4	72.8	80.1	13.9	76.5	K15734
dmpP, poxF, tomA5	phenol/toluene 2-monooxygenase (NADH) P5/A5	10.1	22.2	40.8	59.1	70.3	84	K16246
nifD	nitrogenase molybdenum-iron protein alpha chain	3.7	12.6	66.1	48.4	5.7	141.6	K02586
por	protochlorophyllide reductase	8.1	36.6	41.5	77.4	41.2	73.9	K00218
prmb	propane monooxygenase reductase component	10.1	17.9	38.6	59.1	68.9	84	K18225
tpx	thiol peroxidase, atypical 2-Cys peroxiredoxin	6	28.1	43.1	39.8	71.3	84.8	K11065
cymAb	p-cymene methyl-monooxygenase electron transfer component	9.6	17.9	37.7	59.1	68	83	K18293
por, nifJ	pyruvate-ferredoxin/ferredoxin oxidoreductase	28.7	33.3	56.8	65.3	19.8	87.4	K03737
tphA1	terephthalate 1,2-dioxygenase reductase component	9.6	15	37.7	59.1	66.2	83	K18077
E1.1.1.387	L-serine 3-dehydrogenase (NAD+)	4.1	37.3	88.6	49	6.5	78.7	K19711
bphJ, xylQ, nahO, tesF	acetaldehyde/propanal dehydrogenase	20.4	42.2	82.5	50.6	8.5	72.5	K18366
hsaC	3,4-dihydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione 4,5-dioxygenase	6.6	42	73.4	59.6	15.2	59.5	K16049
nifK	nitrogenase molybdenum-iron protein beta chain	0.3	11.4	62.4	35.3	4.7	133.7	K02591
adh1	alcohol dehydrogenase	5.2	9.7	32.5	73.8	57.3	73.1	K19954
RETSAT	all-trans-retinol 13,14-reductase	8.6	44.6	47	33.7	44	76.3	K09516

Chapter II

hyaB, hybC	hydrogenase large subunit	0.5	14.8	32.2	78.5	49.3	70.5	K06281
hoxF	[NiFe] hydrogenase diaphorase moiety large subunit	11.9	41.7	81.7	36.7	8.9	75.4	K18005
PTGS2, COX2	prostaglandin-endoperoxide synthase 2	4.5	60.1	91.4	46.2	2.5	37.6	K11987
hoxY	NAD-reducing hydrogenase small subunit	2.8	24.4	98	26.7	1.8	84.5	K18007
acdH	short/branched chain acyl-CoA dehydrogenase	9.6	44.1	61.4	72.8	14.7	42.2	K11410
iucD	lysine N6-hydroxylase	0	7.8	36.3	76.5	46.5	64.3	K03897
spnN, oleW	dTDP-3,4-didehydro-2,6-dideoxy-alpha-D-glucose 3-reductase	51.5	66.8	79.1	19.3	15.7	48.3	K13327
actVA5	two-component flavin-dependent monooxygenase	10.9	31.2	77.2	26.5	7.6	73.8	K14630
sad	succinate-semialdehyde dehydrogenase	15.3	37.9	78	16.9	5.3	75.8	K08324
bphC	biphenyl-2,3-diol 1,2-dioxygenase	6.6	40.1	72.8	24.7	15.2	59.5	K00462
PXDN, VPO1	peroxidase	7.1	15.1	34.7	47.3	50.3	60	K19511
tsdA	thiosulfate dehydrogenase	23.1	26.1	42.4	49.5	10.2	72.4	K19713
epmC	elongation factor P hydroxylase	0	7.9	41.9	58.9	8.7	77.2	K09906
todE	3-methylcatechol 2,3-dioxygenase	2.8	30	72	22.8	3.8	59	K16270
dfx	superoxide reductase	0	7.3	38	16.5	39	82.3	K05919
K14330	fatty aldehyde-generating acyl-ACP reductase	1.1	6.8	45.4	20.7	34.9	74.8	K14330
rutF	flavin reductase	0	58.9	65.8	14.7	9	32.8	K09024
E1.12.7.2S	ferredoxin hydrogenase small subunit	0	18.9	29.8	33.5	16.4	79.9	K00534
gfo	glucose-fructose oxidoreductase	6.8	50.5	68	32.5	9.8	16	K00118
DVR	divinyl chlorophyllide a 8-vinyl-reductase	0	24.7	76.3	22.7	0.1	51.6	K19073
caiA	crotonobetainyl-CoA dehydrogenase	0	29.6	52.8	14.9	0.3	38.2	K08297
RDH11	retinol dehydrogenase 11	0	8.2	30.6	23.1	0.9	61.4	K11152
dusC	tRNA-dihydrouridine synthase C	5.2	42.9	58.4	6.1	5.6	6.7	K05541
L2HGDH	2-hydroxyglutarate dehydrogenase	9.1	15.3	15.7	30.8	16.3	31.9	K00109
wbpB	UDP-N-acetyl-2-amino-2-deoxyglucuronate dehydrogenase	0.5	26.7	51.6	13.2	7	9.6	K13016
pdxB	erythronate-4-phosphate dehydrogenase	3.1	28.9	53.4	4	10.2	11.4	K03473
crtP	diaplycopen oxygenase	1.8	4.7	12.2	43.8	16.6	25.7	K10210
soxG	sarcosine oxidase, subunit gamma	8.5	11.7	21.1	44	11.2	12.7	K00305
tauX	taurine dehydrogenase small subunit	8.4	20.2	56	0	1.4	11.3	K07255
NVD, DAF36	cholesterol 7-desaturase	0	30.7	48	3.1	1.4	2.2	K14938
mvhA, vhuA, vhcA	F420-non-reducing hydrogenase large subunit	0.4	17.4	44.9	16.6	1.2	4.2	K14126
andAd	anthranilate 1,2-dioxygenase small subunit	1.1	21.2	22.7	18.5	2.6	11.8	K16320
iaaM	tryptophan 2-monooxygenase	4.4	18.3	42	3.3	0.4	2	K00466
K10253	DOPA 4,5-dioxygenase	10.1	18.3	25.7	1.5	5.6	7.1	K10253
dkgA	2,5-diketo-D-gluconate reductase A	1.3	1.9	6	35.8	1.5	4.4	K06221
RRM1	ribonucleoside-diphosphate reductase subunit M1	7.4	15.9	16.9	0	0	10	K10807
NXN	nucleoredoxin	3.6	10.7	16.2	1	0	5.4	K17609
nagH	salicylate 5-hydroxylase small subunit	0	4	4.2	18.5	0	3.2	K18243
XR	D-xylose reductase	2.9	5.7	5.8	4.6	2.8	8.9	K17743
CMAH	CMP-N-acetylneuraminate monooxygenase	0	2.3	3.2	18.8	0.7	1.1	K08080
pvdA, SIDA	L-ornithine N5-monooxygenase	0	0.6	2.1	22.5	0	0.1	K10531
tphA3	terephthalate 1,2-dioxygenase oxygenase component beta subunit	0	8.4	10.2	0	0	4.1	K18075
MIOX	inositol oxygenase	0.6	5.9	7.9	1.1	2.6	4.7	K00469
AASS	alpha-aminoadipic semialdehyde synthase	0	5	6.3	6.8	0.2	2.9	K14157
TER, TSC13, CER10	very-long-chain enoyl-CoA reductase	0	0.4	0.9	19.4	0	0.2	K10258
DHFR-TS	dihydrofolate reductase / thymidylate synthase	0	3.3	10.9	1.8	0.8	3.6	K13998
padB	phenylacetyl-CoA:acceptor oxidoreductase	3.7	4.3	5.5	7	0.1	2.2	K18361
MESO1, ERG25	methylsterol monooxygenase	0	6	6.3	0	1.4	2.9	K07750
ped	(S)-1-phenylethanol dehydrogenase	0	3.5	9.8	0	0.1	2.8	K14746
IL4I1	L-amino-acid oxidase	0	1.2	1.6	11.1	0	0.4	K03334
folM	dihydropyrimidine reductase / dihydrofolate reductase	0	0.4	5.9	2.5	0	4.6	K13938
SMO2	plant 4alpha-monomethylsterol monooxygenase	0	0.2	7.3	0	0	5.8	K14424
RIOX1, NO66	bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	0	3.9	6.8	0	0	2.5	K16914
MDH1	malate dehydrogenase	2.8	3.7	5.8	1.2	0	2	K00025
SUR2	sphinganine C4-monooxygenase	0	0.2	7.2	0	0	5.2	K04713
JMJD7	peptidyl-lysine (3S)-dioxygenase / protease	0	2.6	6.9	0	0	2.6	K19219
DET2	steroid 5-alpha-reductase	0	0.3	4.5	0	2.6	3.3	K09591
ALDH7A1	aldehyde dehydrogenase family 7 member A1	1.5	3	3.7	0	0.8	2.4	K14085
TDH	threonine 3-dehydrogenase	0	2.7	4	0	0	2	K15789
kdhL	6-hydroxypseudoxyxynicotine dehydrogenase subunit gamma	0	0.7	2.9	0	0	5	K19187
HAO	(S)-2-hydroxy-acid oxidase	0	0.5	2.8	2.6	0	2.5	K11517

Chapter II

RBOH	respiratory burst oxidase	0	2	2.5	2.1	0	1.8	K13447
GPD1	glycerol-3-phosphate dehydrogenase (NAD+)	0	2.7	3.7	0	0	1.9	K00006
luci	renilla-luciferin 2-monooxygenase	0	0.2	5.4	0	0	2.6	K18053
ALKBH8, TRM9	alkylated DNA repair protein alkB homolog 8	0	1.5	2.7	2.5	0	1.4	K10770
SDHB, SDH2	succinate dehydrogenase (ubiquinone) iron-sulfur subunit	0.6	1.2	2.1	0	0.6	3.1	K00235
E1.12.7.2	ferredoxin hydrogenase	1.7	1.9	2.7	0	0.2	2	K00532
DOHH	deoxyhypusine monooxygenase	0	1.8	2.1	0	0.8	1.6	K06072
bdhAB	butanol dehydrogenase	0	0.7	4.5	0	0	1.1	K00100
ADO	cysteamine dioxygenase	0.7	2.5	3	0	0	0.8	K10712
GLDH	L-galactono-1,4-lactone dehydrogenase	0	2	2.8	0	0	1.5	K00225
ACAD8	isobutyryl-CoA dehydrogenase	0	1.3	3.9	0	0	0.9	K11538
CDO1	cysteine dioxygenase	0	1.3	3.8	0	0	0.8	K00456
DUS2	tRNA-dihydrouridine synthase 2	0	0.9	2.8	0	0	1.8	K05543
POR	NADPH-ferrihemoprotein reductase	0	1.2	2.8	0	0	1.3	K00327
cobR	cob(II)yrinic acid a,c-diamide reductase	0	0.8	3.3	0	0	1	K13786
hndD	NADP-reducing hydrogenase subunit HndD	0	1.9	2.3	0	0.1	0.6	K18332
sucD	succinate-semialdehyde dehydrogenase	0	1.1	1.2	0	0	2.5	K18119
NR	nitrate reductase (NAD(P)H)	0.5	1.8	1.8	0	0	1.1	K10534
ERG4	Delta24(24(1))-sterol reductase	0	0.2	0.3	3.7	0	0.5	K00223
DHRSX	dehydrogenase/reductase SDR family member X	0	1.9	2	0	0	0.6	K11170
PCBC	isopenicillin-N synthase	0	1.4	1.7	0	0	0.8	K04126
phdI	1-hydroxy-2-naphthoate dioxygenase	0	0.3	1.5	0	0	2	K11948
PTGS1, COX1	prostaglandin-endoperoxide synthase 1	0	1.1	2.1	0	0	0.5	K00509
hydA	iron-hydrogenase subunit alpha	0	1.5	1.6	0	0.1	0.3	K17997
CBR4	carbonyl reductase 4 / 3-oxoacyl-[acyl-carrier protein] reductase beta subunit	0	1.1	1.6	0	0	0.7	K11539
IYD, DEHAL1	iodotyrosine deiodinase	0	0.2	2.3	0	0	0.7	K17231
CYP6	cytochrome P450 family 6	0	0.8	1.3	0	0	1	K14999
CYP734A1, BAS1	PHYB activation tagged suppressor 1	0	0.9	1.3	0	0	0.8	K15639
DCXR	L-xylulose reductase	0	1	1.4	0	0	0.6	K03331
HIF1AN	hypoxia-inducible factor 1-alpha inhibitor (HIF hydroxylase)	0	0.4	1.7	0	0	0.8	K18055
DHRS13	dehydrogenase/reductase SDR family member 13	0	0.2	1.8	0	0	0.8	K11169
TYRAAT	arogenate dehydrogenase (NADP+), plant	0	0.7	1.6	0	0	0.5	K15227
LOX1_5	linoleate 9S-lipoxygenase	0	0.2	0.6	1.2	0	0.8	K15718
CRYM	thiomorpholine-carboxylate dehydrogenase	0	0.2	1.3	0	0	1.2	K18258
MECR, NRBF1	mitochondrial enoyl-[acyl-carrier protein] reductase / trans-2-enoyl-CoA reductase	0	1	1.1	0	0	0.6	K07512
PHF8, JHDM1F	lysine-specific demethylase PHF8	0	0.9	1.4	0	0	0.4	K19415
CKX	cytokinin dehydrogenase	0	0.4	0.7	0	0	1.2	K00279
kdnB	3-deoxy-alpha-D-manno-octulosonate 8-oxidase	0	0.8	1.1	0	0	0.3	K19714
RRM2	ribonucleoside-diphosphate reductase subunit M2	0	0.2	1.1	0	0	0.6	K10808
ZEP, ABA1	zeaxanthin epoxidase	0	0.2	0.6	0	0	0.4	K09838
PAXM, ATMM, LTMM	FAD dependent monooxygenase	0	0.2	0.6	0	0	0.4	K18386

Table S6 –Tukey test results comparing the cell abundance (cells cm⁻¹) between different pairs of samples. Significant differences (*) were determined at p-value < 0.05.

	diff	lwr	upr	p adj
Plastic:A-Glass:A	681.381	541.865	820.898	0.000*
Glass:B-Glass:A	-7.997	-136.504	120.508	1
Plastic:B-Glass:A	366.369	224.527	508.210	0.000*
Glass:C-Glass:A	-8.815	-136.685	119.052	1
Plastic:C-Glass:A	1258.004	1130.136	1385.873	0.000*
Glass:B-Plastic:A	-689.380	-828.285	-550.475	0.000*
Plastic:B-Plastic:A	-315.013	-466.340	-163.687	0.000*
Glass:C-Plastic:A	-690.198	-828.513	-551.883	0.000*
Plastic:C-Plastic:A	576.622	438.307	714.937	0.000*
Plastic:B-Glass:B	374.366	233.126	515.607	0.000*
Glass:C-Glass:B	-0.817	-128.019	126.383	1
Plastic:C-Glass:B	1266.002	1138.801	1393.203	0.000*
Glass:C-Plastic:B	-375.185	-515.845	-234.524	0.000*
Plastic:C-Plastic:B	891.635	750.974	1032.296	0.000*
Plastic:C-Glass:C	1266.820	1140.263	1393.377	0.000*

Table S7 –Tukey test results comparing (A) the total oxygen consumption ($\mu\text{mol O}_2 \text{ cm}^{-2}$) and (B) the oxygen consumption rates ($\mu\text{mol O}_2 \text{ h}^{-1} \text{ cell}^{-1}$) between different pairs of samples. Significant differences (*) were determined at p-value < 0.05.

		diff	lwr	upr	p adj
A	Control:Ctrl 2-Control:Ctrl	-10.21	-16.451	-3.975	0.001*
	Glass:A-Control:Ctrl	1.653	-4.584	7.891	1
	Plastic:A-Control:Ctrl	20.362	14.124	26.599	0.000*
	Glass:B-Control:Ctrl	4.182	-2.055	10.420	0.405
	Plastic:B-Control:Ctrl	8.884	2.646	15.122	0.002*
	Glass:C-Control:Ctrl	-3.880	-10.117	2.357	0.510
	Plastic:C-Control:Ctrl	22.566	16.328	28.804	0.000*
	Glass:A-Control:Ctrl 2	11.867	5.629	18.104	0.000*
	Plastic:A-Control:Ctrl 2	30.575	24.337	36.813	0.000*
	Glass:B-Control:Ctrl 2	14.396	8.158	20.634	0.000*
	Plastic:B-Control:Ctrl 2	19.097	12.859	25.335	0.000*
	Glass:C-Control:Ctrl 2	6.333	0.095	12.571	0.045
	Plastic:C-Control:Ctrl 2	32.780	26.542	39.018	0.000*
	Plastic:A-Glass:A	18.708	12.470	24.946	0.000*
	Glass:B-Glass:A	2.529	-3.708	8.766	0.934
	Plastic:B-Glass:A	7.230	0.992	13.468	0.016*
	Glass:C-Glass:A	-5.533	-11.771	0.704	0.110
	Plastic:C-Glass:A	20.913	14.675	27.151	0.000*
	Glass:B-Plastic:A	-16.179	-22.417	-9.941	0.000*
	Plastic:B-Plastic:A	-11.478	-17.715	-5.240	0.000*
	Glass:C-Plastic:A	-24.242	-30.480	-18.004	0.000*
	Plastic:C-Plastic:A	2.204	-4.033	8.442	0.974
	Plastic:B-Glass:B	4.701	-1.536	10.939	0.257
	Glass:C-Glass:B	-8.062	-14.300	-1.824	0.006*
	Plastic:C-Glass:B	18.384	12.146	24.622	0.000*
	Glass:C-Plastic:B	-12.764	-19.002	-6.526	0.000*
	Plastic:C-Plastic:B	13.682	7.444	19.920	0.000*
	Plastic:C-Glass:C	26.446	20.209	32.684	0.000*
B	Plastic:A-Glass:A	-1.31E-07	-1.58E-07	-1.03E-07	0.000*
	Glass:B-Glass:A	1.57E-07	1.30E-07	1.85E-07	0.000*
	Plastic:B-Glass:A	-9.20E-08	-1.19E-07	-6.47E-08	0.000*
	Glass:C-Glass:A	-7.57E-08	-1.03E-07	-4.84E-08	0.000*
	Plastic:C-Glass:A	-1.34E-07	-1.61E-07	-1.07E-07	0.000*
	Glass:B-Plastic:A	2.88E-07	2.61E-07	3.15E-07	0.000*
	Plastic:B-Plastic:A	3.87E-08	1.14E-08	6.59E-08	0.005*
	Glass:C-Plastic:A	5.50E-08	2.77E-08	8.23E-08	0.000*
	Plastic:C-Plastic:A	-3.21E-09	-3.05E-08	2.41E-08	0.998
	Plastic:B-Glass:B	-2.49E-07	-2.77E-07	-2.22E-07	0.000*
	Glass:C-Glass:B	-2.33E-07	-2.60E-07	-2.06E-07	0.000*
	Plastic:C-Glass:B	-2.91E-07	-3.18E-07	-2.64E-07	0.000*
	Glass:C-Plastic:B	1.64E-08	-1.09E-08	4.36E-08	0.388
	Plastic:C-Plastic:B	-4.19E-08	-6.92E-08	-1.46E-08	0.003*
	Plastic:C-Glass:C	-5.82E-08	-8.55E-08	-3.10E-08	0.000*

Table S8 –Tukey test results comparing the weight (in mg) of the packaging PE and non-weathered LDPE incubated with the three different microbial communities. Significant differences (*) were determined at p-value < 0.05.

	Non-weathered LDPE				Packaging PE			
	diff	lwr	upr	p adj	diff	lwr	upr	p adj
Control-T0	-0.008	-0.073	0.057	0.997	-0.007	-0.014	0.000	0.035*
A-T0	-0.101	-0.175	-0.027	0.003*	-0.008	-0.015	-0.001	0.021*
B-T0	-0.063	-0.126	0.001	0.053	-0.008	-0.016	-0.001	0.032*
C-T0	-0.114	-0.184	-0.044	0.000*	-0.011	-0.018	-0.004	0.001*
A-Control	-0.093	-0.165	-0.022	0.006*	-0.001	-0.009	0.007	0.996
B-Control	-0.055	-0.116	0.006	0.094	-0.001	-0.009	0.007	0.995
C-Control	-0.106	-0.174	-0.038	0.001*	-0.004	-0.011	0.004	0.556
B-A	0.038	-0.032	0.108	0.520	0.000	-0.009	0.008	1.000
C-A	-0.012	-0.089	0.064	0.989	-0.003	-0.011	0.005	0.804
C-B	-0.051	-0.117	0.016	0.201	-0.003	-0.011	0.005	0.862

Table S9 – ASW recipe and concentrations of respective chemicals. Salts were added to obtain a final salinity of 35.8.

Chemicals	Concentration (mM)
NaCl	355.20
Na ₂ SO ₄	24.48
KCl	7.75
NaHCO ₃	2.02
KBr	0.71
H ₃ BO ₃	0.36
NaF	0.06
MgCl ₂ .6H ₂ O	46.21
CaCl ₂ .2H ₂ O	8.95
SrCl ₂ .6H ₂ O	0.08
NH ₄ Cl	0.01
NaH ₂ PO ₄	0.002

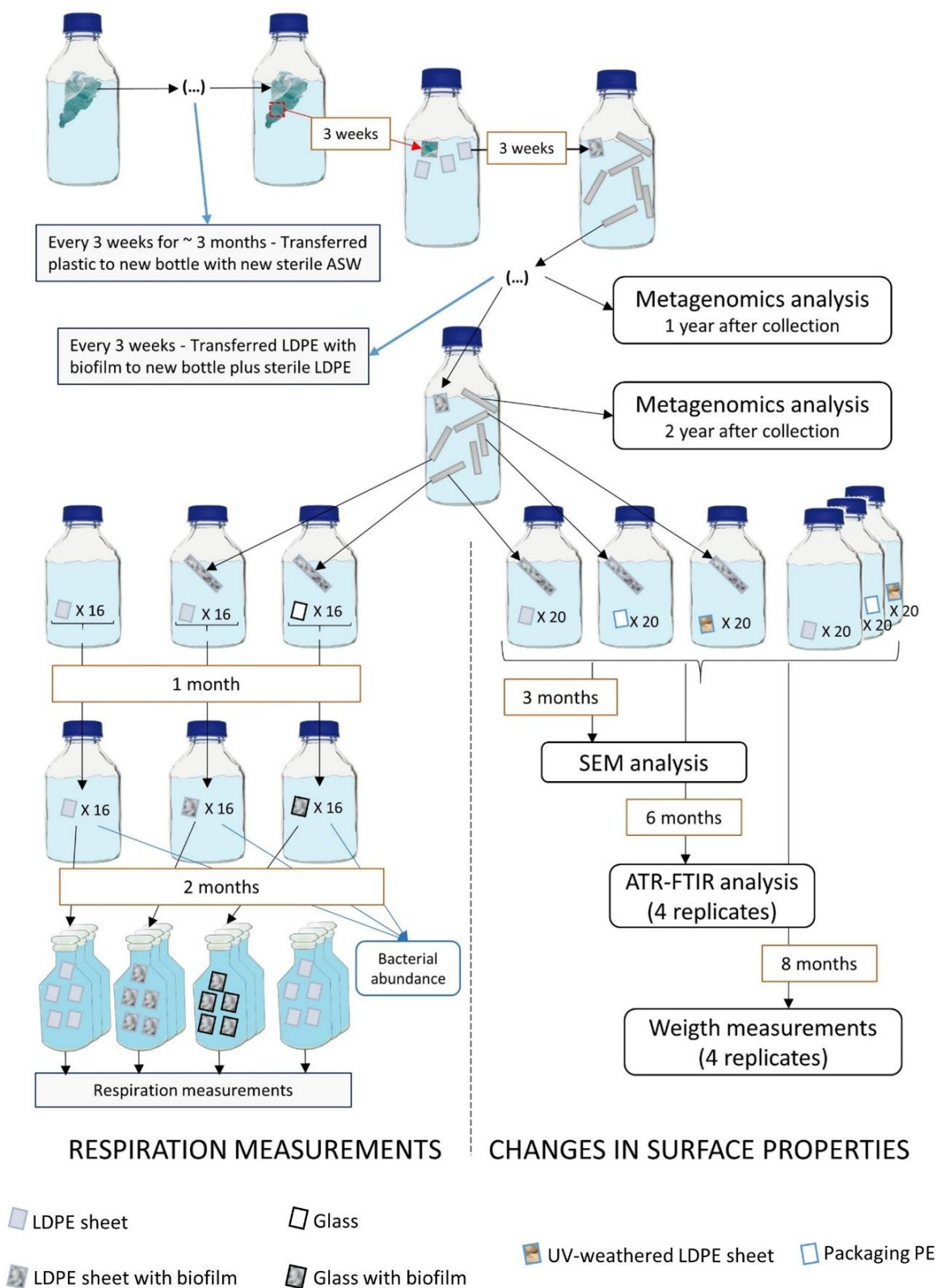


Fig. S1 – Scheme of the experimental setup. All incubations were performed in sterile artificial seawater amended with 2 μM of NaPO_4 and 10 μM of NH_4Cl . All bottles were kept in the dark at room temperature ($\sim 21^\circ\text{C}$). This workflow was performed for each of the three plastics, A, B and C.

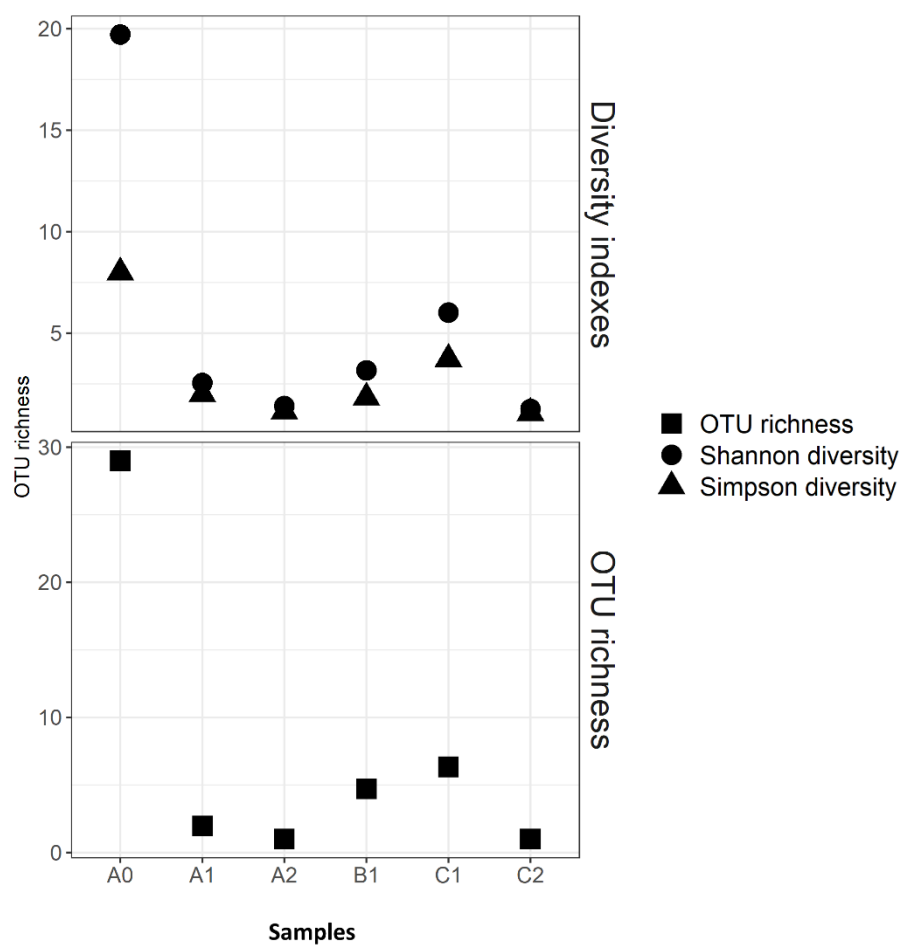


Fig. S2- mOTU diversity indexes and richness of the six metagenomes calculated from the mOTUs obtained with the software mOTUs. Samples were normalized to a coverage of 0.84.

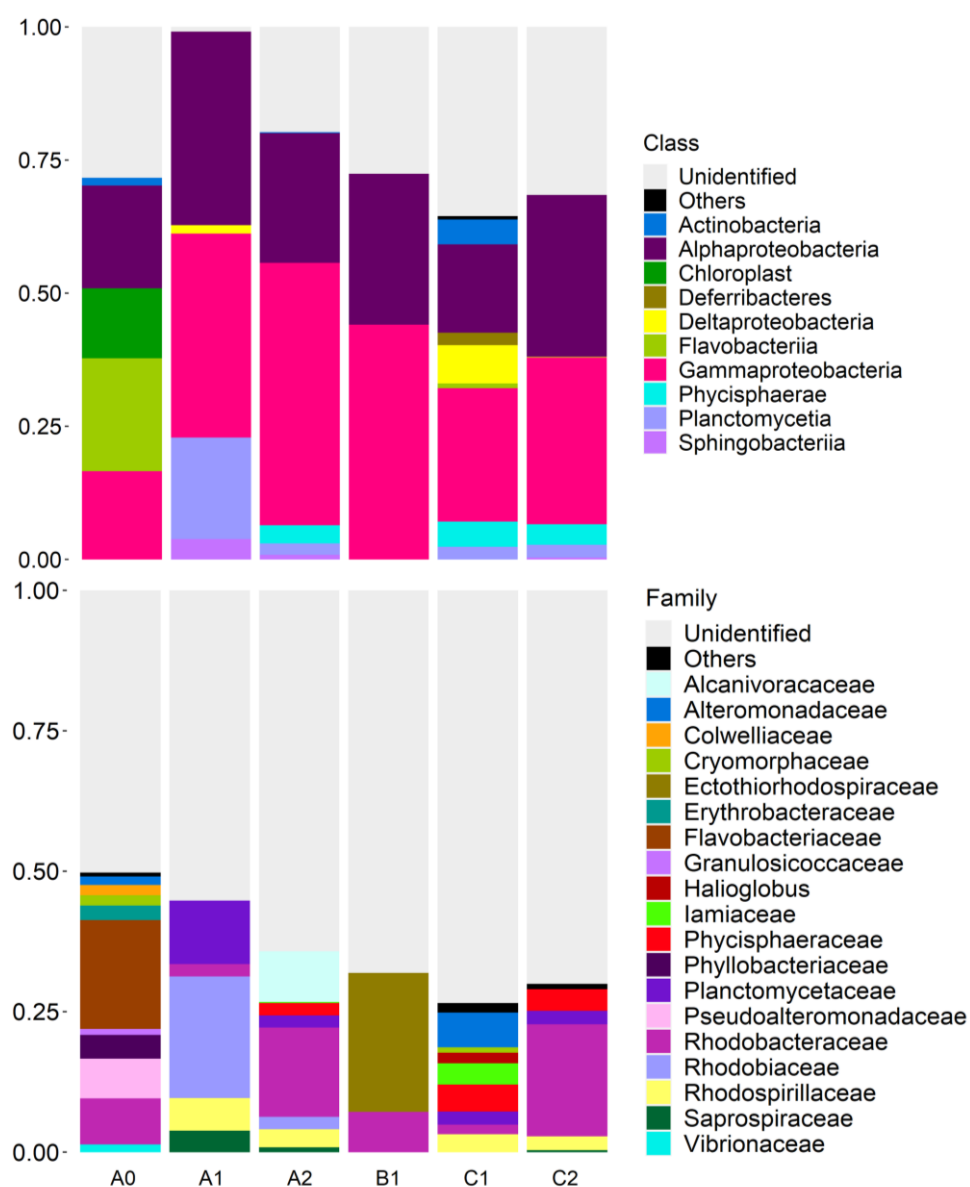


Fig. S3 - Relative abundance of the abundant classified classes and families (>1% relative abundance) in the metagenomes obtained with matam. All classes and families with relative abundance below 1% were grouped in the category “Others”.

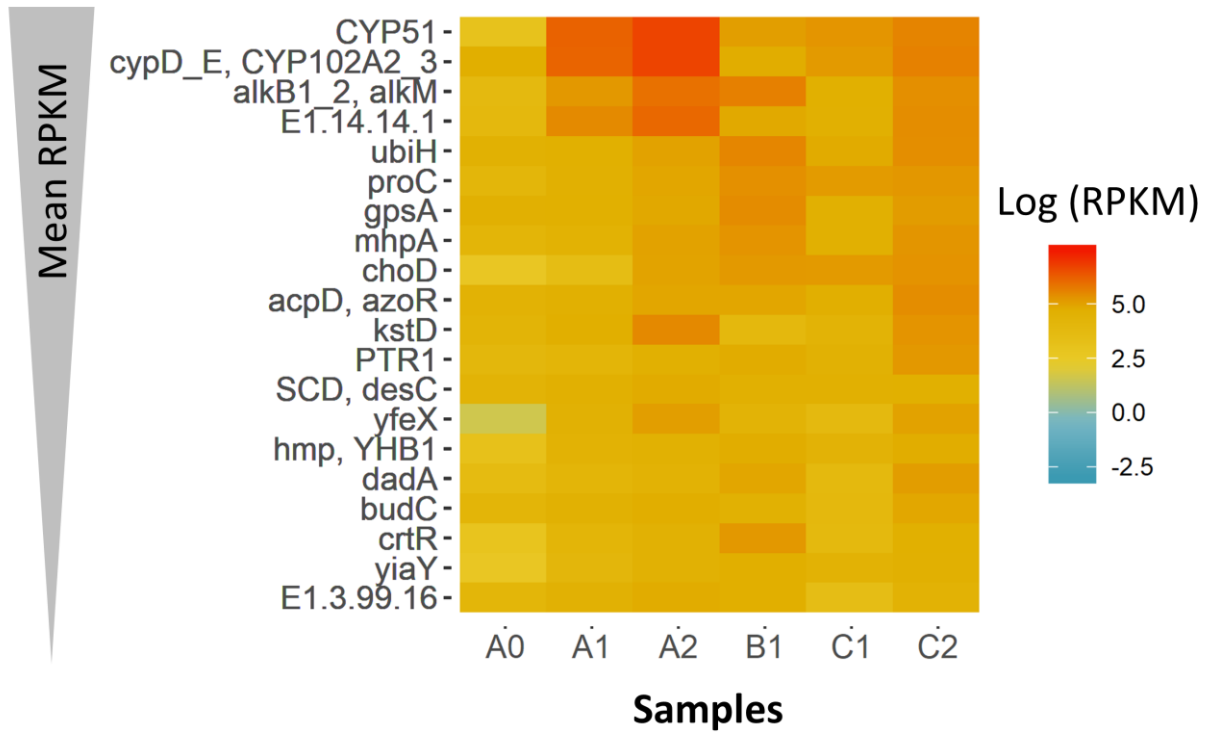


Fig. S4 - Plot showing the RPKM values (in log) of enriched genes encoding for KEGG-annotated oxidoreductases in all six metagenomes. RPKM values of all genes increased from A0 to A1 and further on to A2, and also from C1 to C2. These were the top 20 enriched KEGG-annotated oxidoreductases genes with a higher average of RPKM in all six metagenomes combined (Table S6). They are ordered top to bottom from the most abundant to the less abundant.

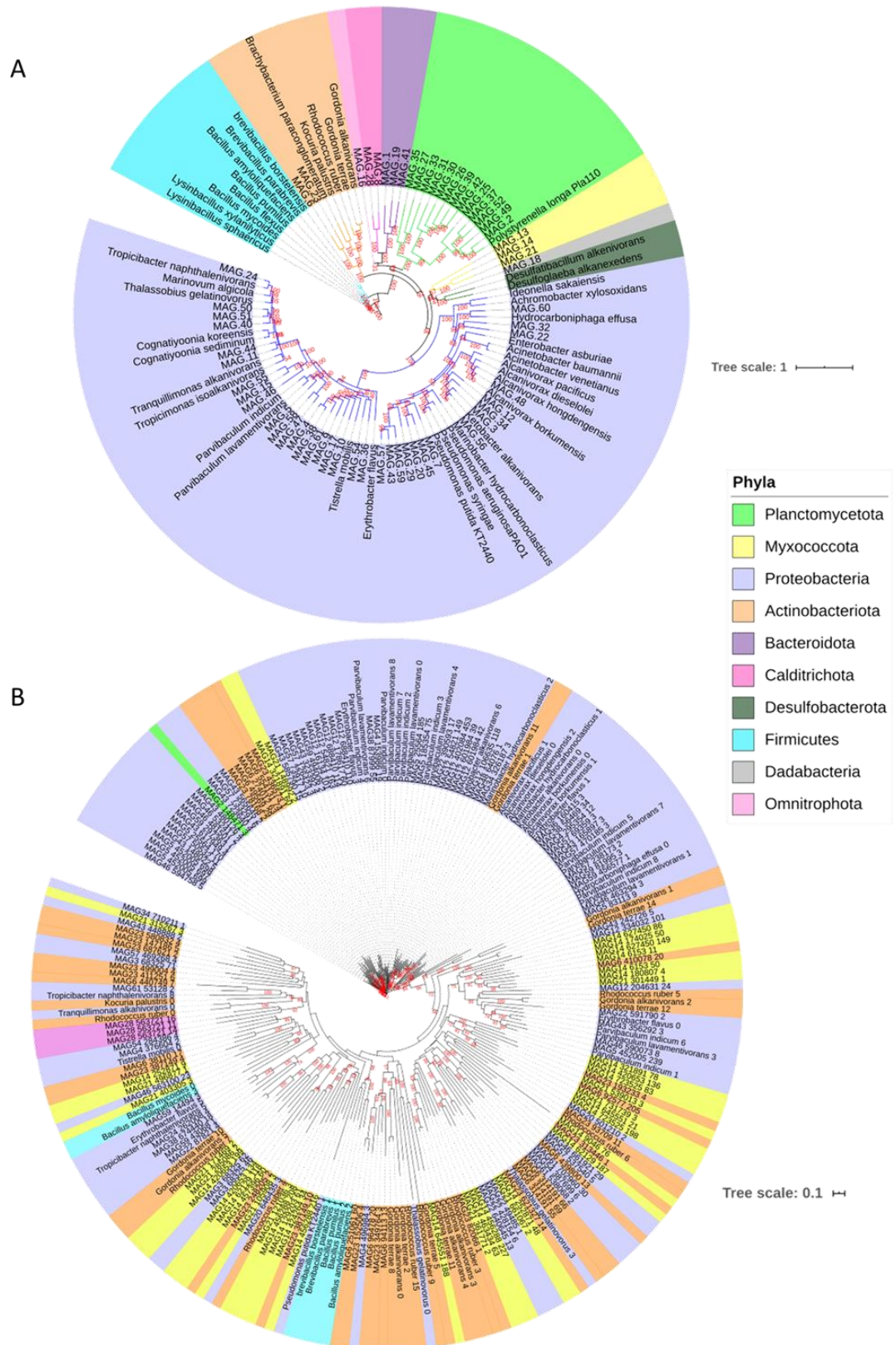


Fig. S5 – Phylogenetic placement of (A) the MAGs and selected genomes (Table S2) and (B) putative CYP153 sequences identified in MAGs and genomes. The bootstrap values are written in red at the respective nodes. Only bootstrap values >50 were considered in B.

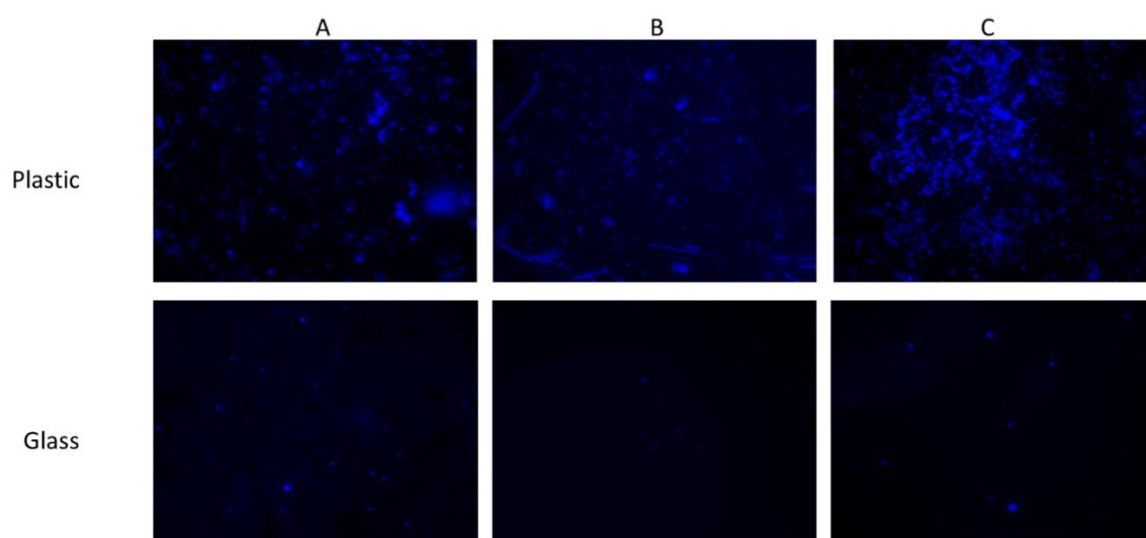


Fig. S6 – Randomly selected fluorescence microscope photos of DAPI stained cells on plastic and glass samples, incubated for three months with communities A2, B2 and C2. The photos were taken right before the respiration measurements.

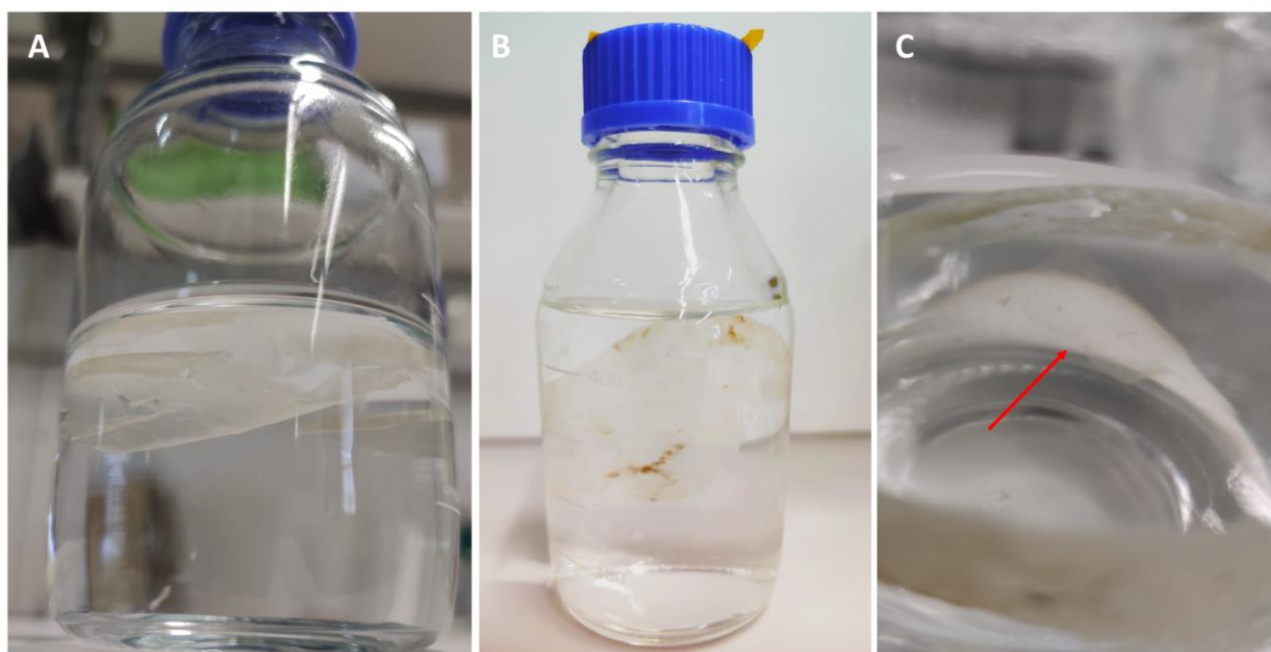


Fig. S7 – Plastics (A) A, (B) B and (C) C.

References

- Artham, T., Sudhakar, M., Venkatesan, R., Madhavan Nair, C., Murty, K.V.G.K., and Doble, M. (2009) Biofouling and stability of synthetic polymers in sea water. *Int Biodeterior Biodegradation* **63**: 884–890.
- Di Cello, F., Pepi, M., Baldi, F., and Fani, R. (1997) Molecular characterization of an n-alkane-degrading bacterial community and identification of a new species, *Acinetobacter venetianus*. *Res Microbiol* **148**: 237–249.
- Cravo-Laureau, C., Matheron, R., Joulian, C., Cayol, J.-L., and Hirschler-Réa, A. (2004) *Desulfatibacillum alkenivorans* sp. nov., a novel n-alkene-degrading, sulfate-reducing bacterium, and emended description of the genus *Desulfatibacillum*. *Int J Syst Evol Microbiol* **54**: 1639–1642.
- Davidova, I.A., Duncan, K.E., Choi, O.K., and Suflita, J.M. (2006) *Desulfoglaeba alkanexedens* gen. nov., sp. nov., an n-alkane-degrading, sulfate-reducing bacterium. *Int J Syst Evol Microbiol* **56**: 2737–2742.
- Esmaeili, A., Pourbabaee, A.A., Alikhani, H.A., Shabani, F., and Esmaeili, E. (2013) Biodegradation of low-density polyethylene (LDPE) by mixed culture of *Lysinibacillus xylanilyticus* and *Aspergillus niger* in soil. *PLoS One* **8**: e71720.
- Gauthier, M.J., Lafay, B., Christen, R., Fernandez, L., Acquaviva, M., Bonin, P., and Bertrand, J.-C. (1992) *Marinobacter hydrocarbonoclasticus* gen. nov., sp. nov., a new, extremely halotolerant, hydrocarbon-degrading marine bacterium. *Int J Syst Evol Microbiol* **42**: 568–576.
- Hadad, D., Geresh, S., and Sivan, A. (2005) Biodegradation of polyethylene by the thermophilic bacterium *Brevibacillus borstelensis*. *J Appl Microbiol* **98**: 1093–1100.
- Harshvardhan, K. and Jha, B. (2013) Biodegradation of low-density polyethylene by marine bacteria from pelagic waters, Arabian Sea, India. *Mar Pollut Bull* **77**: 100–106.
- Harwati, T.U., Kasai, Y., Kodama, Y., Susilaningih, D., and Watanabe, K. (2007) Characterization of diverse hydrocarbon-degrading bacteria isolated from Indonesian seawater. *Microbes Environ* **22**: 412–415.
- Harwati, T.U., Kasai, Y., Kodama, Y., Susilaningih, D., and Watanabe, K. (2008) *Tranquillimonas alkanivorans* gen. nov., sp. nov., an alkane-degrading bacterium isolated from Semarang Port in Indonesia. *Int J Syst Evol Microbiol* **58**: 2118–2121.
- Harwati, T.U., Kasai, Y., Kodama, Y., Susilaningih, D., and Watanabe, K. (2009a) *Tropicibacter naphthalenivorans* gen. nov., sp. nov., a polycyclic aromatic hydrocarbon-degrading bacterium isolated from Semarang Port in Indonesia. *Int J Syst Evol Microbiol* **59**: 392–396.
- Harwati, T.U., Kasai, Y., Kodama, Y., Susilaningih, D., and Watanabe, K. (2009b) *Tropicimonas isoalkanivorans* gen. nov., sp. nov., a branched-alkane-degrading bacterium isolated from Semarang Port in Indonesia. *Int J Syst Evol Microbiol* **59**: 388–391.
- Ibiene, A.A., Stanley, H.O., and Immanuel, O.M. (2013) Biodegradation of polyethylene by *Bacillus* sp. indigenous to the Niger delta mangrove swamp. *Niger J Biotechnol* **26**: 68–78.
- Ingavale, R.R. and Raut, P.D. (2018) Comparative biodegradation studies of LDPE and HDPE using *Bacillus weihenstephanensis* isolated from garbage soil. *Nat Environ Pollut Technol* **17**: 649–655.
- Katayama, Y., Oura, T., Iizuka, M., Orita, I., Cho, K.J., Chung, I.Y., and Okada, M. (2003) Effects of spilled oil on microbial communities in a tidal flat. *Mar Pollut Bull* **47**: 85–90.
- Kim, S.-H., Kim, J.-G., Jung, M.-Y., Kim, S.-J., Gwak, J.-H., Yu, W.-J., et al. (2018) *Ketobacter alkanivorans*

- gen. nov., sp. nov., an n-alkane-degrading bacterium isolated from seawater. *Int J Syst Evol Microbiol* **68**: 2258–2264.
- Kiran, G.S., Sabarathnam, B., Thajuddin, N., and Selvin, J. (2014) Production of glycolipid biosurfactant from sponge-associated marine actinobacterium *Brachybacterium paraconglomeratum* MSA21. *J Surfactants Deterg* **17**: 531–542.
- Kowalczyk, A., Chyc, M., Ryszka, P., and Latowski, D. (2016) *Achromobacter xylosoxidans* as a new microorganism strain colonizing high-density polyethylene as a key step to its biodegradation. *Environ Sci Pollut Res* **23**: 11349–11356.
- Kummer, C., Schumann, P., and Stackebrandt, E. (1999) *Gordonia alkanivorans* sp. nov., isolated from tar-contaminated soil. *Int J Syst Evol Microbiol* **49**: 1513–1522.
- Kyaw, B.M., Champakalakshmi, R., Sakharkar, M.K., Lim, C.S., and Sakharkar, K.R. (2012) Biodegradation of low density polythene (LDPE) by *Pseudomonas* species. *Indian J Microbiol* **52**: 411–419.
- Labasque, T., Chaumery, C., Aminot, A., and Kergoat, G. (2004) Spectrophotometric Winkler determination of dissolved oxygen: re-examination of critical factors and reliability. *Mar Chem* **88**: 53–60.
- Lai, Q., Wang, L., Liu, Y., Fu, Y., Zhong, H., Wang, B., et al. (2011) *Alcanivorax pacificus* sp. nov., isolated from a deep-sea pyrene-degrading consortium. *Int J Syst Evol Microbiol* **61**: 1370–1374.
- Lai, Q., Wang, L., Liu, Y., Yuan, J., Sun, F., and Shao, Z. (2011) *Parvibaculum indicum* sp. nov., isolated from deep-sea water. *Int J Syst Evol Microbiol* **61**: 271–274.
- Liu, C. and Shao, Z. (2005) *Alcanivorax dieselolei* sp. nov., a novel alkane-degrading bacterium isolated from sea water and deep-sea sediment. *Int J Syst Evol Microbiol* **55**: 1181–1186.
- Nicdao, M.A.C. and Rivera, W.L. (2012) Two strains of *Gordonia terrae* isolated from used engine oil-contaminated soil utilize short-to long-chain n-alkanes. *Philipp Sci Lett* **5**: 1–10.
- Palleroni, N.J., Port, A.M., Chang, H.-K., and Zylstra, G.J. (2004) *Hydrocarboniphaga effusa* gen. nov., sp. nov., a novel member of the γ -Proteobacteria active in alkane and aromatic hydrocarbon degradation. *Int J Syst Evol Microbiol* **54**: 1203–1207.
- Peeters, S.H., Wiegand, S., Kallscheuer, N., Jogler, M., Heuer, A., Jetten, M.S.M., et al. (2020) Description of *Polystyrenella longa* gen. nov., sp. nov., isolated from polystyrene particles incubated in the Baltic Sea.
- Pramila, R., Padmavathy, K., Ramesh, K.V., and Mahalakshmi, K. (2012) *Brevibacillus parabrevis*, *Acinetobacter baumannii* and *Pseudomonas citronellolis*-Potential candidates for biodegradation of low density polyethylene (LDPE). *African J Bacteriol Res* **4**: 9–14.
- Rodrigo-Torres, L., Pujalte, M.J., and Arahall, D.R. (2017) Draft genome sequence of *Thalassobius gelatinovorans* CECT 4357T, a roseobacter with the potential ability to degrade polycyclic aromatic hydrocarbons. *Gene Reports* **9**: 32–36.
- Rueden, C.T., Schindelin, J., Hiner, M.C., DeZonia, B.E., Walter, A.E., Arena, E.T., and Eliceiri, K.W. (2017) ImageJ2: ImageJ for the next generation of scientific image data. *BMC Bioinformatics* **18**: 529.
- Schleheck, D., Tindall, B.J., Rossello-Mora, R., and Cook, A.M. (2004) *Parvibaculum lavamentivorans* gen. nov., sp. nov., a novel heterotroph that initiates catabolism of linear alkylbenzenesulfonate. *Int J Syst Evol Microbiol* **54**: 1489–1497.
- Sivan, A., Szanto, M., and Pavlov, V. (2006) Biofilm development of the polyethylene-degrading bacterium *Rhodococcus ruber*. *Appl Microbiol Biotechnol* **72**: 346–352.
- Wang, L., Wang, W., Lai, Q., and Shao, Z. (2010) Gene diversity of CYP153A and AlkB alkane

- hydroxylases in oil-degrading bacteria isolated from the Atlantic Ocean. *Environ Microbiol* **12**: 1230–1242.
- Wang, W. and Shao, Z. (2012) Diversity of flavin-binding monooxygenase genes (*almA*) in marine bacteria capable of degradation long-chain alkanes. *FEMS Microbiol Ecol* **80**: 523–533.
- Wang, W., Wang, L., and Shao, Z. (2010) Diversity and abundance of oil-degrading bacteria and alkane hydroxylase (*alkB*) genes in the subtropical seawater of Xiamen Island. *Microb Ecol* **60**: 429–439.
- Wirth, J.S. and Whitman, W.B. (2018) Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera *Aestuaria*, *Citricella*, *Loktanella*, *Nautella*, *Pelagibaca*, *Ruegeria*, *Thalassobius*, *Thiobacimonas* and *Tropicibacter*, and the proposal . *Int J Syst Evol Microbiol* **68**: 2393–2411.
- Wu, Y., Lai, Q., Zhou, Z., Qiao, N., Liu, C., and Shao, Z. (2009) *Alcanivorax hongdengensis* sp. nov., an alkane-degrading bacterium isolated from surface seawater of the straits of Malacca and Singapore, producing a lipopeptide as its biosurfactant. *Int J Syst Evol Microbiol* **59**: 1474–1479.
- Yakimov, M.M., Golyshin, P.N., Lang, S., Moore, E.R.B., Abraham, W.-R., Lünsdorf, H., and Timmis, K.N. (1998) *Alcanivorax borkumensis* gen. nov., sp. nov., a new, hydrocarbon-degrading and surfactant-producing marine bacterium. *Int J Syst Evol Microbiol* **48**: 339–348.
- Yang, J., Yang, Y., Wu, W.-M., Zhao, J., and Jiang, L. (2014) Evidence of polyethylene biodegradation by bacterial strains from the guts of plastic-eating waxworms. *Environ Sci Technol* **48**: 13776–13784.
- Yoshida, S., Hiraga, K., Takehana, T., Taniguchi, I., Yamaji, H., Maeda, Y., et al. (2016) A bacterium that degrades and assimilates poly(ethylene terephthalate). *Science* **351**: 1196–1199.

CHAPTER III

Putative degraders of low-density polyethylene-derived compounds are ubiquitous members of plastic-associated bacterial communities in the marine environment

Maria Pinto^{1,2*}, Paula Polania Zenner¹, Teresa M. Langer¹, Jesse Harrison^{3†}, Meinhard Simon⁴,
Marta M. Varela⁵, Gerhard J. Herndl^{1,2,6}

¹ Department of Functional and Evolutionary Ecology, University of Vienna, Vienna, Austria

² Research Platform 'Plastics in the Environment and Society', University of Vienna, Vienna, Austria

³ Centre for Microbiology and Environmental Systems Science, University of Vienna, Vienna, Austria

⁴ Institute for Chemistry and Biology of the Marine Environment (ICBM), University of Oldenburg, Oldenburg, Germany

⁵ IEO, Instituto Español de Oceanografía, Centro Oceanográfico de A Coruña, A Coruña, Spain

⁶ NIOZ, Department of Marine Microbiology and Biogeochemistry, Royal Netherlands Institute for Sea Research, Utrecht University, Den Burg, The Netherlands

* Corresponding author: maria.pinto@univie.ac.at

† Current address: CSC – IT Center for Science Ltd., Espoo, Finland

In press in Environmental Microbiology

Abstract

It remains unknown whether and to what extent marine prokaryotic communities are capable of degrading plastic in the ocean. To address this knowledge gap, we combined enrichment experiments employing low-density polyethylene (LDPE) as the sole carbon source with a comparison of bacterial communities on plastic debris in the Pacific, the North Atlantic and the northern Adriatic Sea. A total of 35 OTUs were enriched in the LDPE-laboratory incubations after one year, of which 20 were present with relative abundances > 0.5% in at least one plastic sample collected from the environment. From these, OTUs classified as *Cognatibacter*, *Psychrobacter*, *Roseovarius*, and *Roseobacter* were found in the communities of plastics collected at all oceanic sites. Additionally, OTUs classified as *Roseobacter*, *Pseudophaeobacter*, *Phaeobacter*, *Marinovum* and *Cognatibacter*, also enriched in the LDPE-laboratory incubations, were enriched on LDPE communities compared to the ones associated to glass and polypropylene in *in situ* incubations in the northern Adriatic Sea after one month of incubation. Some of these enriched OTUs were also related to known alkane and hydrocarbon degraders. Collectively, these results demonstrate that there are prokaryotes capable of surviving with LDPE as the sole carbon source living on plastics in relatively high abundances in different water masses of the global ocean.

Introduction

Between 4.8 and 12.7 million metric tons of plastic are entering the ocean each year (Jambeck *et al.*, 2015). Like all solid surfaces in the ocean, plastics are colonized by microbial communities referred to as the plastisphere (Zettler *et al.*, 2013). The term ‘plastisphere’ indicates that the plastic associated microbial community is different in its composition from that found in the surrounding environment (Lobelle and Cunliffe, 2011). This has been shown for plastics collected in different locations (Amaral-Zettler *et al.*, 2015; Oberbeckmann *et al.*, 2015; De Tender *et al.*, 2017; Kettner *et al.*, 2017; Dussud *et al.*, 2018b; Harrison *et al.*, 2018), and has been observed in both seawater (Amaral-Zettler *et al.*, 2015) and sediment habitats (Harrison *et al.*, 2014).

The composition of the plastisphere is also shaped by biogeographic and environmental factors, such as salinity and nutrient availability (Oberbeckmann *et al.*, 2014, 2018; Amaral-Zettler *et al.*, 2015; Kesy *et al.*, 2019). Surface characteristics of the plastic, such

as surface free energy, hydrophobicity, presence of additives, weathering state and molecular composition might also play a role in determining the community composition of plastic-associated biofilms (Cai *et al.*, 2019; Hossain *et al.*, 2019), especially in earlier stages of biofilm development (Pinto *et al.*, 2019). Because some marine bacteria have the ability to degrade hydrocarbons, it has been suggested that a certain fraction of the microbial community colonizing plastics could also be capable of degrading plastics (Jacquin *et al.*, 2019; Roager and Sonnenschein, 2019). For example, the bacterium *Ideonella sakaiensis* produces enzymes capable of efficiently converting poly(ethylene-terephthalate) (PET) into benign monomers (Yoshida *et al.*, 2016).

The two most abundant plastics in the ocean, polyethylene (PE) and polypropylene (PP), show signs of biodegradation when incubated with specific bacteria or fungi under controlled laboratory conditions (Sudhakar *et al.*, 2008; Harshvardhan and Jha, 2013; Paço *et al.*, 2017). Whether these organisms also degrade marine plastics in the oceanic environment, however, remains unclear. The majority of the tested microorganisms, such as *Bacillus* sp. (Harshvardhan and Jha, 2013) and the fungus *Zalerion maritimum* (Paço *et al.*, 2017), while isolated from seawater, were not particularly abundant in plastic-associated biofilms, indicating that they likely play only a minor role in plastic degradation in the marine environment.

However, weight loss has been reported for PE and PP during in situ incubations in the marine environment, indicating either an abiotic loss due to fragmentation and leaching or biotically via microbial action on plastics (Sudhakar *et al.*, 2007). The systematic association of bacteria capable of degrading hydrocarbons, such as members of the families *Alcanivoraceae*, *Rhodobacteraceae* and *Sphingomonadaceae* (Oberbeckmann and Labrenz, 2019; Roager and Sonnenschein, 2019) to plastic surfaces further suggests that specific members of plastic-colonizing microbial communities associated with this plastic might be capable of degrading plastic and/or plastic-derived compounds in the ocean. For example, the family *Alcanivoraceae*, well known for including alkane-degrading taxa (Schneiker *et al.*, 2006; Kim *et al.*, 2018), has been found enriched on polyethylene terephthalate (PET) surfaces compared to glass surfaces (Oberbeckmann *et al.*, 2016). *Alcanivoraceae* also increased in relative abundance in incubations where plastics, such as low density polyethylene (LDPE) and polystyrene (PS), are the only carbon sources (Delacuvellerie *et al.*, 2019; Syranidou *et al.*, 2019). Weight loss of plastics and changes of the chemical properties of their surface, when incubated with specific microorganisms, are indicative of plastic biodegradation

(Oberbeckmann and Labrenz, 2019). However, except for *Ideonella sakaiensis* producing PET-degrading enzymes (Yoshida *et al.*, 2016), the metabolic pathways and associated mechanistic processes involved in the biodegradation of other plastics are yet to be characterized. Therefore, whether oceanic bacteria are capable to degrade plastics remains to be shown.

Recently, the taxonomy of plastic-associated microbial communities has been studied in the Mediterranean Sea (Dussud *et al.*, 2018), the Baltic Sea (Oberbeckmann *et al.*, 2014, 2018; Kettner *et al.*, 2017; Ogonowski *et al.*, 2018; Kesý *et al.*, 2019), the North Sea (De Tender *et al.*, 2017; Kirstein *et al.*, 2019; Oberbeckmann *et al.*, 2014, 2016), the northern Adriatic Sea (Pinto *et al.*, 2019), the Caribbean Sea (Dudek *et al.*, 2020), the western Atlantic Ocean (Zettler *et al.*, 2013; Amaral-Zettler *et al.*, 2015; Debroas *et al.*, 2017), and the North Pacific Gyre (Amaral-Zettler *et al.*, 2015; Bryant *et al.*, 2016). The composition of plastic-associated bacterial communities has been compared using materials collected in the North Sea, the Baltic Sea and Yangtze Estuary (Oberbeckmann and Labrenz, 2019). The community composition of the samples from each of these locations was obtained by the taxonomic classification of the V4 region of the 16S rRNA gene (De Tender *et al.*, 2017; Jiang *et al.*, 2018; Oberbeckmann *et al.*, 2018; Ogonowski *et al.*, 2018; Kesý *et al.*, 2019). While the biofilm samples from different locations did share operational taxonomic units (OTUs), mostly affiliated to *Rhodobacteraceae* and *Sphingomonadaceae* families, the majority of OTUs were location-specific. This suggests that environmental variables are the main factor determining the composition of prokaryotic plastic-associated communities within marine habitats. Most of these studies, however, used different DNA extraction methods, different primers and different sequencing technologies, which might introduce biases in the results and might explain some of the differences in community composition found between locations (Wintzingerode *et al.*, 1997).

In this study, we compare the composition of prokaryotic communities associated with plastics collected in the Pacific, the North Atlantic and the northern Adriatic Sea (Fig. S1, Table S1). If biodegradability of plastics is a factor influencing the composition of plastic-colonizing prokaryotic communities in the ocean, we expect the presence of plastic degraders in plastic-associated biofilms to be independent of the oceanic region. Furthermore, it has been proposed that metabolic pathways involved in the biodegradation of plastics differ between different plastic polymers (Devi *et al.*, 2016). Hence, we hypothesized that different plastic types (e.g. PE, PP) would harbour different plastic-degrading organisms. To determine whether specific bacteria originating from the natural microbial community can utilize LDPE-

derived compounds, we incubated two PE biofilm communities with LDPE as their sole carbon source, one for one year and the other for two years. We then investigated the presence of the bacteria increasing in relative abundance in these incubations and on plastics collected in different regions of the global ocean. We also examined whether the bacteria enriched in the LDPE incubations were present in biofilms associated with PE, PP and glass during an *in situ* incubation experiment taking place in the northern Adriatic Sea (described in Pinto *et al.* 2019). In this previous study, we characterized the composition of bacterial communities on glass and different plastic types after one week, one month and two months using the same molecular and sequencing tools and protocols as used in the present study.

Results

Community composition across different oceanic regions

We analysed the 16S rRNA gene sequences of biofilms associated with 13, 23 and 40 plastic items collected in the North Atlantic, Pacific and northern Adriatic Sea, respectively (Table S2). We could not identify the polymer type of 1 and 6 pieces from the North Atlantic and Pacific, respectively. Thus, they were classified as not identified (NI).

Overall, operational taxonomic unit (OTU) diversity and richness were significantly higher on plastics collected in the northern Adriatic than in the North Atlantic and Pacific, independent of the size of the plastics (Fig. S2, Tables S3-S4).

There was no difference between the taxonomic composition of the bacterial communities colonizing PP and PE (PERMANOVA: $F=0.97$, $p=0.527$). The composition of bacterial communities on plastics, however, significantly differed from that of the surrounding seawater at all sites (Fig. 1, Table S5). Furthermore, the bacterial community composition in plastic-associated biofilms differed between the oceanic basins, i.e. North Atlantic, Pacific and northern Adriatic, and between sampling stations, albeit not in all of them (Fig. 1, Table S5). The bacterial communities on plastics collected in the Pacific at stations 8 and 10 were relatively similar but were significantly different from the communities on plastics collected at any other Pacific stations (Table S5). The bacterial community composition of the plastic-associated biofilms collected in the North Atlantic was relatively similar, with the exception of plastics collected at stations 1 and 5, which significantly differed from each other (PERMANOVA: $F=1.50$, $p<0.05$).

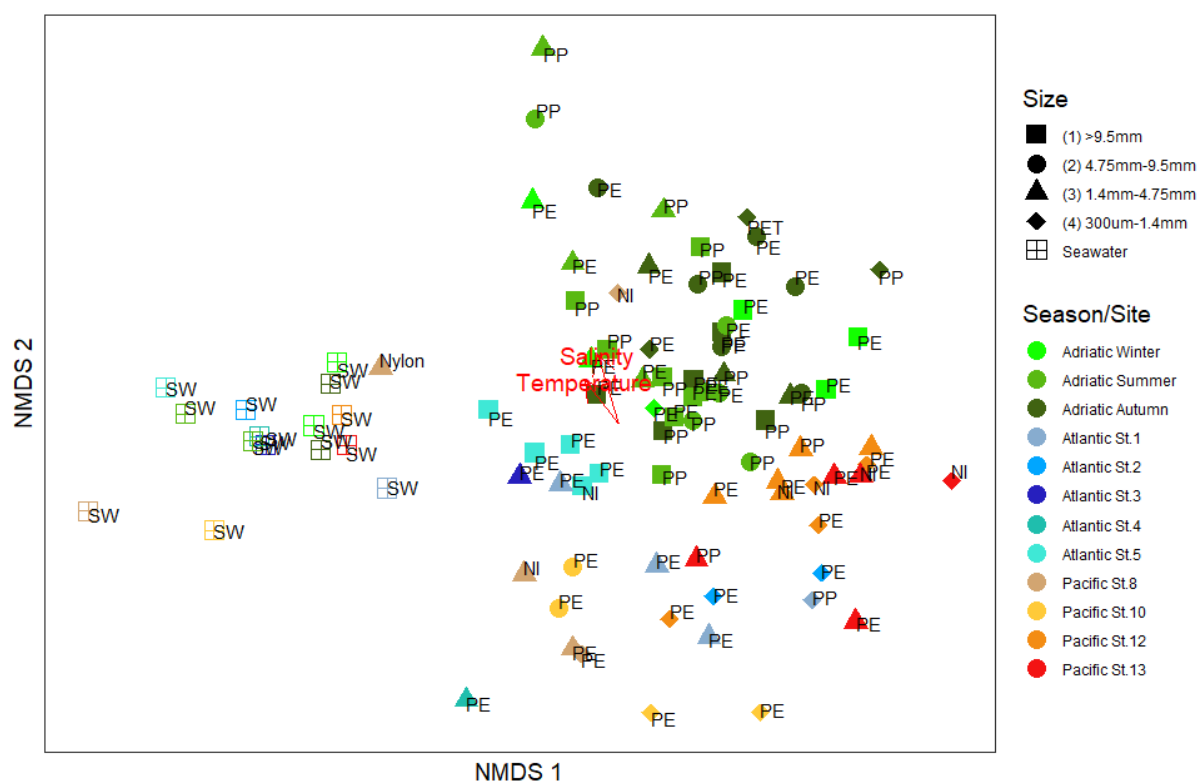


Fig.1- NMDS representation of the prokaryotic community of all plastic and seawater samples collected in the northern Adriatic, North Atlantic and Pacific using Bray-Curtis as the distance measurement. Each symbol represents one sample and the letters next to each symbol indicate the type of plastic (PE, PP, PET and nylon), unidentified polymers (NI) or seawater (SW). The environmental factor vectors were fitted to the NMDS through the envfit function. Envfit results are given in Table S6.

When we fitted environmental vectors to the NMDS scores of all samples, we obtained significant correlations for temperature and salinity ($p < 0.05$), but only when ambient seawater communities were included (Fig. 1 and Table S6). When considering only the northern Adriatic and North Atlantic biofilm samples, NMDS scores were significantly correlated with temperature and NO_2 , NO_3 and PO_4 concentrations (Table S6). However, when examining the correlation between environmental factors and the overall (combined) community composition of biofilm samples from each station, Mantel tests indicated that there was no significant correlation with any of the environmental factors (Table S7). The bacterial community composition of the plastic-associated biofilm collected in the North Atlantic was significantly correlated with the distance between stations ($R^2 = 0.697$, $p < 0.05$). For more details on the taxonomy of the bacterial community on plastics and seawater from the different sampling sites see S1.

We identified 462 OTUs shared between plastics across the different oceanic regions, 57 of them were present only on plastics (Fig. S6A, for taxonomy see Table S9). When

considering only PE biofilms, there were 427 shared OTUs. A total of 471 OTUs with >1% relative abundance was present in at least one sample at each site, distributed between plastics and seawater from the Atlantic, Pacific and northern Adriatic (Fig. S6B, for taxonomy see Table S10). Out of these 481 OTUs only 22 OTUs exhibited a relative abundance of >1% in the plastic biofilm at all three oceanic basins (Fig. S6B, for taxonomy see Table S11) and only 10 OTUs were also shared with ambient seawater. Together, these 19 OTUs contributed a varying percentage to the total classified 16S rRNA gene sequences on plastics collected at the different locations, with a minimum of 7% in one plastic sample collected at Station 4 in the North Atlantic and a maximum of $51\% \pm 0.04\%$ ($n=3$) on plastics collected at Station 13 in the Pacific.

Bacterial communities associated with plastics collected in the northern Adriatic exhibited a higher number of unique OTUs with a relative abundance >1%, 260 OTUs, than corresponding samples collected in the North Atlantic and Pacific, where only 13 and 41 unique OTUs were found, respectively (Fig. S6).

Taxa enriched on plastic-associated communities across different oceanic regions

We identified taxa enriched on plastics in comparison to seawater in the different water masses using DESeq2 analysis. Communities associated to plastics collected in the northern Adriatic harboured more significantly enriched families compared to seawater than plastics collected in the North Atlantic and Pacific. The family *Rhodobacteraceae* was the only family enriched on plastics in all three oceanic regions (Fig. 2). The families *Phormidesmiaceae* and *Hyphomonadaceae* were also enriched on plastics collected in the northern Adriatic and North Atlantic compared to the corresponding seawater. The families *Saprospiraceae*, *Pirellulaceae* and *Oleiphilaceae* were enriched only on plastics collected in the northern Adriatic compared to the ambient water, while *Sphingomonadaceae* and *Rhizobiaceae* were enriched only on plastics collected in the North Atlantic, and *Comamonadaceae* were enriched only on plastics collected in the Pacific compared to the corresponding ambient water (Fig. 2).

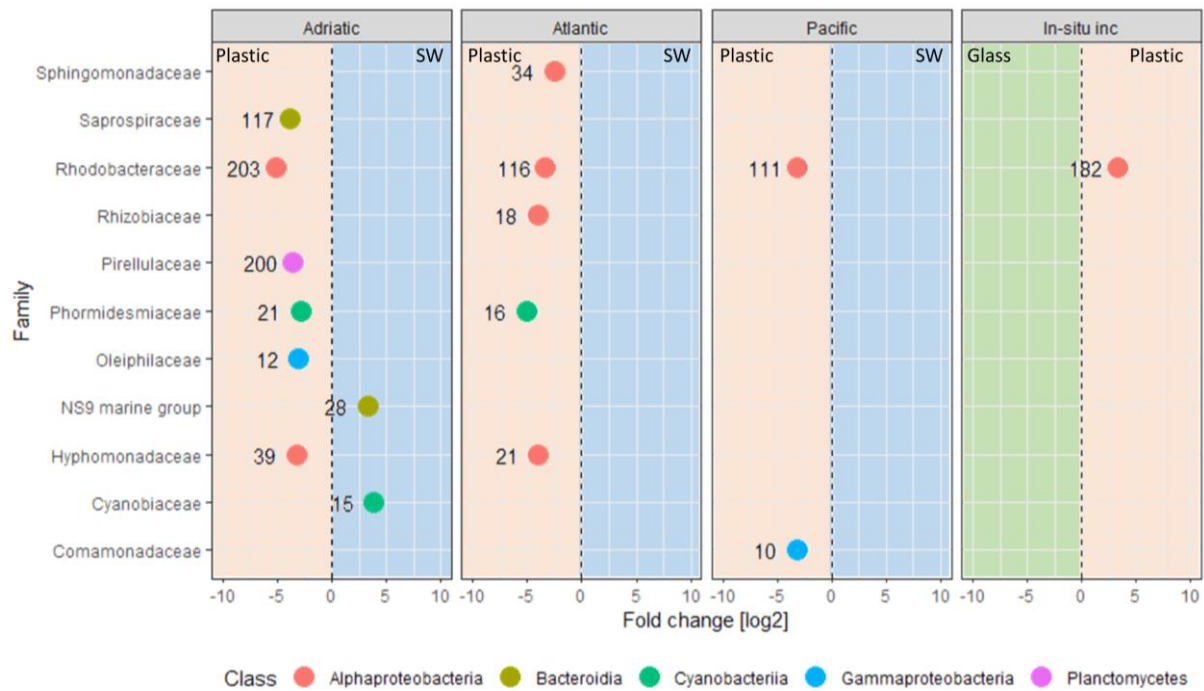


Fig. 2 - Enriched bacterial families between plastics and seawater in the northern Adriatic, the North Atlantic and the Pacific, and between plastics (HDPE + LDPE + PP) and glass in the in-situ incubations (in-situ inc.) in the northern Adriatic. Only significantly enriched taxa were included (adjusted $p < 0.05$). Families enriched on plastics, glass and in seawater (SW) are represented in the red, green and blue areas, respectively. The number associated with each symbol represents the number of OTUs in the family.

The bacterial community associated with PE and PP in the northern Adriatic was enriched in some OTUs (Fig. S7). Four *Flavobacteriaceae* OTUs (OTU 243, OTU 300, OTU 2231 and OTU 5577), one *Microtrichaceae* OTU (OTU 1048), one *Oleiphilaceae* OTU (OTU 49), one *Rhodobacteraceae* OTU (OTU 1457) and three *Sphingomonadaceae* OTUs (OTU 36, OTU 393 and OTU 6729) were enriched on PE, and one *Phormidesmiaceae* OTU (OTU 38), one *Flavobacteriaceae* OTU (OUT 137) and one *Saccharospirillaceae* OTU (OTU 61) were enriched on PP.

Taxa enriched on PE, PP or glass in in-situ incubations in the northern Adriatic

To identify taxa enriched on PE vs. PP vs. glass, we also performed the DESeq2 analysis on 16S rRNA amplicon sequences from the two-month incubation experiment of Pinto *et al.* (2019). *Rhodobacteraceae* was the only enriched family on plastic (PE and PP) compared to glass in the in-situ incubations.

Comparing the bacterial communities on PE (LDPE+HDPE) and glass of the three sampling dates combined, there were no OTUs enriched on either one of the surfaces (DESeq2 analysis, $p > 0.05$). When performing the same analysis comparing the bacterial communities of PE and PP, OTU 6540, classified as *Primorskyibacter sedentarius*, was enriched in PE ($\log_2$

Fold Change = -5.53, $p < 0.05$). However, when analysing only the samples incubated for one month in the in-situ incubations, there were 10 OTUs enriched on the PE (LDPE + HDPE) over glass, and two OTUs enriched on glass over PE. Interestingly, there were four *Rhodobacteraceae* OTUs (OTU 15, OTU 23, OTU 95 and OTU 731) enriched in LDPE biofilms over both PP and glass biofilms (Fig. 3).

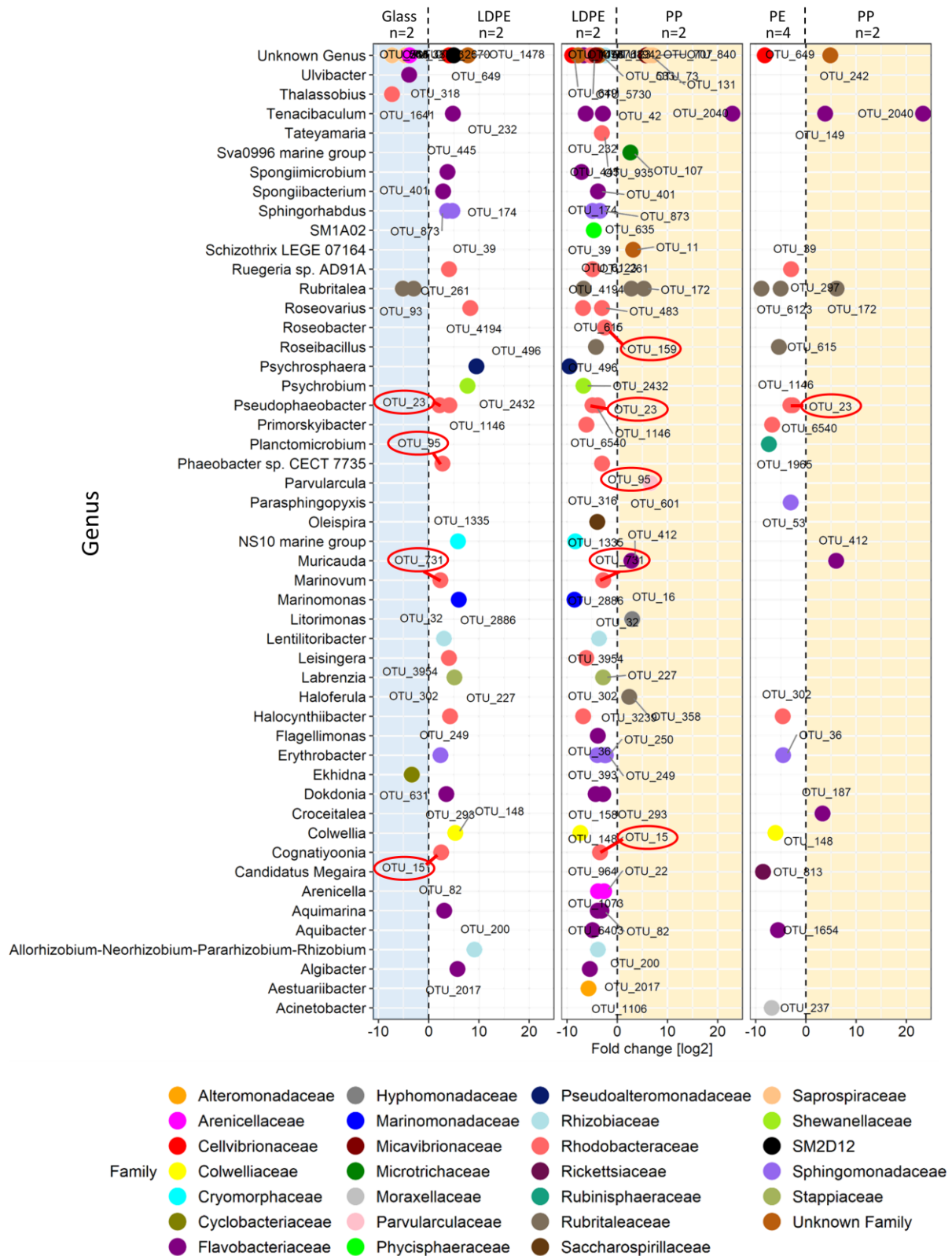
LDPE-laboratory incubations

We incubated two plastics (Fig. S8) collected in the northern Adriatic (incubations A and B) in artificial seawater amended with ammonium and phosphate for two years with LDPE as the sole carbon source. A total of 35 OTUs (Table S12) increased in relative abundance in these incubations after one year compared to the composition of the initial inoculum. These OTUs were also still present in incubation B after two years. Out of these 35 OTUs, only 19 were present in the incubations after one or two years with relative abundances $>0.5\%$ (Fig. S9). OTUs classified as *Cognatiyoonia* (OTU 15), *Parvibaculaceae* (OTU 28), *Cognatishimia* (OTU 40), *Methyloligellaceae* (OTU 55), *Ketobacter* (OTU 60) and *Sneathiella* (OTU 273) were present in both, incubations A and B in relative abundances $>1\%$ after one year and also after two years in incubation B (Fig. S9).

SEM analysis revealed the presence of a biofilm on both incubations A and B after one and two years (Fig. 4 B-E). After removing the biofilm from a plastic piece from incubation A after one year, holes on the plastics surface were visible similar in shape as bacteria (Fig. 4F).

Presence of the OTUs enriched in the LDPE-laboratory incubations on plastics in the ocean

We searched for the 35 OTUs enriched in our LDPE-laboratory incubations on the plastics and seawater collected in the three oceanic regions and on the in-situ incubation in the northern Adriatic Sea. These OTUs represented $4.1 \pm 3.2\%$, $4.8 \pm 4.8\%$ and $7.4 \pm 6.4\%$ of the total bacterial community associated with plastics collected in the northern Adriatic, the North Atlantic and the Pacific, respectively. Sixteen OTUs were present on at least one plastic at all three sampling sites (Fig. S6 C).



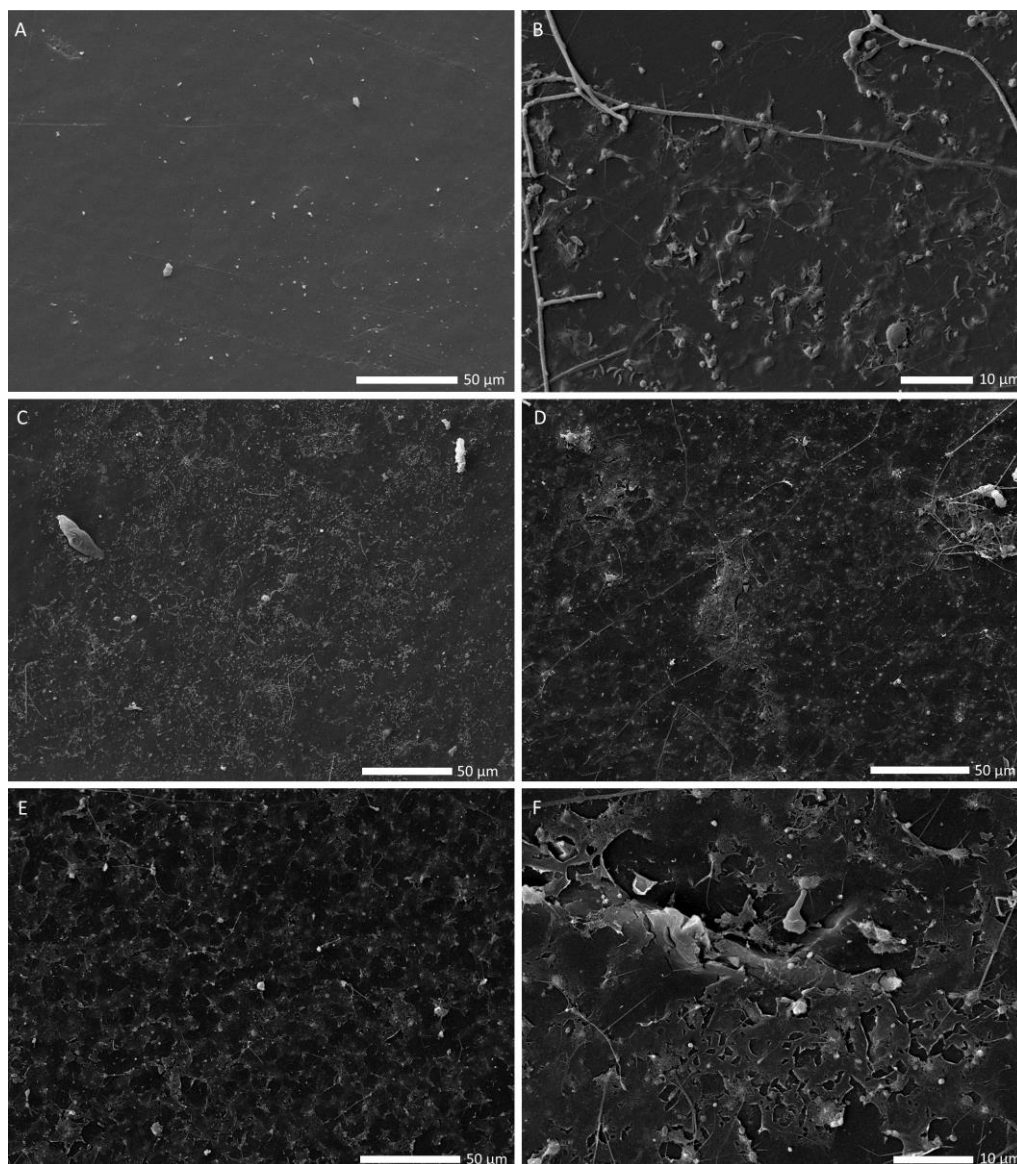


Fig. 4 – SEM pictures of (A) a control plastic incubated in artificial seawater without the addition of a plastic previously covered with a biofilm; (B) plastic A one year after the initial incubation; (C) plastic B one year after the initial incubation; (D) plastic A two years after the initial incubation; (E) plastic B two years after the initial incubation and (F) plastic A one year after the initial incubation after biofilm removal.

From the 35 OTUs, representatives of *Cognatiyoonia*, *Psychrobacter*, *Acinetobacter*, *Roseovarius*, *Roseobacter*, and *Marinovum* were found to be relatively abundant on plastics at all three locations (Fig. 5). OTU 15, affiliated to *Cognatiyoonia*, was found on almost all plastics at all stations (Fig. 6), however, with varying relative abundances of up to 7%. In the ambient seawater, the highest relative abundance of this representative (OTU 15) of the *Cognatiyoonia* was only 0.8%.

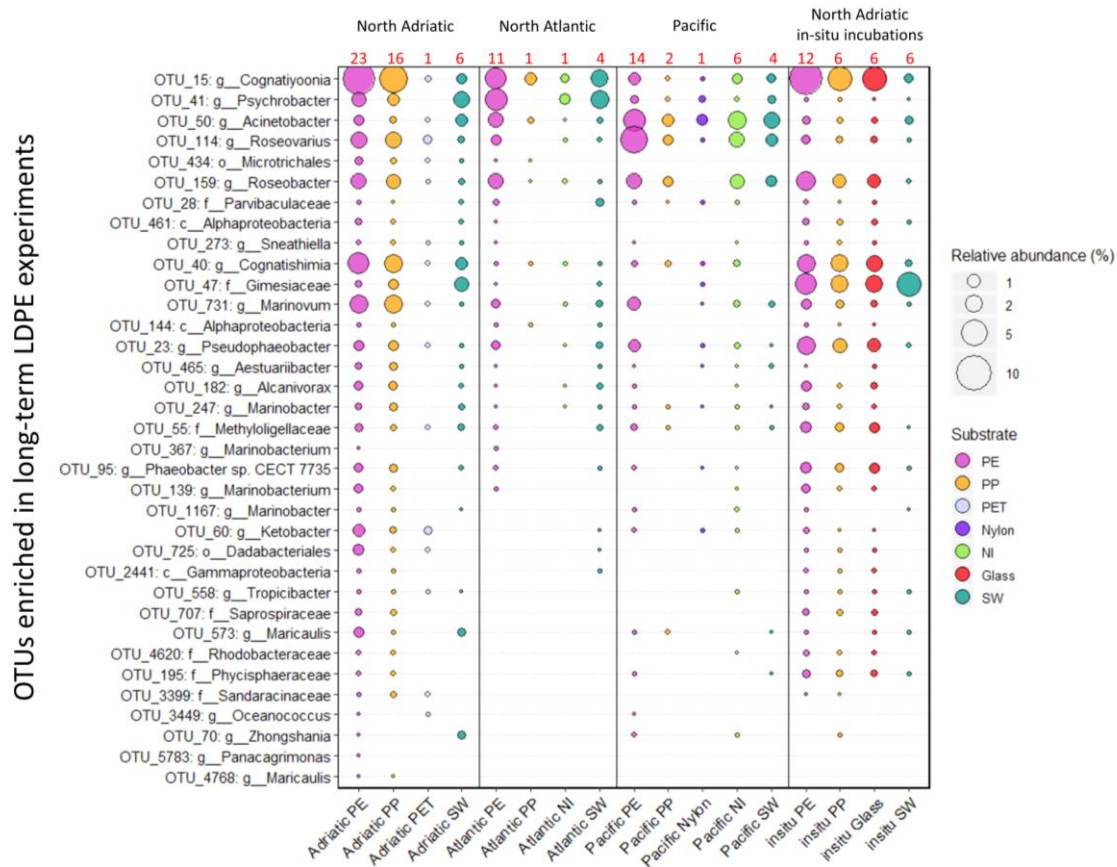


Fig. 5 - Relative abundance of OTUs enriched in the LDPE laboratory long-term incubations in seawater and different surfaces across the different sampling sites. The numbers in red indicate the number of samples. The OTUs represented on the y-axis are the ones enriched on LDPE biofilms after one year of incubation in artificial seawater with LDPE as their sole carbon source.

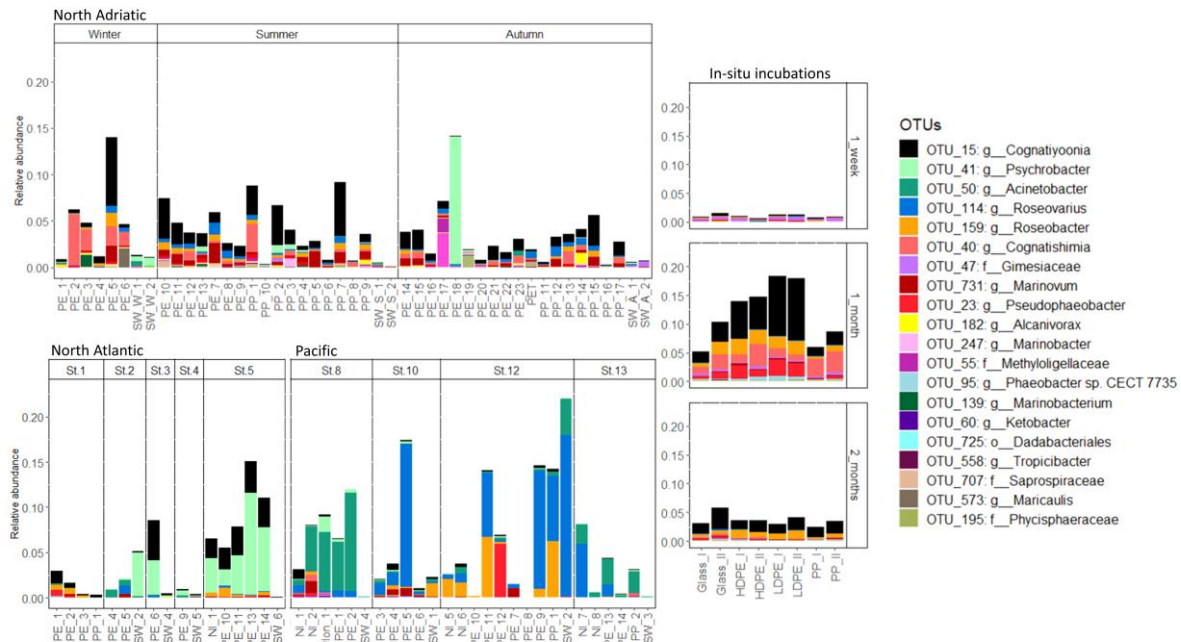


Fig. 6 – Stacked plots of the relative abundance of the OTUs enriched in the long-term LDPE incubations after one year incubated in ASW with LDPE as sole carbon source. Only OTUs that occurred with > 0.5% relative abundance in at least one of the samples are shown. The x-axis represents each individual sample collected in the northern Adriatic, North Atlantic, Pacific and on the different surfaces incubated for two months in the northern Adriatic (Pinto *et al.*, 2019). The y-axis indicates the relative abundance of the classified 16S rRNA genes from 0%-23%. The labels represent the number of the OTU followed by its lowest taxonomic classification.

This difference, however, was not detectable anymore after two months in the in-situ incubation. From the 35 OTUs, representatives of *Cognatiyoonia* and *Psychrobacter* (OTUs 15 and 41, respectively) were the two most abundant OTUs in the plastic associated biofilm in the North Atlantic (Fig. 5). *Acinetobacter* and *Roseovarius* (OTUs 50 and 114, respectively) were the two most abundant OTUs in the biofilm from plastics collected in the Pacific (Fig. 5).

The four *Rhodobacteraceae* OTUs enriched on LDPE sheets in the in-situ incubations (OTU 15, OTU 23, OTU 95 and OTU 731) when compared to PP and glass after one month of incubation were also enriched in the laboratory LDPE-incubations (Fig. 6). However, this enrichment was not detectable anymore after two months of incubation. OTU 15 was particularly abundant on LDPE after one month of incubation compared to the biofilm of PP and glass. OTU 159, also enriched in the laboratory incubations, was also enriched on LDPE compared to PP. OTU 36, classified as *Erythrobacter*, was enriched on PE over PP in both the Adriatic and in the in-situ incubations after one month of incubation (DESeq2 plot PE vs. PP Adriatic).

Discussion

There has been discussion on whether there is a core plastic biofilm community and whether plastic degraders are part of it (Debroas *et al.*, 2017). Our study reveals that while there is high variability in bacterial community composition even between plastics collected at the same site, certain taxa are consistently present on plastics even when collected in different oceanic regions (Fig. 1). Some of these taxa that are ubiquitous on plastics were enriched in our incubations with LDPE as the sole carbon source, suggesting that they might utilize LDPE-derived compounds as a carbon source.

The bacterial community composition on PE and PP was different from that of the ambient water (Fig. 1), similar to what has been shown in previous studies (Dussud *et al.*, 2018; Amaral-Zettler *et al.*, 2020) but was relatively similar between the two polymers at the different sites. For a more detailed discussion on the comparison of the bacterial community composition of plastic-associated biofilms collected at the different sites, see S2. Some OTUs, however, were preferentially colonizing or growing on either PE or PP in the northern Adriatic (Fig. S6). For example, OTUs classified as *Erythrobacter* sp. (OTU 36, OTU 393 and OTU 6729) and *Oleiphilus* sp. (OTU 49) were enriched in PE over PP. Members of these genera have been shown to harbour genes encoding alkane monooxygenases and to play an important role in oil

degradation in the ocean (Wang *et al.*, 2010; Toshchakov *et al.*, 2017). Alkane degradation pathways have been suggested as the most probable PE degradation pathway given the similar chemical structure of PE and alkanes (Devi *et al.*, 2016). Interestingly, OTU 36 (affiliated to *Erythrobacter* sp.) was also enriched on PE compared to PP in the in-situ incubations after one month (Fig. 4). In the Baltic Sea, *Erythrobacter* sp. was also abundant especially on PE (Oberbeckmann *et al.*, 2018), and one *Erythrobacter* OTU was exclusively associated with PE collected in the Baltic and the North Sea (Oberbeckmann and Labrenz, 2019). The enrichment of alkane-degraders on PE in comparison to PP is consistent with the possibility that certain organisms discriminate for certain plastics either due to their ability to degrade plastic-derived hydrocarbons or utilize specific plastic additives.

Members of the *Sphingomonadaceae*, such as *Erythrobacter* sp., and *Rhodobacteraceae* have been regularly found associated with plastics (Bryant *et al.*, 2016; Debroas *et al.*, 2017; Curren and Leong, 2019). Additionally, Oberbeckmann and Labrenz (2019) found that some OTUs from these families made up more than half of the only 45 OTUs present on plastics collected in four different studies. Our study provides further evidence that members of the *Rhodobacteraceae* family are in fact enriched on plastics compared to seawater and other surfaces across different water masses. This is not surprising since members of the *Rhodobacteraceae* family are key members of biofilms developing on different surfaces in the marine environment (Elifantz *et al.*, 2013). As revealed in our *in-situ* incubations, however, some of them, such as *Cognatiyoonia* sp. (OTU 15), *Pseudophaeobacter* sp. (OTU 23), *Phaeobacter* sp. (OTU 95) and *Roseobacter* sp. (OTU 159) have a preference for LDPE over glass and PP. This might be due to their ability to degrade LDPE-related hydrocarbons as indicated by their enrichment in our laboratory incubations with LDPE as the sole carbon source after one year. However, whether they have the ability to degrade the LDPE hydrocarbon backbone or associated plastic additives (Wright *et al.*, 2020) remains unknown. Furthermore, it is important to note that only duplicate samples were collected in the *in-situ* incubations in northern Adriatic, precluding rigorous statistical analyses.

Cognatiyoonia is a new genus within the *Rhodobacteraceae* family (Wirth and Whitman, 2018) to reclassify *Loktanella koreensis* and *Loktanella sediminum*. The genus *Loktanella* has been previously found to be enriched on plastics over non-plastic surfaces (Ogonowski *et al.*, 2018) and particularly abundant on PET and LDPE (Delacuvellerie *et al.*, 2019). In our study, OTU 15, classified as *Cognatiyoonia*, was present in the biofilm of almost all plastics (Fig. 6). Also, OTU 15 exhibited a high relative abundance in the laboratory incubations with LDPE as

the sole organic carbon source after one year. This might indicate that OTU 15 has the ability to utilize plastic-derived hydrocarbons, especially those related to alkanes. Certain *Loktanella* strains have the ability to degrade n-alkanes between C₁₀ and C₂₂ (Harwati *et al.*, 2007). Furthermore, they have been found enriched in oil degradation experiments (Lanfranconi *et al.*, 2010; Sanni *et al.*, 2015). The potential of *Cognatiyoonia* sp. to degrade hydrocarbons and plastics is uncertain, but its ubiquitous presence on plastics collected at different locations and the ability to survive on LDPE as sole carbon source suggest that it might play a role in the degradation of plastics in the ocean.

The above mentioned genera *Pseudophaeobacter* sp. (OTU 23), *Phaeobacter* sp. (OTU 95) and *Roseobacter* sp. (OTU 159), also enriched in the long-term incubations with LDPE as the only carbon source, have also been associated with hydrocarbon degradation (Bacosa *et al.*, 2018; Brakstad *et al.*, 2018). Even though they were present in lower relative abundance than OTU 15, they were still present on plastics collected at all the different oceanic regions (Fig. 6).

As suggested by the *in-situ* incubation, the relative abundance of the OTUs enriched in the LDPE-laboratory incubations varies between different stages of biofilm development, especially on LDPE. The putative LDPE-degrading OTUs were most prevalent during the early stages of biofilm development after about one month of incubation and significantly decreased in relative abundance after two months (Fig. 6). Also, after one month of incubation the largest differences in bacterial community composition between different plastic types were observed in the *in-situ* incubations (Pinto *et al.*, 2019). Microbes with a preference for a specific type of plastic are dominant in the biofilm layers which are in close contact with the plastic surface (Kirstein *et al.*, 2019). In subsequently formed layers when the biofilm thickens, the bacterial community is most likely shaped by internal biofilm processes and micro-environmental factors rather than by microbes selected due to surface properties. For example, Pinto *et al.* (2019) reported that after a one- and two-month incubation period the composition of the bacterial communities growing on different plastics were more similar to each other than after one week of incubation. This might explain the decrease in relative abundance of organisms potentially capable of degrading LDPE-originating compounds in the later stages of biofilm development. This agrees with studies reporting similar bacterial community compositions on different polymers after prolonged incubation periods (Kirstein *et al.*, 2018). The decrease in the number of OTUs with preference for a specific surface in later stages of the biofilm development might be the result of changes in the biofilm

environment, no longer favouring microbes with the ability to metabolize plastic-originating compounds. The development of a thicker biofilm creates a diverse habitat with a plethora of organic carbon compounds (Dang and Lovell, 2016) probably more readily accessible to bacteria than plastic-derived hydrocarbons (Min *et al.*, 2020). Nevertheless, in the *in-situ* incubations even after two months, OTUs enriched in our LDPE-laboratory incubations were still present in the biofilms obtained from all plastics (Fig. 6).

Taken together, degraders of plastic-derived compounds are recruited early in the development of the biofilm on plastic surfaces (Kirstein *et al.*, 2019) and attain high relative abundance at the early stage of biofilm formation, but decrease in relative abundance with further biofilm development. These putative plastic-compound degraders remain in the plastic-associated biofilm in low relative abundances, potentially in the layers that are tightly connected to the plastic surface. Whether these bacteria do degrade the plastics remains unknown. For example, members of the *Rhodobacteraceae* family are known to exhibit high metabolic versatility (Michael *et al.*, 2016) and are capable of occupying different metabolic niches when environmental conditions change.

In conclusion, through a combination of *in-situ* incubations, laboratory long-term incubations with LDPE as the sole organic carbon source and analyses of collected plastics from three oceanic basins, strong evidence is provided for the ubiquitous presence of bacteria capable of utilizing LDPE-derived compounds as a carbon source within plastic biofilms in the global ocean.

Material and Methods

Sampling

Sampling was conducted at four stations in the Pacific, five stations in the North Atlantic and at one location in the northern Adriatic Sea (Fig. S1, Table S1). The Pacific samples were collected aboard R/V *Sonne* during the SO248 expedition with a bongo net and a mesh size of 300 μm in May-June 2016. The net was kept at the sea surface by attaching one float on each side of the net (Fig. S8). The North Atlantic samples were collected aboard the R/V *Rámon Margalef* during the RadProf 2017 expedition belonging to the time series RADIALES-PROFUNDOS in July 2017 (Prieto *et al.*, 2015). The northern Adriatic Sea samples were collected in February, August and November of 2016. Samples from the North Atlantic and the northern Adriatic Sea were collected with a net for microplastic sampling (Hydrobios,

Germany) with a mesh size of 500 μm . At all locations, the net was towed with 2 knots for 30-45 min (detailed information of sampling at each station is given in Table S1). Water samples (2-5 L) from all locations were also collected and immediately filtered through 0.2 μm polycarbonate filters and stored at -80°C .

The plastics were collected from the cod end of the net into a bucket filled with seawater (SW) from the same location and immediately taken to the laboratory for processing. To separate the collected plastic material by size, the samples were passed through a series of sieves with mesh size of 9.5 mm, 4.5 mm, 1.4 mm and 300 μm and rinsed with 0.2 μm freshly filtered SW. The content collected in each sieve was immediately transferred to petri dishes with 0.2 μm filtered SW. Each plastic piece was collected from the Petri dishes, washed three times in 0.2 μm filtered SW to remove all organisms not tightly attached to the plastic biofilm, put in a Greiner tube and immediately stored at -80°C .

Inorganic nutrient analyses and environmental data

Inorganic nutrient concentrations (NO_3^- , NO_2^- and PO_4^{3-}) were determined only on SW samples collected with Niskin bottles just below the sea surface. In the northern Adriatic Sea, surface seawater was filtered through combusted Whatman GF/F filters and stored in polyethylene bottles at -20°C . Nutrient analyses were performed within one month following standard protocols (Strickland and Parsons, 1972). Surface seawater samples collected in the North Atlantic were frozen on board until the inorganic nutrients were measured in the laboratory using a QuAAtri auto-analyser (SEAL Analytical) following published protocols (Coverly *et al.*, 2012). Most nutrient concentrations at the Pacific stations were below the detection limit using standard methods. Therefore, they were excluded from this study.

Temperature and salinity measurements from the northern Adriatic Sea were made available from the sampling station RV001 located off the coast of Rovinj by the *Ruđer Bošković* Centre for Marine Research at Rovinj, Croatia. Temperature and salinity data from the stations in the Pacific and North Atlantic were obtained from the sensors mounted on the CTD sampling rosette deployed at each station. Data from the Pacific are available at Pangaea (<https://doi.pangaea.de/10.1594/PANGAEA.864673>).

Colonization pattern of LDPE and other plastics incubated in-situ in the northern Adriatic Sea

To investigate the presence of putative LDPE degraders in biofilms on different surfaces over a two-month incubation period in the northern Adriatic Sea, we used 16S rRNA amplicon sequencing of the prokaryotic communities collected during incubations exposed to solar radiation, downloaded from the NCBI Sequence Read Archive (SRA) database (BioProject: PRJNA515271). Details of the experimental setup are given elsewhere (Pinto *et al.*, 2019).

The samples comprised duplicates of 4 cm² sized pieces of virgin polypropylene (PP), LDPE and HDPE, with approximately 0.5 mm thickness, glass slides of 1 cm², with approximately 1 mm thickness, and seawater samples. The different substrates were mounted on a floating frame in the northern Adriatic Sea, approximately 500m off the coast of Rovinj, Croatia, over a three-month period (November 2016—January 2017) and the samples were taken after one week, one month and two months of incubation. Processing of the samples, the DNA extraction method, PCR primers and sequencing technology and specifications used were the same as described previously (Pinto *et al.*, 2019).

Enrichment of bacterial communities living on LDPE as sole carbon source

Plastic material was collected in August 2016 off the coast of Rovinj, Croatia, and rinsed with 0.2 µm filtered seawater. Two large plastic pieces (Fig. S8) were incubated each in a 1 L borosilicate bottle filled with artificial seawater (ASW) amended with 10 µM NH₄Cl and 2 µM Na₂PO₄ (incubations A and B), however, without an organic carbon source other than that contained in the plastic material. The incubations were held at room temperature in the dark. For a scheme of the experimental setup see Fig. S9. After three weeks, each plastic was transferred to a new bottle with the same conditions. After repeating this procedure for three months, a small piece of the plastic of approximately 2.25 cm² was cut and transferred to a new bottle with ASW amended with ammonium and phosphate added in the form of NH₄Cl and Na₂PO₄, respectively, using the same concentrations as mentioned above, and 1 cm² sterile LDPE sheets were added as a carbon source. The LDPE sheets were purchased from Goodfellow. The same transfer procedure was repeated with new LDPE sheets every three weeks for a total period of two years. After one and two years of the initial incubation, one square from each flask which had the biofilm developing for one month was taken for 16S rRNA gene amplicon sequencing of the biofilm community. Due to low quality sequencing

output, the sample after two years of incubation A was excluded from further analysis. Two plastic pieces from the same flasks were also taken for scanning electron microscopy (SEM) analysis after one and two years. One piece was used to analyze the intact biofilm, and the second was used to analyze the surface of the plastic after removal of the biofilm. To remove the biofilm, the piece was submerged in Milli-Q water, vortexed for 30 sec, then submerged in 4% SDS buffer at room temperature for 4 h. Subsequently, the plastic was submerged again two times in fresh Milli-Q water, vortexed for 30 sec and gently dried on clean paper. A control plastic that was incubated in a separate bottle with the same ASW as incubations A and B for one month was also stored for SEM analysis.

SEM analysis

Samples for SEM were incubated in 2% glutaraldehyde for 10 min and then stored at -80°C until processing. The samples were then dehydrated with an ethanol dilution series of 30%, 50%, 70%, 80%, 90%, 95% each for 10 min and three times in 100% absolute ethanol for 10 min. The dehydrated samples were CO₂ critical-point dried with a CPD 300 auto critical-point dryer (Leica Microsystems). The dried pieces were gold-coated using a JFC-2300HR sputter coater (JEOL Ltd.) for 80 sec. Pictures were taken using a secondary electron detector with a JEOL JSM-IT300 scanning electron microscope with a 15kV acceleration voltage in ultra-high vacuum.

DNA extraction and 16S rRNA sequencing

DNA extraction of all samples was performed using the modified bead-beating approach in combination with the Puregene Tissue DNA extraction kit (Qiagen, Valencia, CA) (Debeljak *et al.*, 2017). DNA extraction and sequencing were performed in four batches. The first one comprised all the northern Adriatic samples, the second the laboratory LDPE incubations after one-year incubation and the Pacific samples, and the third the laboratory LDPE incubations after two years incubation and the North Atlantic samples. For each batch, we added a blank that was extracted, PCR amplified and sequenced at the same time as the samples using the same protocols (Fig. S12).

The primer pair 341F (5'- CCT ACG GGN GGC WGC AG-3') and 802R (5'- TAC HVG GGT ATC TAA TCC-3') was used to PCR amplify the V3-V4 hypervariable region of the 16S rRNA gene, resulting in fragments of ~460 bp. Each PCR was performed in a total volume of 52 µL containing 25 µL Library Amplification Ready Mix 2xMM (Kapa Biosystems), 1 µL of each 25

μM primer, 23 μL of sterile water and 2 μL of extracted DNA. Amplification was done on a Mastercycler Pro (Eppendorf AG, Germany). The conditions consisted of an initial denaturation at 95°C for 3 min, followed by 20 cycles at 98°C for 20 s, at 56°C for 30 s and at 72°C for 30 s, and a final elongation at 72°C for 5 min.

PCR products were then purified in a 96-well plate using the Agencourt AMPure XP Purification kit and protocol (Beckman Coulter Life Sciences). These purified PCR products were barcoded and an additional 10-cycle PCR was done, followed by paired-end next-generation amplicon sequencing (2 x 250 bp) using Illumina MiSeq technology at Microsynth AG, Switzerland. All raw sequence files were submitted to the NCBI Sequence Read Archive (SRA) database (BioProject: PRJNA623496).

Identification of plastic types using Raman microspectroscopy

After DNA extraction, each plastic was dried on a clean paper and its chemical nature was identified using a LabRAM HR800 confocal Raman spectroscopy system (Horiba Jobin-Yvon). Excitation for Raman scattering was provided by a 532 nm NdYAG laser. The Raman spectrum was obtained for the range of 400-3,200 cm⁻¹. Each sample was compared with reference scans from plastics of known composition. The polymers, which could not be identified were classified as not identified (NI). Most NI polymers were coloured.

Processing of sequencing data

Merging of paired-end reads, quality filtering (max. error of 1 in 100 nucleotides), elimination of singletons, chimera filtering, mapping and clustering of operational taxonomic unit (OTU) were performed using usearch tools, with OTU clustering being performed by UPARSE (Edgar, 2013). Taxonomic assignments of OTUs were done using blastn against the SILVA_138_SSURef_NR99 reference database with a threshold of 97% similarity between the query and reference sequences. Samples with less than 1000 classified reads were excluded from further analysis. All OTUs classified as chloroplasts were excluded from further analysis.

Statistical analysis

All statistical analyses were performed using R version 3.5.1 in RStudio version 1.1.456. All plots were done using R package “ggplot2” version 3.3.1 (Wickham, 2016), unless stated otherwise. Venn diagrams were built using the R package “VennDiagram” version 1.6.20 (Chen and Boutros, 2011). OTU diversity and richness indexes were calculated with the R package

“iNext” version 2.0.20 (Hsieh *et al.*, 2016) using a coverage base rarefaction of 97%, corresponding to the lower coverage calculated for a sample.

To visualise the similarity of the prokaryotic communities of all samples, not including the in-situ or the laboratory incubation samples, non-metric multidimensional scaling (nMDS) was performed with Bray-Curtis dissimilarity as the distance measurement. The environmental factors (temperature, salinity and PO₄, NO₃ and NO₂ concentrations) were fitted to the ordination plots using the ‘envfit’ function of the vegan package in R. A Mantel test was performed to evaluate correlations between the prokaryotic community composition of the biofilms of polymers and the different environmental factors. An additional Mantel test was performed to determine correlations between the relative abundance of the 35 OTUs enriched in the laboratory incubations and environmental factors. Euclidian distance matrices were used for the environmental factors and a Bray-Curtis dissimilarity matrix was used for the community composition. A PERMANOVA was performed to determine whether the prokaryotic community composition was significantly different between sampling regions (e.g. Atlantic Ocean, Pacific Ocean and northern Adriatic Sea), sampling stations or sample type (e.g. PE, PP, PET, nylon and ambient seawater). PERMANOVA analysis was also performed just with the 35 OTUs enriched in the laboratory experiments after one year of incubation. Samples from polymers remaining unclassified were not considered in this analysis. We also evaluated differences in community composition between different sites, stations and plastic types using homogeneity of dispersions tests on Bray-Curtis dissimilarity matrices (‘betadisper’ from R package ‘vegan’ version 2.5.6). Pair-wise PERMANOVAs were performed to each of the above-mentioned factors to determine differences between stations, oceanic basins or sample types. Differences were considered significant if $p < 0.05$.

The fold-change in abundance of each OTU between sample types for each location was calculated using the R package “DESeq2” (Love *et al.*, 2014), which fits negative binomial generalized linear models for each OTU and tests significance using the Wald test.

Acknowledgments

We thank the crew and onboard scientists of R/V *Rámon Margalef* and the R/V *Sonne* assisting us during the Radprof 2017 and the SO248 campaigns, respectively. We acknowledge César González Pola for organizing the RAD-PROF 2017 expedition. We also thank the Ruđer Bošković Center for Marine Research for accommodating us during our stays in Rovinj, Croatia.

We especially thank Mirjana, Dario, Ingrid, Marino and Paolo for all the help provided during sampling in the Adriatic. Financial support was provided by a Doctoral Fellowship (DOC scholarship) from the Austrian Academy of Sciences (ÖAW) awarded to MP, the ARTEMIS project of the Austrian Science Fund (P 28781-B21) to GJH and the research platform PLENTY financially supported by the University of Vienna, Austria. Cruise SO248 was funded by the German Federal Ministry of Education and Research (BMBF) within the BacGeoPac project (03G0248A) and by the Deutsche Forschungsgemeinschaft within the Collaborative Research Center *Roseobacter* (TRR51) awarded to MS. The RAD-PROF campaign was funded by the RADIALES-PROFUNDAS project (RAD-PROF, Instituto Español de Ocenografía). Furthermore, we thank the anonymous reviewers for their constructive criticism, which helped to improve the manuscript.

References

- Amaral-Zettler, L.A., Zettler, E.R., and Mincer, T.J. (2020) Ecology of the plastisphere. *Nat Rev Microbiol* **1**–13.
- Amaral-Zettler, L.A., Zettler, E.R., Slikas, B., Boyd, G.D., Melvin, D.W., Morrall, C.E., et al. (2015) The biogeography of the Plastisphere: implications for policy. *Front Ecol Environ* **13**: 541–546.
- Bacosa, H.P., Erdner, D.L., Rosenheim, B.E., Shetty, P., Seitz, K.W., Baker, B.J., and Liu, Z. (2018) Hydrocarbon degradation and response of seafloor sediment bacterial community in the northern Gulf of Mexico to light Louisiana sweet crude oil. *ISME J* **12**: 2532–2543.
- Brakstad, O.G., Davies, E.J., Ribicic, D., Winkler, A., Brønner, U., and Netzer, R. (2018) Biodegradation of dispersed oil in natural seawaters from Western Greenland and a Norwegian fjord. *Polar Biol* **41**: 2435–2450.
- Bryant, J.A., Clemente, T.M., Viviani, D.A., Fong, A.A., Thomas, K.A., Kemp, P., et al. (2016) Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. *mSystems* **1**: e00024–16.
- Cai, L., Wu, D., Xia, J., Shi, H., and Kim, H. (2019) Influence of physicochemical surface properties on the adhesion of bacteria onto four types of plastics. *Sci Total Environ* **671**: 1101–1107.
- Chen, H. and Boutros, P.C. (2011) VennDiagram: a package for the generation of highly-customizable Venn and Euler diagrams in R. *BMC Bioinformatics* **12**: 35.
- Coverly, S., K  rouel, R., and Aminot, A. (2012) A re-examination of matrix effects in the segmented-flow analysis of nutrients in sea and estuarine water. *Anal Chim Acta* **712**: 94–100.
- Curren, E. and Leong, S.C.Y. (2019) Profiles of bacterial assemblages from microplastics of tropical coastal environments. *Sci Total Environ* **655**: 313–320.
- Dang, H. and Lovell, C.R. (2016) Microbial Surface Colonization and Biofilm Development in Marine Environments. *Microbiol Mol Biol Rev* **80**: 91–138.
- Debeljak, P., Pinto, M., Proietti, M., Reisser, J., Ferrari, F.F., Abbas, B., et al. (2017) Extracting DNA from ocean microplastics: a method comparison study. *Anal Methods* **9**: 1521–1526.
- Debroas, D., Mone, A., and Ter Halle, A. (2017) Plastics in the North Atlantic garbage patch: A boat-microbe for hitchhikers and plastic degraders. *Sci Total Environ* **599–600**: 1222–1232.
- Delacuvellerie, A., Cyriaque, V., Gobert, S., Benali, S., and Wattiez, R. (2019) The plastisphere in marine ecosystem hosts potential specific microbial degraders including *Alcanivorax borkumensis* as a key player for the low-density polyethylene degradation. *J Hazard Mater* **380**: 120899.
- Devi, R.S., Kannan, V.R., Natarajan, K., Nivas, D., Kannan, K., Chandru, S., and Antony, A.R. (2016) The role of microbes in plastic degradation. *Environ Waste Manag* **341**.
- Dudek, K.L., Cruz, B.N., Polidoro, B., and Neuer, S. (2020) Microbial colonization of microplastics in the Caribbean Sea. *Limnol Oceanogr Lett* **5**–17.
- Dussud, C., Hudec, C., George, M., Fabre, P., Higgs, P., Bruzard, S., et al. (2018) Colonization of Non-biodegradable and Biodegradable Plastics by Marine Microorganisms. *Front Microbiol* **9**: 1571.
- Dussud, C., Meistertzheim, A.L., Conan, P., Pujo-Pay, M., George, M., Fabre, P., et al. (2018) Evidence of niche partitioning among bacteria living on plastics, organic particles and surrounding seawaters. *Environ Pollut* **236**: 807–816.
- Edgar, R.C. (2013) UPARSE: highly accurate OTU sequences from microbial amplicon reads. *Nat Meth* **10**: 996–998.
- Elifantz, H., Horn, G., Ayon, M., Cohen, Y., and Minz, D. (2013) Rhodobacteraceae are the key members of the microbial community of the initial biofilm formed in Eastern Mediterranean coastal seawater. *FEMS Microbiol Ecol* **85**: 348–357.
- Harrison, J.P., Hoellein, T.J., Sapp, M., Tagg, A.S., Ju-Nam, Y., and Ojeda, J.J. (2018) Microplastic-associated biofilms: a comparison of freshwater and marine environments. In *Freshwater Microplastics*. Springer, Cham, pp. 181–201.
- Harrison, J.P., Schratzberger, M., Sapp, M., and Osborn, A. (2014) Rapid bacterial colonization of low-density polyethylene microplastics in coastal sediment microcosms. *BMC Microbiol* **14**: 232.

- Harshvardhan, K. and Jha, B. (2013) Biodegradation of low-density polyethylene by marine bacteria from pelagic waters, Arabian Sea, India. *Mar Pollut Bull* **77**: 100–106.
- Harwati, T.U., Kasai, Y., Kodama, Y., Susilaningih, D., and Watanabe, K. (2007) Characterization of diverse hydrocarbon-degrading bacteria isolated from Indonesian seawater. *Microbes Environ* **22**: 412–415.
- Hossain, M.R., Jiang, M., Wei, Q., and Leff, L.G. (2019) Microplastic surface properties affect bacterial colonization in freshwater. *J Basic Microbiol* **59**: 54–61.
- Hsieh, T.C., Ma, K.H., and Chao, A. (2016) iNEXT : an R package for rarefaction and extrapolation of species diversity (Hill numbers). 1451–1456.
- Jacquin, J., Cheng, J., Odobel, C., Pandin, C., Conan, P., Pujo-Pay, M., et al. (2019) Microbial Ecotoxicology of Marine Plastic Debris: A Review on Colonization and Biodegradation by the “Plastisphere”. *Front Microbiol* **10**: 865.
- Jambeck, J.R., Geyer, R., Wilcox, C., Siegler, T.R., Perryman, M., Andrady, A., et al. (2015) Plastic waste inputs from land into the ocean. *Science* **347**: 768–771.
- Jiang, P., Zhao, S., Zhu, L., and Li, D. (2018) Microplastic-associated bacterial assemblages in the intertidal zone of the Yangtze Estuary. *Sci Total Environ* **624**: 48–54.
- Kesy, K., Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2019) Spatial Environmental Heterogeneity Determines Young Biofilm Assemblages on Microplastics in Baltic Sea Mesocosms . *Front Microbiol* **10**: 1665.
- Kettner, M.T., Rojas-Jimenez, K., Oberbeckmann, S., Labrenz, M., and Grossart, H.-P. (2017) Microplastics alter composition of fungal communities in aquatic ecosystems. *Environ Microbiol* **19**: 4447–4459.
- Kim, S.-H., Kim, J.-G., Jung, M.-Y., Kim, S.-J., Gwak, J.-H., Yu, W.-J., et al. (2018) Ketobacter alkanivorans gen. nov., sp. nov., an n-alkane-degrading bacterium isolated from seawater. *Int J Syst Evol Microbiol* **68**: 2258–2264.
- Kirstein, I. V., Wichels, A., Krohne, G., and Gerdt, G. (2018) Mature biofilm communities on synthetic polymers in seawater - Specific or general? *Mar Environ Res* **142**: 147–154.
- Kirstein, I.V., Wichels, A., Gullans, E., Krohne, G., and Gerdt, G. (2019) The Plastisphere – Uncovering tightly attached plastic “specific” microorganisms. *PLoS One* **14**: e0215859.
- Lanfranconi, M.P., Bosch, R., and Nogales, B. (2010) Short-term changes in the composition of active marine bacterial assemblages in response to diesel oil pollution. *Microb Biotechnol* **3**: 607–621.
- Lobelle, D. and Cunliffe, M. (2011) Early microbial biofilm formation on marine plastic debris. *Mar Pollut Bull* **62**: 197–200.
- Love, M.I., Huber, W., and Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* **15**: 550.
- Michael, V., Frank, O., Bartling, P., Scheuner, C., Göker, M., Brinkmann, H., and Petersen, J. (2016) Biofilm plasmids with a rhamnose operon are widely distributed determinants of the ‘swim-or-stick’ lifestyle in roseobacters. *ISME J* **10**: 2498–2513.
- Min, K., Cuiffi, J.D., and Mathers, R.T. (2020) Ranking environmental degradation trends of plastic marine debris based on physical properties and molecular structure. *Nat Commun* **11**: 727.
- Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2018) Environmental Factors Support the Formation of Specific Bacterial Assemblages on Microplastics. *Front Microbiol* **8**: 2709.
- Oberbeckmann, S. and Labrenz, M. (2019) Marine Microbial Assemblages on Microplastics: Diversity, Adaptation, and Role in Degradation. *Ann Rev Mar Sci*.
- Oberbeckmann, S., Löder, M.G.J., and Labrenz, M. (2015) Marine microplastic-associated biofilms—a review. *Environ Chem* **12**: 551–562.
- Oberbeckmann, S., Loeder, M.G.J., Gerdt, G., and Osborn, A.M. (2014) Spatial and seasonal variation in diversity and structure of microbial biofilms on marine plastics in Northern European waters. *FEMS Microbiol Ecol* **90**: 478–492.
- Oberbeckmann, S., Osborn, A.M., and Duhaime, M.B. (2016) Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. *PLoS One* **11**: e0159289.

- Ogonowski, M., Motiei, A., Ininbergs, K., Hell, E., Gerdes, Z., Udekwu, K.I., et al. (2018) Evidence for selective bacterial community structuring on microplastics. *Environ Microbiol* **20**: 2796–2808.
- Paço, A., Duarte, K., da Costa, J.P., Santos, P.S.M., Pereira, R., Pereira, M.E., et al. (2017) Biodegradation of polyethylene microplastics by the marine fungus *Zalerion maritimum*. *Sci Total Environ* **586**: 10–15.
- Pinto, M., Langer, T.M., Hüffer, T., Hofmann, T., and Herndl, G.J. (2019) The composition of bacterial communities associated with plastic biofilms differs between different polymers and stages of biofilm succession. *PLoS One* **14**: e0217165.
- Prieto, E., González-Pola, C., Lavín, A., and Holliday, N.P. (2015) Interannual variability of the northwestern Iberia deep ocean: Response to large-scale North Atlantic forcing. *J Geophys Res Ocean* **120**: 832–847.
- Roager, L. and Sonnenschein, E.C. (2019) Bacterial Candidates for Colonization and Degradation of Marine Plastic Debris. *Environ Sci Technol* **53**: 11636–11643.
- Sanni, G.O., Coulon, F., and McGenity, T.J. (2015) Dynamics and distribution of bacterial and archaeal communities in oil-contaminated temperate coastal mudflat mesocosms. *Environ Sci Pollut Res* **22**: 15230–15247.
- Schneiker, S., dos Santos, V.A.P.M., Bartels, D., Bekel, T., Brecht, M., Buhrmester, J., et al. (2006) Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium *Alcanivorax borkumensis*. *Nat Biotechnol* **24**: 997–1004.
- Strickland, J.D.H. and Parsons, T.R. (1972) A practical handbook of seawater analysis.
- Sudhakar, M., Doble, M., Murthy, P.S., and Venkatesan, R. (2008) Marine microbe-mediated biodegradation of low- and high-density polyethylenes. *Int Biodeterior Biodegradation* **61**: 203–213.
- Sudhakar, M., Trishul, A., Doble, M., Suresh Kumar, K., Syed Jahan, S., Inbakandan, D., et al. (2007) Biofouling and biodegradation of polyolefins in ocean waters. *Polym Degrad Stab* **92**: 1743–1752.
- Syranidou, E., Karkanorachaki, K., Amorotti, F., Avgeropoulos, A., Kolvenbach, B., Zhou, N.-Y., et al. (2019) Biodegradation of mixture of plastic films by tailored marine consortia. *J Hazard Mater* **375**: 33–42.
- De Tender, C., Devriese, L.I., Haegeman, A., Maes, S., Vangeyte, J., Cattijse, A., et al. (2017) Temporal dynamics of bacterial and fungal colonization on plastic debris in the North Sea. *Environ Sci Technol* **51**: 7350–7360.
- Toshchakov, S. V., Korzhnikov, A.A., Chernikova, T.N., Ferrer, M., Golyshina, O. V., Yakimov, M.M., and Golyshin, P.N. (2017) The genome analysis of *Oleiphilus messinensis* ME102 (DSM 13489T) reveals backgrounds of its obligate alkane-devouring marine lifestyle. *Mar Genomics* **36**: 41–47.
- Wang, L., Wang, W., Lai, Q., and Shao, Z. (2010) Gene diversity of CYP153A and AlkB alkane hydroxylases in oil-degrading bacteria isolated from the Atlantic Ocean. *Environ Microbiol* **12**: 1230–1242.
- Wickham, H. (2016) ggplot2: elegant graphics for data analysis, Springer.
- Wintzingerode, V.F., Göbel, U.B., and Stackebrandt, E. (1997) Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. *FEMS Microbiol Rev* **21**: 213–229.
- Wirth, J.S. and Whitman, W.B. (2018) Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera *Aestuariivita*, *Citricella*, *Loktanella*, *Nautella*, *Pelagibaca*, *Ruegeria*, *Thalassobius*, *Thiobacimonas* and *Tropicibacter*, and the proposal. *Int J Syst Evol Microbiol* **68**: 2393–2411.
- Wright, R.J., Bosch, R., Gibson, M.I., and Christie-Oleza, J.A. (2020) Plasticizer Degradation by Marine Bacterial Isolates: A Proteogenomic and Metabolomic Characterization. *Environ Sci Technol* **54**: 2244–2256.
- Yoshida, S., Hiraga, K., Takehana, T., Taniguchi, I., Yamaji, H., Maeda, Y., et al. (2016) A bacterium that degrades and assimilates poly(ethylene terephthalate). *Science* **351**: 1196–1199.
- Zettler, E.R., Mincer, T.J., and Amaral-Zettler, L. (2013) Life in the “plastisphere”: Microbial communities on plastic marine debris. *Environ Sci Technol* **47**: 7137–7146.

Supplementary Information

S1- Results of the taxonomy of the prokaryotic community on plastics and seawater across oceanic regions.

S2- Discussion on the comparison of the prokaryotic community composition of plastic biofilms collected at different sites.

Table S1 - Information on the sampling site.

Table S2 - Information on the samples.

Table S3 - Results of the ANOVA tests comparing diversity and richness indexes of the prokaryotic communities between the different sites, stations, season (in the case of the North Adriatic samples) and size of the plastics.

Table S4 - Results of the post-hoc Tukey tests performed on the ANOVAs comparing richness and diversity indexes of the different sampling sites (Table S3).

Table S5 – Results of the PERMANOVA, betadisper tests and pair-wise PERMANOVAs comparing the prokaryotic community composition between different polymer types, sampling site, sampling station and season in the case of the North Adriatic samples.

Table S6 – Envfit test results of fitted environmental factors to the ordination scores (NMDS) of samples dependent on their prokaryotic community composition.

Table S7 - Mantel tests identifying correlations between the community composition of all polymers and the distance between sampling stations and environmental factors.

Table S8 – Relative abundance of families present with more than 1% relative abundance in at least one samples across the three sampling sites.

Table S9 – OTUs found in plastics from all sampling sites, but not in SW.

Table S10 – OTUs with more than 1% relative abundance in at least one sample.

Table S11 – OTUs with more than 1% relative abundance in at least one sample of each sampling site.

Table S12 – OTUs that were enriched in the laboratory LDPE incubations after one year incubation, and that were still present in incubation B after two years.

Table S13 – ASW recipe.

Fig. S1- Sampling stations in (A) the Pacific Ocean, (B) the North Atlantic and (C) the northern Adriatic Sea.

Fig. S2- OTU richness and diversity indexes of samples collected across the three different sites. Each symbol represents one sample.

Fig. S3 - Venn diagrams displaying the relatively abundant families (>1% relative abundant in at least one sample of that site) shared between the biofilm of plastics collected from the different sampling sites and seawater.

Fig. S4 - Stacked plot of all genera present in at least one sample with a relative abundance >10% in the samples collected in the northern Adriatic.

Fig. S5- Stacked plot of all genera that were present at least in one sample with relative abundance >10% in the samples collected in the (A) North Atlantic and (B) Pacific.

Fig. S6 - Venn diagrams displaying OTUs shared between different sites.

Fig. S7 - Enriched bacterial families between the PE and PP samples collected in the northern Adriatic.

Fig. S8 – Photos of the Original plastics A and B collected from the northern Adriatic Sea.

Fig. S9- Stacked plot of OTUs that increased in relative abundance in the LDPE-incubations over time.

Fig. S10 - Sampling nets used to collect plastics in different sites.

Fig. S11 – Scheme of the LDPE-laboratory incubations.

Fig. S12 – Stacked plots of the relative abundance of the OTUs with relative abundance >0.7% found in each blank.

S1 – Taxonomy of the prokaryotic community on plastics and seawater across oceanic regions

There were 11 families that had a relative abundance $> 1\%$ in at least one plastic particle in all sampling sites (Fig. S3); these were *Cyanobiaceae*, *Flavobacteriaceae*; *Hyphomonadaceae*, *Moraxellaceae*, *Phormidesmiaceae*, *Pirellulaceae*, *Pseudoalteromonadaceae*, *Rhodobacteraceae*, *Sphingomonadaceae*, *Planococcaceae*, and *Rhizobiaceae*. In contrast to the other families, the latter two were only abundant on plastic and not in any of the seawater samples. Families that were relatively abundant ($>1\%$ relative abundance) on almost all plastics were *Rhodobacteraceae*, *Rhizobiaceae*, *Moraxellaceae* and *Hyphomonadaceae* (Table S8). Together, these 11 families represented a minimum of $45\% \pm 26\%$ ($n=8$) of the total classified 16S rRNA gene sequences of the biofilm communities in the northern Adriatic during the winter and a maximum of $88\% \pm 5\%$ ($n=4$) on plastics collected at Station 5 in the North Atlantic.

Erythrobacter were relatively abundant in almost all plastic samples across the three oceanic regions (Fig. S4 and Fig. S5). Microbes classified as *Yoonia-Loktanella* were abundant in almost all plastic samples across the Atlantic and Pacific (Fig. S5). Certain taxa like *Sulfitobacter* and *Phormidesmis* were more abundant in the plastics collected in the Atlantic, while others like *Roseovarius* and *Woeseia* were more abundant on plastics collected in the Adriatic (Fig. S4).

S2- Comparison of the prokaryotic community composition of plastic biofilms collected at different sites

For the plastic material collected in the different oceanic regions, it is unknown for how long these plastics were floating at the sea-surface. Therefore, the developmental stage of the plastic biofilm cannot be determined. Plastics collected at more coastal sites in the northern Adriatic and in the North Atlantic at Station 5 are more likely to have been in the water for shorter periods of time than plastics collected in the open ocean, like at the Pacific stations (Brandon et al., 2016). This could explain why the community composition differed between stations in the North Atlantic but not in the Pacific samples and why there was a significant correlation between the community composition and distance to land in the North Atlantic (Table S7). The stations in the North Atlantic ranged from more coastal to open ocean, while the Pacific stations were all in the open ocean (Fig. S1). Coastal stations are also more likely to harbour a mixture of plastics with some floating at the surface already for a long time, while

other plastics might be in the water for only a short period. A higher variability in the time the plastics collected in the northern Adriatic spent in the water could also explain the higher variability in the community composition and OTU diversity between different seasons (Fig. 1, Fig. S2). However, the lack of correlations between environmental factors and the prokaryotic community composition at the stations in the Pacific and North Atlantic could also be the result of plastics present in the water at a specific site for a variable period of time. Thus, biofilms could have been collected at different stages of development and differently influenced by environmental factors. Furthermore, plastic exposure to UV radiation (Pinto et al., 2019), presence of eukaryotes (von Ammon et al., 2018) and plastic-related characteristics, such as the presence of additives and other leachable compounds (Romera-Castillo et al., 2018; Tetu et al., 2019), sorption of compounds from the water (Rochman et al., 2013) and physico-chemical properties (Gross et al., 2016) are also likely to shape the microbial community of plastics biofilms.

Table S1 - Information on the sampling site.

Site	Station/ Season	Longitude	Latitude	PO4 (μM)	NO3 (μM)	NO2 (μM)	Temperature ($^{\circ}\text{C}$)	Salinity	Total plastics analysed	n° PEs	n° PPs	n° PET	n° Nylon	n° NI
Adriatic	Summer	13.62	45.09	0.04	0.07	0.02	23.84	37.85	17	7	10	0	0	0
Adriatic	Autumn	13.62	45.09	0.06	1.10	0.60	16.41	37.82	17	10	6	1	0	0
Adriatic	Winter	13.62	45.09	0.00	0.44	0.38	9.81	38.47	6	6	0	0	0	0
Pacific	St.8	179.00	11.00	-	-	-	27.828	34.435	5	2	0	0	1	2
Pacific	St.10	178.32	21.00	-	-	-	25.206	35.353	4	4	0	0	0	0
Pacific	St.12	177.33	33.00	-	-	-	15.763	34.599	9	6	1	0	0	2
Pacific	St.13	177.33	40.00	-	-	-	11.897	33.98	5	2	1	0	0	2
Atlantic	St.1	-10.33	42.00	0.024	0.06	0.038	18.084	35.74	4	3	1	0	0	0
Atlantic	St.2	-11.11	43.04	0.022	0.03	0.007	18.618	35.79	2	2	0	0	0	0
Atlantic	St.3	-13.90	42.00	0.040	0.01	0.017	19.1061	35.8	1	1	0	0	0	0
Atlantic	St.4	-16.33	42.79	0.029	0.04	0.029	19.7772	35.81	1	1	0	0	0	0
Atlantic	St.5	-8.75	43.49	0.018	0.10	0.105	19.6531	35.81	5	4	0	0	0	1

Table S2 - Information on the samples.

Sample	Site	Type	Season/Station	Size
PE_1	Adriatic	PE	Winter	(1) >9.5mm
PE_2	Adriatic	PE	Winter	(1) >9.5mm
PE_3	Adriatic	PE	Winter	(3) 1.4mm-4.75mm
PE_4	Adriatic	PE	Winter	(3) 1.4mm-4.75mm
PE_5	Adriatic	PE	Winter	(4) 300um-1.4mm
PE_6	Adriatic	PE	Winter	(1) >9.5mm
SW_W_1	Adriatic	SW	Winter	Seawater
SW_W_2	Adriatic	SW	Winter	Seawater
PE_10	Adriatic	PE	Summer	(2) 4.75mm-9.5mm
PE_11	Adriatic	PE	Summer	(2) 4.75mm-9.5mm
PE_12	Adriatic	PE	Summer	(3) 1.4mm-4.75mm
PE_13	Adriatic	PE	Summer	(3) 1.4mm-4.75mm
PE_7	Adriatic	PE	Summer	(1) >9.5mm
PE_8	Adriatic	PE	Summer	(1) >9.5mm
PE_9	Adriatic	PE	Summer	(2) 4.75mm-9.5mm
PP_1	Adriatic	PP	Summer	(1) >9.5mm
PP_10	Adriatic	PP	Summer	(3) 1.4mm-4.75mm
PP_2	Adriatic	PP	Summer	(1) >9.5mm
PP_3	Adriatic	PP	Summer	(1) >9.5mm
PP_4	Adriatic	PP	Summer	(1) >9.5mm
PP_5	Adriatic	PP	Summer	(1) >9.5mm
PP_6	Adriatic	PP	Summer	(2) 4.75mm-9.5mm
PP_7	Adriatic	PP	Summer	(2) 4.75mm-9.5mm
PP_8	Adriatic	PP	Summer	(2) 4.75mm-9.5mm
PP_9	Adriatic	PP	Summer	(3) 1.4mm-4.75mm
SW_S_1	Adriatic	SW	Summer	Seawater
SW_S_2	Adriatic	SW	Summer	Seawater
PE_14	Adriatic	PE	Autumn	(1) >9.5mm
PE_15	Adriatic	PE	Autumn	(1) >9.5mm
PE_16	Adriatic	PE	Autumn	(1) >9.5mm
PE_17	Adriatic	PE	Autumn	(1) >9.5mm
PE_18	Adriatic	PE	Autumn	(2) 4.75mm-9.5mm
PE_19	Adriatic	PE	Autumn	(2) 4.75mm-9.5mm
PE_20	Adriatic	PE	Autumn	(2) 4.75mm-9.5mm
PE_21	Adriatic	PE	Autumn	(3) 1.4mm-4.75mm
PE_22	Adriatic	PE	Autumn	(3) 1.4mm-4.75mm
PE_23	Adriatic	PE	Autumn	(4) 300um-1.4mm
PET	Adriatic	PET	Autumn	(4) 300um-1.4mm
PP_11	Adriatic	PP	Autumn	(1) >9.5mm
PP_12	Adriatic	PP	Autumn	(1) >9.5mm
PP_13	Adriatic	PP	Autumn	(2) 4.75mm-9.5mm
PP_14	Adriatic	PP	Autumn	(2) 4.75mm-9.5mm
PP_15	Adriatic	PP	Autumn	(3) 1.4mm-4.75mm
PP_16	Adriatic	PP	Autumn	(4) 300um-1.4mm
SW_A_1	Adriatic	SW	Autumn	Seawater
SW_A_2	Adriatic	SW	Autumn	Seawater
PE_1	Atlantic	PE	St.1	(3) 1.4mm-4.75mm
PE_2	Atlantic	PE	St.1	(3) 1.4mm-4.75mm
PE_3	Atlantic	PE	St.1	(3) 1.4mm-4.75mm
PP_1	Atlantic	PP	St.1	(4) 300um-1.4mm
SW_1	Atlantic	SW	St.1	Seawater
PE_4	Atlantic	PE	St.2	(4) 300um-1.4mm
PE_5	Atlantic	PE	St.2	(4) 300um-1.4mm
SW_2	Atlantic	SW	St.2	Seawater
PE_6	Atlantic	PE	St.3	(3) 1.4mm-4.75mm
SW_4	Atlantic	SW	St.3	Seawater

PE_9	Atlantic	PE	St.4	(3) 1.4mm-4.75mm
SW_5	Atlantic	SW	St.4	Seawater
NI_1	Atlantic	NI	St.5	(1) >9.5mm
PE_10	Atlantic	PE	St.5	(1) >9.5mm
PE_11	Atlantic	PE	St.5	(1) >9.5mm
PE_13	Atlantic	PE	St.5	(1) >9.5mm
PE_14	Atlantic	PE	St.5	(1) >9.5mm
SW_6	Atlantic	SW	St.5	Seawater
NI_1	Pacific	NI	St.8	(3) 1.4mm-4.75mm
NI_2	Pacific	NI	St.8	(4) 300um-1.4mm
Nylon_1	Pacific	Nylon	St.8	(3) 1.4mm-4.75mm
PE_1	Pacific	PE	St.8	(3) 1.4mm-4.75mm
PE_2	Pacific	PE	St.8	(4) 300um-1.4mm
SW_4	Pacific	SW	St.8	Seawater
PE_3	Pacific	PE	St.10	(2) 4.75mm-9.5mm
PE_4	Pacific	PE	St.10	(2) 4.75mm-9.5mm
PE_5	Pacific	PE	St.10	(4) 300um-1.4mm
PE_6	Pacific	PE	St.10	(4) 300um-1.4mm
SW_1	Pacific	SW	St.10	Seawater
NI_5	Pacific	NI	St.12	(4) 300um-1.4mm
NI_6	Pacific	NI	St.12	(3) 1.4mm-4.75mm
PE_7	Pacific	PE	St.12	(3) 1.4mm-4.75mm
PE_8	Pacific	PE	St.12	(3) 1.4mm-4.75mm
PE_12	Pacific	PE	St.12	(4) 300um-1.4mm
PE_9	Pacific	PE	St.12	(4) 300um-1.4mm
PE_10	Pacific	PE	St.12	(4) 300um-1.4mm
PE_11	Pacific	PE	St.12	(3) 1.4mm-4.75mm
PP_1	Pacific	PP	St.12	(3) 1.4mm-4.75mm
SW_2	Pacific	SW	St.12	Seawater
NI_8	Pacific	NI	St.13	(3) 1.4mm-4.75mm
NI_7	Pacific	NI	St.13	(4) 300um-1.4mm
PE_11	Pacific	PE	St.13	(3) 1.4mm-4.75mm
PE_12	Pacific	PE	St.13	(3) 1.4mm-4.75mm
PP_2	Pacific	PP	St.13	(3) 1.4mm-4.75mm
SW_3	Pacific	SW	St.13	Seawater

Table S3- Results of the ANOVA tests comparing diversity and richness indexes of the prokaryotic communities between the different sites, stations, season (in the case of the northern Adriatic samples) and size of the plastics. * indicates $p < 0.05$.

	OTU Richness		Shannon index		Simpson index	
	F value	p-value	F value	p-value	F value	p-value
Site	29.888	2.04E-09*	26.258	1.19E-08*	22.378	9.00E-08*
Season/Station	0.787	0.629	0.753	0.659	0.72	0.689
Size	1.11	0.353	1.476	0.232	2.153	0.105
Site:Size	0.171	0.916	0.273	0.844	0.37	0.775
Season/Station:Size	1.621	0.16	1.339	0.256	1.621	0.16

Table S4 – Results of the post-hoc Tukey tests performed on the ANOVAs comparing richness and diversity indexes of the different sampling sites (Table S3). * indicates $p < 0.05$.

	OTU Richness		Shannon index		Simpson	
	diff	p adj	diff	p adj	diff	p adj
Atlantic-Adriatic	-45.221	5.22E-05*	-26.149	1.76 E-04*	-14.467	7.40E-04*
Pacific-Adriatic	-56.812	0.000*	-33.457	0.000*	-19.140	2E-07*
Pacific-Atlantic	-11.590	0.512	-7.3085	0.507546	-4.672	0.481

Table S5 – Results of the (A) PERMANOVA, (B) betadisper tests and (C) pair-wise PERMANOVAs, comparing the prokaryotic community composition between different polymer types, sampling site, sampling station and season in the case of the North Adriatic samples. * indicates $p < 0.05$.

A

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
type	5	5.876	1.1753	3.9225	0.16086	0.001*
site	2	3.345	1.67249	5.5819	0.09156	0.001*
seas_stat	9	4.497	0.49963	1.6675	0.12309	0.001*
type:site	5	1.913	0.38265	1.2771	0.05237	0.009*
type:seas_stat	13	3.823	0.29404	0.9813	0.10463	0.609
Residuals	57	17.079	0.29963		0.46749	
Total	91	36.533			1	

B

	Df	SumsOfSqs	MeanSq	F	N. Perm	Pr(>F)	Location
Type	5	0.83	0.17	20.15	999	0.001*	All
Site	2	0.02	0.01	1.69	999	0.212	
Stations	11	0.33	0.03	2.18	999	0.029*	
Stations	2	0	0	0.32	999	0.733	Northern
Type	3	0.44	0.15	21.53	999	0.001*	Adriatic
Stations	4	0.04	0.01	0.58	999	0.681	North
Type	3	0.51	0.17	9.64	999	0.002*	Atlantic
Stations	3	0.12	0.04	1.67	999	0.21	Pacific
Type	4	0.34	0.09	11.53	999	0.001*	

C

Pairs	F.Model	R2	p.value
<i>Comparison between locations</i>			
Atlantic vs Adriatic	4.07	0.06	0.001*
Atlantic vs Pacific	3.42	0.07	0.001*
Adriatic vs Pacific	3.55	0.05	0.001*
<i>Comparison between different plastics and SW</i>			
PE vs PP	0.97	0.01	0.53
PE vs SW	6.42	0.09	0.001*
PE vs PET	1.06	0.02	0.33
PE vs Nylon	1.14	0.02	0.06
PP vs SW	6.05	0.15	0.001*
PP vs PET	1.07	0.05	0.29
PP vs Nylon	1.21	0.06	0.09
SW vs PET	1.97	0.12	0.08

SW vs Nylon	1.46	0.09	0.07
<i>Comparison between stations</i>			
Atlantic St. 3 vs Atlantic St. 4	0.57	0.22	0.66
Atlantic St. 3 vs Atlantic St. 1	0.91	0.15	0.62
Atlantic St. 3 vs Atlantic St. 5	1.32	0.18	0.10
Atlantic St. 3 vs Atlantic St. 2	0.74	0.2	0.6
Atlantic St. 3 vs Adriatic Autumn	1.41	0.07	0.022*
Atlantic St. 3 vs Adriatic Winter	1.03	0.11	0.49
Atlantic St. 3 vs Adriatic Summer	1.31	0.06	0.035*
Atlantic St. 3 vs Pacific St. 12	1.7	0.14	0.031*
Atlantic St. 3 vs Pacific St.8	1.37	0.19	0.16
Atlantic St. 3 vs Pacific St. 13	1.47	0.2	0.07
Atlantic St. 3 vs Pacific St.10	1.11	0.18	0.18
Atlantic St. 4 vs Atlantic St. 1	1.2	0.19	0.15
Atlantic St. 4 vs Atlantic St. 5	1.73	0.22	0.07
Atlantic St. 4 vs Atlantic St. 2	0.77	0.2	0.6
Atlantic St. 4 vs Adriatic Autumn	1.42	0.07	0.023*
Atlantic St. 4 vs Adriatic Winter	1.02	0.11	0.49
Atlantic St. 4 vs Adriatic Summer	1.38	0.07	0.039*
Atlantic St. 4 vs Pacific St. 12	1.67	0.14	0.032*
Atlantic St. 4 vs Pacific St.8	1.31	0.18	0.25
Atlantic St. 4 vs Pacific St. 13	1.43	0.19	0.07
Atlantic St. 4 vs Pacific St.10	1.05	0.17	0.39
Atlantic St. 1 vs Atlantic St. 5	1.5	0.14	0.032*
Atlantic St. 1 vs Atlantic St. 2	0.9	0.13	0.69
Atlantic St. 1 vs Adriatic Autumn	2.18	0.09	0.001*
Atlantic St. 1 vs Adriatic Winter	1.55	0.12	0.002*
Atlantic St. 1 vs Adriatic Summer	2.01	0.08	0.001*
Atlantic St. 1 vs Pacific St. 12	2.32	0.15	0.001*
Atlantic St. 1 vs Pacific St.8	2.09	0.19	0.005*
Atlantic St. 1 vs Pacific St. 13	1.84	0.17	0.005*
Atlantic St. 1 vs Pacific St.10	1.48	0.16	0.008*
Atlantic St. 5 vs Atlantic St. 2	1.56	0.18	0.08
Atlantic St. 5 vs Adriatic Autumn	3.05	0.11	0.001*
Atlantic St. 5 vs Adriatic Winter	2.18	0.15	0.004*
Atlantic St. 5 vs Adriatic Summer	2.82	0.11	0.001*
Atlantic St. 5 vs Pacific St. 12	3.57	0.2	0.002*
Atlantic St. 5 vs Pacific St.8	2.99	0.23	0.003*
Atlantic St. 5 vs Pacific St. 13	2.87	0.22	0.005*
Atlantic St. 5 vs Pacific St.10	2.42	0.21	0.003*
Atlantic St. 2 vs Adriatic Autumn	1.49	0.07	0.014*
Atlantic St. 2 vs Adriatic Winter	1.06	0.11	0.34
Atlantic St. 2 vs Adriatic Summer	1.45	0.07	0.034*
Atlantic St. 2 vs Pacific St. 12	1.61	0.13	0.017*
Atlantic St. 2 vs Pacific St.8	1.43	0.17	0.08
Atlantic St. 2 vs Pacific St. 13	1.31	0.16	0.15
Atlantic St. 2 vs Pacific St.10	1.14	0.16	0.12
Adriatic Autumn vs Adriatic Winter	1.18	0.04	0.15
Adriatic Autumn vs Adriatic Summer	1.09	0.03	0.25

Adriatic Autumn vs Pacific St. 12	2.62	0.09	0.001*
Adriatic Autumn vs Pacific St.8	2.34	0.09	0.001*
Adriatic Autumn vs Pacific St. 13	2.25	0.09	0.001*
Adriatic Autumn vs Pacific St.10	1.92	0.08	0.001*
Adriatic Winter vs Adriatic Summer	1.25	0.05	0.11
Adriatic Winter vs Pacific St. 12	1.95	0.11	0.005*
Adriatic Winter vs Pacific St.8	1.69	0.12	0.006*
Adriatic Winter vs Pacific St. 13	1.66	0.12	0.025*
Adriatic Winter vs Pacific St.10	1.4	0.11	0.016*
Adriatic Summer vs Pacific St. 12	2.88	0.1	0.001*
Adriatic Summer vs Pacific St.8	2.3	0.09	0.001*
Adriatic Summer vs Pacific St. 13	2.42	0.1	0.001*
Adriatic Summer vs Pacific St.10	1.9	0.08	0.001*
Pacific St. 12 vs Pacific St.8	2.64	0.16	0.002*
Pacific St. 12 vs Pacific St. 13	1.41	0.09	0.038*
Pacific St. 12 vs Pacific St.10	1.81	0.12	0.018*
Pacific St.8 vs Pacific St. 13	2.4	0.19	0.004*
Pacific St.8 vs Pacific St.10	1.27	0.12	0.15
Pacific St. 13 vs Pacific St.10	1.69	0.16	0.008*
<i>Comparison between stations excluding the SW samples</i>			
Atlantic St. 3 vs Atlantic St. 1	0.88	0.23	0.8
Atlantic St. 3 vs Atlantic St. 5	1.72	0.3	0.17
Atlantic St. 3 vs Atlantic St. 2	1.02	0.5	0.33
Atlantic St. 3 vs Adriatic Autumn	1.3	0.07	0.049*
Atlantic St. 3 vs Adriatic Summer	1.26	0.07	0.17
Atlantic St. 3 vs Adriatic Winter	1.08	0.18	0.29
Atlantic St. 3 vs Pacific St. 12	1.6	0.17	0.10
Atlantic St. 3 vs Pacific St.8	1.55	0.28	0.17
Atlantic St. 3 vs Pacific St. 13	1.65	0.29	0.17
Atlantic St. 3 vs Pacific St.10	1.16	0.28	0.2
Atlantic St. 4 vs Atlantic St. 1	1.38	0.32	0.2
Atlantic St. 4 vs Atlantic St. 5	2.67	0.4	0.17
Atlantic St. 4 vs Atlantic St. 2	1.19	0.54	0.33
Atlantic St. 4 vs Adriatic Autumn	1.42	0.08	0.07
Atlantic St. 4 vs Adriatic Summer	1.45	0.08	0.043*
Atlantic St. 4 vs Adriatic Winter	1.18	0.19	0.16
Atlantic St. 4 vs Pacific St. 12	1.72	0.18	0.13
Atlantic St. 4 vs Pacific St.8	1.6	0.29	0.17
Atlantic St. 4 vs Pacific St. 13	1.74	0.3	0.17
Atlantic St. 4 vs Pacific St.10	1.19	0.28	0.2
Atlantic St. 1 vs Atlantic St. 5	1.92	0.22	0.008*
Atlantic St. 1 vs Atlantic St. 2	0.98	0.2	0.6
Atlantic St. 1 vs Adriatic Autumn	2.25	0.1	0.001*
Atlantic St. 1 vs Adriatic Summer	2.13	0.1	0.001*
Atlantic St. 1 vs Adriatic Winter	1.57	0.16	0.006*
Atlantic St. 1 vs Pacific St. 12	2.45	0.18	0.003*
Atlantic St. 1 vs Pacific St.8	2.41	0.26	0.016*
Atlantic St. 1 vs Pacific St. 13	2.06	0.23	0.019*
Atlantic St. 1 vs Pacific St.10	1.54	0.2	0.026*

Atlantic St. 5 vs Atlantic St. 2	2.47	0.33	0.037*
Atlantic St. 5 vs Adriatic Autumn	3.52	0.14	0.001*
Atlantic St. 5 vs Adriatic Summer	3.31	0.14	0.001*
Atlantic St. 5 vs Adriatic Winter	2.68	0.23	0.002*
Atlantic St. 5 vs Pacific St. 12	4.36	0.27	0.004*
Atlantic St. 5 vs Pacific St.8	3.94	0.33	0.008*
Atlantic St. 5 vs Pacific St. 13	3.88	0.33	0.007*
Atlantic St. 5 vs Pacific St.10	3.05	0.3	0.011*
Atlantic St. 2 vs Adriatic Autumn	1.57	0.08	0.015*
Atlantic St. 2 vs Adriatic Summer	1.59	0.09	0.01*
Atlantic St. 2 vs Adriatic Winter	1.22	0.17	0.04*
Atlantic St. 2 vs Pacific St. 12	1.7	0.16	0.015*
Atlantic St. 2 vs Pacific St.8	1.78	0.26	0.046*
Atlantic St. 2 vs Pacific St. 13	1.57	0.24	0.103
Atlantic St. 2 vs Pacific St.10	1.3	0.25	0.07
Adriatic Autumn vs Adriatic Summer	1.14	0.03	0.19
Adriatic Autumn vs Adriatic Winter	1.11	0.05	0.19
Adriatic Autumn vs Pacific St. 12	2.92	0.1	0.001*
Adriatic Autumn vs Pacific St.8	2.66	0.11	0.002*
Adriatic Autumn vs Pacific St. 13	2.56	0.11	0.002*
Adriatic Autumn vs Pacific St.10	2.08	0.09	0.001*
Adriatic Summer vs Adriatic Winter	1.17	0.05	0.13
Adriatic Summer vs Pacific St. 12	3.21	0.12	0.001*
Adriatic Summer vs Pacific St.8	2.63	0.12	0.001*
Adriatic Summer vs Pacific St. 13	2.78	0.12	0.001*
Adriatic Summer vs Pacific St.10	2.07	0.1	0.001*
Adriatic Winter vs Pacific St. 12	1.98	0.13	0.001*
Adriatic Winter vs Pacific St.8	1.96	0.18	0.001*
Adriatic Winter vs Pacific St. 13	1.91	0.17	0.002*
Adriatic Winter vs Pacific St.10	1.52	0.16	0.004*
Pacific St. 12 vs Pacific St.8	3.09	0.2	0.002*
Pacific St. 12 vs Pacific St. 13	1.61	0.12	0.015*
Pacific St. 12 vs Pacific St.10	1.97	0.15	0.008*
Pacific St.8 vs Pacific St. 13	3	0.27	0.009*
Pacific St.8 vs Pacific St.10	1.68	0.19	0.05
Pacific St. 13 vs Pacific St.10	1.97	0.22	0.019*

Table S6- Envfit test results of fitted environmental factors to the ordination scores (NMDS) of samples dependent on their prokaryotic community composition. NMDS analyses were conducted for all samples (Fig. 1), all polymer samples excluding seawater samples, and for only the polymers we could identify. * indicates $p < 0.05$.

		Pacific		Atlantic		Adriatic		Atlantic + Adriatic		All	
		R2	p-value	R2	p-value	R2	p-value	R2	p-value	R2	p-value
All samples	Temperature	0.431	0.002*	0.276	0.075	0.113	0.072	0.059	0.157	0.063	0.049*
	Salinity	0.010	0.864	0.218	0.154	0.045	0.33	0.051	0.192	0.120	0.002*
	NO2	-	-	0.349	0.038*	0.096	0.117	0.431	0.001*	-	-
	NO3	-	-	0.309	0.064	0.076	0.19	0.489	0.001*	-	-
	PO4	-	-	0.278	0.099	0.021	0.619	0.316	0.001*	-	-
Just polymers	Temperature	0.111	0.319	0.128	0.519	0.092	0.179	0.169	0.013*	0.034	0.284
	Salinity	0.231	0.062	0.101	0.585	0.092	0.179	0.107	0.056	0.066	0.076
	NO2	-	-	0.436	0.055	0.092	0.179	0.473	0.001*	-	-
	NO3	-	-	0.504	0.032*	0.092	0.179	0.471	0.001*	-	-
	PO4	-	-	0.444	0.053	0.092	0.179	0.015	0.001*	-	-
Polymers excluding NI	Temperature	0.066	0.613	0.16	0.47	0.092	0.179	0.115	0.042*	0.073	0.06
	Salinity	0.080	0.552	0.081	0.68	0.092	0.179	0.065	0.178	0.063	0.108
	NO2	-	-	0.610	0.012*	0.092	0.179	0.441	0.001*	-	-
	NO3	-	-	0.615	0.012*	0.092	0.179	0.461	0.001*	-	-
	PO4	-	-	0.247	0.294	0.092	0.179	0.221	0.003*	-	-

Table S7- Mantel tests identifying correlations between the community composition of all polymers and the distance between sampling stations and environmental factors. SW samples were excluded from this analysis. The analysis was repeated considering only the relative abundance of the OTUs enriched in the laboratory LDPE incubations (potential LDPE degraders). Pacific samples were excluded from all the inorganic nutrients analyses (indicated with [†]). * indicates $p < 0.05$.

		Pacific		Atlantic		Adriatic		All	
		R2	p-value	R2	p-value	R2	p-value	R2	p-value
All OTUs (n=3352)	Temperature	-0.142	0.75	0.103	0.391	-0.5	0.833	-0.344	0.99
	Salinity	0.942	0.083	-0.284	0.633	-0.5	0.833	-0.197	0.847
	NO2	-	-	-0.454	0.866	0.5	0.5	-0.188 [†]	0.691 [†]
	NO3	-	-	-0.329	0.725	1	0.167	-0.046 [†]	0.479 [†]
	PO4	-	-	0.309	0.283	-0.5	0.833	-0.166 [†]	0.658 [†]
	Distance	-0.371	0.916	0.697	0.025*	-	-	-0.003	0.435
	Distance to land	-	-	0.951	0.008*	-	-	-	-
Potential LDPE degraders (n=35)	Temperature	-0.085	0.682	-0.393	0.925	-0.5	0.833	-0.284	0.976
	Salinity	-0.142	0.5	-0.49	0.991	1	0.166	-0.088	0.636
	NO2	-	-	-0.103	0.6	-1	1	-0.255 [†]	0.845 [†]
	NO3	-	-	0.122	0.375	-0.5	0.833	-0.153 [†]	0.632 [†]
	PO4	-	-	0.927	0.008*	1	0.166	0.039 [†]	0.417 [†]
	Distance	0.257	0.291	0.684	0.066	-	-	0.068	0.276
	Distance to land	-	-	0.952	0.008*	-	-	-	-

Table S8 – Relative abundance of families present with more than 1% relative abundance in at least one samples across the three sampling sites.

Site	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic	Atlantic
Sample	PE_6	PE_9	PP_1	PE_10	PE_11	NI_1	PE_13	PE_14	PE_1	PE_2	PE_3	PE_4	PE_5
Season/stations	St.3	St.4	St.1	St.5	St.5	St.5	St.5	St.5	St.1	St.1	St.1	St.2	St.2
Actinomarinaceae	0.05	0.06	0	0	0.05	0.08	0.02	0	0.28	0.01	0.02	0	0
AEGEAN-169 marine group	0.97	0.01	0	0.13	0.79	0.19	0.71	0.2	0.53	0.06	0.19	0	0
Alcanivoraceae	0	0	0	0	0.01	0.01	0	0	0	0	0	0	0
Alteromonadaceae	0.19	0	0	0.05	0.53	0.15	0.94	0.17	0.08	0.02	0.42	0.12	0
Arcobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Arenicellaceae	0	0	0	0	0.02	0	0.01	0.02	0.03	0	0	0	0
Balneolaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Bdellovibrionaceae	0.03	0.01	0.05	0.08	0.06	0.07	0.14	0.07	0.14	0.03	0	0.09	0
Beljerinckiaceae	0.97	0.42	0.08	0.01	0	0	0	0	1.140	0.03	0	0.4	0
Blastocatellaceae	0	0	0	0	0	0	0	0	0	0	0.13	0	0
Caldilineaceae	0	0.11	0.03	0	0	0	0	0	0	0	0	0.03	0
Caulobacteraceae	1.220	5.170	0.2	0.08	0.06	0.26	0.51	0.02	0.77	0.06	0.3	3.340	5.680
Cellvibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Chromatiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade I	0.07	0	0	0.01	0.04	0	0.03	0.02	0.09	0	0.02	0	0
Clade II	0.04	0	0	0.01	0.02	0	0.01	0.04	0.01	0	0.01	0	0
Clade III	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade IV	0.01	0	0	0.01	0.02	0	0.12	0	0.11	0.01	0.01	0	0
Clostridiaceae	0	0	0	0	0	0	0	0	0	0	0	1.170	0.1
Colwelliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Comamonadaceae	0	0.01	0.01	0	0	0	0.01	0	0.04	0	0.01	0.65	0.02
Crocinitomicaceae	0.11	0	0	0	0.03	0.01	0.04	0.02	0.09	0.01	0.01	0	0
Cryomorphaceae	0	0	0	0.01	0	0.02	0.04	0.11	0.01	0.02	0.01	0	0
Cyanobiaceae	6.390	0.91	0.08	2.300	3.170	2.530	6.540	2.680	8.450	0.73	0.51	0.56	0.07
Cyclobacteriaceae	0.04	0.01	0.05	0.02	0.01	0.02	0.03	0.02	0.19	0.05	0.02	0	0
DEV007	0.05	0.74	0.05	0.01	0.02	0.03	0.01	0	0	0.01	0	0.09	0.07
Exiguobacteraceae	0.3	0.2	0.01	0.01	0.01	0	0.13	0	0.17	0.02	0	0	0
Flavobacteriaceae	1.830	0.84	1.000	1.940	3.730	2.000	4.930	3.900	1.700	0.4	0.44	1.700	0.96
Fokinaceae	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Gemmataceae	0	0	0	0	0.01	0.02	0	0	0.01	0	0	0	1.230
Granulosicoccaceae	0	0	0	0	0	0	0	0.04	0	0	0	0	0
Hahellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Halieaceae	0	0	0	0.01	0.01	0.02	0.04	0.02	0	0.01	0.01	0	0
Halomonadaceae	0.02	0	0	0.07	0.16	0.11	0.63	0	0.01	0	0	0	0
Hyphomicrobiaceae	0.42	0	0	0	0.01	0	0	0	0	0	0	0	0
Hyphomonadaceae	5.100	1.380	10.370	11.060	3.630	2.310	2.740	5.390	10.640	7.480	19.660	1.920	3.440
Illumatobacteraceae	0.29	0.04	0.08	0.35	0.23	0.33	0.65	0.33	0.79	0.13	0	0.19	0
Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Kiloniellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
marine metagenome	0	0	0	0	0	0	0	0	0	0	0	0	0
Marinobacteraceae	0	0	0	0	0	0.01	0.01	0	0	0	0	0	0
metagenome	0	0	0	0.13	0	0.26	0.04	0.2	1.320	0.02	0	0	0
Methyloiligellaceae	0	0	0	0	0.01	0	0.04	0.02	0	0	0	0.03	0
Methylophilaceae	0	0	0	0	0	0	0	0	0.02	0	0	0	0
Micavibrionaceae	0.14	0	0.01	0	0.02	0.02	0.01	0.04	0.02	0	0	0	0
Microbacteriaceae	0.13	0.31	0	0.01	0	0	0	0	0.02	0	0	0	0
Microcystaceae	0.26	0.01	0	0	0.03	0.05	0.09	0	0.34	0.03	0	0.03	0
Microscillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Microtrichaceae	0	0.01	0	0.05	0.02	0	0.01	0.17	0.06	0	0	0	0
Moraxellaceae	6.900	0.84	0.04	2.000	4.470	4.440	12.650	7.740	0.2	0.01	0.12	1.210	0.89
Nisaeaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Nitricolaceae	0	0	0	0	0	0	0.01	0	0	0	0	0	0.07
Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Nostocaceae	0	0	0	5.160	0.22	14.240	0.01	0.02	1.170	29.370	0.08	0.22	19.430
NS9 marine group	0.01	0.01	0	0	0.01	0	0.01	0	0.03	0	0	0	0
Obscuribacteraceae	0.42	0.09	0.02	0.06	0.01	0.04	0.3	0.04	0.54	0.03	0.01	1.210	1.870
Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
OCS116 clade	0	0	0	0	0.02	0.1	0	0	0.09	0	0	0	0
Oleiphilaceae	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Oscillatoriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Parvularculaceae	0	0	0	0.11	0	0.16	0.01	0	0	0.14	0	0.03	0.3
Phormidemiaceae	16.270	0.03	62.380	33.090	35.830	24.140	1.700	8.400	6.200	25.070	12.680	70.800	37.710
Phycisphaeraceae	0.82	7.140	11.880	0.43	0.59	0.29	0.57	0.22	1.390	0.5	0.02	0	1.130
Pirellulaceae	4.210	0.56	0	2.000	1.890	1.660	4.760	5.450	3.310	0.13	0.9	0.03	0.42
Planococcaceae	0.32	2.330	0	0	0.02	0.01	0.03	0.02	0.08	0.01	0	0	0
Porticocccaceae	0.01	0	0	0	0	0	0.02	0	0.02	0	0	0	0
Propionibacteriaceae	1.270	0.07	0.05	0.08	0.1	0.08	0.14	0.2	0.27	0.01	0.01	0	0.3

Chapter III

PS1 clade	0.03	0	0	0	0	0	0	0	0.06	0.01	0	0	0
Pseudoalteromonadaceae	3.910	0.02	0.02	0.21	1.660	0.45	1.510	0.28	0.07	0.01	0.06	0	0.07
Pseudohongiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudomonadaceae	0.31	0.18	0.02	0.03	0.6	0.02	0.57	0.04	0.87	0.02	0.03	0	0.07
Puniceococcaceae	0.26	0.01	0	0.01	0.07	0.01	0.18	0	0.07	0.01	0.02	0	0
Rhizobiaceae	17.050	0.04	2.350	6.330	2.140	6.630	0.7	1.440	7.140	2.570	5.040	8.680	2.560
Rhizobiales Incertae Sedis	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhodobacteraceae	23.600	71.410	7.360	27.810	34.800	33.270	51.430	40.010	37.460	14.750	48.300	2.350	14.710
Rhodothermaceae	0	0	0	0.01	0	0	0	0.02	0	0	0	0	0
Rubinisphaeraceae	0.07	0.06	0	0.03	0.07	0.05	0.09	0.15	0.2	0	0	0	0.02
Rubritaleaceae	0.58	0.12	0	0.55	1.350	0.68	2.600	2.140	0.8	0.08	0.21	0.06	1.530
Rubrobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
S25-593	0	0	0	0	0.01	0.01	0	0	0	0	0	0	0
Saccharimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Saccharospirillaceae	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Saprospiraceae	0.13	0.06	0.29	0.22	0.21	0.28	0.37	0.57	0.13	0.19	0.46	0.03	0.27
SAR116 clade	0.03	0.01	0	0	0.11	0	0.15	0	0.25	0.09	0.06	0	0
Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
SM2D12	0	0	0	0	0	0	0	0	0	0	0	0	0
Sphingomonadaceae	2.900	4.760	0.34	3.870	1.140	2.060	2.990	7.370	11.360	2.830	8.450	2.660	6.350
Sphingibacteraceae	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Stappiaceae	0	0	0	0.02	0.02	0	0.01	0.02	0.01	0	0.2	0	0
Synechococcales Incertae Sedis	0	0	2.950	1.030	1.380	1.350	0.07	11.230	0.32	14.230	0.57	0	0
Tenderiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Thermoanaerobaculaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Thioglobaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Thiotrichaceae	0	0.01	0	0.01	0.01	0	0	0	0.01	0	0	0	0
Vibrionaceae	0.62	0.02	0	0.01	0.04	0.02	0.06	0	0.07	0	0.02	0	0
Woeseiaceae	0	0	0	0.01	0.05	0.06	0.01	0.02	0	0.01	0	0	0
Xanthobacteraceae	0.05	0.02	0.07	0.02	0	0	0.3	0	0	0	0.27	1.360	0.05
Xenococcaceae	0.13	0	0.15	0.24	0.29	1.270	0.07	0.57	0.15	0.7	0.37	0.03	0

Site	Atlantic	Atlantic	Atlantic	Atlantic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic
Sample	SW_2	SW_4	SW_5	SW_6	SW_A_1	PE_14	PE_15	PE_16	PE_17	PP_11	PP_12	PE_18	PE_19
Season/stations	St.2	St.3	St.4	St.5	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn
Actinomarinaceae	1.930	1.390	2.460	1.290	11.200	0	0.01	0	0	0.01	0	0	0
AEGEAN-169 marine group	2.080	11.990	9.250	1.260	5.220	0.01	0	0	0	0	0.02	0	0
Alcanivoracaceae	0	0.05	0.01	0	0	0	0	0.04	0.16	0	0.01	0.01	1.610
Alteromonadaceae	0.07	0.06	0.12	0	0.06	1.720	3.150	0.54	0.04	0.03	0.14	0.02	5.510
Arcobacteraceae	0	0	0	0	0.06	0	0	0	0	0	0	0	0.04
Arenicellaceae	0	0	0	0	0	0.13	0.47	0.62	0.8	0.08	0.16	0.85	0.07
Balneolaceae	0	0.01	0	0	0.04	0.01	0	0	0	0	0.02	0	0.02
Bdellovibrionaceae	0.02	0.01	0.02	0.01	0.08	0.34	0.82	0.07	0.13	1.150	0.38	0	0.06
Beijerinckiacae	0	0	0.07	0	0	0	0	0	0.03	0.01	0	0	0
Blastocatellaceae	0.02	0	0.01	0	0	0.07	0.01	0.16	0.19	0.05	0	0	0.01
Caldilineaceae	0	0	0	0	0	0	0	0.07	0.67	0.02	0.01	0.01	0
Caulobacteraceae	0.05	0.02	0.04	0	0	0	0.01	0	0	0	0	0.03	0.12
Cellvibrionaceae	0	0	0	0	0	0.02	0.03	0.01	0.03	0	0	0	0.17
Chromatiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade I	0.35	3.570	3.790	0.77	11.820	0	0	0	0	0	0	0.01	0
Clade II	0.07	0.93	0.9	0.12	1.910	0	0	0	0	0	0	0.03	0
Clade III	0	0	0.01	0	0.17	0	0	0	0	0	0	0.01	0
Clade IV	0.37	1.250	1.960	0.22	0.6	0	0	0	0	0	0	0.04	0
Clostridiaceae	0.02	0	0.01	0	0	0.01	0.01	0	0.11	0.02	0	0.26	0
Colwelliaceae	0	0	0	0	0.02	0.72	2.520	0.86	0.04	0.02	0.01	0.01	0.21
Comamonadaceae	0	0	0	0	0.04	0	0.06	0.14	0	0.02	0.02	0.25	0.07
Crocinitomicaceae	0.02	0.13	0.01	0.04	0.15	0.07	0.04	2.460	0.05	0.05	0.06	0.22	0.16
Cryomorphaceae	0.02	0.01	0	0	0.25	0.09	0.28	0.34	0.07	0.02	0.19	0	0.16
Cyanobiaceae	67.530	52.190	58.590	86.410	26.620	0.05	0.03	0.01	0.07	0.15	0.78	2.480	0.01
Cyclobacteriaceae	0	0.01	0.02	0	0.02	1.790	0.18	0.57	1.690	0.05	0.77	0.43	2.600
DEV007	0	0.05	0.01	0	0.02	0.7	0.06	0.52	1.210	0.17	0.19	0.47	0.21
Exiguobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0.01
Flavobacteriaceae	1.360	1.640	3.330	0.5	0.87	25.160	15.900	24.760	5.060	5.240	11.670	14.270	3.090
Fokiniaceae	0	0.01	0	0	0.02	0.03	0	0	0	0	0	0	0
Gemmataceae	0	0	0	0	0	0	0	0	0.04	0	0	0	0
Granulosicoccaceae	0	0	0	0	0	0.21	0.05	0.36	0.01	0.11	0.56	0	0.08
Hahellaceae	0	0	0	0	0	0.01	0	0	0	0	0	0	1.200
Halieaceae	0.05	0.09	0.16	0.11	0.15	0.4	0.3	0.16	0.88	0.18	0.51	0.15	0.06
Halomonadaceae	0.3	0.04	0.06	0	0	0	0	0	0	0	0	0	0.18
Hyphomicrobiaceae	0	0	0	0	0	1.030	0.01	1.770	2.600	0.74	2.430	1.370	0.02
Hyphomonadaceae	0	0.03	0.04	0.02	0.08	4.440	1.530	8.000	1.340	10.610	7.140	0.43	7.290
Ilumatobacteraceae	0	0.07	0.01	0.05	0.44	0.11	0.03	0.36	0.59	0.32	0.06	0.52	0.02

Chapter III

Intrasporangiaceae	0.15	0.06	0.03	0	0	0	0	0	0	0	0	0	0
Kiloniellaceae	0	0	0	0	0.02	0	0	0.02	0.43	0	0.01	0	0.31
marine metagenome	0	0.01	0.01	0.01	2.630	0.01	0.01	0.02	0	0	0.03	0	0
Marinobacteraceae	0	0.01	0.01	0	0.04	0	0.04	0	0.1	0.01	0	0.01	0.95
metagenome	0.02	0.11	0.41	0	0.48	0	0.03	0	0.03	0	0.07	0	0
Methyloligellaceae	0	0	0.04	0	0.02	0.85	0.03	1.570	2.880	0.11	0.13	0.21	0.01
Methylophilaceae	0	0.05	0.04	0.01	0	0	0	0	0.21	0	0	0	0
Micavibrionaceae	0	0	0.02	0	0	0.1	0.16	0.02	0.39	0.34	0.42	0	0.11
Microbacteriaceae	0.05	0.01	0.03	0	0.17	0.01	0.01	0	0.01	0	0.01	0	0.36
Microcystaceae	6.390	0.33	0.1	0.2	0	0	0	0	0	0	0	0	0
Microscillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.01
Microtrichaceae	0	0.35	0.01	0.08	1.240	1.120	0.06	6.590	6.810	1.160	0.14	0.31	0.11
Moraxellaceae	5.820	0.26	0.24	0.01	0.29	0.01	0.07	0	0.01	0.02	0.02	16.050	0.2
Nisaeaceae	0.07	0.08	0.05	0.09	1.140	0	0	0	0	0	0	0	0
Nitrincolaceae	0	0	0	0	0.04	0.03	0.04	0	0.02	0.03	0.01	0	0.19
Nitrospiraceae	0	0	0	0	0	0	0	0.01	0.25	0	0	0.2	0
Nostocaceae	0	0.01	0.1	0.02	0.06	0	0	0	0	0	0	0	0
NS9 marine group	0.05	0.05	0.03	0.01	0.41	0.05	0.11	0.05	0.02	0.02	0.18	0.02	0.06
Obscuribacteraceae	0	0	0.01	0	0	0	0	0	0.06	0	0	0	0.02
Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
OCS116 clade	0.05	0.08	0.13	0.25	1.240	0	0	0	0	0	0	0	0
Oleiphilaceae	0	0	0	0	0	0.06	0.13	0.46	0.02	0.09	0.01	0.03	35.170
Oscillatoriaceae	0	0	0	0	0	0.92	0.3	0.52	0	0	0.35	0	0
Parvularculaceae	0	0	0	0	0.02	0.4	0.5	0.4	0.6	2.310	1.280	0.01	0.27
Phormidesmiaceae	0	0.05	0.08	0.05	0.29	0.15	0.26	0.19	1.060	11.990	7.490	0	0.02
Phycisphaeraceae	0.15	1.000	0.02	0.48	1.220	0.02	0	0.03	0.23	0.21	0.07	0.09	0.45
Pirellulaceae	0.35	2.300	0.39	1.110	1.180	5.650	0.36	8.320	14.190	0.65	6.150	7.250	2.910
Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	1.750	0.04
Porticoccaceae	0	0.05	0.09	0.03	0.02	0	0	0.01	0.02	0	0	0	0
Propionibacteriaceae	0.1	0.22	0.21	0.04	0	0	0.17	0.02	0	0.06	0.03	0.03	0.02
PS1 clade	0.07	0.1	0.18	0.02	0.21	0.01	0	1.310	3.420	0.07	0	0.12	0.03
Pseudoalteromonadaceae	1.340	0.18	0.17	0	0.04	0.28	0.48	1.090	0.03	0.1	0.02	0.12	0.71
Pseudohongiellaceae	0	0	0	0	0.02	0.03	0	0.03	0.1	0.02	0	0.02	0.05
Pseudomonadaceae	0.64	0.1	0.02	0	0	0	0	0	0	0	0	0.02	2.540
Puniceicoccaceae	0.02	0.17	0.31	0.05	0.19	0.04	0.01	0.1	0.45	5.460	0.41	0.07	0.03
Rhizobiaceae	0	0.01	0.06	0.01	0.23	2.820	0.95	9.090	5.610	15.040	3.660	9.370	1.660
Rhizobiales Incertae Sedis	0	0	0	0	0	1.680	0	0.22	0.45	0.04	0.01	4.180	0.02
Rhodobacteraceae	4.060	7.950	6.530	3.410	8.670	29.810	50.790	10.830	16.070	26.890	23.960	1.370	6.880
Rhodothermaceae	0	0	0	0	0	0.42	0.03	0.05	0.27	0	0.01	0	0.02
Rubinisphaeraceae	0.02	0.01	0	0.06	0.17	0.41	0.02	1.700	2.010	0.06	3.420	0.2	0.33
Rubritaleaceae	0.5	1.190	0.72	1.570	0.27	0.07	0.02	0.47	0.19	0.09	0.13	0.17	0.04
Rubrobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
S25-593	0.1	0.42	0.29	0	0.93	0	0	0	0	0.01	0	0	0
Saccharimonadaceae	0	0	0	0	0	0	0	0	0	0.01	0	0.02	0.12
Saccharospirillaceae	0	0	0.01	0	0	0.02	0.11	0.04	0.03	0.04	0	0.03	14.620
Saprospiraceae	0	0	0.03	0	0.08	5.150	3.530	2.540	2.090	0.66	12.820	0.21	0.22
SAR116 clade	0.79	3.160	4.370	0.64	3.150	0.01	0	0.03	0	0.06	0	0	0.09
Shewanellaceae	0	0	0	0	0.02	0	0	0.07	0	0.01	0	0.01	0.05
SM2D12	0	0	0	0	0.08	0	0	0	0	0	0.15	0	0
Sphingomonadaceae	1.190	1.070	0.54	0.02	0.02	5.560	10.990	3.030	1.320	10.140	8.960	0.39	2.910
Spongiibacteraceae	0	0	0	0	0	0.04	0.01	0.47	0.04	0.01	0	0.12	0.08
Stappiaceae	0	0.25	0.01	0.1	0.17	0.02	0.03	0.01	0.06	0.1	0.1	0	0.91
Synechococcales Incertae Sedis	0	0.01	0	0.01	0	0.12	0.16	0.08	0.02	1.460	1.090	0.13	0.03
Tenderiaceae	0	0	0	0	0.04	0.01	0	0.26	3.110	0	0.07	0.02	0.01
Thermoanaerobaculaceae	0	0	0	0	0	0.03	0	0.09	0.13	0.02	0	0.13	0
Thioglobaceae	0	0	0	0	0.12	0	0	0	0	0	0	0	0
Thiotrichaceae	1.140	0.79	0.75	0.46	0.27	0.03	0.18	0.03	0.02	0.02	0.01	0	0.03
Vibrionaceae	0	0.03	0.05	0	0	0.8	1.290	0.16	0.08	0.17	0.33	0.28	0.16
Woeseiaceae	0	0	0	0	0.02	1.550	0	1.720	5.160	0.1	0.14	13.040	0.09
Xanthobacteraceae	0	0	0.02	0	0	0	0	0	0	0	0	0	0
Xenococcaceae	0.15	0.03	0	0	0.02	0.81	0.02	0.05	0	0.61	0.04	0.13	0

Site	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic
Sample	PP_13	SW_W_2	PP_14	PE_21	PE_22	PP_15	PE_23	PET	PP_16	SW_A_2	SW_S_1	PE_7	PE_8
Season/stations	Autumn	Winter	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn	Autumn	Summer	Summer	Summer
Actinomarinaceae	0.01	3.750	0	0.01	0	0	0.04	0	0.03	10.420	1.670	0	0
AEGEAN-169 marine group	0	2.210	0	0.01	0	0	0	0	0	3.460	14.100	0	0
Alcanivoracaceae	0	0.03	2.150	0	1.700	0.01	0.07	1.420	0	0	0.03	0.11	0
Alteromonadaceae	3.750	0.42	0.11	0.81	0.31	0.12	8.910	0.09	0.24	0.15	0.24	0.88	3.150
Arcobacteraceae	0	0.11	0.17	0	0	0.01	0	0	0.04	0.09	0.01	0	0
Arenicellaceae	0.48	0.02	2.850	0.1	0.74	6.610	0.15	0.67	1.090	0.03	0	1.370	0.07

Chapter III

Balneolaceae	0	0	0	0	0	0.28	0	0	0	0.35	0.25	0.53	0.01
Bdellovibrionaceae	0.05	0.12	0.07	0.13	0.02	0.25	0.96	0	0.03	0.19	0.02	0.17	0.47
Beijerinckiaceae	0	0	0	0	0	0	0	0.02	0.01	0	0	0	0
Blastocatellaceae	0.32	0	0	0	0.01	0	0	0.24	0.01	0	0	0.01	0
Caldiineaceae	0.01	0	0.02	0	0	0.02	0	0.01	0	0.01	0	0.11	0.03
Caulobacteraceae	0	0.1	0	0.01	0.03	0	0	0.03	0	0	0.01	0	0
Cellvibrionaceae	0	0	0.09	0	0.08	0	0	5.320	0	0	0	0.52	0.02
Chromatiaceae	0.02	0	0	0	0	0	0	0	0.18	0	0	0.05	0.01
Clade I	0.01	11.010	0	0	0	0.01	0	0	0	9.270	0.34	0	0
Clade II	0.01	2.370	0	0	0	0.01	0	0	0	2.290	0.64	0	0
Clade III	0	0.02	0	0	0	0	0	0	0	0.17	0.28	0	0
Clade IV	0	1.150	0.02	0	0	0	0	0	0	0.49	0	0	0
Clostridiaceae	0.03	0	0	0	0	0	0.04	0.01	0	0.02	0.01	0.02	0
Colwelliaceae	2.070	0.02	0.52	0.02	0.43	0.09	1.520	0	0.11	0.45	0	0.27	1.010
Comamonadaceae	0.05	0.01	0.08	0	8.950	0.11	0.07	0.38	0.04	0	0	0.02	0
Crocinitomicaceae	0.41	0.69	0.34	0.44	3.430	1.900	0.11	0.25	0.26	1.750	0	0.16	0.03
Cryomorphaceae	0.1	1.050	0.14	0.36	0.36	0.4	0.11	0	0.51	2.190	0.05	0.16	0.2
Cyanobiaceae	0.14	11.300	0.01	0.28	0	0.02	0	0.01	0.06	13.970	56.880	0.02	0.23
Cyclobacteriaceae	0.86	0.17	0.16	5.500	0.3	1.170	0.11	3.540	0.31	0.27	0.01	1.050	0.3
DEV007	0.3	0.06	0.24	0.18	0.03	0.33	0.07	0.32	0.17	1.010	0.02	0.28	0.1
Exiguobacteraceae	0	0	0	0	0	0	0	0.09	0	0	0	0	0
Flavobacteriaceae	26.040	3.750	5.420	12.690	49.910	19.070	10.160	6.020	42.950	9.530	0.92	13.290	7.620
Fokiniaceae	0.1	0	0	0.01	0	0.01	0	0	0.19	0.01	0.03	0.02	0
Gemmataceae	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Granulosicoccaceae	1.410	0	0.26	0	0.04	0.31	0.07	0.02	0	0	0	0.06	0.1
Hahellaceae	0	0	0.01	0	0	0.03	0	0	0	0	0	0.01	0
Halieaceae	1.090	0.4	0.18	0.32	0.01	0.34	0.26	0.04	0.14	2.410	0.33	0.31	0.62
Halomonadaceae	0	0.1	0.03	0	0	0	0.04	0	0	0	0	0.04	0
Hyphomicrobiaceae	0.82	0.02	0.4	1.110	0.38	0.07	0.96	2.310	0.29	0.02	0.01	0.57	2.250
Hyphomonadaceae	1.580	0.01	7.690	4.810	1.110	5.370	0.41	2.320	0.31	0.04	0.94	4.250	3.430
Ilumatobacteraceae	0.38	0.05	0.97	0.14	0.1	1.460	1.000	0.52	0.11	0.61	0.02	0.61	0.12
Intrasporangiaceae	0	0.02	0	0	0	0	0	0	0	0	0	0	0
Kiloniellaceae	0.05	0.02	0.05	0.03	0.01	0.02	0	2.240	0	0	0	0.42	0
marine metagenome	0	0.37	0.09	0.01	0.04	0.04	0	0	0	0.85	0.02	0.05	0.05
Marinobacteraceae	0	0.03	0.45	0	0.01	0.95	0.04	0.01	0	0	0	3.620	0.01
metagenome	0	0.1	0.14	0.03	0	0.05	0	0	0	0.18	0	2.790	0.05
Methyloiligellaceae	0.24	0	0.43	0.23	0.09	0.02	0.92	0.18	0.28	0.02	0.11	0.08	0.17
Methylophilaceae	0	0.53	0	0	0	0	0	0	0	0.05	0	0	0
Micavibrionaceae	0	0.09	0.11	1.180	0	0.08	0.3	1.240	0.16	0	0	0.36	0.22
Microbacteriaceae	0	0.01	0.25	0	0	0	0	0	0.01	0.21	2.270	0.02	0
Microcystaceae	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Microscillaceae	0	0	0	1.800	0.01	0	0.04	0	0	0	0	0	0.16
Microtrichaceae	0.56	0.65	3.570	0.14	0.16	1.750	0.22	9.190	0.11	1.040	0.03	0.58	0.2
Moraxellaceae	0.05	2.570	0.1	0.03	0.02	0.02	0.48	0.19	0.07	0.02	0.23	0.02	0.03
Nisaeaceae	0	0.11	0	0	0	0	0	0	0	0.49	0	0	0
Nitrincolaceae	0.12	0	0.57	0.01	0.01	0.02	0	0.06	0.02	0.86	0.01	0.1	0.02
Nitrospiraceae	0	0	0.06	0	0	0	0	0	0.01	0	0	0.05	0
Nostocaceae	0	0	0	0	0	0	1.180	0	0	0	0.01	0.01	0.07
NS9 marine group	0.04	2.010	0.05	0.08	0.03	0.08	0	0	0.04	3.210	0.03	0.11	0.04
Obscuribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
OCS116 clade	0	0.72	0	0	0	0	0	0	0.01	0.49	0	0	0
Oleiphilaceae	0.14	0.01	2.370	0.05	0.26	8.080	0.41	0.19	0.12	0.03	0	0.74	0.3
Oscillatoriaceae	1.290	0	0	0	0.01	0	0	0	0	0	0	0.21	0.39
Parvularculaceae	0.3	0	0.57	0.13	0.17	0.06	0.92	1.400	0.01	0	0.01	0.86	2.300
Phormidiesmiaceae	0.02	0.01	0.02	1.330	0.06	0.07	6.870	0.02	0.12	0	0.02	6.810	12.030
Phycisphaeraceae	0	0.1	0.04	0.28	0	0.11	0	0.04	0.1	0.28	0.11	0.12	0.2
Pirellulaceae	3.210	0.47	1.170	1.250	0.82	1.270	0.92	7.660	0.53	2.990	0.59	1.960	6.990
Planococcaceae	0	0	0	0	0	0	0	0.02	0	0	0.01	0	0
Porticoccaceae	0	0.07	0.01	0	0	0	0	0	0	0.09	0.01	0	0
Propionibacteriaceae	0.33	0.01	0.01	0.01	0.07	0.03	0.07	3.970	0.01	0	0	0.01	0
PS1 clade	0.1	0	0.27	0.02	0.03	0.04	0	0.6	0.03	0.06	0.61	0.04	0
Pseudoalteromonadaceae	0.6	32.290	0.44	1.440	2.280	0.42	0.26	0.08	0.72	0.3	0.04	2.350	0.7
Pseudohongiellaceae	0	0.13	0.31	0.01	0	0.28	0	1.530	0	0.41	0.02	0.32	0.01
Pseudomonadaceae	0	0.1	0.01	0	0.01	0.03	0.11	0.14	0.02	0	0.02	0.08	0.01
Puniceicoccaceae	0.05	0.04	0.06	0.97	0.01	0.25	0	0.01	0.27	0.45	0.15	0.17	0.19
Rhizobiaceae	4.440	0.09	7.570	12.570	0.64	6.440	1.880	7.270	0.49	0.05	0.8	2.580	2.540
Rhizobiales Incertae Sedis	3.770	0	0.6	0.02	0.22	0.07	0	0.96	1.030	0.01	0	0.1	0
Rhodobacteraceae	18.630	5.880	23.930	35.340	7.790	26.280	24.170	10.150	1.200	6.440	8.460	24.200	29.600
Rhodothermaceae	0.1	0.01	0.08	0	0.01	0.06	0.26	0.82	0	0.03	0	0.08	0.01
Rubinisphaeraceae	0.18	0.06	0.74	0.09	0.16	1.210	0.96	2.060	0.04	0.39	0	1.030	5.450
Rubritaleaceae	0.39	0.04	0.09	0.27	0.39	0.14	0.3	0.09	0.17	3.170	0.11	0.14	0.16
Rubrobacteriaceae	0	0.01	0	0	0	0	0	0	0	0	0	0	0
S25-593	0	0.21	0.02	0	0	0.01	0	0	0	0.68	0.99	0	0

Chapter III

Saccharimonadaceae	0	0.98	0	0	0	0	0	0	0	0	0	0	0
Saccharospirillaceae	0.02	0.07	0.29	0.01	0.12	0.14	0.11	0.15	0.26	0	0	0.77	0.1
Saprospiraceae	3.580	0.12	1.630	2.600	0.43	5.370	6.910	0.6	0.21	0.44	0.11	2.190	5.600
SAR116 clade	0	1.350	0	0.01	0.01	0.02	0	0	0.02	2.650	6.250	0	0.01
Shewanellaceae	0	0.01	0.21	0.01	0.24	0.05	0	0	0.03	0.02	0	0.15	0.01
SM2D12	0	0	0	0.47	0	0	0	0	0	0	0	0.03	0.01
Sphingomonadaceae	3.310	2.980	3.610	2.980	14.800	3.690	10.900	4.880	0.3	0.03	0.05	6.120	4.720
Spongilbacteraceae	0	0.01	0.3	0.05	0.01	0.22	0.04	1.660	0.02	0.01	0.19	0.5	0.02
Stappiaceae	0.07	0.02	0	0.99	0	0.02	0.04	0.02	0.01	0.08	0.42	0.05	0.13
Synechococcales Incertae Sedis	0.27	0	0.01	2.970	0	0.03	1.220	0.05	0.06	0	0.07	2.970	1.890
Tenderiaceae	0	0	0.02	0	0.03	0	0	0.09	0	0.03	0.33	0	0.03
Thermoanaerobaculaceae	0.02	0	0.07	0.02	0	0.02	0	2.140	0.07	0.01	0	0.47	0
Thioglobaceae	0	1.080	0	0	0	0	0	0	0	1.020	0	0	0
Thiotrichaceae	1.040	0.16	0.74	0.01	0.02	0.02	0.26	0.19	35.430	0.16	0.01	0.11	0.05
Vibrionaceae	1.600	1.410	0.27	0.13	0.21	0.07	1.000	0.05	1.490	0.25	0	0.71	1.380
Woeseiaceae	4.710	0.15	15.610	0.15	0.19	0.24	0.18	6.150	3.470	0.34	0	5.220	0.18
Xanthobacteraceae	0	0	0	0	0	0	0	0.03	0	0	0	0	0
Xenococcaceae	0.12	0.03	0	0.12	0.08	0.09	11.420	0.03	0.03	0	0	0.22	0.65

Site	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic
Sample	PP_1	PP_2	PP_3	PP_4	PP_5	PE_9	PE_10	PE_11	PP_6	PP_7	PP_8	PE_12	PE_13
Season/stations	Summer	Summer	Summer	Summer	Summer	Summer	Summer	Summer	Summer	Summer	Summer	Summer	Summer
Actinomarinaceae	0	0.09	0	0	0	0.18	0	0	0	0	0	0	0
AEGEAN-169 marine group	0	0.01	0	0	0	0.02	0	0	0	0	0.01	0	0
Alcanivoraceae	0	0.05	0.1	0.12	0	0	0.15	0.18	0	0.05	0.01	0	0.48
Alteromonadaceae	2.470	2.150	9.100	0.24	0.41	0.69	0.15	0.5	0.22	0.25	26.610	6.600	3.450
Arcobacteraceae	0.02	0.03	0.02	0	0	0.06	0.01	0	0	0	0	0	0.84
Arenicellaceae	0.47	0.34	0.12	0.86	0.03	2.460	0.91	0.51	0.07	0.86	0.08	0.23	0.21
Balneolaceae	0.02	0.01	0	0	0.01	0.02	0.02	0.01	0	0	0.02	0	0.01
Bdellovibrionaceae	0.08	0.14	0	0.11	0.66	0	0.19	0.15	0.04	0.36	0.03	0.72	0.09
Beijerinckiaceae	0	0.05	0	0.03	0.02	0.02	0.01	0.05	0	0.04	0	0	0
Blastocatellaceae	0.29	0.06	0	0.09	0	0.08	0.06	0.15	0	0.08	0.01	0	0.01
Caldilineaceae	0.12	0.06	0	0.02	0	0.06	0.02	0.07	0.01	0	0	0	0.01
Caulobacteraceae	0	0.03	0.2	0.02	0.01	0	0.01	0.02	0.01	0.03	0	0	0.04
Cellvibrionaceae	0.07	0.06	0.06	0.33	0	0.28	0	0.06	0	0	0	0.13	0.16
Chromatiaceae	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Clade I	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade II	0	0	0	0	0	0	0	0	0.02	0	0	0	0
Clade III	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade IV	0	0	0	0	0	0	0	0	0	0	0	0	0
Clostridiaceae	0.01	0.05	0	0.09	0.01	0	0.02	0	0	0	0.01	0	0.04
Colwelliaceae	1.590	0.68	0.14	0.33	0.02	4.040	0.01	0.04	0.01	0	0.65	3.320	4.980
Comamonadaceae	0.01	0.4	0.1	0.05	0.03	0.06	0	0.18	0.02	0.51	0	0.01	0.01
Crocinitomicaceae	0.26	1.910	0.43	2.210	0.01	3.000	0.05	0.05	0	0	0.05	0.02	0.55
Cryomorphaceae	0.2	0.73	0.16	0	0.02	0.67	0.08	0.15	0.07	0.4	0.03	0.25	0.16
Cyanobiaceae	0.21	0.4	0.02	0	0.01	0.04	0.07	0.04	0.12	0.02	0.14	0.1	0.02
Cyclobacteriaceae	0.55	0.77	0.33	0.62	0.72	0.75	2.130	0.95	0.18	0.22	0.75	0.4	0.37
DEV007	0.84	0.65	0.02	0.14	0.02	1.120	0.54	0.41	0.97	0.05	0.01	0.04	0.21
Exiguobacteraceae	0.03	0	0	0	0	0	0	0	0	0.01	0	0.01	0.02
Flavobacteriaceae	10.100	16.260	16.320	3.070	9.140	6.740	10.750	23.230	2.180	7.540	44.200	23.210	12.100
Fokinaceae	0	0	0	0	0	0	0	0.03	0.05	0.07	0	0	0
Gemmataceae	0	0	0	0	0	0.02	0	0	0	0	0	0	0
Granulosioccaceae	0.02	0.32	0.02	0.11	0.02	0	0.03	0.11	0	0.05	0	0.03	0.13
Hahellaceae	0	0.48	0.16	0.09	0	0.02	0	0	0	0	0	0.02	1.040
Halieaceae	0.65	0.59	0	0.21	0.11	0.85	0.94	0.5	0.06	2.100	0.06	0.24	0.11
Halomonadaceae	0	0.08	0.78	0.14	0	0	0	0	0.01	0	0.01	0	0.24
Hyphomicrobiaceae	0.91	0.02	0	6.220	0.08	0.39	3.240	0.91	4.850	0.33	0.1	0.03	0.01
Hyphomonadaceae	4.840	2.990	14.460	1.630	0.63	1.480	7.770	5.090	12.130	4.590	0.22	1.520	0.36
Ilumatobacteraceae	0.4	0.85	0.02	0.12	0.19	0.32	1.000	0.39	0.02	0.23	0.01	0.02	0.17
Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Kiloniellaceae	0.02	0.07	0	0.62	0	0.97	0.05	0.1	0	0	0	0	0.01
marine metagenome	0.02	0.03	0.02	0.03	0	0	0.05	0.01	0	0	0	0.02	0.05
Marinobacteraceae	0.01	0.52	1.880	0.21	0.01	0.08	0.02	0.1	0	0	0.01	0.01	7.890
metagenome	0.01	0	0	0.21	0.43	0	0.16	0	0	0.28	0	0	0.16
Methyloligellaceae	0.48	0.02	0	0.39	0	0.41	0.45	0.2	0.05	0.05	0.01	0	0.01
Methylophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Micavibrionaceae	0.13	0.01	0.14	0.05	0.01	0	0.35	0.46	0.02	0.64	0	0.09	0.13
Microbacteriaceae	0.01	0.11	0.18	0.02	0	0.12	0	0	0	0	0.01	0	0
Microcystaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Microscillaceae	0.02	0.12	0	0	0	0	0.02	0.02	0	0	0.06	0	0
Microtrichaceae	2.200	1.110	0.06	7.030	0.1	3.690	3.510	1.580	0.02	1.290	0.01	0.1	0.1
Moraxellaceae	0.05	1.090	0.47	0.21	0.04	0.12	0	0	0	0.23	0.01	0.03	1.370

Chapter III

Nisaeaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Nitrincolaceae	0.21	0.17	0.1	0.36	0	0.57	0	0.04	0	0	0.02	0.27	0.52
Nitrospiraceae	0	0	0.02	0.33	0	0.14	0	0	0	0	0	0	0.01
Nostocaceae	0	0.11	0	0	0.07	0	0	0	0.08	0	0	0.01	0
NS9 marine group	0.41	0.23	0	0	0.09	0.18	0.06	0.11	0.02	0.23	0.01	0.13	0.01
Obscuribacteraceae	0.01	0	0	0.02	0	0.02	0.01	0	0	0	0	0	0
Oceanospirillaceae	0.02	0	0	0	0	0	0	0.02	0	0	0	0.03	0
OCS116 clade	0	0	0	0	0	0	0	0	0	0	0	0	0
Oleiphilaceae	0.27	2.910	7.650	0.62	0.02	3.880	0.19	0.11	0.01	1.640	0.03	0.18	3.740
Oscillatoriaceae	0.52	0.05	0	0	0	0	0.19	0	0.01	0	0.03	0.75	0
Parvularculaceae	0.32	0.09	0.02	0.27	6.260	0.91	0.81	1.030	0.32	0.28	0.04	0.32	0.22
Phormidesmiaceae	0.26	0.43	0.06	0.03	26.180	0.1	0.35	0.09	13.850	2.200	0.04	0.69	0.01
Phycisphaeraceae	0.36	0.35	0.04	0.39	0	0.35	0.18	0.31	0.06	0.26	0.01	0.01	0.04
Pirellulaceae	6.720	2.370	0.8	7.150	0.62	8.020	5.130	5.730	2.110	3.490	0.51	0.58	0.91
Planococcaceae	0	0.01	0	0	0	0	0	0	0	0	0	0	0.19
Portiococcaceae	0	0.02	0	0.03	0	0	0	0.15	0	0	0	0	0.01
Propionibacteriaceae	0.01	0.07	0	0.05	0.02	0.04	0	0.01	0.01	0.07	0	0	0
PS1 clade	0.57	0	0.04	0.47	0	0.43	0.51	0.26	0.03	0	0.01	0	0
Pseudoalteromonadaceae	0.6	11.720	5.870	0.74	0.05	5.870	0.04	0.2	0.04	0.05	20.930	0.76	14.210
Pseudohongiellaceae	0.04	0.14	0	2.360	0	1.040	0.13	1.360	0	0.02	0	0	0.13
Pseudomonadaceae	0	0.68	2.330	0.11	0	0.2	0	0	0	0	0	0	1.060
Puniceicoccaceae	0.08	0.02	0.02	0	0	0.95	0.17	0.08	0	0.07	0.01	0.02	0
Rhizobiaceae	4.720	5.880	1.840	8.540	0.59	5.520	11.010	3.330	6.600	4.830	0.12	2.360	0.58
Rhizobiales Incertae Sedis	0.07	0.1	0	2.330	0	1.160	0.43	0.45	0	0.05	0.05	0	0
Rhodobacteraceae	34.260	21.800	24.350	13.140	17.090	10.620	30.470	26.820	39.340	40.190	2.300	41.870	19.380
Rhodothermaceae	0.05	0.08	0.02	0.18	1.730	0.24	0.09	0.46	0	1.550	0.01	0.57	0.98
Rubinisphaeraceae	0.92	0.58	0.2	0.87	0.01	2.130	1.150	1.040	0.04	1.040	0.02	0.09	0.79
Rubritaleaceae	0.13	0.89	0	0.05	0.04	1.540	0.14	0.01	0.05	0	0.08	0.07	0.08
Rubrobacteriaceae	0	0.01	0	0	0	0	0	0	0	0	0	0	0
S25-593	0	0	0	0	0	0	0	0	0.02	0	0	0	0
Saccharimonadaceae	0	0.23	0	0	0	0	0	0	0	0	0	0	0.08
Saccharospirillaceae	0.15	0.54	4.390	9.240	0.01	1.320	0.01	0.07	0	0	0.04	0.05	3.940
Saprosiraceae	9.650	2.030	0.67	1.320	6.750	2.720	5.780	9.920	10.850	13.230	0.64	4.100	1.390
SAR116 clade	0	0.02	0.1	0	0	0.12	0	0.01	0.01	0	0.01	0	0.02
Shewanellaceae	0	0.31	0.06	0.45	0	0.3	0.01	0.02	0.01	0	0	0	0.46
SM2D12	0.01	0	0	0	0	0	0	0	0.02	0.14	0	0	0
Sphingomonadaceae	3.320	6.130	1.940	1.040	11.000	2.090	3.850	4.470	3.570	5.510	0.27	5.250	3.700
Spongibacteraceae	0.01	0.06	0.26	1.070	0	0.63	0.11	0.22	0	0.14	0	0	0.04
Stappiaceae	0.32	0.22	0	0.27	0.07	0	0.02	0.09	0.01	0	0.03	0.05	0.01
Synechococcales Incertae Sedis	0.1	0.1	0.26	0.03	11.600	0.1	0.33	0.03	0.13	1.760	0.04	0.43	0
Tenderiaceae	0.36	0.01	0	0.05	0	0	0.15	0.02	0	0	0.01	0	0
Thermoanaerobaculaceae	0.02	0	0.02	0.12	0	0.53	0.08	0.11	0	0	0	0	0
Thioglobaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Thiotrichaceae	0.28	0.11	0.14	0.14	0.01	0.06	0.08	0.02	0.01	0	0.03	0.2	3.340
Vibrionaceae	2.690	0.87	0.84	1.490	0.06	1.660	0.05	0.15	0.11	0.14	0.58	2.280	1.180
Woeseiaceae	0.49	0.42	0.08	5.360	0.02	5.360	0.82	1.090	0.68	0	0	0.01	0.12
Xanthobacteraceae	0	0	0	0	0.02	0	0	0.01	0	0	0	0	0
Xenococcaceae	0.01	0.28	0.02	0	4.480	0.02	0.09	0.04	0.04	0.06	0	0.26	0.01

Site	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Adriatic	Pacific	Pacific
Sample	PP_9	PP_10	SW_S_2	SW_W_1	PE_1	PE_2	PE_3	PE_4	PE_5	PE_6	PP_17	PE_3	PE_4
Season/stations	Summer	Summer	Summer	Winter	Winter	Winter	Winter	Winter	Winter	Winter	Autumn	St.10	St.10
Actinomarinaceae	0	0.05	0.95	8.800	0.07	0	0	0.02	0	0	0	0.08	0.08
AEGEAN-169 marine group	0	0.05	6.880	3.260	0.07	0	0	0	0	0	0	0.01	0.02
Alcanivoraceae	1.000	0.05	0	0.02	0.52	0	0	0	0.06	0	0	0.01	0.1
Alteromonadaceae	7.850	14.270	0.15	0.23	0.88	1.360	1.180	0.85	0.62	2.510	1.220	0.16	0.1
Arcobacteraceae	0.03	0	0.13	0.12	0	0.13	7.500	0	0.08	0	0.08	0	0
Arenicellaceae	2.030	0.05	0.01	0.02	2.120	2.510	0.03	2.100	0.36	0.44	0.08	0.04	0.06
Balneolaceae	0.03	0	3.170	0	0	0	0.01	0	0	0	0	0	0
Bdellovibrionaceae	0.08	0	0.04	0.09	0	0	0.02	0.02	0.54	0	0.08	0.12	0.36
Beijerinckiaceae	0	0	0	0	0.23	0	0.01	0	0	0	0	0	0
Blastocatellaceae	0.62	0	0	0	0	0	0	0	0.01	0.23	0	0	0
Caldilineaceae	0.08	0	0	0	0	0	0	0.02	0	0	0	0	0
Caulobacteraceae	0.01	0.05	0	0.12	0	0.06	0.01	0	0.01	0.02	0	0.01	0
Cellvibrionaceae	1.620	0.05	0	0	0	0	0.15	0.02	0.05	0	0	0	0
Chromatiaceae	0	0.1	0	0	0.1	0.04	0	0	0.01	0	0	0	0
Clade I	0	0.05	1.530	12.810	0.07	0	0	0.02	0	0	0	0.04	0.13
Clade II	0	0	4.890	1.510	0	0	0	0	0	0	0	0	0
Clade III	0	0	2.310	0.1	0	0	0	0	0	0	0	0	0
Clade IV	0	0	0.02	0.94	0.03	0	0	0	0	0	0	0	0
Clostridiaceae	0	0	0.01	0.02	0	0	0.02	0.02	0.01	0.08	0	0.02	0

Chapter III

Colwelliaceae	0.52	0.19	0.17	0	0.03	0.01	5.210	0	0.13	0.25	0	0.03	0
Comamonadaceae	0.03	0	0	0.02	0.68	0.1	0.04	0.16	0.01	0.06	0	0.02	0.02
Crocinitomicaceae	0.24	0	0	0.21	1.140	0.34	0.02	0.36	0.59	0.03	0.65	0.01	0
Cryomorphaceae	0.08	0	0.99	0.35	1.110	0	0.49	0.11	0.21	0.12	0.33	1.230	0.06
Cyanobiaceae	0	0.05	34.870	43.410	1.630	0.08	0.4	1.560	0.04	0.58	0.16	1.710	0.75
Cyclobacteriaceae	1.530	0.05	0.07	0.14	0.26	0.04	0.06	0.36	0.03	1.830	4.970	0.1	0.02
DEV007	1.520	0	0.01	0.07	0	0	0.01	0.42	0.13	0.09	0.08	0.01	0.02
Exiguobacteraceae	0	0	0.01	0.02	0	0	28.230	0	0.02	0.01	0.08	0	0
Flavobacteriaceae	4.180	0.24	9.350	1.910	2.900	1.940	2.170	24.930	13.840	18.360	11.000	40.840	3.140
Fokiniaceae	0	0	0	0	0	1.360	0.08	0	0.01	0	0	0	0
Gemmataceae	0.04	0	0	0	0	0	0	0	0	0	0	0	0
Granulosicoccaceae	2.620	0	0	0	0	0.01	0.02	0	0.06	1.570	0	0	0.02
Hahellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Halieaceae	1.200	0	4.070	0.12	0.82	0.43	0.04	0.13	0.46	0.23	0.49	0.14	0.04
Halomonadaceae	0.24	0.29	0	0.05	0	0	0	0	0.01	0	0	0	0
Hyphomicrobiaceae	1.030	0.05	0.02	0.03	0.03	0.03	0.86	0.07	1.050	5.370	0.98	0	0
Hyphomonadaceae	1.650	0	0.35	0.05	5.970	5.360	0.43	7.550	4.000	5.460	3.990	3.980	3.200
Ilumatobacteraceae	0.41	0	0.02	0	0.1	0.09	0.01	0.67	0.2	0.01	0.16	0	0
Intrasporangiaceae	0	0	0	0.12	0	0	0	1.160	0	0	0	0	0
Kiloniellaceae	0.59	0	0	0.02	0	0.05	0	0	0	0.01	0	0.06	0
marine metagenome	0	0	0.36	0.88	0	0	0.27	0	0.08	0	0.08	0.01	0
Marinobacteraceae	0.59	0.14	0	0.03	0	0	0.01	0.07	0.03	0	0	0.01	0
metagenome	0.09	0	0	0.12	0	0	0.01	0	0.02	0	0	0.01	0
Methyloigellaceae	0.25	0	0	0.03	0	0	0.02	0	0.29	0.1	0.16	0.02	0.19
Methylophilaceae	0	0	0.01	0.19	0	0	0	0	0	0	0	0	0
Micavibrionaceae	0.03	0.05	0	0.02	0	0	0.03	0	0.24	0	0.73	0	0.02
Microbacteriaceae	0	0	2.210	0.03	0	0	0.03	0	0	0	0	0	0
Microcystaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.1
Microsillaceae	0	0	0	0	0	0	0	0	0	0	0.9	0	0
Microtrichaceae	0.82	0.1	0.02	0.94	1.270	0.19	0.02	0.02	0.67	1.690	0	0	0.02
Moraxellaceae	0.1	0.19	0.01	1.370	1.500	0.03	0.27	0.09	0.36	0	0	0.75	0.52
Nisaeaceae	0	0	0.01	0.23	0	0	0	0	0	0	0	0	0
Nitrincolaceae	0	0	0.17	0	0	0	12.090	0.04	0.29	0.05	0	0	0
Nitrospiraceae	0.84	0	0	0	0	0	0	0	0	0.01	0	0	0
Nostocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.02
NS9 marine group	0	0.05	0.35	0.5	0.16	0.11	0.04	0.13	0.42	0.48	0.08	0	0
Obscuribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Oceanospirillaceae	0	0	0	0	0	0	1.020	0	0.03	0	0	0	0
OCS116 clade	0	0	0	1.010	0	0	0	0	0	0	0	0	0
Oleiphilaceae	0.2	4.650	0.02	0.02	18.490	69.970	0.21	0.29	0.71	0.38	0.65	0.07	0
Oscillatoriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Parvularculaceae	1.650	0.05	0.01	0.02	0	0.2	0.06	1.990	0.07	0.38	0.08	0	0
Phormidiesmiaceae	0.04	0.1	0	0.02	28.340	0.01	0.04	10.590	0.03	0.08	0.73	0.32	0.08
Phycisphaeraceae	0.09	0	0.03	0.17	0.26	0	0.01	0.07	0.19	0.01	0	0.3	0.36
Pirellulaceae	10.020	0.05	1.550	0.83	1.730	0.22	0.81	1.430	3.600	3.510	1.140	0.21	0.27
Planococcaceae	0	0	0	0.02	0	0	0.44	0	0	0	0	0.14	0
Porticoccaceae	0	0	0.28	0.02	0.03	0	0	0	0	0	0	0.02	0.02
Propionibacteriaceae	0	0.05	0	0.02	0.78	0.13	0.01	0	0.02	0.28	0	0.05	0.06
PS1 clade	0.08	0	0.46	0	0	0	0	0	0.04	0.84	0	0.01	0
Pseudoalteromonadaceae	1.290	2.010	0	0.45	1.110	0	5.970	0.11	0.09	0.35	1.220	0.02	0.06
Pseudohongiellaceae	0.86	0.05	0.05	0.02	0	0	0	0	0.02	0	0	0	0
Pseudomonadaceae	0.2	0.24	0	0.02	0.03	0	0.06	0	0.01	0	0	0.07	0.02
Puniceicoccaceae	0.3	0	1.120	0.02	3.880	0	0.01	0.02	0	0.03	0.24	0	0
Rhizobiaceae	4.230	0.81	0.44	0.1	7.110	0.8	0.58	0.78	3.030	4.630	16.140	13.790	24.070
Rhizobiales Incertae Sedis	1.250	0	0	0.03	0	0.01	0	0	0	3.840	0.08	0	0
Rhodobacteraceae	19.100	2.010	10.010	8.820	5.060	8.820	10.000	20.820	49.050	23.150	40.910	28.540	58.250
Rhodothermaceae	0	0	0	0.02	0	0	0	1.010	0.04	0.09	0	0	0
Rubinisphaeraceae	8.580	0	0	0.12	0.03	0.03	0.04	1.900	0.18	0.02	0	0.02	0
Rubritaleaceae	0.09	0	0.4	0	0	0.1	0.03	0.02	0.01	0.09	0.16	0.08	0
Rubrobacteriaceae	0	0	0	0.07	0	0	0	4.070	0	0	0	0	0
S25-593	0	0	0.94	0.12	0.03	0.03	0	0	0	0	0	0	0
Saccharimonadaceae	0	0.14	0	1.020	0	0	0	0	0	0	0	0	0
Saccharospirillaceae	2.470	67.050	0.01	0.02	0	0.01	1.280	0	0.34	0.01	0	0	0
Saprospiraceae	1.220	0.14	0.32	0	2.670	0.47	1.620	1.120	9.100	3.060	2.530	2.890	2.530
SAR116 clade	0	0	4.640	1.180	0.03	0.09	0.01	0	0	0	0	0.04	0.13
Shewanellaceae	0.13	0	0	0	0	0	2.940	0	0.05	0.01	0.08	0	0
SM2D12	0	0	0	0	0	0	0	0	0.01	0	0.08	0	0
Sphingomonadaceae	0.76	0.1	0.01	1.700	2.770	3.790	0.69	9.270	4.370	1.920	1.960	1.120	4.310
Spongiibacteraceae	0.51	0	0.02	0.02	0	0	0	0.02	0.03	0	0	0	0.17
Stappiaceae	0	0	0.14	0.03	0.03	0	0.01	0	0	0.23	1.390	0	0
Synechococcales Incertae Sedis	0.03	0	0	0.14	1.790	0	0	0.04	0.02	0.04	2.440	0.03	0.08
Tenderiaceae	0.14	0	0.15	0	0.03	0	0	0	0.02	0	0	0	0
Thermoanaerobaculaceae	0.05	0	0	0	0	0	0	0	0	0.34	0	0	0
Thioglobaceae	0	0	0	0.35	0	0	0	0	0	0	0	0	0

Chapter III

Thiotrichaceae	0.03	0.19	0.01	0.1	0.1	0.01	0.18	0.22	0.08	0.01	0	0	0.02
Vibrionaceae	0.86	0	0.36	0.03	0.07	0	12.830	0.22	1.030	0.2	0.08	0	0
Woeseiaceae	4.900	0.05	0	0	0.03	0.14	0.02	0.04	0.02	2.530	0.08	0	0
Xanthobacteraceae	0	0	0	0	0	0.04	0	0	0	0	0	0	0
Xenococcaceae	0	0	0	0	0.13	0.06	0.03	3.170	0	0	0	0.01	0

Site	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific
Sample	PE_5	Nylon_1	NI_1	PE_1	PE_2	NI_2	PE_6	SW_1	NI_5	PE_9	PE_10	PP_1	PE_11
Season/stations	St.10	St.8	St.8	St.8	St.8	St.8	St.10	St.10	St.12	St.12	St.12	St.12	St.12
Actinomarinaceae	0.06	1.660	0	0.01	0	0	0	0	0	0	0	0	0
AEGEAN-169 marine group	0	0.3	0.1	0.01	0	0	0	0	0	0.01	0	0.1	0
Alcanivoraceae	0.08	0.18	0.02	0	0	0	0.09	0	0	0	0	0	0
Alteromonadaceae	0.03	39.780	0.2	0.49	1.140	0.57	2.060	0	0.65	0.11	0	0	0
Arcobacteraceae	0	0	0	0	0	7.430	0.13	0	0	0	0	0	0
Arenicellaceae	0.03	0	0	0.01	0	0.27	2.140	0	0.15	0	0	0	0
Balneolaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Bdellovibrionaceae	0.79	0.1	0.08	0.16	0.08	0.48	1.120	0.04	0.03	0.04	0	0	0
Beijerinckiaceae	0	0.04	0.3	0.02	0.13	0.02	0	0.02	0	0.03	0.03	0	0
Blastocatellaceae	0	0	0	0	0.08	0	0	0	0	0	0	0	0
Caldilineaceae	0	0	0	0	0	9.060	0	0	0	0	0	0	0
Caulobacteraceae	0	0.27	0.2	0.02	0	0	0	0	0	0	0	0	0
Cellvibrionaceae	0	0	0	0	0	1.050	0	0	0	0	0	0	0
Chromatiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade I	0	0.42	0.06	0.01	0	0	0	0	0	0	0	0.07	0
Clade II	0	0.05	0	0	0	0	0	0	0	0	0	0.01	0
Clade III	0	0	0	0	0	0	0	0	0	0	0	0	0
Clade IV	0	0	0	0	0	0	0	0	0	0	0	0.03	0
Clostridiaceae	0	0	0.32	0	0	0.05	0	0.02	0	0	0	0	0
Colwelliaceae	0	0.03	0	0	0	1.570	3.000	0	0.04	0	0	0	0.01
Comamonadaceae	0.03	0.32	0.1	1.270	2.070	1.190	0.04	0.02	0.05	0.06	0.1	0.03	0.02
Crocinitomicaceae	0	0.1	0	0.01	0.01	0.07	0.26	0.13	0.04	0	0	0	0
Cryomorphaceae	0.71	0.1	0.02	0.21	0	0	0.45	5.240	0.07	0.31	0	0.07	0.01
Cyanobiaceae	0.2	17.150	2.090	0.23	0.07	0.41	0.09	0.02	0.06	0.1	0.3	0.84	0
Cyclobacteriaceae	0	0.04	0.02	0.05	0.01	0.35	8.940	0.11	0.41	2.450	0	0.01	0.16
DEV007	0.08	0	0	0.01	0	1.120	0.04	0.02	0.11	0.1	0	0.01	0
Exiguobacteraceae	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Flavobacteriaceae	0.62	0.5	0.12	5.980	3.450	3.280	7.180	0.62	2.700	0.53	0.39	5.160	5.250
Fokiniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Granulosicoccaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Hahellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Halieaceae	0	0.93	0	0.08	0.24	0.11	0	0	0.03	0.04	0	0.01	0
Halomonadaceae	0	0.1	0	0.01	0.01	0.04	0.02	0	0	0.01	0	0.01	0
Hyphomicrobiaceae	0	0.01	0.98	0.8	0.25	0.18	0	0	0.01	0.12	0	0.01	0
Hyphomonadaceae	6.060	0.23	14.550	8.030	6.420	0.02	4.390	0.25	3.480	25.700	1.780	1.980	0.37
Ilumatobacteraceae	0	0	0	0	0	0	0.04	0	0.01	2.780	0	0	0
Intrasporangiaceae	0	0	0.02	0	0	0	0	0	0	0	0	0	0
Kiloniellaceae	0.34	0	0	0	0	1.050	0	0	0	0	0	0	0
marine metagenome	0	0.12	0	0.03	0.01	0	0.02	0	0	0	0	0	0
Marinobacteraceae	0	0.17	0	0	0.05	0.01	0.04	0	0.01	0.02	0	0.01	0
metagenome	0.03	0.06	0	0	0	0	0.04	0	0	0	0	1.260	1.290
Methylophilaceae	0.2	0	0	0	0	0.13	0	0.02	0	0	0.07	0	0
Methylophilaceae	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Micavibrionaceae	0.03	0	0	0.04	0	0	0.06	0	0	0	0	0.13	0
Microbacteriaceae	0	0.18	0.16	0	0	0.01	0	0	0	0	0	0	0
Microcystaceae	0	0.01	0.04	0.01	0	0	0	0	0	0	0	0.06	0
Microscillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Microtrichaceae	0	0.09	1.540	0.34	0.26	4.270	0	0	1.350	0	0	0.01	0
Moraxellaceae	0.45	10.600	0.78	6.270	12.120	5.380	0.26	0.74	0.22	0.51	0.03	0.54	0.21
Nisaeaceae	0	0.25	0	0	0	0	0	0	0.01	0	0	0	0
Nitrincolaceae	0.03	0.33	0	0	0	3.900	0	0	0	0	0	0	0
Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Nostocaceae	0.03	0.01	0	0	0	0	0.02	0.02	0	0.02	0	0.03	0
NS9 marine group	0	0.25	0	0.08	0.01	0	0	0	0	0	0	0	0
Obscuribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Oceanospirillaceae	0	0.02	0	0	0	0.03	0	0	0	0	0	0	0
OCS116 clade	0	0.14	0.02	0	0	0	0	0	0	0	0	0	0
Oleiphilaceae	0	0	0	0	0	0	0.79	0	0.01	0	0	0	0
Oscillatoriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Parvularculaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Phormidiesmiaceae	1.220	0.04	0.12	0.02	0.04	0.02	0.13	0.08	0.06	0.05	0.03	0.41	43.100
Phycisphaeraceae	2.830	0	0	0.24	0.46	0.51	0.22	0	0.03	0.25	0	0.89	0

Chapter III

Pirellulaceae	0	0.12	0	0	0.01	2.080	0.11	0.02	0.02	0.01	0	0.13	0
Planococcaceae	0	7.610	0.56	0.68	1.450	1.090	0	0	0.02	0	0	0.01	0
Porticoccaceae	0	0	0	0.01	0	0.11	0.07	0	0.03	0	0	0	0
Propionibacteriaceae	0	0.52	0.76	0.03	0.05	0.08	0	0	0.01	0.02	0.1	0	0.01
PS1 clade	0	0	0.28	0.02	0.02	0	0	0	0	0	0	0	0
Pseudalteromonadaceae	0.08	4.370	0.14	0.29	0.52	0.81	1.590	0.02	0.47	0.18	0	0.03	0
Pseudohongiellaceae	0	0.03	0	0	0	0	0	0	0	0	0	0	0
Pseudomonadaceae	0	0.28	0	0.19	0.37	0.12	0.11	0	0.06	0.02	0	0.01	0.01
Puniceococcaceae	0	0	0	0	0	0.2	0	0	0.02	0	0	0.01	0
Rhizobiaceae	5.550	0.14	0.48	0.08	0.06	11.480	11.210	62.180	2.170	2.210	46.980	5.160	0.86
Rhizobiales Incertae Sedis	0	0	0	0	0	0.18	0	0	0	0	0	0	0
Rhodobacteraceae	74.480	4.320	69.610	53.080	54.110	16.950	36.440	25.230	50.440	54.380	49.670	74.170	46.940
Rhodothermaceae	0	0	0	0	0	0.16	0	0	0	0	0	0	0
Rubinisphaeraceae	0	0	0	0	0	0.03	0	0.08	0	0	0	0	0
Rubritaleaceae	0.03	0.1	0	0.02	0.01	0.08	0.04	0	0.07	0	0	0.04	0.01
Rubrobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
S25-593	0	0	0.02	0.03	0	0	0	0	0	0	0	0	0
Saccharimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Saccharospirillaceae	0	0	0	0.01	0	0.05	0	0	0	0	0	0	0
Saprospiraceae	0.17	0.11	0	0.12	0.11	5.140	13.050	2.250	20.400	5.580	0	0.88	0.03
SAR116 clade	0	0.55	0.12	0.01	0	0.11	0.02	0.02	0	0	0	0.01	0
Shewanellaceae	0	0	0	0	0	0	0.45	0.02	0	0	0	0	0
SM2D12	0	0	0	0	0	0	0.09	0	0.48	0.27	0	0	0
Sphingomonadaceae	2.690	1.190	4.670	17.940	12.790	2.630	1.740	2.040	0.35	1.410	0.36	3.680	1.450
Spongiibacteraceae	0.08	0	0	0	0	0	0.02	0	0.01	0	0	0	0
Stappiaceae	0.06	0.19	0.62	0.11	0.09	2.750	0	0.02	0	0	0	0.01	0
Synechococcales Incertae Sedis	0.03	0	0	0	0.04	0	0.04	0.17	0	0	0	0	0
Tenderiaceae	0	0	0	0	0	0.42	0	0	0	0	0	0	0
Thermoanaerobaculaceae	0	0	0	0	0	0	0	0	0	0	0	0	0
Thioglobaceae	0	0.18	0	0	0	0	0	0	0	0	0	0	0
Thiotrichaceae	0	0.01	0	0	0	0	0	0	0	0	0	0.01	0
Vibrionaceae	0	0.23	0	0	0.01	8.970	0	0.02	0.54	0.33	0	0.03	0
Woeseiaceae	0	0	0	0	0	0.03	0	0	0	0	0	0	0
Xanthobacteraceae	0	0.06	0.12	0.02	0.02	0	0	0	0	0	0	0	0
Xenococcaceae	0	0	0	0	0	0	0.02	0	0	0	0	0	0

Site	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific	Pacific
Sample	PE_12	NI_6	PE_7	PE_8	SW_2	NI_7	PP_2	PE_13	NI_8	PE_14	SW_3	SW_4	
Season/stations	St.12	St.12	St.12	St.12	St.12	St.13	St.13	St.13	St.13	St.13	St.13	St.8	
Actinomarinaceae	0	0	0.39	0.43	0	0	0	0	7.890	2.060	13.230	8.640	
AEGEAN-169 marine group	0	0	0.12	0.11	0.02	0.01	0	0	4.090	3.340	3.930	7.160	
Alcanivoracaceae	0	0	0	0	0	0.02	0	0.02	0	0	0	0	
Alteromonadaceae	0.03	0.09	0.12	0.01	0.52	0.12	0.62	0.24	0.32	0.72	0.35	0.01	
Arcobacteraceae	0	0	0	0	0	0	0	0	0	0.01	0.02	0	
Arenicellaceae	1.970	0.58	0	0	0.17	0	5.200	0.01	0	0	0	0	
Balneolaceae	0	0	0	0	0	0	0	0	0	0	0	0.03	
Bdellovibrionaceae	0	0	0.06	1.120	1.140	0	0.05	0	0.18	0.09	0	0.29	
Beijerinckiaceae	0	0	0	0	0.26	0.02	0.22	0.26	0	0	0	0	
Blastocatellaceae	0	0	0	0	0	0	0	0	0	0	0	0	
Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0.05	0	
Caulobacteraceae	0.02	0	0	0.15	0.26	0.02	0.12	0.28	0	0	0	0	
Cellvibrionaceae	0	0	0	0	0	0	0	0	0	0	0.02	0	
Chromatiaceae	0	0	0	0	0	0	0	0	0	0	0	0	
Clade I	0	0	0.15	0.06	0.01	0	0	0	7.240	6.110	22.190	6.390	
Clade II	0	0	0	0	0	0	0	0	1.750	1.200	1.390	2.350	
Clade III	0	0	0	0	0	0	0	0	0	0	0	0.03	
Clade IV	0	0	0	0.03	0	0	0	0	0.75	0.21	4.590	0.91	
Clostridiaceae	0	0	0	0	0	0	0.03	0	0	0	0	0	
Colwelliaceae	0.23	0.17	0	0	0	0	0.34	0.01	0	0	0.02	0	
Comamonadaceae	0.09	0.33	0	0	1.550	0.85	0.83	1.230	0.02	0.02	0	0	
Crocinitomicaceae	0.01	0.02	0	0	2.850	0	0.01	0	0	0.67	0.02	0.26	
Cryomorphaceae	0	0.09	0	0	0	0.01	0.07	0	0	0.1	0.03	0.09	
Cyanobiaceae	0.29	0.07	4.710	3.040	0.03	0.24	0.02	0.01	66.250	9.610	32.180	56.200	
Cyclobacteriaceae	1.000	0.23	0.01	0.01	0.02	0.21	0.36	0.14	0.02	0.33	0.02	0.01	
DEV007	0.02	0	0	0.15	0	10.880	0.07	3.210	0	0.13	0	0.46	
Exiguobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	
Flavobacteriaceae	16.730	9.510	0.13	0	4.060	15.640	11.710	5.060	0.37	14.120	0.97	2.970	
Fokiniaceae	0	0	0	0	0	0	0	0	0	0.01	0	0	
Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	
Granulosicoccaceae	0	0	0	0	0	0	0	0	0	0	0	0	
Hahellaceae	0	0	0	0	0	0	0	0	0	0	0	0	
Halieaceae	0.01	0.02	0.11	0	0.49	0.29	0.23	0.05	0.03	0.26	0.03	0.03	

Chapter III

Halomonadaceae	0	0	0	0	0	0.01	0.01	0	1.460	1.330	0	0
Hyphomicrobiaceae	0	0	0	0.01	0	0	0	0	0.03	0	0	0
Hyphomonadaceae	5.370	0.58	54.710	1.430	3.160	17.850	2.090	8.880	0.06	0.05	0.03	0.02
Ilumatobacteraceae	0	0	0.01	0	0.02	0.24	0	0.01	0	0.01	0	0
Intrasporangiaceae	0	0	0.02	0	0	0	0	0	0	0	0	0
Kiloniellaceae	0	0	0	0	0	0	0	0	0	0	0	0
marine metagenome	0	0	0	0.03	0	0	0	0	0.27	0.35	0.06	0.36
Marinobacteraceae	0.04	0.02	0	0	0.01	0	0.16	0.02	0.13	0.04	0	0.01
metagenome	0	0.19	0	0	0	0	0	0.01	0.02	0.01	0	0.14
Methyloiligellaceae	0	0	0	0.02	0.01	0.01	0.03	0	0	0.01	0	0
Methylophilaceae	0	0	0	0	0	0	0	0	0	1.070	0.05	0
Micavibrionaceae	0	0.02	0	0	0.14	0.2	0.52	0	0	0.01	0	0
Microbacteriaceae	0	0	0.09	0.02	0	0	0	0.06	0	0	0	0
Microcystaceae	0.01	0	0	0.49	0	18.630	0.16	0	0.13	0.01	0	0
Microscillaceae	0	0	0	0.02	0	0	0.01	0	0	0	0	0
Microtrichaceae	0	0.01	0.01	0.09	0	0.04	0	0.01	0.05	0.18	0.11	0
Moraxellaceae	0.57	1.010	0.05	0.01	4.270	2.300	5.140	5.020	1.110	0.46	0.16	0.11
Nisaeaceae	0	0	0.13	0	0	0	0	0	0.05	0.25	0.32	0.07
Nitrincolaceae	0	0.01	0	0	0.01	0	0	0	0	0	0	0
Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0
Nostocaceae	0.01	0	0	0.03	0.01	0.94	0.01	0.04	0.1	0.02	0.02	0.02
NS9 marine group	1.370	0	0	0	0	0	0	0	0.08	4.010	0.3	0.55
Obscuribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0
OCS116 clade	0	0	0.01	0.05	0	0	0	0	0.05	4.530	2.480	0.43
Oleiphilaceae	0	0	0	0	0	0	0.65	0	0	0	0	0
Oscillatoriaceae	0	0	0	0	0	0	0	0	0	0	0	0
Parvularculaceae	0	0	0.32	0	0	0.04	0	0	0	0	0	0
Phormidemiaceae	0.21	1.360	0	0.55	0.01	0.01	0.25	0.35	0.24	0	0.06	0.01
Phycisphaeraceae	0	0.07	3.180	0.1	0.08	7.510	0.57	0	0.21	0.25	0.14	0.28
Pirellulaceae	0.03	0.08	0.35	0.28	0.23	6.610	0.41	0.13	0	1.010	1.290	0.18
Planococcaceae	0.02	0.02	0.01	0.01	0	0	0	0	0	0.01	0.02	0
Porticoccaceae	0	0	0	0	0	0	0	0	0	2.710	0.1	0.14
Propionibacteriaceae	0.07	0.03	0.07	0.4	0.33	0.19	0.35	0.72	0.02	0.06	0	0.01
PS1 clade	0	0	0	0	0.11	0	0.01	0	0.05	0	0	0.11
Pseudoalteromonadaceae	0.05	0.01	0	0	0.03	0.01	0.48	0	0.25	0.13	0.03	0.06
Pseudohongiellaceae	0	0	0	0	0.01	0	0	0	0	0.03	0.02	0.01
Pseudomonadaceae	0.03	0.07	0	0.01	0.52	0.21	0.85	0.67	0	0.03	0.02	0.02
Puniceicoccaceae	0.01	0	0.01	0	0	0	0	0	0.08	0.1	0.03	0.14
Rhizobiaceae	8.750	18.360	8.790	1.570	0.23	3.370	2.660	0.29	0.02	0.02	0.21	0.01
Rhizobiales Incertae Sedis	0	0	0	0	0	0.07	0	0	0	0	0	0
Rhodobacteraceae	60.250	60.140	24.690	88.110	29.250	9.310	20.590	52.290	1.320	20.870	8.310	1.630
Rhodothermaceae	0	0	0	0	0	0	0	0	0	0	0	0
Rubinisphaeraceae	0.01	0.03	0.02	0	30.480	2.270	0.01	9.420	0	0.01	0	0
Rubritaleaceae	0.41	0.02	0	0	0.01	0	0.08	0	0	0.24	0.06	0.22
Rubrobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
S25-593	0	0	0	0.01	0	0	0	0	1.100	0.1	0.02	1.090
Saccharimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0
Saccharospirillaceae	0	0	0	0	0	0	0.13	0	0	0	0	0.01
Saprospiraceae	0.5	2.750	0	0.1	1.910	0.92	4.450	0.27	0.05	0.77	0	0.03
SAR116 clade	0	0	0.12	0.03	0.08	0.01	0	0	2.930	2.550	4.700	2.810
Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0
SM2D12	0.62	0	0	0	0	0	23.080	0.23	0	0	0	0
Sphingomonadaceae	0.09	0.19	0.33	1.050	0.49	0.09	1.770	0.42	0.29	0.07	0.14	0
Spongiibacteraceae	0.16	0.02	0	0	0	0.01	0	0.01	0.02	0.01	0	0
Stappiaceae	0	0	0.8	0	15.830	0.02	11.710	0.01	0	0	0	0.02
Synechococcales Incertae Sedis	0	0	0	0	0.03	0	0	0.01	0	0.01	0	0
Tenderiaceae	0	0	0	0	0	0	0	0	0	0	0	0
Thermoanaerobaculaceae	0	0	0	0	0	0	0	0	0	0	0	0
Thioglobaceae	0	0	0	0	0	0	0	0	0	3.420	0.03	0
Thiotrichaceae	0.01	0	0.06	0	0	0	0	0	0.1	1.870	1.150	0.05
Vibrionaceae	0	0.01	0	0	0.05	0.01	0.01	0	0	0.01	0.02	0.06
Woeseiaceae	0	0	0.02	0	0	0	0	0	0	0.36	0.02	0.01
Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0.02	0
Xenococcaceae	0	0	0	0	0.01	0	0.01	0	0	0.01	0	0

Table S9 – OTUs found in plastics from all sampling sites, but not in SW.

Taxonomy	OTUId
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Micavibrionales; f__uncultured; g__uncultured bacterium	OTU_2533
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Micavibrionales; f__Micavibrionaceae; g__uncultured; s__uncultured bacterium	OTU_6040
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__Filomicrobium; s__uncultured Alphaproteobacteria bacterium	OTU_698
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens; s__Psychroserpens damuponensis	OTU_1947
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_598
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Pir4 lineage; s__uncultured bacterium	OTU_1787
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Gammaproteobacteria Incertae Sedis; f__Unknown Family; g__Acidibacter; s__uncultured bacterium	OTU_5718
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_1213
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Actibacterium; s__uncultured bacterium	OTU_2316
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_611
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Micavibrionales; f__Micavibrionaceae; g__uncultured; s__uncultured bacterium	OTU_5962
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__uncultured Pseudomonas sp.	OTU_2291
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Fretibacter; s__Fretibacter rubidus	OTU_2250
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrocolaceae; g__Marinobacterium; s__Neptuniibacter sp.	OTU_1071
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium sensu stricto 13; s__uncultured bacterium	OTU_1058
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_1773
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Pelomonas; s__uncultured bacterium	OTU_921
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__uncultured bacterium	OTU_6709
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Tepidimonas; s__uncultured bacterium	OTU_2176
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter; s__uncultured bacterium	OTU_4960
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingobium; s__Sphingomonas sp. ML1	OTU_5740
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__Reichenbachiella; s__uncultured Flammeovirgaceae bacterium	OTU_2285
k__Bacteria; p__Bdellovibrionota; c__Bdellovibrionia; o__Bdellovibrionales; f__Bdellovibrionaceae; g__Bdellovibrio; s__uncultured bacterium	OTU_1356
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Aureispira; s__Saprospira sp. CNJ640	OTU_168
k__Bacteria; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae; g__SM1A02; s__uncultured organism	OTU_3223
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella; s__uncultured bacterium	OTU_964
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Muricauda; s__uncultured bacterium	OTU_1100
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Anoxybacillus; s__Anoxybacillus flavithermus	OTU_2548
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tropicimonas; s__Bacteroidetes bacterium	OTU_500
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__Marinoscillum; s__metagenome	OTU_2599

k__Bacteria; p__Patescibacteria; c__Parcubacteria; o__Candidatus Kaiserbacteria; f__marine metagenome	OTU_2492
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_4706
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Parvularculaceae; g__Parvularcula; s__Parvularcula oceani	OTU_1198
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Rubidimonas; s__uncultured Saprospiraceae bacterium	OTU_1547
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Spongiivirga; s__Spongiivirga citrea	OTU_126
k__Bacteria; p__Planctomycetota; c__OM190; o__uncultured planctomycete	OTU_374
k__Bacteria; p__Bdellovibrionota; c__Bdellovibrionia; o__Bdellovibrionales; f__Bdellovibrionaceae; g__OM27 clade; s__uncultured bacterium	OTU_753
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Dokdonia; s__Dokdonia sp. U1371-101202-SW230	OTU_293
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__marine bacterium MSC1	OTU_266
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pontivivens; s__bacterium	OTU_989
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__uncultured; s__uncultured bacterium	OTU_2208
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter; s__uncultured bacterium	OTU_3161
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Algimonas; s__Algimonas ampicilliniresistens	OTU_1926
k__Bacteria; p__Planctomycetota; c__OM190; o__uncultured bacterium	OTU_1892
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter; s__Octadecabacter sp. LPB0143	OTU_1331
k__Bacteria; p__Bdellovibrionota; c__Bdellovibrionia; o__Bdellovibrionales; f__Bdellovibrionaceae; g__Bdellovibrio; s__uncultured bacterium	OTU_4997
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Cryomorphaceae; g__Vicingus; s__uncultured Owenweeksia sp.	OTU_2418
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__uncultured bacterium	OTU_6397
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Portibacter; s__Portibacter lacus	OTU_2245
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_5723
k__Bacteria; p__WPS-2; c__hydrothermal vent metagenome	OTU_3284
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Magnetospiraceae; g__uncultured; s__uncultured marine bacterium	OTU_1298
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__uncultured; s__uncultured bacterium	OTU_508
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__Flavobacterium plurextorum	OTU_6759
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroflexus; s__Flavobacteriaceae bacterium	OTU_2877
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium sensu stricto 10; s__uncultured bacterium	OTU_2917
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tropicimonas; s__Bacteroidetes bacterium	OTU_1380

Table S10 - OTUs with more than 1% relative abundance in at least one sample.

Taxonomy	OTUId
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Gemmatales; f__Gemmataceae; g__Fimbriiglobus; s__uncultured planctomycete	OTU_1194
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Caulobacter; s__uncultured bacterium	OTU_100
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; s__Sphingomonas dokdonensis	OTU_156
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; s__uncultured bacterium	OTU_344
k__Bacteria; p__Cyanobacteria; c__Vampirivibrionia; o__Obscuribacteriales; f__Obscuribacteriaceae; g__uncultured bacterium	OTU_224
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Pseudahrensia; s__uncultured bacterium	OTU_134
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Psychrosphaera; s__marine bacterium Tw-3	OTU_496
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Paracoccus; s__uncultured Paracoccus sp.	OTU_2
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Cognatyyoonia; s__uncultured Alphaproteobacteria bacterium	OTU_15
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Leptolyngbya sp. LEGE 07075	OTU_7
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured microorganism	OTU_1921
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Ruegeria sp. AD91A	OTU_39
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Synechococcus CC9902; s__uncultured marine cyanobacterium	OTU_1
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured Rhodobacteraceae bacterium	OTU_171
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Leptolyngbya sp. LEGE 07075	OTU_201
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Synechococcus CC9902; s__unidentified marine bacterioplankton	OTU_3982
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Psychrobacter; s__uncultured Psychrobacter sp.	OTU_41
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sulfitobacter; s__Sulfitobacter sp. EE-36	OTU_1304
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_280
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Aestuariicoccus; s__uncultured bacterium	OTU_4719
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Vibrio; s__Vibrio splendidus	OTU_1028
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas; s__Pseudoalteromonas sp. 12	OTU_54
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__AEGEAN-169 marine group; g__uncultured marine bacterium	OTU_64
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_37
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Prochlorococcus MIT9313; s__Prochlorococcus marinus str. EQPAC1	OTU_86
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Yoonia-Loktanelia; s__Thalassobium sp. R2A62	OTU_309
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured bacterium	OTU_9
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__uncultured; s__unidentified marine bacterioplankton	OTU_320
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__Filomicrobium; s__uncultured Alphaproteobacteria bacterium	OTU_169
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Primorskyibacter; s__Primorskyibacter sedentarius	OTU_6540
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Dinoroseobacter; s__unidentified marine bacterioplankton	OTU_2188
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Synechococcus sp. PCC 7335	OTU_8
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacteriales; f__Microcystaceae; g__Atelocyanobacterium (UCYN-A); s__Candidatus Atelocyanobacterium thalassa isolate ALOHA	OTU_269
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Ahrensia; s__uncultured bacterium	OTU_89

k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Amylibacter; s__Amylibacter sp. ECD29	OTU_80
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Yoonia-Loktanelia; s__uncultured bacterium	OTU_29
k__Bacteria; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae; g__Algisphaera; s__Algisphaera agarilytica	OTU_13
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Shimia; s__Shimia sp. SK013	OTU_141
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter junii CIP 64.5	OTU_50
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured microorganism	OTU_497
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Silicimonas; s__uncultured bacterium	OTU_3272
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Pseudahrensia; s__uncultured bacterium	OTU_135
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_36
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__uncultured organism	OTU_114
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sulfitobacter; s__uncultured Rhodobacterales bacterium	OTU_143
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Litoreibacter; s__uncultured marine microorganism	OTU_72
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__bacterium SH1-10	OTU_68
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Rubripirellula; s__uncultured planctomycete 6N14	OTU_33
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Pseudoanabaena minima SAB031701	OTU_44
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Marinibacterium; s__uncultured bacterium	OTU_30
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured bacterium	OTU_27
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Hellea; s__Hellea balneolensis DSM 19091	OTU_105
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Planomicrobium; s__Planomicrobium okeanokoites	OTU_211
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter radioresistens DSM 6976 = NBRC 102413 = CIP 103788	OTU_237
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Litorimonas; s__Arctic bacterium NP26	OTU_16
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; s__uncultured Caulobacterales bacterium	OTU_162
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC- 6307; s__Synechococcus sp. RCC307	OTU_104
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__uncultured; s__uncultured bacterium	OTU_2279
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter; s__uncultured bacterium	OTU_299
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_249
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas; s__Pseudoalteromonas marina	OTU_1720
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Synechococcus CC9902; s__uncultured bacterium	OTU_5917
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae; g__Roseibacillus; s__uncultured organism	OTU_125
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Pseudahrensia; s__Ahrensia sp. R2A130	OTU_103
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Acrophormium PCC-7375; s__uncultured bacterium	OTU_38
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Actinomarinales; f__Actinomarinaceae; g__Candidatus Actinomarina; s__uncultured marine bacterium	OTU_56
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Silicimonas; s__uncultured Alphaproteobacteria bacterium	OTU_99
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Croceitalea; s__Croceitalea sp. U1371-101227-XH137	OTU_58
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae; g__Roseibacillus; s__Verrucomicrobia bacterium SCGC AAA164-L15	OTU_48
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__Erythrobacter vulgaris	OTU_52

k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseobacter clade NAC11-7 lineage; s__uncultured bacterium	OTU_678
k__Bacteria; p__Firmicutes; c__Bacilli; o__Exiguobacterales; f__Exiguobacteraceae; g__Exiguobacterium; s__Exiguobacterium profundum	OTU_183
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Crocinitomicaceae; g__Fluviicola; s__uncultured marine bacterium	OTU_215
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__AEGEAN-169 marine group; g__uncultured Alphaproteobacteria bacterium	OTU_258
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Algimonas; s__uncultured bacterium	OTU_129
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured bacterium	OTU_123
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured bacterium	OTU_112
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Thalassobius; s__uncultured bacterium	OTU_777
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__NS4 marine group; s__uncultured marine bacterium	OTU_246
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Vibrio; s__Vibrio owensii	OTU_285
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured bacterium	OTU_397
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter; s__Octadecabacter sp. UDC483	OTU_995
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__Filomicrobium; s__uncultured Alphaproteobacteria bacterium	OTU_698
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tateyamaria; s__uncultured bacterium	OTU_935
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Nitrobacter; s__uncultured Alphaproteobacteria bacterium	OTU_820
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Synechococcus CC9902; s__uncultured bacterium	OTU_5343
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter; s__Polaribacter sp. BM10	OTU_582
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Psychrobacter; s__uncultured Psychrobacter sp.	OTU_287
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__Erythrobacter sp. U1370-101126-SW175	OTU_278
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__Erythrobacter seohaensis	OTU_393
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens; s__Psychroserpens mesophilus	OTU_121
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Boseongicola; s__Boseongicola aestuarii	OTU_69
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured Bacteroidetes bacterium	OTU_274
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacteriales; f__Xenococcaceae; g__Pleurocapsa PCC-7319; s__uncultured bacterium	OTU_228
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__NS2b marine group; s__uncultured marine bacterium	OTU_1211
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Crocinitomicaceae; g__Fluviicola; s__unidentified marine bacterioplankton	OTU_292
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Ilumatobacteraceae; g__Ilumatobacter; s__Ilumatobacter nonamiensis YM16-303	OTU_311
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tropicimonas; s__uncultured bacterium	OTU_1778
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Cognatishimia; s__uncultured Alphaproteobacteria bacterium	OTU_3128
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured organism	OTU_779
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseobacter; s__uncultured bacterium	OTU_159
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Clade I; g__Clade Ia; s__marine metagenome	OTU_67
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__SAR86 clade; f__unidentified marine bacterioplankton	OTU_218
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Formosa; s__uncultured bacterium	OTU_229
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_598
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured bacterium	OTU_6239

k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured bacterium	OTU_31
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Vibrio; s__Vibrio fortis	OTU_440
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__uncultured; s__uncultured bacterium	OTU_74
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_6729
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__uncultured; s__uncultured marine bacterium	OTU_124
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Gramella; s__metagenome	OTU_463
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__unidentified marine bacterioplankton	OTU_3493
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_1213
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured bacterium	OTU_438
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Arcticiflavibacter; s__uncultured Bacteroidetes bacterium	OTU_265
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_611
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum aiptasiae	OTU_42
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Schizotrichaceae cyanobacterium TAU-MAC 1315	OTU_290
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Clade II; g__uncultured marine bacterium	OTU_193
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanella; s__Cognatiyoonia sediminum	OTU_447
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Lacimonas; s__uncultured bacterium	OTU_803
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter; s__uncultured bacterium	OTU_888
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Puniceispirillales; f__SAR116 clade; g__uncultured bacterium	OTU_1182
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__uncultured Bacteroidetes bacterium	OTU_188
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Clade IV; g__uncultured marine bacterium	OTU_593
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacteriales; f__Nostocaceae; g__Rivularia PCC-7116; s__Calothrix parasitica NIES-267	OTU_3
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__NS2b marine group; s__uncultured marine bacterium	OTU_301
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Olleya; s__Olleya sp. R18-12	OTU_208
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Alteromonas; s__Alteromonas genovensis	OTU_6
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__Planctomicrobium; s__uncultured bacterium	OTU_528
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__Roseovarius aestuarii	OTU_483
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Cognatishimia; s__uncultured bacterium	OTU_40
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_62
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__Erythrobacter sp. NAP1	OTU_697
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured bacterium	OTU_307
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Dokdonia; s__Dokdonia donghaensis DSW-1	OTU_142
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Puniceispirillales; f__SAR116 clade; g__uncultured bacterium	OTU_422
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aurantivirga; s__Flavobacterium sp. SCGC AAA160-P02	OTU_243
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__NS2b marine group; s__marine metagenome	OTU_612
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae; g__uncultured; s__uncultured marine bacterium	OTU_219
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__uncultured; s__Cladosiphon okamuranus	OTU_510

k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Marivita; s__uncultured bacterium	OTU_231
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Marinovum; s__uncultured bacterium	OTU_731
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__uncultured; f__uncultured bacterium	OTU_893
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Actinomarinales; f__Actinomarinaceae; g__Candidatus Actinomarina; s__uncultured bacterium	OTU_83
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Gammaproteobacteria Incertae Sedis; f__Unknown Family; g__Marinicella; s__uncultured gamma proteobacterium	OTU_167
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Acrophormium PCC-7375; s__Leptolyngbya cf. ectocarpi LEGE 11479	OTU_2713
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Verrucomicrobiales; f__DEV007; g__uncultured bacterium	OTU_178
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_66
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__uncultured Bacteroidetes bacterium	OTU_78
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Yoonia-Loktanella; s__uncultured bacterium	OTU_400
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Planktomarina; s__uncultured marine bacterium	OTU_2790
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Lentibacter; s__uncultured bacterium	OTU_259
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__Winogradskyella thalassocola	OTU_424
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured bacterium	OTU_848
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Lentilitoribacter; s__uncultured bacterium	OTU_32
k__Bacteria; p__Bdellovibrionota; c__Bdellovibrionia; o__Bdellovibrionales; f__Bdellovibrionaceae; g__Bdellovibrio; s__uncultured marine bacterium	OTU_1527
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Litorimonas; s__uncultured Alphaproteobacteria bacterium	OTU_77
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Qipengyuania; s__uncultured bacterium	OTU_2242
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Maribius; s__Maribius sp. MOLA 401	OTU_2069
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Puniceispirillales; f__SAR116 clade; g__alpha proteobacterium SCGC AAA015-N04	OTU_120
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_250
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Limimanicola; s__Limimanicola hongkongensis	OTU_451
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium; s__Agrobacterium radiobacter	OTU_370
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella; s__uncultured proteobacterium	OTU_22
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__NS4 marine group; s__uncultured bacterium	OTU_190
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tateyamaria; s__uncultured bacterium	OTU_542
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiales Incertae Sedis; g__Andersenella; s__uncultured bacterium	OTU_102
k__Bacteria; p__Deinococcota; c__Deinococci; o__Deinococcales; f__Trueperaceae; g__Truepera; s__uncultured bacterium	OTU_1429
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas; s__Halomonas sp. H1-55	OTU_1508
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Flavobacteria bacterium S1-62	OTU_798
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Synechococcales Incertae Sedis; g__Schizothrix LEGE 07164; s__uncultured bacterium	OTU_11
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured cyanobacterium	OTU_239
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__Oceaniserpentilla; s__gamma proteobacterium Yb007	OTU_12
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__Reichenbachella; s__uncultured bacterium	OTU_453
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Clade IV; g__uncultured bacterium	OTU_225
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquimarina; s__Aquimarina amphilecti	OTU_82
k__Bacteria; p__Bdellovibrionota; c__Bdellovibrionia; o__Bdellovibrionales; f__Bdellovibrionaceae; g__Bdellovibrio; s__uncultured bacterium	OTU_1356

k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__uncultured; s__uncultured Rhodobacterales bacterium	OTU_295
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Shimia; s__uncultured bacterium	OTU_6475
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Porticoccaceae; g__SAR92 clade; s__uncultured bacterium	OTU_1015
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae; g__Colwellia; s__uncultured bacterium	OTU_1604
k__Bacteria; p__Cyanobacteria; c__Sericytochromatia; o__uncultured bacterium	OTU_254
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__Litorimonas; s__Litorimonas cladophorae	OTU_2940
k__Bacteria; p__Patescibacteria; c__Parcubacteria; o__Candidatus Kaiserbacteria; f__metagenome	OTU_323
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Thalassobaculales; f__Nisaeaceae; g__OM75 clade; s__uncultured bacterium	OTU_395
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter; s__uncultured bacterium	OTU_561
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured bacterium	OTU_35
k__Bacteria; p__Bacteroidota; c__Rhodothermia; o__Rhodothermales; f__Rhodothermaceae; g__Rubrivirga; s__Rubrivirga profundus	OTU_1944
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_369
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum sp.	OTU_149
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__Rhodobacterales bacterium JY-7	OTU_556
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudophaeobacter; s__uncultured marine bacterium	OTU_23
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured bacterium	OTU_385
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__PeM15; f__uncultured bacterium	OTU_116
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Subsaxibacter; s__Aquaticitalea lipolytica	OTU_1569
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__Winogradskyella echinorum	OTU_1251
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__Roseovarius nanhaiticus	OTU_1114
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_664
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Parvularculaceae; g__Parvularcula; s__Parvularcula luteaensis	OTU_601
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter; s__Pibocella sp. UDC543	OTU_119
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Jannaschia; s__Jannaschia sp.	OTU_897
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__Fokiniaceae; g__MD3-55; s__uncultured bacterium	OTU_377
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Dokdonia; s__uncultured bacterium	OTU_4131
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Pseudahrensia; s__Pseudahrensia aquimaris	OTU_1498
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Amylibacter; s__uncultured Alphaproteobacteria bacterium	OTU_906
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacteriales; f__Woeseiaceae; g__Woeseia; s__uncultured bacterium	OTU_688
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_230
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacteriales; f__Woeseiaceae; g__Woeseia; s__uncultured bacterium	OTU_3045
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Cryomorphaceae; g__Cryomorpha; s__uncultured organism	OTU_1205
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Synechococcales Incertae Sedis; g__Schizothrix LEGE 07164; s__uncultured bacterium	OTU_872
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Meridianimaribacter; s__Meridianimaribacter flavus	OTU_51
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Dinoroseobacter; s__uncultured bacterium	OTU_421
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tateyamaria; s__uncultured marine bacterium	OTU_5397
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Kordia; s__Kordia ulvae	OTU_275

k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Cellulophaga; s__Cellulophaga sp. NBRC 101309	OTU_428
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tateyamaria; s__uncultured Alphaproteobacteria bacterium	OTU_5559
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__uncultured; s__uncultured Acidimicrobiales bacterium	OTU_506
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Nonlabens; s__Nonlabens antarcticus	OTU_305
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter; s__metagenome	OTU_2822
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_2811
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Salinimonas; s__Salinimonas sp. N102	OTU_1933
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Pseudofulvibacter; s__Pseudofulvibacter geojedonensis	OTU_26
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Portibacter; s__uncultured bacterium	OTU_1140
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Parvularculaceae; g__Amphiplicatus; s__uncultured Alphaproteobacteria bacterium	OTU_926
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__Marivita sp. CZ-AX3	OTU_1045
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured bacterium	OTU_2778
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Olleya; s__Olleya aquimaris	OTU_5577
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Rhodopirellula; s__unidentified marine bacterioplankton	OTU_192
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_1101
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Halieaceae; g__OM60(NOR5) clade; s__uncultured bacterium	OTU_410
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__Photobacterium profundum 3TCK	OTU_175
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvibaculales; f__OCS116 clade; g__uncultured bacterium	OTU_207
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sulfitobacter; s__marine bacterium ATAM407_2031	OTU_4863
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured organism	OTU_632
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured marine bacterium	OTU_569
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_1060
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__uncultured Rhodobacteraceae bacterium	OTU_92
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__S25-593; g__uncultured bacterium	OTU_555
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Pibocella; s__uncultured bacterium	OTU_1740
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter; s__uncultured bacterium	OTU_357
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methylobacteriaceae; g__uncultured; s__uncultured bacterium	OTU_733
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter; s__Octadecabacter sp. LPB0143	OTU_1331
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Croceitalea; s__Croceitalea bacterium PAORIC-8	OTU_1553
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae; g__Alcanivorax; s__uncultured Alcanivorax sp.	OTU_182
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__uncultured; s__uncultured bacterium	OTU_942
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Crocinitomicaceae; g__Salinirepens; s__uncultured marine bacterium	OTU_97
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella; s__uncultured bacterium	OTU_223
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Rheinheimera; s__Rheinheimera baltica	OTU_296
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Thalassobius; s__Thalassobius mediterraneus	OTU_1755
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Cryomorphaceae; g__Vicingus; s__uncultured bacterium	OTU_76

k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__uncultured; s__uncultured planctomycete	OTU_25
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__uncultured gamma proteobacterium	OTU_2046
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Defluviimonas; s__uncultured bacterium	OTU_709
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__uncultured; s__uncultured bacterium	OTU_1153
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_714
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured gamma proteobacterium	OTU_338
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methyloiligellaceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_55
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pontivivens; s__Pontivivens insulae	OTU_1020
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Marinobacteraceae; g__Marinobacter; s__Marinobacter lipolyticus SM19	OTU_317
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Cryomorphaceae; g__uncultured; s__uncultured marine bacterium	OTU_475
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__uncultured; s__uncultured Bacteroidetes bacterium	OTU_1308
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Parasphingopyxis; s__uncultured bacterium	OTU_53
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maritimimonas; s__uncultured marine bacterium	OTU_106
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacteriales; f__Xenococcaceae; g__Pleurocapsa PCC-7319; s__Xenococcaceae cyanobacterium CENA345	OTU_1255
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured bacterium	OTU_1183
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_5723
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Muriicola; s__Muriicola jejuensis	OTU_843
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__uncultured; s__uncultured bacterium	OTU_616
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Rhodopirellula; s__planctomycete MS30D1	OTU_186
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__Sva0996 marine group; s__uncultured Acidimicrobiales bacterium	OTU_180
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter; s__Ulvibacter litoralis	OTU_1368
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Pseudofulvibacter; s__uncultured bacterium	OTU_741
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__SAR86 clade; f__uncultured marine bacterium	OTU_1294
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Aureispira; s__uncultured bacterium	OTU_1173
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured planctomycete	OTU_4671
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella; s__Arenicella chitinivorans	OTU_170
k__Archaea; p__Thermoplasmatota; c__Thermoplasmata; o__Marine Group II; f__uncultured archaeon	OTU_217
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__uncultured; g__uncultured bacterium	OTU_2180
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Nereida; s__uncultured Nereida sp.	OTU_748
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae; g__Haloferula; s__uncultured Verrucomicrobiae bacterium	OTU_358
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Parvularculaceae; g__Parvularcula; s__Parvularcula oceani	OTU_1736
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__uncultured; f__uncultured bacterium	OTU_800
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitricolaceae; g__Marinobacterium; s__uncultured Marinobacterium sp.	OTU_139
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__Hymenobacter sp. PDD-47b-5	OTU_5364
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Frankiales; f__uncultured; g__uncultured bacterium	OTU_3408
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__NS9 marine group; g__uncultured bacterium	OTU_252
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__uncultured marine bacterium	OTU_537
k__Bacteria; p__Actinobacteriota; c__Rubrobacteria; o__Rubrobacterales; f__Rubrobacteriaceae; g__Rubrobacter; s__uncultured bacterium	OTU_1638

k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella; s__uncultured Bacteroidetes bacterium	OTU_234
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__SAR86 clade; f__uncultured marine bacterium	OTU_3122
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__NS4 marine group; s__uncultured bacterium	OTU_2406
k__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Arcobacteraceae; g__uncultured; s__uncultured bacterium	OTU_717
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__Sva0996 marine group; s__uncultured bacterium	OTU_199
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__Fuerstia; s__uncultured bacterium	OTU_330
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__SAR86 clade; f__uncultured bacterium	OTU_138
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__Pseudomonas xinjiangensis	OTU_812
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Micrococcales; f__Intrasporangiaceae; g__Arsenicicoccus; s__uncultured bacterium	OTU_1472
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__Oleibacter; s__uncultured bacterium	OTU_57
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Parvularculaceae; g__Marinicaulis; s__uncultured bacterium	OTU_315
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Paraglaciecola; s__Paraglaciecola aestuariivivens	OTU_3853
k__Bacteria; p__Bacteroidota; c__Rhodothermia; o__Balneolales; f__Balneolaceae; g__Balneola; s__uncultured bacterium	OTU_347
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Henriciella; s__Henriciella sp. LA220	OTU_534
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Puniceispirillales; f__SAR116 clade; g__marine metagenome	OTU_795
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Vibrio; s__Vibrio antiquarius	OTU_638
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Psychrobium; s__uncultured bacterium	OTU_2432
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__Roseovarius sp.	OTU_643
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae; g__Ketobacter; s__uncultured bacterium	OTU_60
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiomicrospirales; f__Thioglobaceae; g__SUP05 cluster; s__uncultured gamma proteobacterium	OTU_205
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Clade III; g__uncultured bacterium	OTU_802
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Gammaproteobacteria Incertae Sedis; f__Unknown Family; g__Marinicella; s__Marinicella sp. F2	OTU_1560
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__Oleibacter; s__uncultured bacterium	OTU_61
k__Bacteria; p__Dadabacteria; c__Dadabacteriia; o__Dadabacteriales; f__uncultured bacterium	OTU_725
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Halieaceae; g__OM60(NOR5) clade; s__uncultured bacterium	OTU_1396
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Porticoccaceae; g__SAR92 clade; s__uncultured SAR92 cluster bacterium	OTU_1735
k__Archaea; p__Thermoplasmatota; c__Thermoplasmata; o__Marine Group II; f__marine metagenome	OTU_1068
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured bacterium	OTU_212
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__Sva0996 marine group; s__marine metagenome	OTU_381
k__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__DS001; s__marine metagenome	OTU_603
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rickettsiales; f__SM2D12; g__uncultured bacterium	OTU_160
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrincolaceae; g__uncultured; s__uncultured bacterium	OTU_411
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured Rhodobacteraceae bacterium	OTU_321
k__Bacteria; p__Bdellovibrionota; c__Bdellovibrionia; o__Bdellovibrionales; f__Bdellovibrionaceae; g__Bdellovibrio; s__uncultured marine bacterium	OTU_3275
k__Bacteria; p__Marinimicrobia (SAR406 clade); c__uncultured marine bacterium	OTU_392
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Stappiaceae; g__Labrenzia; s__Labrenzia alexandrii DFL-11	OTU_227
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Diaphorobacter; s__uncultured bacterium	OTU_332
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae; g__Thalassotalea; s__Thalassotalea eurytherma	OTU_267
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__uncultured bacterium	OTU_209

k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum geojense	OTU_1518
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured bacterium	OTU_2440
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Robiginitomaculum; s__uncultured Alphaproteobacteria bacterium	OTU_1033
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquibacter; s__uncultured Bacteroidetes bacterium	OTU_5474
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_614
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__uncultured; s__uncultured bacterium	OTU_746
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum sp. SZ-18	OTU_260
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__uncultured; s__uncultured bacterium	OTU_857
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacterales; f__Oscillatoriaceae; g__uncultured; s__uncultured bacterium	OTU_668
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__Fuerstia; s__uncultured bacterium	OTU_84
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacterales; f__Xenococcaceae; g__Chroococcidiopsis PCC-6712; s__uncultured cyanobacterium	OTU_1090
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum sp. U1368-101106-SW106	OTU_770
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__Filomicrobium; s__uncultured bacterium	OTU_1628
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__uncultured; s__uncultured bacterium	OTU_840
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured bacterium	OTU_492
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrospiraceae; g__Amphritea; s__Amphritea balenae	OTU_1643
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__uncultured; f__uncultured bacterium	OTU_482
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Actibacterium; s__uncultured bacterium	OTU_1332
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_1026
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Lewinella; s__uncultured bacterium	OTU_1327
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__SZB50; f__uncultured gamma proteobacterium	OTU_1557
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured gamma proteobacterium	OTU_361
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aureicoccus marinus	OTU_81
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Paraglaciacola; s__bacterium QM22	OTU_1064
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Zeaxanthinibacter; s__uncultured Flavobacterium sp.	OTU_380
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__pltb-vmat-80; f__uncultured bacterium	OTU_525
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Granulosicoccales; f__Granulosicoccaceae; g__Granulosicoccus; s__uncultured gamma proteobacterium	OTU_1202
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured bacterium AD12-E7	OTU_5
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum litopenaei	OTU_474
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__uncultured; f__uncultured Alphaproteobacteria bacterium	OTU_442
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured Planctomycetales bacterium	OTU_5434
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Donghicola sp. OG05	OTU_437
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Nonlabens; s__Nonlabens sp. MIC269	OTU_333
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae; g__Leucothrix; s__Leucothrix mucor DSM 2157	OTU_459
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Maricaulis; s__Maricaulis maris MCS10	OTU_573
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__Rubidimonas; s__uncultured bacterium	OTU_905
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Opitutales; f__Puniceicoccaceae; g__Lentimonas; s__uncultured bacterium	OTU_355

k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Cytophaga sp. MBIC04665	OTU_389
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Gilvibacter; s__Gilvibacter sediminis	OTU_2385
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Oceanicola; s__Oceanicola litoreus	OTU_477
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured gamma proteobacterium	OTU_922
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Woeseiaceae; g__Woeseia; s__uncultured bacterium	OTU_1352
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Psychrosphaera; s__uncultured bacterium	OTU_176
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Blastopirellula; s__uncultured bacterium	OTU_1155
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__Microtrichaceae; g__uncultured; s__uncultured bacterium	OTU_1455
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__uncultured; s__uncultured bacterium	OTU_17
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__uncultured; s__uncultured bacterium	OTU_1156
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__uncultured; s__uncultured planctomycete	OTU_2939
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_1093
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquibacter; s__uncultured bacterium	OTU_24
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Muricauda; s__Flavobacteriaceae bacterium B7	OTU_412
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Gammaproteobacteria Incertae Sedis; f__Unknown Family; g__uncultured; s__uncultured bacterium	OTU_1881
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Granulosicoccales; f__Granulosicoccaceae; g__Granulosicoccus; s__uncultured gamma proteobacterium	OTU_4016
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Gammaproteobacteria Incertae Sedis; f__Unknown Family; g__Alkalimarinus; s__uncultured bacterium	OTU_45
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Spongiibacteraceae; g__BD1-7 clade; s__uncultured gamma proteobacterium	OTU_1161
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Granulosicoccales; f__uncultured; g__uncultured bacterium	OTU_1059
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured Oleiphilus sp.	OTU_517
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Bythopirellula; s__uncultured planctomycete	OTU_1316
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Micavibrionales; f__uncultured; g__uncultured Rhizobiales bacterium	OTU_894
k__Bacteria; p__Acidobacteriota; c__Blastocatellia; o__Blastocatellales; f__Blastocatellaceae; g__Blastocatella; s__uncultured bacterium	OTU_1670
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Micavibrionales; f__Micavibrionaceae; g__uncultured; s__uncultured bacterium	OTU_454
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_1457
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae; g__Thalassotalea; s__uncultured bacterium	OTU_572
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__uncultured; s__uncultured bacterium	OTU_833
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_1703
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvibaculales; f__PS1 clade; g__uncultured bacterium	OTU_325
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Eudoraea; s__uncultured bacterium	OTU_300
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Rubinisphaeraceae; g__Fuerstia; s__Fuerstia marisgermanicae	OTU_1172
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__uncultured; s__Sphingomonadaceae bacterium BL116	OTU_3127
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Silicimonas; s__uncultured bacterium	OTU_5916
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_1074
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Limibaculum; s__uncultured bacterium	OTU_1582
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Algimonas; s__uncultured bacterium	OTU_3889

k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Mesoflavibacter; s__Mesoflavibacter sp. NBRC 110217	OTU_65
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__uncultured; s__uncultured bacterium	OTU_831
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Tenderiales; f__Tenderiaceae; g__Candidatus Tenderia; s__uncultured bacterium	OTU_544
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured bacterium	OTU_49
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__NS9 marine group; g__uncultured bacterium	OTU_809
k__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__JGI 0000069-P22; f__uncultured bacterium	OTU_1617
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae; g__Leucothrix; s__uncultured bacterium	OTU_222
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Hydrogenophaga; s__Hydrogenophaga sp. N8S-2-6	OTU_363
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens; s__Psychroserpens sp. KLE1228	OTU_2231
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Oceanospirillum; s__uncultured Oceanospirillum sp.	OTU_2307
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Marinobacteraceae; g__Marinobacter; s__Marinobacter nanhaiticus D15-8W	OTU_1132
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter; s__uncultured bacterium	OTU_137
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Granulosicoccales; f__uncultured; g__uncultured bacterium	OTU_486
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Ponticaulis; s__uncultured organism	OTU_730
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Oceanicola; s__Oceanicola granulosus HTCC2516	OTU_1644
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__Oleiphilus sp. HI0043	OTU_20
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Algicola; s__Algicola bacteriolytica	OTU_1534
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kiloniellales; f__Kiloniellaceae; g__uncultured; s__uncultured bacterium	OTU_662
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Robiginitalea; s__bacterium AMSU	OTU_627
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae; g__Colwellia; s__uncultured bacterium	OTU_148
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Opitutales; f__Puniceicoccaceae; g__Lentimonas; s__uncultured bacterium	OTU_6705
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__Litoribacillus; s__gamma proteobacterium 25	OTU_1031
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__Oleispira; s__uncultured Antarctic sea ice bacterium	OTU_316
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter; s__uncultured Bacteroidetes bacterium	OTU_2641
k__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Rubritaleaceae; g__Roseibacillus; s__uncultured bacterium	OTU_1376
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__uncultured; s__uncultured bacterium	OTU_387
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Colwelliaceae; g__Colwellia; s__unidentified marine eubacterium	OTU_3615
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__uncultured; g__uncultured planctomycete	OTU_507
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured bacterium	OTU_1603
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiales Incertae Sedis; g__Andersenella; s__uncultured Alphaproteobacteria bacterium	OTU_937
k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Actinomarinales; f__uncultured; g__uncultured bacterium	OTU_878
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas; s__Pseudoalteromonas sp. JL1130	OTU_489
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__Ekhidna; s__uncultured Flammeovirgaceae bacterium	OTU_466
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Crocinitomicaceae; g__Crocinitomix; s__uncultured bacterium	OTU_2891
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Chromatiaceae; g__Candidatus Thiobios; s__uncultured organism	OTU_826
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kiloniellales; f__Kiloniellaceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium	OTU_577

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured bacterium	OTU_2256
k__Bacteria; p__Dadabacteria; c__Dadabacteriia; o__Dadabacteriales; f__uncultured bacterium	OTU_607
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Mesorhizobium; s__Mesorhizobium sp. 55(2013)	OTU_2399
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiotrichales; f__Thiotrichaceae; g__Cocleimonas; s__uncultured bacterium	OTU_71
k__Bacteria; p__Desulfobacterota; c__Desulfuromonadia; o__PB19; f__uncultured bacterium	OTU_1576
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacteriales; f__Hyphomonadaceae; g__Hirschia; s__uncultured bacterium	OTU_289
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured Rhodobacteraceae bacterium	OTU_993
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_738
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Pseudohongiellaceae; g__Pseudohongiella; s__uncultured sediment bacterium	OTU_6269
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__uncultured; s__marine metagenome	OTU_2491
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Palleronia-Pseudomaribius; s__Palleronia soli	OTU_904
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Maritimimonas; s__uncultured Bacteroidetes bacterium	OTU_146
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrincolaceae; g__Neptunomonas; s__Neptunomonas concharum	OTU_700
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Granulosicoccales; f__Granulosicoccaceae; g__Granulosicoccus; s__uncultured bacterium	OTU_1326
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrincolaceae; g__Marinobacterium; s__uncultured bacterium	OTU_4176
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas; s__Pseudoalteromonas sp. '520P1 No. 423'	OTU_6381
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Stappiaceae; g__Labrenzia; s__Labrenzia marina	OTU_977
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured cyanobacterium	OTU_4442
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Crocinitomicaceae; g__Crocinitomix; s__uncultured bacterium	OTU_1554
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__uncultured; f__uncultured bacterium	OTU_2673
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__Oceaniserpentilla; s__uncultured bacterium	OTU_263
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Paraglacicola; s__Paraglacicola mesophila KMM 241	OTU_718
k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Pirellulales; f__Pirellulaceae; g__Rhodopirellula; s__Pirellula sp.	OTU_3505
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Gammaproteobacteria Incertae Sedis; f__Unknown Family; g__uncultured; s__uncultured bacterium	OTU_1262
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Pseudohongiellaceae; g__Pseudohongiella; s__uncultured gamma proteobacterium	OTU_4309
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Aestuariicella; s__Pseudomaricurvus alcaniphilus	OTU_4038
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__NS9 marine group; g__uncultured bacterium	OTU_903
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae; g__Alcanivorax; s__uncultured bacterium	OTU_815
k__Bacteria; p__Acidobacteriota; c__Thermoanaerobaculia; o__Thermoanaerobaculales; f__Thermoanaerobaculaceae; g__Subgroup 10; s__uncultured Acidobacteria bacterium	OTU_1614
k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Microscillaceae; g__Microscilla; s__uncultured Microscilla sp.	OTU_832
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Actibacterium; s__uncultured Alphaproteobacteria bacterium	OTU_3278
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Leptolyngbya ectocarpi SABCO12402	OTU_760
k__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Candidatus Peregrinibacteria; f__uncultured bacterium	OTU_3281

Table S11 - OTUs with more than 1% relative abundance in at least one sample of each sampling site.

Taxonomy	OTUId	Only on plastic
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Pseudahrensia; s__uncultured bacterium	OTU_134	x
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__Leptolyngbya sp. LEGE 07075	OTU_7	
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Synechococcus CC9902; s__uncultured marine cyanobacterium	OTU_1	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured Rhodobacteraceae bacterium	OTU_171	
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Psychrobacter; s__uncultured Psychrobacter sp.	OTU_41	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured; s__uncultured bacterium	OTU_280	x
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas; s__Pseudoalteromonas sp. 12	OTU_54	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured bacterium	OTU_9	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Yoonia-Loktanella; s__uncultured bacterium	OTU_29	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_36	x
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Litoreibacter; s__uncultured marine microorganism	OTU_72	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Marinibacterium; s__uncultured bacterium	OTU_30	
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Planomicrobium; s__Planomicrobium okeanoikoites	OTU_211	x
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_249	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__Erythrobacter vulgaris	OTU_52	x
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Algimonas; s__uncultured bacterium	OTU_129	x
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__uncultured; s__uncultured bacterium	OTU_112	
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseobacter; s__uncultured bacterium	OTU_159	
k__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Phormidesmiales; f__Phormidesmiaceae; g__Phormidesmis ANT.LACV5.1; s__uncultured bacterium	OTU_31	x
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter; s__uncultured bacterium	OTU_6729	x
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured Rhodobacterales bacterium	OTU_295	x
k__Bacteria; p__Patescibacteria; c__Parcubacteria; o__Candidatus Kaiserbacteria; f__metagenome	OTU_323	x

Table S12 - OTUs that were enriched in the laboratory LDPE incubations after one year incubation, and that were still present in incubation B after two years.

OTUId	Taxonomy
OTU_15	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Cognatyyoonia; s__uncultured Alphaproteobacteria bacterium
OTU_41	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Psychrobacter; s__uncultured Psychrobacter sp.
OTU_50	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter junii CIP 64.5
OTU_114	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseovarius; s__uncultured organism
OTU_434	k__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__uncultured; g__uncultured bacterium
OTU_159	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseobacter; s__uncultured bacterium
OTU_28	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Parvibaculales; f__Parvibaculaceae; g__Mf105b01; s__alpha proteobacterium Mf 1.05b.01
OTU_461	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__NRL2; f__alpha proteobacterium DG1294
OTU_273	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sneathiellales; f__Sneathiellaceae; g__Sneathiella; s__uncultured bacterium
OTU_40	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Cognatishimia; s__uncultured bacterium
OTU_47	k__Bacteria; p__Planctomycetota; c__Planctomycetes; o__Planctomycetales; f__Gimesiaceae; g__uncultured; s__uncultured bacterium
OTU_731	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Marinovum; s__uncultured bacterium
OTU_144	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__NRL2; f__uncultured marine bacterium
OTU_23	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudophaeobacter; s__uncultured marine bacterium
OTU_465	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Aestuariibacter; s__Aestuariibacter aggregatus
OTU_182	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae1; g__Alcanivorax; s__uncultured Alcanivorax sp.
OTU_247	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Marinobacteraceae; g__Marinobacter; s__uncultured bacterium
OTU_55	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methyloigellaceae; g__uncultured; s__uncultured Alphaproteobacteria bacterium
OTU_367	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrocolaceae; g__Marinobacterium; s__Marinobacterium jannaschii
OTU_95	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Phaeobacter sp. CECT 7735
OTU_139	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Nitrocolaceae; g__Marinobacterium; s__uncultured Marinobacterium sp.
OTU_1167	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Marinobacteraceae; g__Marinobacter; s__Marinobacter litoralis
OTU_60	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Alcanivoracaceae; g__Ketobacter; s__uncultured bacterium
OTU_725	k__Bacteria; p__Dadabacteria; c__Dadabacteriia; o__Dadabacteriales; f__uncultured bacterium
OTU_2441	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__JTB23; f__uncultured bacterium
OTU_558	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tropicibacter; s__uncultured bacterium

OTU_707	k__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Saprospiraceae; g__uncultured; s__uncultured bacterium
OTU_573	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Maricaulis; s__Maricaulis maris MCS10
OTU_4620	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__uncultured bacterium
OTU_195	k__Bacteria; p__Planctomycetota; c__Phycisphaerae; o__Phycisphaerales; f__Phycisphaeraceae; g__SM1A02; s__marine metagenome
OTU_3399	k__Bacteria; p__Myxococcota; c__Polyangia; o__Polyangiales; f__Sandaracinaceae; g__uncultured; s__uncultured bacterium
OTU_3449	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Salinisphaerales; f__Solimonadaceae; g__Oceanococcus; s__gamma proteobacterium APT1
OTU_70	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Spongiibacteraceae; g__Zhongshania; s__gamma proteobacterium DSW25-13
OTU_5783	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Salinisphaerales; f__Solimonadaceae; g__Panacagrimonas; s__uncultured bacterium
OTU_4768	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Maricaulis; s__Maricaulis salignorans

Table S13 – ASW recipe and concentrations of respective chemicals. Salts were added to obtain a final salinity of 35.8. Final pH was 8.1.

Chemicals	Concentration (mM)
NaCl	355.20
Na ₂ SO ₄	24.48
KCl	7.75
NaHCO ₃	2.02
KBr	0.71
H ₃ BO ₃	0.36
NaF	0.06
MgCl ₂ .6H ₂ O	46.21
CaCl ₂ .2H ₂ O	8.95
SrCl ₂ .6H ₂ O	0.08
NH ₄ Cl	0.01
NaH ₂ PO ₄	0.002

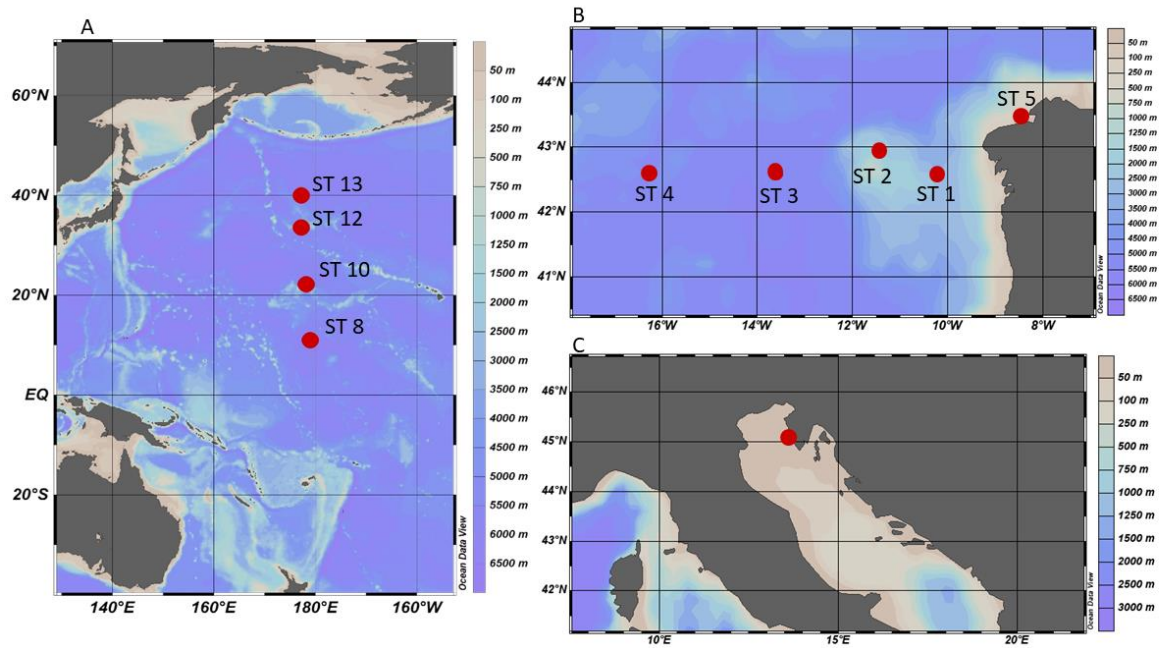


Fig. S1- Sampling stations in (A) the Pacific Ocean, (B) the North Atlantic and (C) the northern Adriatic Sea.

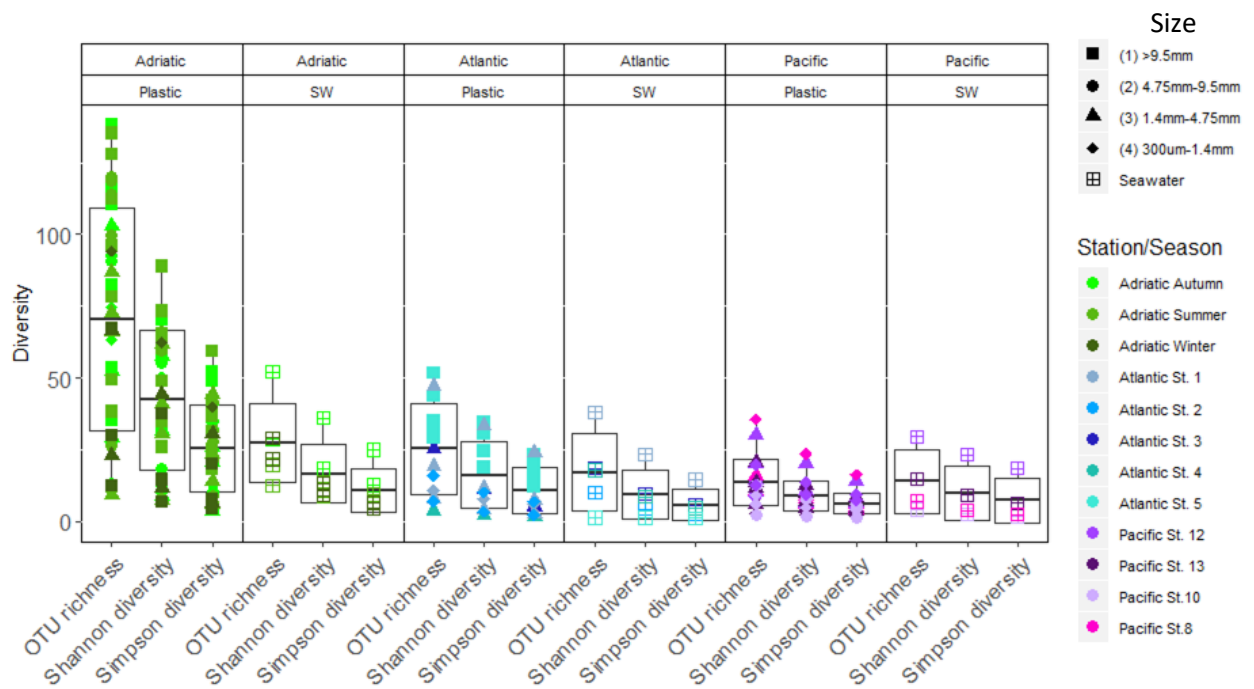


Fig. S2- OTU richness and diversity indexes of samples collected across the three different sites. Each symbol represents one sample. The boxplots represent the mean $\pm$ SD and the whiskers represent the minimum and maximum values.

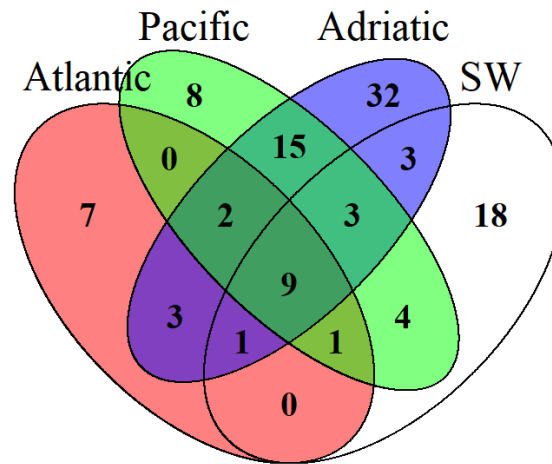


Fig. S3 - Venn diagrams displaying the relatively abundant families (>1% relative abundant in at least one sample of that site) shared between the biofilm of plastics collected from the different sampling sites and seawater (SW). The SW category includes all seawater samples from the considered sites combined.

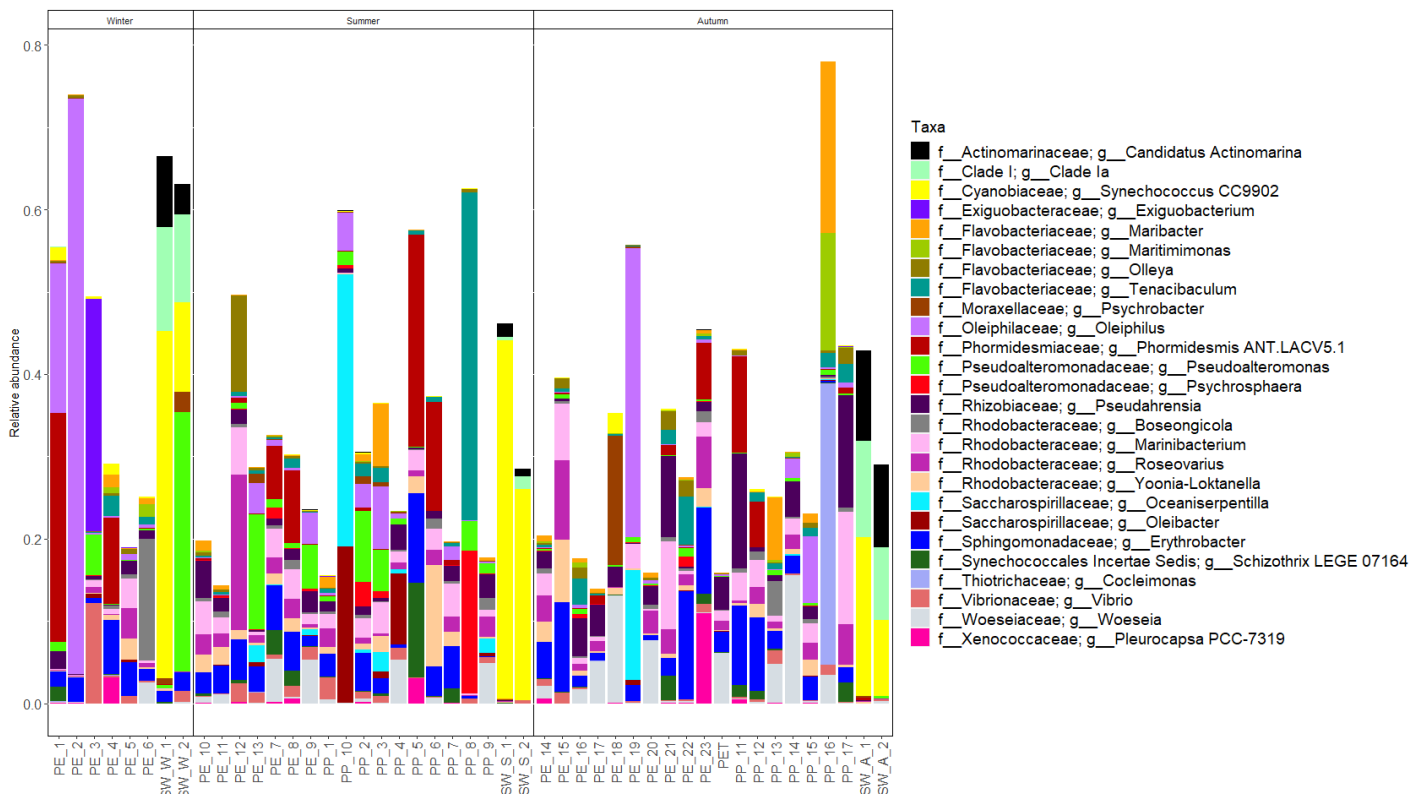


Fig. S4 - Stacked plot of genera present in at least one sample with a relative abundance >10% in the samples collected in the northern Adriatic.

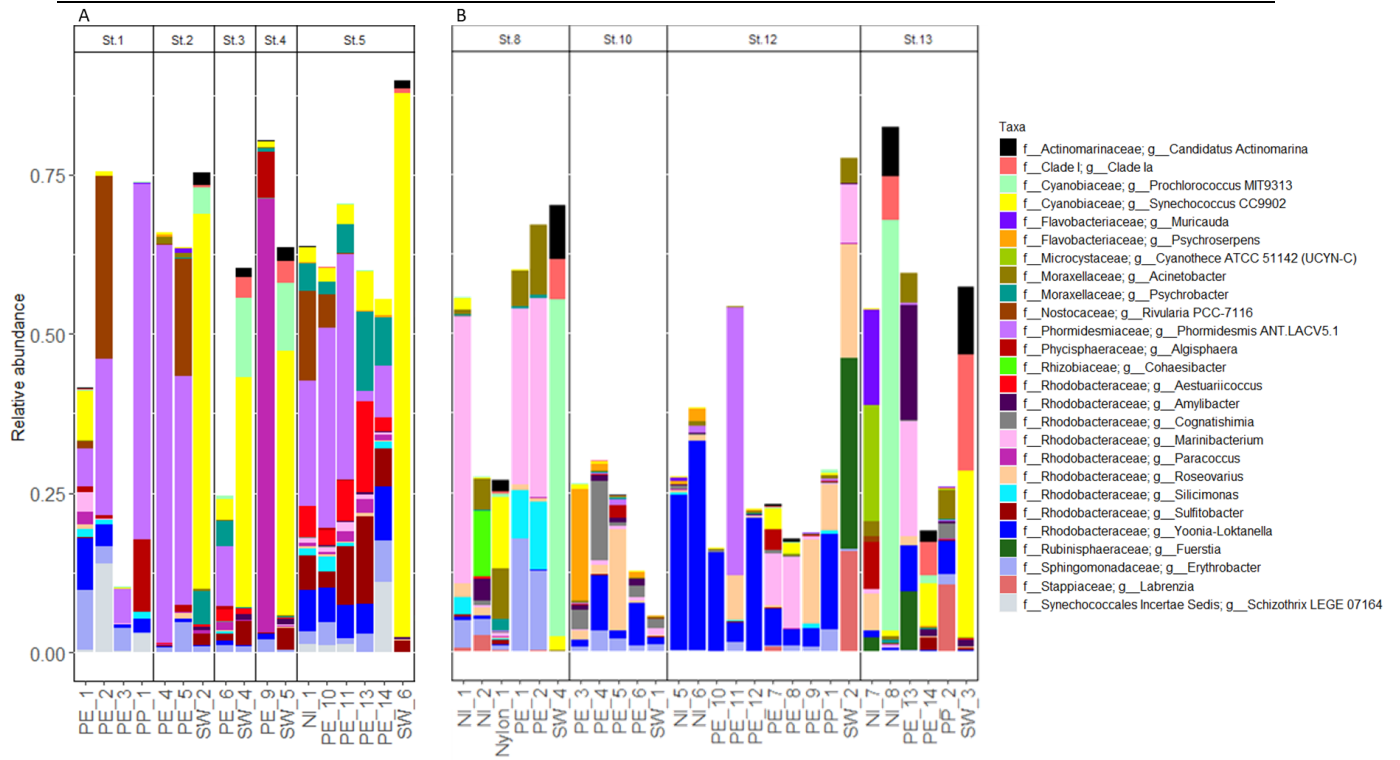


Fig. S5- Stacked plot of the genera present in at least one sample with relative abundance >10% in the samples collected in the (A) North Atlantic and (B) Pacific.

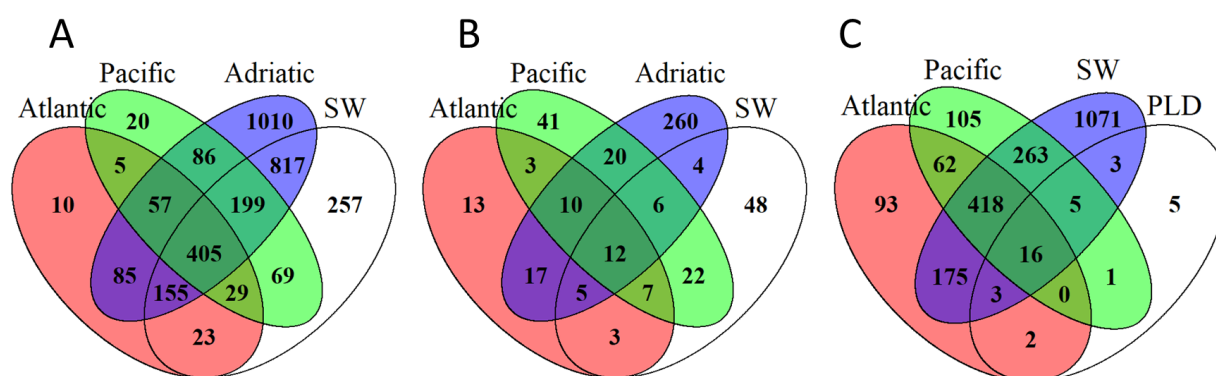


Fig. S6 - Venn diagrams displaying: (A) the OTUs shared between the biofilm of plastics collected at the different sampling sites and seawater; (B) the relatively abundant OTUs (>1% relative abundance in at least one sample at the specific site) shared between the biofilm of plastics collected at the different sampling sites and seawater, and (C) the potential LDPE-degrading OTUs (PLD) enriched in the LDPE laboratory incubations and the OTUs from the biofilms of plastics collected in the Pacific and North Atlantic. The SW category included all seawater samples from the respective sites combined.

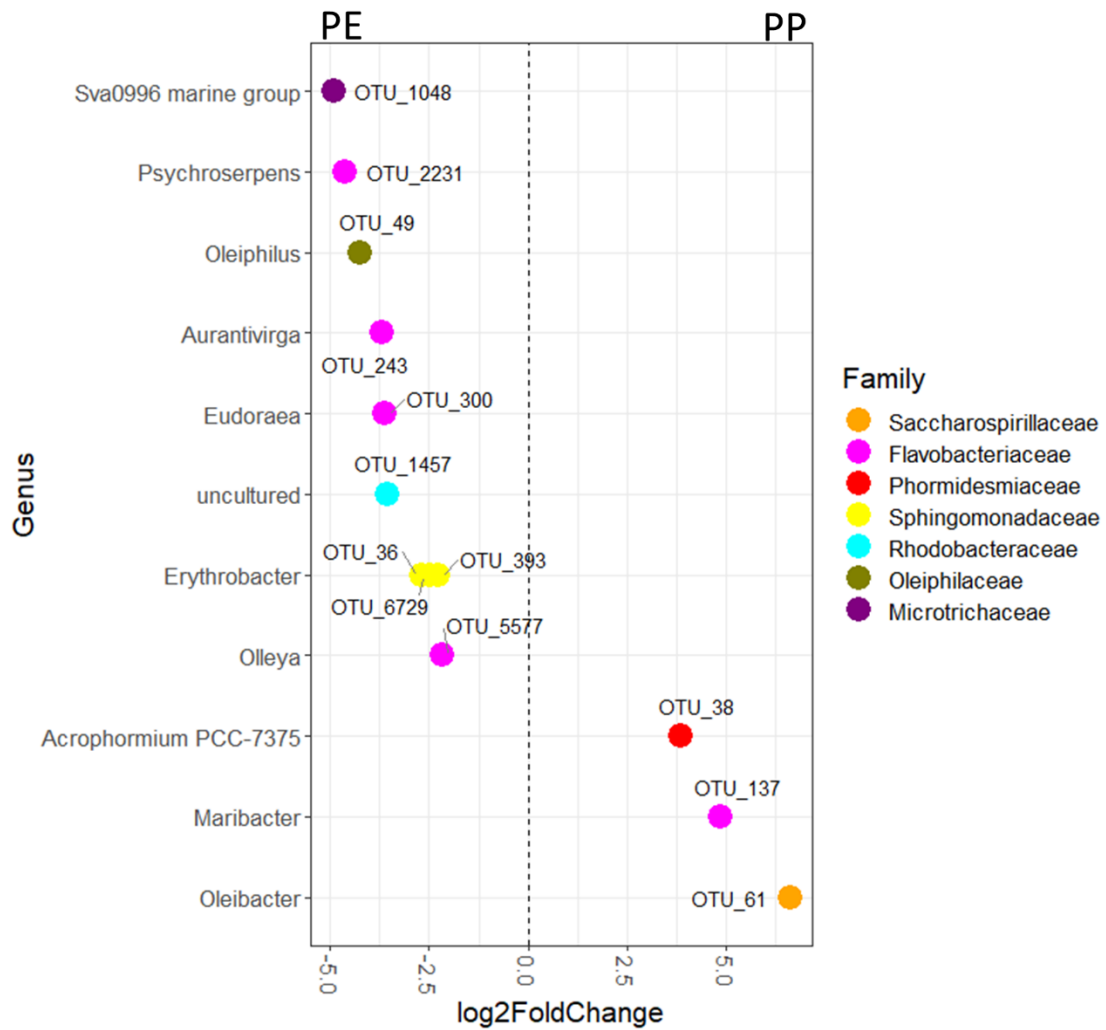


Fig. S7 - Enriched bacterial families between the PE and PP samples collected in the northern Adriatic. OTUs with fold change > 0 were enriched in PP, and OTUs with fold change < 0 were enriched in PE. Each symbol represents one OTU. Only statistically and significantly enriched taxa were included (adjusted p-value < 0.05).

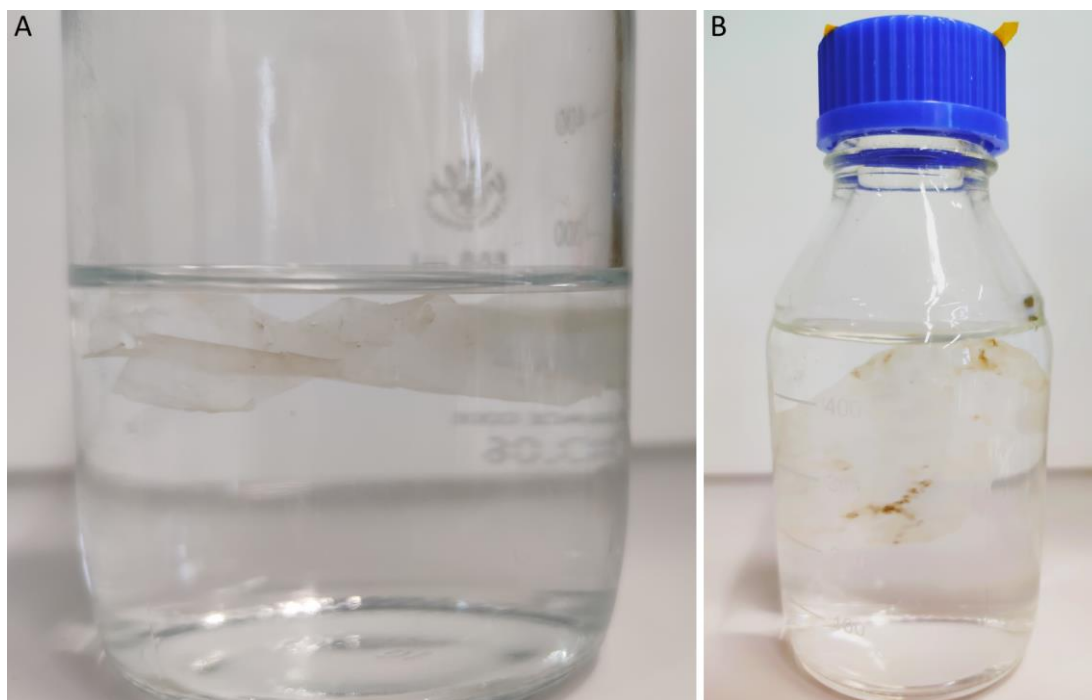


Fig. S8 – Original plastics A (A) and B (B) collected from the northern Adriatic Sea.

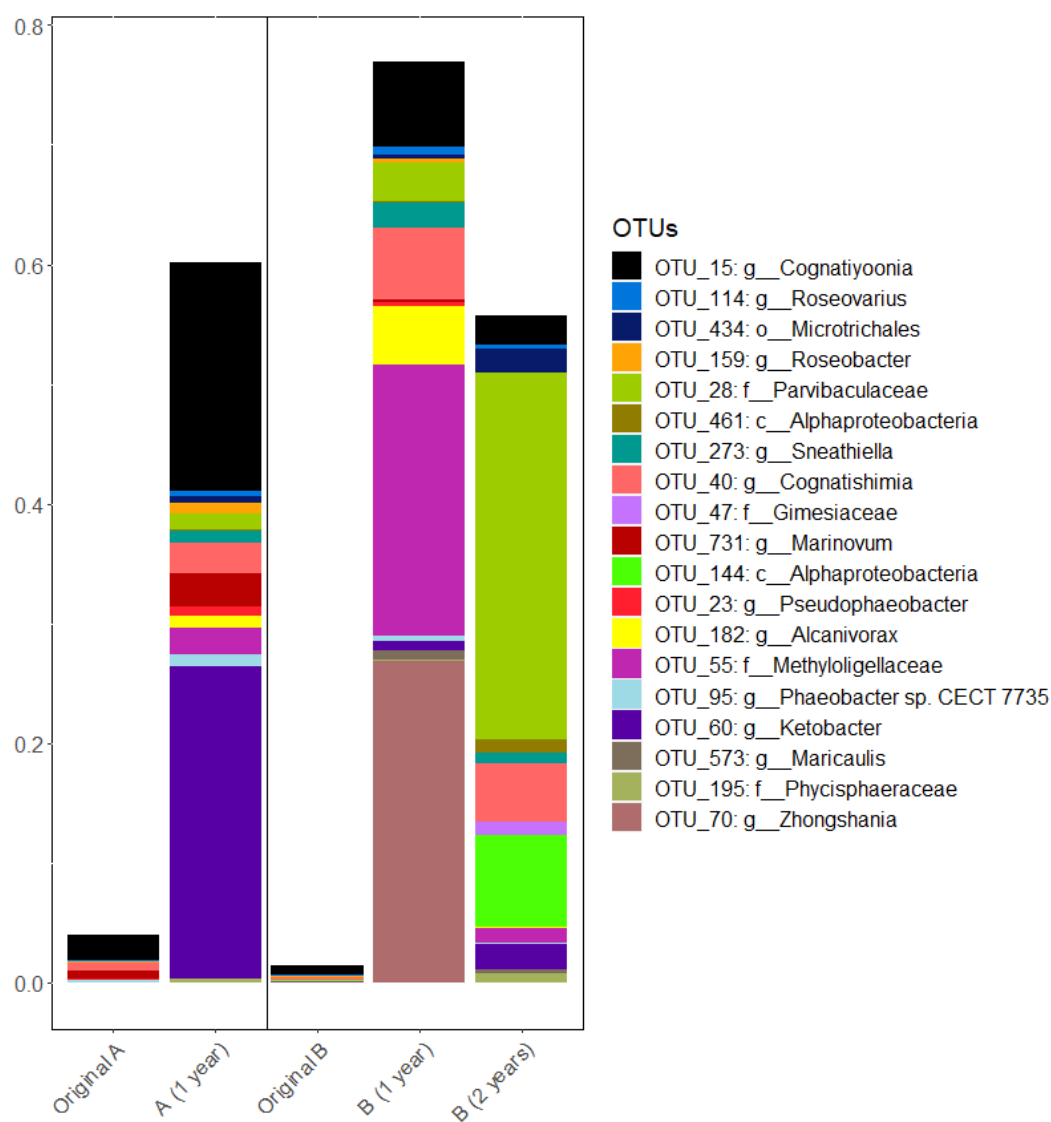


Fig. S9- Stacked plot of the potential LDPE-degrading OTUs. Potential LDPE-degrading OTUs are tentatively defined as OTUs that increased in relative abundance in the biofilm of both LDPE incubations A and B after one year and present in incubation B after two years. The y-axis represents the relative abundance, and the x-axis represents the different stages of incubations A and B. Original A and B samples refer to the original prokaryotic community of the biofilm of the original plastics collected in the North Adriatic. Only OTUs that occurred with relative abundance >0.5% in at least one of the samples are represented.

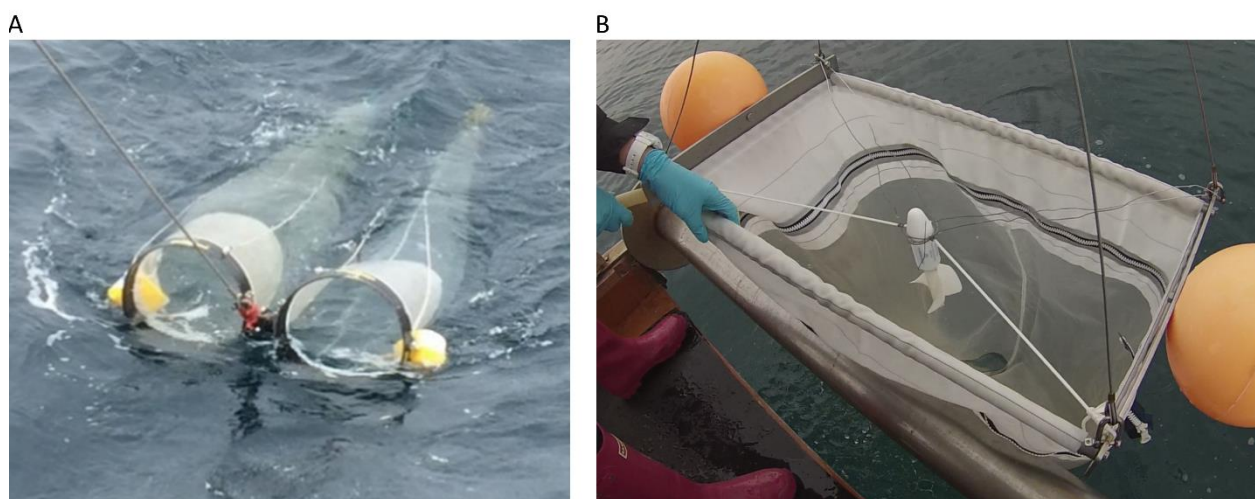


Fig. S10 - Sampling nets used to collect plastics in different sites. (A) Bongo net used to collect plastic samples during the SO248 expedition in the Pacific. (B) Manta net for collecting microplastics used for sampling in the northern Adriatic and during the Radprof expedition in the North Atlantic.

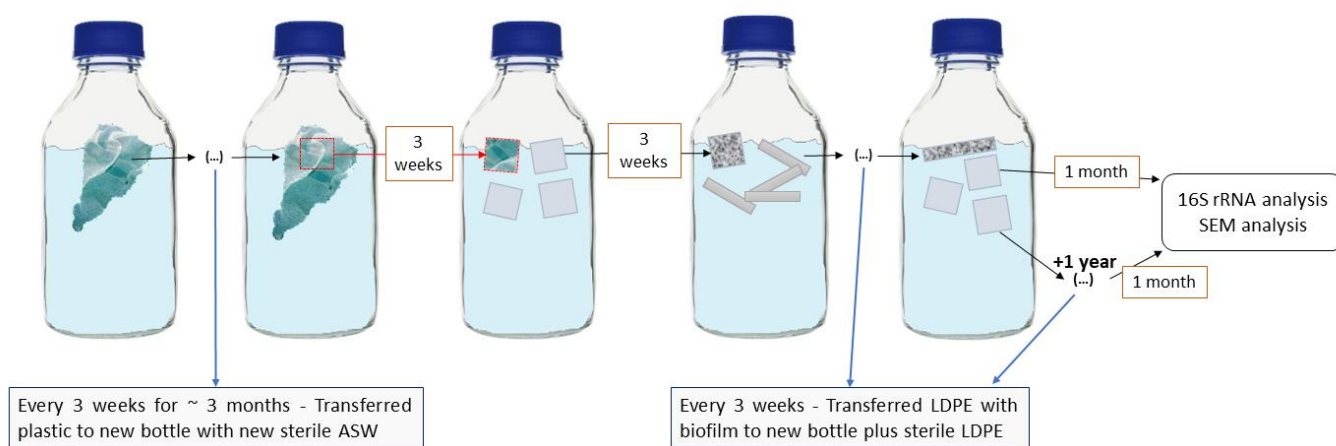


Fig. S11 – Scheme of the LDPE-laboratory incubations. The shapes with a black and white pattern represent LDPE pieces with biofilm.

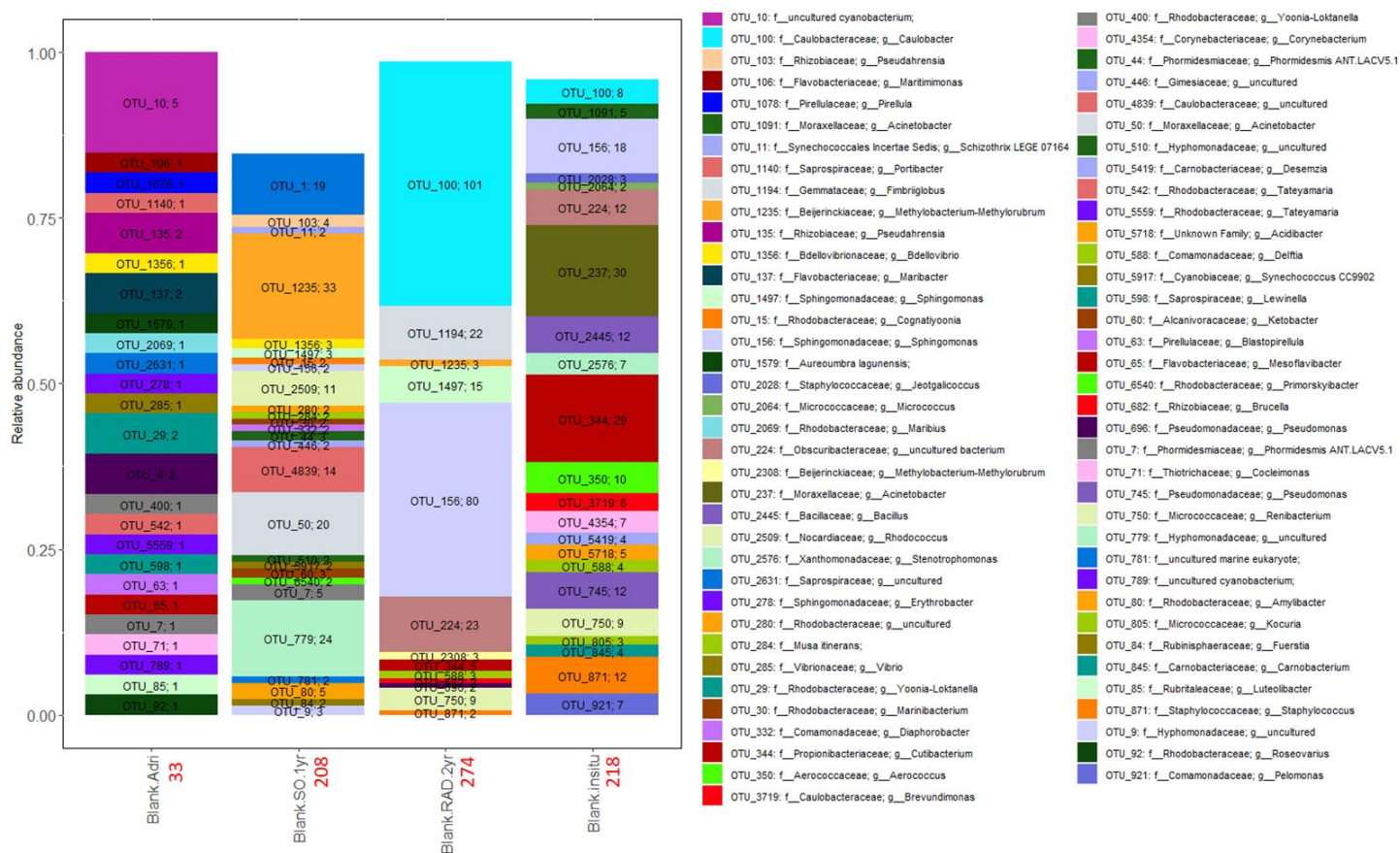


Fig. S12 – Relative abundance of the OTUs with relative abundance >0.7% found in each blank.

The text in the plot refers to the OTU number and the number of respective classified reads.

The red numbers represent the total number of analysed reads of each sample.

References

- Brandon, J., Goldstein, M., & Ohman, M. D. (2016). Long-term aging and degradation of microplastic particles: Comparing in situ oceanic and experimental weathering patterns. *Mar Pollut Bull* **110**: 299–308.
- Gross, M., Zhao, X., Mascarenhas, V., & Wen, Z. (2016). Effects of the surface physico-chemical properties and the surface textures on the initial colonization and the attached growth in algal biofilm. *Biotechnol Biofuels* **9**: 38.
- Pinto, M., Langer, T. M., Hüffer, T., Hofmann, T., & Herndl, G. J. (2019). The composition of bacterial communities associated with plastic biofilms differs between different polymers and stages of biofilm succession. *PLoS One* **14**: e0217165.
- Rochman, C. M., Hoh, E., Hentschel, B. T., & Kaye, S. (2013). Long-term field measurement of sorption of organic contaminants to five types of plastic pellets: implications for plastic marine debris. *Environ Sci Technol* **47**: 1646–1654.
- Romera-Castillo, C., Pinto, M., Langer, T. M., Álvarez-Salgado, X. A., & Herndl, G. J. (2018). Dissolved organic carbon leaching from plastics stimulates microbial activity in the ocean. *Nat Commun* **9**: 1–7.
- Tetu, S. G., Sarker, I., Schrameyer, V., Pickford, R., Elbourne, L. D. H., Moore, L. R., & Paulsen, I. T. (2019). Plastic leachates impair growth and oxygen production in *Prochlorococcus*, the ocean's most abundant photosynthetic bacteria. *Commun Biol* **2**: 1–9.
- von Ammon, U., Wood, S. A., Laroche, O., Zaiko, A., Tait, L., Lavery, S., *et al.* (2018). The impact of artificial surfaces on marine bacterial and eukaryotic biofouling assemblages: a high-throughput sequencing analysis. *Mar Environ Res* **133**: 57–66.

CHAPTER IV

Dissolved organic carbon leaching from plastics stimulates microbial activity in the ocean

Cristina Romera-Castillo^{1,2*}, Maria Pinto¹, Teresa M. Langer¹, Xosé Antón Álvarez-Salgado³ & Gerhard J. Herndl^{1,4*}

¹ Department of Limnology and Bio-Oceanography, Center of Functional Ecology, University of Vienna, Althanstraße 14, 1090, Vienna, Austria

² CSIC Institut de Ciències del Mar, Passeig Marítim de la Barceloneta 37-49, 08003, Barcelona, Spain

³ CSIC Instituto de Investigaciones Mariñas, Eduardo Cabello 6, 36208, Vigo, Spain

⁴ NIOZ, Department of Marine Microbiology and Biogeochemistry, Royal Netherlands Institute for Sea Research, Utrecht University, Den Burg, The Netherlands

*Corresponding authors: crisrc@icm.csic.es and gerhard.herndl@univie.ac.at

Published in Nature communications

Abstract

Approximately 5.25 trillion plastic pieces are floating at the sea surface. The impact of plastic pollution on the lowest trophic levels of the food web, however, remains unknown. Here we show that plastics release dissolved organic carbon (DOC) into the ambient seawater stimulating the activity of heterotrophic microbes. Our estimates indicate that globally up to 23,600 metric tons of DOC are leaching from marine plastics annually. About 60% of it is available to microbial utilization in less than 5 days. If exposed to solar radiation, however, this DOC becomes less labile. Thus, plastic pollution of marine surface waters likely alters the composition and activity of the base of the marine food webs. It is predicted that plastic waste entering the ocean will increase by a factor of ten within the next decade, resulting in an increase in plastic-derived DOC that might have unaccounted consequences for marine microbes and for the ocean system.

Introduction

Plastic debris represents a contemporary environmental problem affecting marine fauna from small copepods to large mammals (Andrady, 2011). Some animals mistake plastic for food (Savoca *et al.*, 2016) and, among other impacts, the ingestion of plastic might cause stress, false satiation, reduced growth rates and can affect reproduction (Auta *et al.*, 2017). However, the impact of plastics on the lower levels of the food web, dominated by marine microbes, remains largely unknown. Plastic can undergo natural abiotic degradation processes of chemical and mechanical nature, collectively called weathering, leading to its fragmentation. Moreover, biodegradation processes by microbes might also contribute to the degradation of plastics (Andrady, 2011). Plastic litter on beaches and floating in seawater is exposed to solar radiation resulting in the formation of surface cracks and fragmentation into progressively smaller particles, ultimately reaching microscopic sizes (Andrady, 2011; Kalogerakis *et al.*, 2017). Around 35,000 metric tons (MT) of all the plastics floating in the ocean are smaller than 5 mm (microplastics) (Cózar *et al.*, 2014). Microplastics can also be directly derived from personal care and cosmetic products or textile fibres entering the marine environment via wastewater discharge (Fendall and Sewell, 2009). To increase their performance and durability, commercial plastic frequently contains additives. In contact with

water, these additives can leach from the plastic into the surrounding water (Suhrhoﬀ and Scholz-Böttcher, 2016). In this paper, the term leachate is used for any compound (additive or organic substance derived from polymer degradation including any nano-particle that might break off from the plastic surfaces) released from the plastic into the seawater. It has been shown that photo-degradation of plastic can release submicron particles into the aquatic media (Lambert and Wagner, 2016). With decreasing particle size, the surface to volume ratio of the particle increases, potentially increasing also the concentration of leachates in the surrounding water.

The oceanic DOC pool is one of the largest reduced carbon pools on Earth (662 Pg C) (Hansell *et al.*, 2009) and it is of similar size as the atmospheric CO₂ (828 Pg C) (Prather *et al.*, 2012). Oceanic DOC is mainly derived from phytoplankton and forms the basic substrate for the microbial food web fuelling micro-heterotrophic growth (Hansell *et al.*, 2009; Romera-Castillo *et al.*, 2016). In this study, we hypothesize that the estimated 250,000 MT of plastics currently floating in the ocean (Eriksen *et al.*, 2014; van Sebille *et al.*, 2015) also contribute to the oceanic DOC pool via leaching. If bioavailable these plastic-leachates might stimulate microbial carbon flux in the ocean, especially in the surface layer. Here we use the term bioavailable DOC for the DOC which is used by heterotrophic bacteria within days. In this regard, it is expected that particles of synthetic polymers are not bioavailable in the timescale of the experiment but only the truly dissolved leachate. Most of the marine studies on plastics focus on the distribution of plastic size classes in the surface ocean (Andrady, 2011; Auta *et al.*, 2017). The role of plastics releasing DOC into the ambient seawater, their biodegradation and effects on the marine biota, however, remain largely unknown.

In the present study, the potential contribution of DOC leaching from microplastics to the surface oceanic DOC pool is estimated and the bioavailability of the plastic-derived DOC determined. We calculate that up to 23,600 MT of DOC is annually released by marine plastic litter. In highly contaminated areas, where plastics can be found in concentrations up to 2500 g km⁻², the leached DOC could make up to 10% of the DOC in the surface microlayer (top 40 µm of the water column). About 60% of the DOC leached from plastics is bioavailable in less than 5 days. However, if exposed to solar radiation, this plastic-derived DOC becomes less labile. Plastic leaching likely gives rise to local hot spots of DOC that can be rapidly remineralized by marine microbes. However, we do not know the fate of the 40% that is not taken up rapidly by bacteria. Taken together, we conclude that increasing plastic waste

entering the oceans will have consequences for the marine microbial food web and for the carbon cycling.

Results

DOC leaching from plastics

Experiments were performed using commercially available low- and high-density polyethylene (LDPE and HDPE) as well as polypropylene (PP) and polyethylene (PE) from supermarket packaging (see Methods section). PP and PE were used because they represent the most abundant plastics found in the ocean (Cózar *et al.*, 2014; Suaria *et al.*, 2016). The plastics were added to autoclaved artificial seawater (ASW) and exposed to artificial solar radiation over a period of 6 days and/or 30 days. Dark treatments and controls without plastics were also performed at the same time in all the experiments. DOC was measured before and after the irradiation period from unfiltered samples. Therefore, in this study DOC includes all the organic carbon compounds released by plastic, from truly dissolved substances to any polymeric nano-plastic that might have been also fragmented from the plastic surface. All plastic types used here leached DOC into the ambient water whether they were irradiated or held in the dark. To calculate the total DOC leaching from the plastics, the DOC concentration of the ASW prior to adding the plastics was used as initial concentration (Table 1).

LDPE and HDPE, either after 6 days or after 1 month of sterile incubation, leached between 2.4 and 8.9 $\mu\text{g C cm}^{-2}$ of plastic surface (total DOC leached; Table 1). Plastics used as packing material released less DOC amounting to 0.26–0.31 $\mu\text{g C cm}^{-2}$ and 1.6–2.2 $\mu\text{g C cm}^{-2}$ plastic surface for PE and PP, respectively. A time course experiment conducted in the dark using LDPE added to artificial seawater confirmed that the highest leaching of DOC from plastics occurs initially, when plastics get in contact with seawater (Fig. 1). Thereafter, DOC concentration exponentially decreased (about 45%) until reaching a constant leaching of about 5.5 $\mu\text{g C cm}^{-2}$, roughly similar to the total DOC leached in our irradiation experiments (Table 1). The first-order constant of DOC lost was -0.0135 h^{-1} , i.e., half of the missing leached DOC was lost in about 50 h (Fig. 1).

Table 1 - DOC concentration leached from plastics during the light and dark incubations. Instantaneous DOC leached is the DOC released right after the addition of the plastic to the artificial seawater and prior to the exposure to the artificial solar radiation. Total DOC leached: DOC at the end of the irradiation period minus DOC in artificial seawater before the plastic addition; Incubation DOC leached: DOC at the end of the irradiation period minus DOC after the plastic addition and prior incubation. DOC consumption during microbial incubation: DOC at the end of the microbial experiment minus DOC at the initial time of the microbial experiment. * only one sample of the three replicates. *HDPE* high-density polyethylene, *LDPE* low-density polyethylene, *PE* polyethylene, *PP* polypropylene.

Plastic type	Incubation time (d)	Treatment	Total DOC leached ($\mu\text{g cm}^{-2}$)	Instantaneous DOC leached ($\mu\text{g cm}^{-2}$)	Incubation DOC leached ($\mu\text{g cm}^{-2}$)	DOC consumption during microbial incubation ($\mu\text{mol L}^{-1}$)
LDPE	6	Light	5.8 ± 0.51	3.50 ± 0.51	2.3 ± 0.07	74.0 ± 4.39
		Dark	6.02 ± 1.75	2.81 ± 1.80	3.21 ± 0.41	94.6 ± 16.74
HDPE	6	Light	2.41 ± 0.94	2.03 ± 0.94	0.39 ± 0.05	53.7 ± 5.62
		Dark	2.74*	1.56*	1.18 ± 0.5	104.1 ± 1.50
LDPE	30	Light	6.67 ± 0.90	0.67 ± 1.39	6.00 ± 1.06	92.1 ± 3.74
		Dark	8.92 ± 0.29	8.13 ± 0.59	0.79 ± 0.52	150.4 ± 17.62
HDPE	30	Light	6.28 ± 0.96	5.16 ± 0.96	1.12 ± 0.03	136.3 ± 0.54
		Dark	2.79 ± 0.34	2.42 ± 0.45	0.37 ± 0.29	69.6 ± 17.34
PE packaging	30	Light	0.31 ± 0.16	0.09 ± 0.17	0.22 ± 0.02	27.2 ± 1.16
		Dark	0.26 ± 0.20	0.52 ± 0.39	-0.26 ± 0.33	30.9 ± 3.49
PP packaging	30	Light	2.17 ± 0.13	1.10 ± 0.42	1.07 ± 0.40	55.0 ± 1.77
		Dark	1.61 ± 0.15	1.10 ± 0.20	0.51 ± 0.14	52.5 ± 2.25

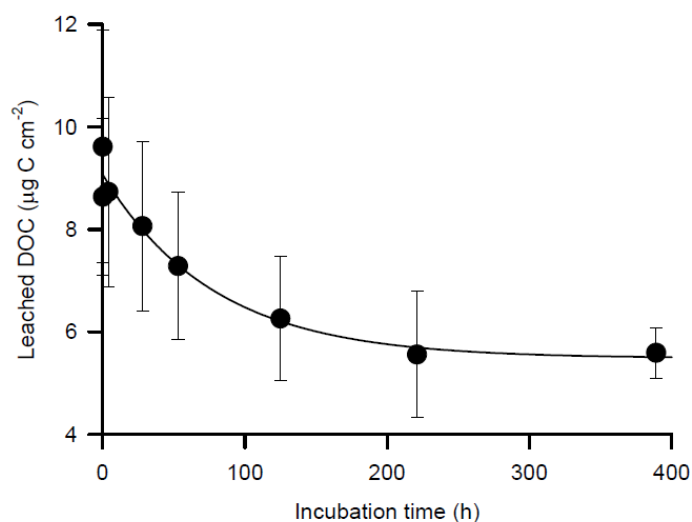


Fig.1 - Loss of DOC over time using LDPE. The original DOC concentration of the artificial seawater before plastic addition was subtracted from all the points. Thus, the first point represents the maximum leaching after the plastic addition. Error bars show the standard deviation of the mean of three replicates. First order rate constant = $-0.013 \text{ h}^{-1} \pm 0.003$; $R^2 = 0.97$; $p < 0.001$. LDPE low-density polyethylene, DOC dissolved organic carbon.

Accordingly, the effect of artificial solar radiation on the leaching of DOC from plastics floating in sterile seawater was also determined (Incubation DOC leached; Table 1). The DOC concentration immediately after adding the plastics was used as initial DOC concentration. The effect of artificial solar radiation varied depending on the plastic material and the duration of exposure. Over a 6-day incubation period under artificial solar radiation, we measured less DOC leached from LDPE and HDPE (2.30 and $0.39 \mu\text{g C cm}^{-2}$ of plastic surface, respectively) than from their corresponding dark treatments (3.21 and $1.18 \mu\text{g C cm}^{-2}$, respectively). For HDPE, however, the differences were not significant (t test, $p > 0.05$). In contrast, over 1-month incubation period, irradiated LDPE and HDPE released significantly more DOC (t test, $p < 0.05$) (6 and $1.12 \mu\text{g C cm}^{-2}$, respectively) than their corresponding dark treatments (0.79 and $0.37 \mu\text{g C cm}^{-2}$, respectively). The packaging plastic (PE and PP) did not exhibit significant differences in the DOC leaching between artificial solar radiation and the corresponding dark controls (t test, $p > 0.05$).

Microbial utilization of DOC leached from plastics

As plastics floating at the sea surface release DOC, we aimed at determining the bioavailability of plastic-derived DOC and its influence on the microbial community. Therefore, after removing the plastic pieces from the seawater incubated in the previous experiments, we inoculated this water with a natural bacterial community from surface waters of the Adriatic Sea (nine parts of water with plastic-leachate: one part of inoculum). The samples were incubated in the dark until microbes reached stationary phase.

In the treatments previously containing plastics (thereafter plastic treatments) and held in the dark, bacteria grew faster than in the previously irradiated plastic treatments or in the controls without plastics (Fig. 2). In general, in the irradiated plastic samples, bacterial abundance reached higher values (Fig. 2c, d) than in the irradiated control without plastic but in some cases, the differences were low or not significant (t test, $p < 0.05$; Fig. 2a, b, e, f). The higher bacterial abundance in the plastic treatments held in the dark regarding the irradiated and no-plastic treatments was also consistent with higher leucine incorporation rates (a proxy for biomass production) (Fig. 3). After 24 h of incubation, leucine incorporation in LDPE and HDPE held in the dark ($0.26 \text{ nmol Leu L}^{-1} \text{ h}^{-1}$ and $0.34 \text{ nmol Leu L}^{-1} \text{ h}^{-1}$, respectively) was at least one order of magnitude higher (t test, $p < 0.05$) than in the irradiated treatments (0.75×10^{-2} and $1.67 \times 10^{-2} \text{ nmol Leu L}^{-1} \text{ h}^{-1}$, Fig. 3a). This trend was also observed after 48 h of incubation (Fig. 3b).

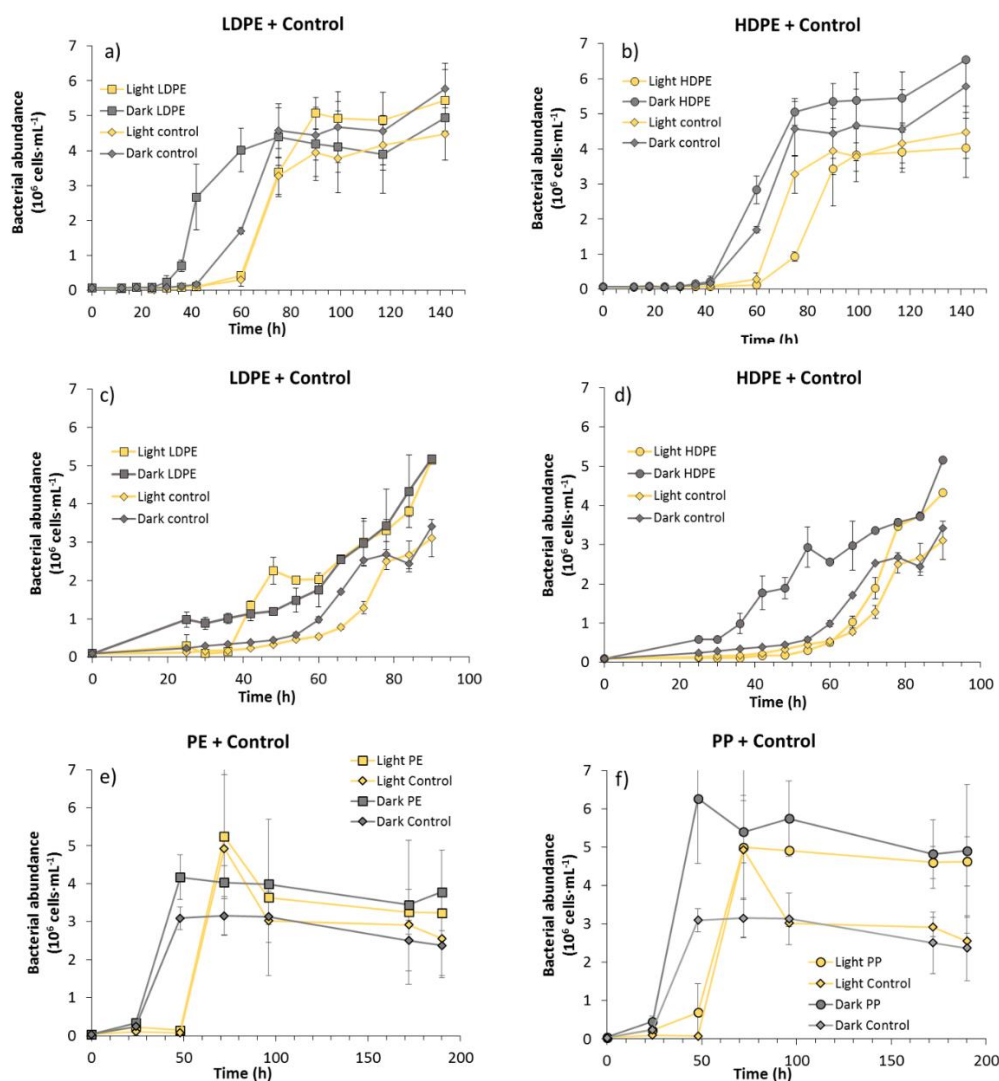


Fig. 2- Bacterial abundance during incubation with plastic leachates. Bacterial abundance (cell mL^{-1}) during the incubation with DOC leached from plastics previously irradiated for 6 days using a LDPE and b HDPE; for 30 days using c LDPE and d HDPE; for 30 days using e PE and f PP. Error bars represent the standard deviation of the mean of the triplicate cultures. HDPE high-density polyethylene, LDPE low-density polyethylene, PE polyethylene, PP polypropylene.

At the end of the bacterial incubation experiments, there were no significant differences ($p < 0.05$) in bacterial abundance between plastic treatments and the controls without plastics (Fig. 2). Also, there was no clear pattern in the maximum bacterial abundance reached among the different types of plastics. All the treatments reached a maximum bacterial abundance of about $6 \times 10^6 \text{ cells mL}^{-1}$. Bacteria started to grow slightly earlier in the LDPE and packaging PE and PP than in the HDPE treatments (Fig. 2). After 24 h of incubation, bacterial leucine incorporation was significantly higher ($p < 0.05$) in the plastic treatments than in the non-plastic treatments, especially under dark conditions. When packaging plastic was used, leucine incorporation rates measured after 24 h of incubation were lower than in the other plastic types. Nevertheless, leucine incorporation in the dark plastic treatments

(7.41×10^{-2} and 0.12×10^{-2} nmol Leu L⁻¹ h⁻¹ for PE and PP, respectively) was higher than in the corresponding irradiated (4.25×10^{-3} and 4.97×10^{-3} nmol Leu L⁻¹ h⁻¹ for PE and PP, respectively) treatments (Fig. 3c). After 48 h of incubation, bacterial leucine incorporation in the dark treatments was significantly higher ($p < 0.05$) than in the irradiated treatments. However, the dark control was not significantly different from the dark treatments containing plastics (Fig. 3d).

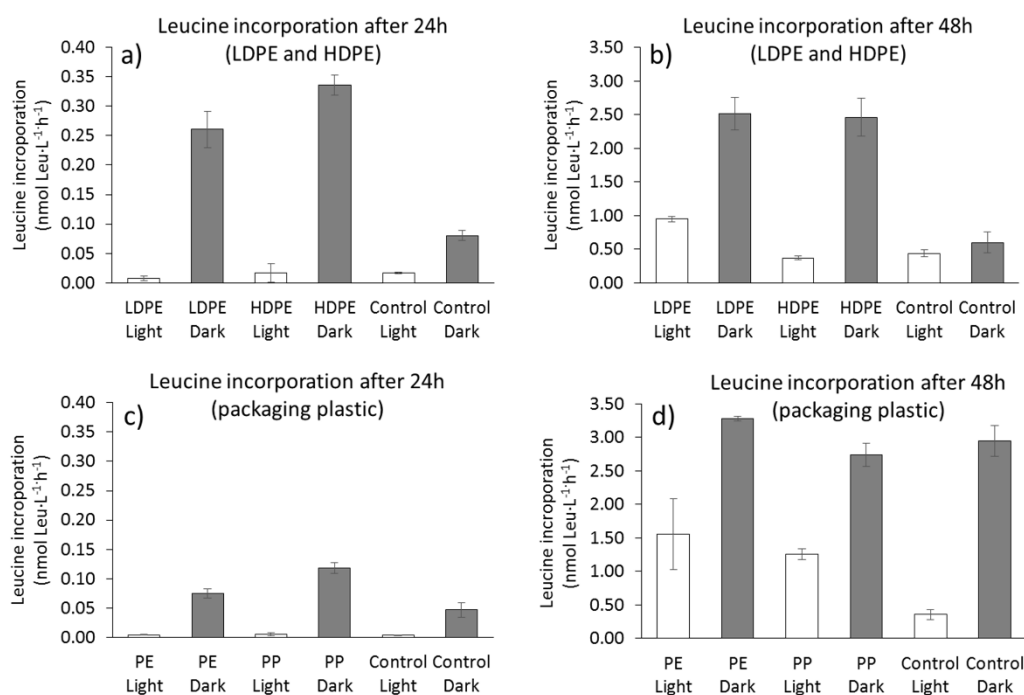


Fig. 3 - Leucine incorporation in the 30-days plastic leaching experiments. Leucine incorporation (nmol Leu L⁻¹ h⁻¹) for: LDPE and HDPE treatments after a 24 h and b 48 h of incubation; PE and PP packaging plastic after c 24 h and d 48 h of incubation. Error bars represent the standard deviation of the mean of the triplicate cultures. HDPE high-density polyethylene LDPE low-density polyethylene, PE polyethylene, PP polypropylene.

The bacterial growth efficiency (BGE, as %) was calculated from the increase in bacterial carbon biomass and the concomitant decrease in DOC in the incubations over time. An average BGE of $12\% \pm 10\%$ was obtained for plastics (irradiated and dark treatments) and $19\% \pm 8\%$ for the control treatments (irradiated and dark) without plastics. No significant differences were found in the BGE between treatment with and without plastic neither for irradiated and dark treatments. These BGE values are comparable with those of coastal waters (del Giorgio and Cole, 1998).

A strong positive linear relationship between DOC leaching and bacterial DOC consumption ($R^2 = 0.87$; $p < 0.001$; $N = 46$, all plastic experiments included, Model II regression, Fig. 4) indicated that DOC leaching from plastics, either irradiated or held in the

dark, is utilized by marine microbes. The regression slope indicates that $58\% \pm 3\%$ of the (Rohlf *et al.*, 1973) leached DOC is taken up by microbes at the time scale of the incubations.

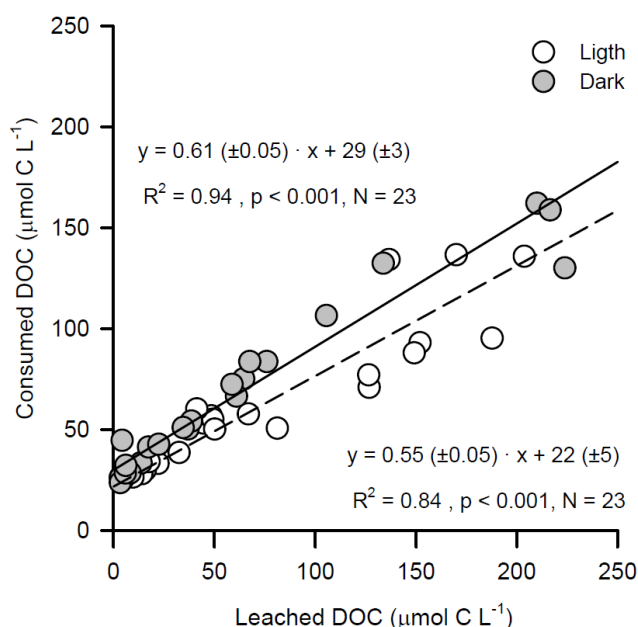


Fig. 4 - Relation between DOC consumption by microbes and DOC leaching from plastics. DOC in $\mu\text{mol C L}^{-1}$. Linear regression equation (Model II) using all data: $Y = 0.58 (\pm 0.03) \cdot X + 45.43 (\pm 3.03)$ ($R^2 = 0.87$; $p < 0.001$; $N = 46$). Open circles: irradiated samples; Gray circles: non-irradiated samples. DOC dissolved organic carbon

Discussion

All plastic types used here leached DOC into seawater with a major fraction being released in the initial phase when plastics first have contact with seawater ($60\% \pm 26\%$; see Instantaneous DOC leached in Table 1). About 45% of the leached DOC is progressively lost during the first 200 h as shown in the kinetic experiment conducted in the dark (Fig. 1). Since in this experiment photo-oxidation cannot be the cause of the DOC decline, the loss of DOC could be due to sorption onto the plastic, a loss of volatile leachates or a combination of both. The sorption–desorption capacity of plastics is well documented (Karapanagioti and Klontza, 2008); thus a part of the DOC might re-adsorb onto plastics until an equilibrium is reached. The sorption of organic compounds onto plastic can be a fast process. Bakir *et al.* (2014) found that some organic pollutants absorbed onto polyethylene floating in seawater reaching an equilibrium within 24–48 h. However, other studies determined a longer period (>20 days) to reach equilibration for organic pollutants absorbing onto polyethylene and polypropylene (Karapanagioti and Klontza, 2008). In our study, the equilibrium was reached after about 200 h. That could include the sorption of the DOC that was already present in seawater.

However, in our study, this amounted to only 5% of the total DOC before it started to decrease. So, if some sorption of the DOC from seawater happened in our experiments, this was minimal compared to the DOC leachate. In nature, the sorption of natural DOC onto plastics could compete with microbial DOC uptake disrupting the natural lower trophic level processes. Another explanation for the observed loss of DOC might be the production of volatile organic compounds resulting from degradation of plastics (Curran and Strlič, 2015). The strong plastic specific smell at the end of our incubation experiments (both in the irradiated and non-irradiated) suggests that some of the leached DOC is volatile. In irradiated samples, in addition to the possible direct release of organic volatiles from the plastics, solar radiation might have caused photo-degradation of the released non-volatile compounds resulting in CO, CO₂, or organic volatiles not measurable with our method to determine DOC. Possible photo-degradation products from plastic are propane, propene, ethane, ethylene, butane, and hexene (Gewert *et al.*, 2015) among others. The method for measuring DOC applied in this study only accounts for the non-volatile fraction because the seawater samples are sparged with N₂ gas prior to the analysis to remove all the inorganic carbon which, however, also results in the loss of the volatile DOC fraction (see Methods section). Thus, it is likely that plastics exposed to solar radiation leach more DOC than is measured with the approach used here.

It has been estimated that between 4.8×10^{12} and 12.7×10^{12} MT of plastics entered the ocean in the year of 2010 (Jambeck *et al.*, 2015). Assuming that floating plastics have an average density of 0.96 g cm^{-3} (see Methods section) and given our range of DOC leaching ($0.26\text{--}8.92 \text{ } \mu\text{g C cm}^{-2}$; Table 1), we estimate that between 260 and 23,600 MT of DOC year⁻¹ leach from those plastics. Previous estimates indicate that 5.25×10^{12} pieces of plastic particles weighing 268,940 MT are currently floating at the sea surface (Cózar *et al.*, 2014; Eriksen *et al.*, 2014), i.e., much less than the plastic entering the ocean annually (Jambeck *et al.*, 2015). This indicates that the majority of the plastics entering the ocean is not floating at the surface. Missing plastic likely sunk in the water column and is buried in marine sediments or it is too small to be caught by the commonly used nets to collect marine plastics (about $200 \text{ } \mu\text{m}$) (Cózar *et al.*, 2014). In the subtropical gyres, plastic concentrations can be as high as 2500 g km^{-2} (Cózar *et al.*, 2014; Eriksen *et al.*, 2014). By extrapolating our results to the concentration of plastics in the ocean, we estimate that 2500 g km^{-2} of plastics would leach between 0.14 and $4.65 \text{ g DOC km}^{-2}$. Considering a $40 \text{ } \mu\text{m}$ thick surface microlayer in which these plastics are floating and leaching, 2500 g km^{-2} of plastics leach between 0.28 and

9.68 $\mu\text{mol C L}^{-1}$ within 5 days. DOC concentrations of about 110 $\mu\text{mol L}^{-1}$ have been measured in the surface microlayer of the oligotrophic gyre of the North Atlantic (Reinthal *et al.*, 2008). Thus, up to $10 \pm 0.3\%$ of the DOC in the surface microlayer might originate from plastics. This could create local hot spots of high DOC concentrations stimulating microbial activity.

Even if the plastic types used in our experiments are the most abundant plastics found in the ocean (polyethylene and polypropylene) (Suaria *et al.*, 2016), there is a high diversity of plastic polymers in the ocean. Other plastic types might release different amounts of DOC than those examined here. Therefore, the values presented here are only tentative estimates. Aging and degradation of plastic causes its breakdown into small piece (GESAMP, 2015), a mechanism, which could potentially increase DOC leaching due to the increase in surface area relative to its volume. The plastics used in our experiments did not show any signs of aging to the naked eye after the exposure to artificial solar radiation. Moreover, since the missing plastic mentioned above is not taken into account here, our estimates of DOC leaching from plastics are likely very conservative.

Plastics could also contribute to the DOC measurements through their direct presence in the samples. Nanoplastics ($<100\text{ nm}$) are either derived from fragmentation of larger particles or directly from products for personal care, cosmetics, or textile fibers (Fendall and Sewell, 2009; Browne *et al.*, 2011; Koelmans *et al.*, 2015). A recent study showed that plastic particles smaller than $2\text{ }\mu\text{m}$ are generated upon exposure of polystyrene to solar radiation (Lambert and Wagner, 2016). A high number of these polymer particles were found to be smaller than 800 nm (Lambert and Wagner, 2016). In our experiments, any nanoparticle formed would be included in the DOC pool since we did not filter the sample before and after the irradiation experiment. However, we did not find significant differences in DOC leaching between irradiated and dark samples in most of the experiment, indicating that sub-micrometer particles from photo-degradation were not generated to a significant extent in our experiments. DOC is operationally defined as the fraction of organic matter passing through a $0.2\text{--}0.7\text{ }\mu\text{m}$ filter (Hansell and Carlson, 2014). Therefore, any particle smaller than 700 nm would pass the most commonly used filters for DOC analysis (Whatman GF/F, $0.7\text{ }\mu\text{m}$ pore size) and consequently, will contribute to the measured DOC. Thus, special care should be taken when collecting DOC samples in plastic contaminated areas.

Leaching of DOC from plastics influences the microbial activity and carbon cycling in the ocean. The bioavailable fraction of the leached DOC was (insignificantly) higher when the

plastic was kept in the dark than under artificial solar radiation ($61\% \pm 3\%$ in the dark vs. $55\% \pm 5\%$ in the light treatments). Even in the treatments with only low levels of DOC leaching (e.g., PE packaging plastic), dark conditions stimulated the response of the bacterial community, as indicated by the DOC utilization and by an earlier increase in microbial abundance in the plastic incubations than in the controls without plastic. Even where no differences in the DOC leaching between the light and dark treatments were observed, microbial growth started earlier in the dark treatments containing plastics indicating that irradiated DOC derived from plastics might undergo photochemical transformation affecting microbial growth. Photodegradation of plastics is known to produce free radicals (Gewert *et al.*, 2015) potentially inhibiting bacterial growth (Anesio *et al.*, 2005). Therefore, the lower bacterial abundance and leucine incorporation in the treatments exposed to artificial solar radiation might be due to the formation of microbial inhibitors. The large amount of plastics potentially present in the deeper water layers or in sediments (Cózar *et al.*, 2014) is not exposed to solar radiation. Thus, plastic-derived DOC could also potentially enhance microbial growth in layers well below the oceanic surface layer. Our leaching experiments were performed under abiotic conditions. In the ocean, however, microbes will have access to the plastic-derived DOC immediately upon its release, resulting in $\sim 45\%$ more DOC, potentially available, than the estimates given in Table 1 (Total leached DOC). Thus, re-sorption of leached DOC onto the plastics would be largely prevented if microbes would efficiently take up the DOC as soon as it is released from the plastics.

DOC leaching from plastics and its effect on microbial activity might be important in areas with high plastic concentrations (e.g., subtropical gyres or near shore waters), especially in the surface microlayer. The quantity of plastic waste entering the oceans is predicted to increase by up to one order of magnitude by the year 2025 (20) resulting in plastic-derived DOC of up to 236,000 MT per year in the global ocean, with potential major consequences for marine microbes and the carbon cycling in the oceanic system.

Material and Methods

Plastic leaching experiments

A total of six experiments were performed using four different types of plastics (low density polyethylene (LDPE), high density polyethylene (HDPE), polyethylene (PE), and

polypropylene (PP)) and two exposure times with artificial solar radiation, 6 days and 30 days. An additional experiment to study the kinetics of DOC leaching from plastics was performed in the dark using LDPE.

Artificial photosynthetic active radiation (PAR) was provided by a HQI-T Powerstar lamp (250 W, Osram), UV-A radiation by 2 Philips TL100W/10 R fluorescent tubes, and UV-B radiation by 2 UVA-340 fluorescent lamps (Q-Panel Company, UK). The radiation intensity for each wavelength or wavelength range was as follows: PAR (400–700 nm), $700 \mu\text{mol m}^{-2} \text{s}^{-1}$; 380 nm, $28.47 \mu\text{W cm}^{-2} \text{nm}^{-1}$; 340 nm, $16.31 \mu\text{W cm}^{-2} \text{nm}^{-1}$; 320 nm, $7.95 \mu\text{W cm}^{-2} \text{nm}^{-1}$; 305 nm, $1.09 \mu\text{W cm}^{-2} \text{nm}^{-1}$. The radiation dose rate represents the solar radiation in the subtropical North Atlantic Gyre measured at noon at 15 m depth (Obernosterer *et al.*, 2001). Artificial solar radiation was measured at 305, 320, 340, 380 nm, and PAR with a Biospherical PUV-510 radiometer using a correction factor for the 305 nm channel as suggested by Kirk (1994). The light treatments received continuous artificial solar radiation.

Polyethylene plastic (LDPE and HDPE) was obtained from GoodFellow as plastic film (LDPE, 0.5 mm thickness) and pellets (HDPE, ~4 mm diameter). PE from fruit bags and PP from fruit packaging, both translucent, were obtained from a local supermarket in Vienna (Austria). LDPE, PE, and PP were cut into ~7 mm squares. Plastic pieces (63 squares for LDPE, PE and PP, and 123 pellets for HDPE experiments) were added to 250 mL of sterilized (autoclaved at 121 °C for 20 min) artificial seawater in quartz tubes for the treatments receiving artificial solar radiation. Dark controls were established in the same way but using borosilicate bottles wrapped in aluminium foil. Light and dark controls without plastics were also performed in the same way as the samples with plastics. All the treatments and controls were performed in triplicate. Light and dark samples were placed in the solar simulator under the radiation conditions described above during 6 days (LDPE and HDPE) and 30 days (LDPE, HDPE, PE and PP). A flow-through water bath maintained the temperature of the incubation flasks at 23 °C.

DOC was measured from the unfiltered artificial seawater before and after the incubation period to estimate the DOC leaching from the plastic material and the effect of the radiation on it. DOC released was normalized to the surface area of the whole plastic used in every flask. Bacterial abundance was measured at the end of the experiment to check whether bacterial growth took place in the plastic leaching experiments. However, bacterial abundance in these experiments was always below 10^4 mL^{-1} .

Bioavailability of DOC leaching from plastics

Following the exposure to artificial solar radiation, plastic pieces were removed from the incubation flasks and 0.8 μm filtered surface seawater from the North Adriatic Sea was added to the incubation water at a ratio of 9:1 (incubation water: 0.8 μm filtered). The treatments were amended with NH_4Cl and NaH_2PO_4 to a final concentration of 10 and 2 $\mu\text{mol L}^{-1}$, respectively, to avoid growth limitation by either nitrogen or phosphorus availability. The flasks were incubated in the dark at 23 °C until the mixed microbial community reached stationary phase. Samples for microbial abundance were collected every 6–12 h for the LDPE and HDPE experiments and daily for the PE and PP experiments. DOC samples were collected at the beginning of the incubation and at the end of the exponential growth phase of the microbial community. At the end of this incubation experiment, DOC samples were filtered through combusted Whatman GF/F filters to remove bacteria. In the 30 days experiments with different types of plastics (LDPE, HDPE, PE, and PP), heterotrophic microbial production was measured 24 and 48 h after inoculating the microbial community as described below.

An additional experiment was performed to study the kinetics of the DOC leaching from plastics in which 63 LDPE squares were added to 300 mL of artificial seawater. The samples were kept in the dark at 23 °C and DOC samples were collected at different times over a 2-weeks period, with a higher frequency in the initial phase of the kinetic study.

DOC and microbial analysis

DOC samples were collected unfiltered for the initial and final time of the irradiation experiment as well as the kinetic experiment. However, they were filtered at the end of the microbial incubation experiment (Whatman GF/F filters pre-combusted at 450 °C for 4 h) to remove bacteria. Water for DOC analyses was collected in pre-combusted 20 mL glass vials, acidified with concentrated HCl to $\text{pH} < 2$ and stored at 4 °C until analysis. DOC was measured with a Shimadzu TOC-V organic carbon analyser (Álvarez-Salgado and Miller, 1998) after removal of CO_2 by vigorous sparging with high purity N_2 . Therefore, only the non-volatile fraction of DOC is measured. The accuracy was tested daily with the DOC reference materials provided by D.A. Hansell (University of Miami). We obtained average concentrations of $43.3 \pm 0.3 \mu\text{mol L}^{-1}$ for the deep ocean reference (Batch 16—2016) minus blank reference materials. The nominal DOC value provided by the reference laboratory was 43–45 $\mu\text{mol L}^{-1}$.

The global budget of DOC leaching from plastic in the ocean was calculated assuming a plastic density of 0.96 g cm^{-3} , a plastic thickness of 0.1 mm and the two sides of the plastic film.

Bacterial abundance was measured collecting aliquots of 1.5–2 mL from each bottle, fixed with 0.5% glutaraldehyde (final concentration, Sigma-Aldrich), stored in the dark for 10 min and subsequently frozen at -80°C until further processing. Bacterial abundance was measured by flow cytometry (BD FACSAria IIu) following the method described elsewhere (Giorgio *et al.*, 1996).

Leucine incorporation rates of the microbial communities were measured by adding 20 nmol L^{-1} $[3\text{H}]$ -leucine (final concentration, specific activity $120 \text{ Ci mmol L}^{-1}$) to triplicate 1.5 mL samples. Duplicate TCA (trichloroacetic acid)-killed blanks (5% final concentration) were treated in the same way as the samples (Smith and Azam, 1992). Samples and blanks were incubated in the dark at 20°C for 2 h. Incubations were terminated by adding TCA (5% final concentration) to the samples. Bacterial proteins were precipitated by two successive centrifugation steps ($12,000 \times g$ for 10 min), including a washing step with 1 mL of 5% TCA. The samples were air-dried before adding 1 mL of liquid scintillation cocktail. After 24 h, the radioactivity was determined in a scintillation counter (Packard Tri-Carb 1600TR). The disintegrations per minute (DPMs) of the blanks were subtracted from the mean DPMs of the respective samples and the resulting DPMs converted into leucine incorporation rates.

Acknowledgements

The authors thank Eva Sintes for assistance with the bacterial abundance analyses and M.J. Pazo for the DOC analyses. This research was supported by the Austrian Science Fund (FWF) projects Z194-B17 and P28781-B21. X.A.A.-S was funded by the project MODMED (CSIC–PIE, 201730E020) project.

References

- Álvarez-Salgado, X.A. and Miller, A.E.J. (1998) Simultaneous determination of dissolved organic carbon and total dissolved nitrogen in seawater by high temperature catalytic oxidation: conditions for precise shipboard measurements. *Mar Chem* **62**: 325–333.
- Andrady, A.L. (2011) Microplastics in the marine environment. *Mar Pollut Bull* **62**: 1596–605.
- Anesio, A.M., Granéli, W., Aiken, G.R., Kieber, D.J., and Mopper, K. (2005) Effect of Humic Substance Photodegradation on Bacterial Growth and Respiration in Lake Water. *Appl Environ Microbiol* **71**: 6267–6275.
- Auta, H.S., Emenike, C.U., and Fauziah, S.H. (2017) Distribution and importance of microplastics in the marine environment: A review of the sources, fate, effects, and potential solutions. *Environ Int* **102**: 165–176.
- Bakir, A., Rowland, S.J., and Thompson, R.C. (2014) Transport of persistent organic pollutants by microplastics in estuarine conditions. *Estuar Coast Shelf Sci* **140**: 14–21.
- Browne, M.A., Crump, P., Niven, S.J., Teuten, E., Tonkin, A., Galloway, T., and Thompson, R. (2011) Accumulation of Microplastic on Shorelines Worldwide: Sources and Sinks. *Environ Sci Technol* **45**: 9175–9179.
- Cózar, A., Echevarría, F., González-Gordillo, J.I., Irigoien, X., Úbeda, B., Hernández-León, S., et al. (2014) Plastic debris in the open ocean. *Proc Natl Acad Sci* **111**: 10239–10244.
- Curran, K. and Strlič, M. (2015) Polymers and volatiles: Using VOC analysis for the conservation of plastic and rubber objects. *Stud Conserv* **60**: 1–14.
- Eriksen, M., Lebreton, L., Carson, H., Thiel, M., Moore, C., Borerro, J., et al. (2014) Plastic Pollution in the World's Oceans: More than 5 Trillion Plastic Pieces Weighing over 250,000 Tons Afloat at Sea. *PLoS One* **9**: e111913.
- Fendall, L.S. and Sewell, M.A. (2009) Contributing to marine pollution by washing your face: Microplastics in facial cleansers. *Mar Pollut Bull* **58**: 1225–1228.
- GESAMP (2015) Sources, fate and effects of microplastic in the marine environment: a global assessment.
- Gewert, B., Plassmann, M.M., and MacLeod, M. (2015) Pathways for degradation of plastic polymers floating in the marine environment. *Environ Sci Process Impacts* **17**: 1513–1521.
- Giorgio, P.A. del, Bird, D.F., Prairie, Y.T., and Planas, D. (1996) Flow cytometric determination of bacterial abundance in lake plankton with the green nucleic acid stain SYTO 13. *Limnol Oceanogr* **41**: 783–789.
- Giorgio, P.A. and Cole, J.J. (1998) Bacterial growth efficiency in natural aquatic systems. *Annu Rev Ecol Syst* **29**: 503–541.
- Hansell, D.A. and Carlson, C.A. (2014) Biogeochemistry of marine dissolved organic matter, Academic Press.
- Hansell, D.A., Carlson, C.A., Repeta, D.J., and Schlitzer, R. (2009) Dissolved organic matter in the ocean. *Oceanography* **22**: 202–211.
- Jambeck, J.R., Geyer, R., Wilcox, C., Siegler, T.R., Perryman, M., Andrady, A., et al. (2015) Plastic waste inputs from land into the ocean. *Science* **347**: 768–771.
- Kalogerakis, N., Karkanorachaki, K., Kalogerakis, G.C., Triantafyllidi, E.I., Gotsis, A.D., Partsinevelos, P., and Fava, F. (2017) Microplastics Generation: Onset of Fragmentation of Polyethylene Films in Marine Environment Mesocosms. *Front Mar Sci* **4**: 84.
- Karapanagioti, H.K. and Klontza, I. (2008) Testing phenanthrene distribution properties of virgin plastic pellets and plastic eroded pellets found on Lesbos island beaches (Greece). *Mar Environ Res* **65**: 283–290.
- Kirk, J.T.O. (1994) Optics of UV-B radiation in natural waters. *Ergeb Limnol Ocean* **43**: 1–16.
- Koelmans, A.A., Besseling, E., and Shim, W.J. (2015) Marine anthropogenic litter, 2nd ed. Bergmann, M., Gutow, L., and Klages, M. (eds) Springer Nature.
- Lambert, S. and Wagner, M. (2016) Characterisation of nanoplastics during the degradation of polystyrene. *Chemosphere* **145**: 265–268.

- Obernosterer, I., Ruardij, P., and Herndl, G.J. (2001) Spatial and diurnal dynamics of dissolved organic matter (DOM) fluorescence and H₂O₂ and the photochemical oxygen demand of surface water DOM across the subtropical Atlantic Ocean. *Limnol Oceanogr* **46**: 632–643.
- Prather, M.J., Holmes, C.D., and Hsu, J. (2012) Reactive greenhouse gas scenarios: Systematic exploration of uncertainties and the role of atmospheric chemistry. *Geophys Res Lett* **39**.
- Reinthal, T., Sintes, E., and Herndl, G.J. (2008) Dissolved organic matter and bacterial production and respiration in the sea-surface microlayer of the open Atlantic and the western Mediterranean Sea. *Limnol Oceanogr* **53**: 122–136.
- Rohlf, F.J., Sokal, R., and James, F. (1973) Introduction to biostatistics, WH Freeman San Francisco.
- Romera-Castillo, C., Letscher, R.T., and Hansell, D.A. (2016) New nutrients exert fundamental control on dissolved organic carbon accumulation in the surface Atlantic Ocean. *Proc Natl Acad Sci* **113**: 10497–10502.
- Savoca, M.S., Wohlfeil, M.E., Ebeler, S.E., and Nevitt, G.A. (2016) Marine plastic debris emits a keystone infochemical for olfactory foraging seabirds. *Sci Adv* **2**: e1600395.
- van Sebille, E., Wilcox, C., Lebreton, L., Maximenko, N., Hardesty, B.D., van Franeker, J.A., et al. (2015) A global inventory of small floating plastic debris. *Environ Res Lett* **10**: 124006.
- Smith, D.C. and Azam, F. (1992) A simple, economical method for measuring bacterial protein synthesis rates in seawater using 3H-leucine. *Mar Microb food webs* **6**: 107–114.
- Suaria, G., Avio, C.G., Mineo, A., Lattin, G.L., Magaldi, M.G., Belmonte, G., et al. (2016) The Mediterranean Plastic Soup: synthetic polymers in Mediterranean surface waters. *Sci Rep* **6**: 37551.
- Suhrhoff, T.J. and Scholz-Böttcher, B.M. (2016) Qualitative impact of salinity, UV radiation and turbulence on leaching of organic plastic additives from four common plastics — A lab experiment. *Mar Pollut Bull* **102**: 84–94.

GENERAL DISCUSSION

This thesis contributes to the understanding of the interaction between microbial communities and plastic pollution in the ocean. It provides insight into biofilm development on different plastic types, the taxonomy of bacteria with the potential for metabolizing LDPE-related compounds, and the respective metabolic pathways that might be involved. It also sheds light on the impact of plastic leachates on microbial growth and activity in seawater, and therefore on oceanic biogeochemical cycles. The following section is intended to synthesize the findings of the four chapters and emphasize their importance to the field of microbial oceanography and marine plastic pollution research.

Plastic colonization by prokaryotes at the sea surface

The term *plastisphere* has been coined to refer to the biofilm habitat and community that establish on plastics in the ocean (Zettler *et al.*, 2013), however it is still unclear if there is a core *plastisphere* shared between plastics across oceans. There is increasing evidence that the overall biofilm development on plastics in the ocean is mainly shaped by internal biofilm processes and environmental factors rather than by the specific surface properties of the plastic (Oberbeckmann *et al.*, 2015). However, there appears to be a part of the *plastisphere* also influenced by plastic properties, with different types of plastics hosting different microbial communities (Chapter I; Dudek *et al.*, 2020). The portion of the community which is shaped by plastic properties probably depends on a combination of factors, such as the stage of biofilm development (Chapter I), environmental factors (Oberbeckmann *et al.*, 2016) and the characteristics of the plastics (Chapter I). There was a clear difference between the prokaryotic composition of the biofilm on PVCs compared to other plastics (HDPE, LDPE and PP) and glass, but there was little difference between the prokaryotic community of the biofilm of LDPE, HDPE, PP and glass after the plastics were one week, one and two months incubated at the sea surface (Chapter I). This reveals that the influence of the surface properties of PVC was stronger on the development of the biofilm than those of the other plastics. A recent study, however, found no significant difference between the prokaryotic community composition of the biofilm of several different plastic types, including PVC, when

incubated for one, three and six weeks in the Caribbean Sea (Dudek *et al.*, 2020). This suggests that geographical and environmental factors also play an important role in determining how much of the community is influenced by the plastic surface (Oberbeckmann *et al.*, 2018).

It appears that the influence of the colonized surfaces on the attached bacterial community is also dependent on the stage of biofilm development, being stronger in the earlier stages (Chapter I). In earlier stages of biofilm development, the organisms are in direct contact with the surface. A study revealed that in a 21 months incubation, microorganisms tightly attached to the plastic surfaces were composed of relatively rare taxa differing in their composition between different types of plastic (Kirstein *et al.*, 2019). This further supports the notion of the existence of a surface type-specific community, which is most likely decreasing in relative abundance when biofilm becomes thicker. This also explains why in plastics collected in the environment there are always certain taxa that discriminate for certain plastic types even when the overall community composition between them is statistically similar (Chapters I and III). For example, the two most common plastics at the sea surface, PE and PP, have been systematically shown to exhibit a relatively similar bacterial community composition across different water masses (Amaral-Zettler *et al.*, 2015; Chapter III), even at earlier stages of biofilm development (Chapter I). Nevertheless, there are certain taxa that appear to discriminate for one or the other plastic type (Chapter III). For example, members of the *Rhodobacteraceae* family have been found in relatively higher abundances in PE biofilms than in PP and glass (Chapter II). When comparing samples from different water masses, members of this family have also been identified as core members of the PE biofilm community (Oberbeckmann *et al.*, 2015).

The reason why certain bacterial taxa discriminate for certain plastic types is still unclear. Physico-chemical properties like surface free energy, hydrophobicity and roughness are usually important factors in biofilm development at any surface (Hunt and Parry, 1998; Teughels *et al.*, 2006; Myint *et al.*, 2010) and might affect the community composition. But other plastic type-specific characteristics, like the presence and composition of additives and biodegradability are also candidate factors influencing the community composition of plastics in the ocean (Roager and Sonnenschein, 2019). The impact of plastic leachates on the activity and growth of microbial communities (Chapter IV) and the fact that there are organisms on the biofilm of PE that can putatively utilize LDPE-derived carbon (Chapter II) further support the idea that plastic-associated compounds could select for specific organisms. Additionally,

the fact that some of the putative degraders of LDPE-related compounds discriminated for PE and LDPE over glass and PP after one month incubated in the North Adriatic Sea (Chapter III) can be an indication that the ability of some bacteria to utilize plastic-derived carbon might also be involved in shaping at least partly the bacterial community developing on plastics in the ocean.

A recent study has identified marine bacterial species with the ability of degrading certain plastic additives (Wright *et al.*, 2020). In contrast, plastic leachates have also been shown to impair the growth of *Prochlorococcus* (Tetu *et al.*, 2019). The potential negative or positive impact plastic additives and other leachates have on certain species is likely to shape the plastic colonizing community and provoke differences in the community composition between plastics with different concentrations and types of additives. This could also be the reason why the microbial community on PVCs was strikingly different from the microbial community on other surfaces under both ambient and dim light conditions (Chapter I). While the PVC pellets had concentrations between 33% and 41% (w/w) of phthalate additives, the other surfaces did not contain measurable phthalate concentrations. It is possible that the other plastic surfaces had other non-phthalate additives, however, the concentration of additives for any of the other types of plastic usually is less than 3% (Cherif Lahimer *et al.*, 2017).

Plastic biofilms typically also harbor a large eukaryotic community, which is also likely influenced by both the plastics surface and environmental factors (Dudek *et al.*, 2020). While the interaction between eukaryotes and prokaryotes on plastic biofilms is not well studied, it is likely that it plays a role in shaping both parts of the community (Dudek *et al.*, 2020). Taken together, the community composition of plastic biofilms is probably determined by the interaction between a network of biological and environmental factors and physico-chemical properties of the plastic.

Influence of plastic-derived compounds on marine microbial communities

The impact of compounds leaching from plastics in marine ecosystems has become a concern over the last years. We know that plastics can leach additives (Suhrrhoff and Scholz-Böttcher, 2016; Hermabessiere *et al.*, 2017), and produce methane and ethylene when

exposed to solar radiation (Royer *et al.*, 2018). It is now clear that plastic leachates can affect the marine biota (Hermabessiere *et al.*, 2017) and impact primary production and consequently, biogeochemical cycles in the ocean (Tetu *et al.*, 2020). Bacteria are major drivers of oceanic biogeochemical cycles. Thus, the effect of plastic leachates on bacterial growth and activity could have implications on the transfer of carbon, nitrogen and other nutrients to the food web (Chapter IV; Seeley *et al.*, 2020). This will likely be exacerbated in the future with the annual increase of plastic production (PlasticsEurope), and the increasing plastic accumulation in the oceans (Ostle *et al.*, 2019).

Plastics are differently distributed throughout the water column, with buoyant plastics accumulating at the sea surface and denser plastics sinking through the water column and eventually accumulating on the sea floor (Krause *et al.*, 2020). Plastic leachates are likely to differently affect microbial communities at different depths. A higher microbial activity and growth when plastics are kept in the dark suggest that plastic leachates might also have a strong impact on the microbial activity in dark deeper layers of the ocean (Chapter IV). However, there are other factors that might influence the leaching of compounds from plastics and their uptake by the microbial communities in the deep, such as the microbial community composition, hydrostatic pressure, temperature and nutrient availability.

The release of significant concentrations of dissolved organic carbon (DOC) from plastics to the surrounding water might create hotspots of high DOC concentration (Chapter IV), especially in plastic accumulation zones. Typical accumulation zones are oceanic gyres and relatively enclosed water masses with high coastal activity and slow water-replacement, like the Mediterranean Sea (Eriksen *et al.*, 2014). How this increase in plastic-derived DOC will impact the affected areas is unknown. Nevertheless, with the ability microbial communities have to utilize this plastic-derived DOC under both light and dark conditions (Chapter IV) changes to the carbon cycle in these areas could be expected.

Bacteria and metabolic pathways putatively involved in the degradation of LDPE-originating compounds

Low-density polyethylene (LDPE) with its high hydrophobicity and tensile strength is highly resistant to biodegradation (Min *et al.*, 2020). However, prior thermal or (photo)chemical oxidation by environmental factors can reduce the hydrophobicity of the

polymer creating polar groups and facilitating microbial action on plastics (Orr *et al.*, 2004; Esmaeili *et al.*, 2013; Da Costa *et al.*, 2018).

The survival of certain bacteria in incubations kept in the dark where plastic was the sole carbon source were accompanied with a decrease in plastic weight and changes to the plastic surface (Sudhakar *et al.*, 2008; Syranidou, Karkanorachaki, Amorotti, Franchini, *et al.*, 2017; Syranidou, Karkanorachaki, Amorotti, Repouskou, *et al.*, 2017; Chapter II), this suggests that some bacteria might have the potential to biodegrade plastic in the ocean even under dark conditions. The discovery of the PET-degrading bacterium *Ideonella sakaiensis* and its associated PET degrading enzymes (Yoshida *et al.*, 2016) reinforces the idea that there are bacteria in the environment with the ability to breakdown some of these complex polymers to benign monomers. While several fungal and bacterial species have been reported to alter LDPE in terrestrial environments (Yoon *et al.*, 2012; Esmaeili *et al.*, 2013; Das and Kumar, 2014; Muhonja *et al.*, 2018; Bardaji *et al.*, 2020), only a few from marine environments have been identified (Sudhakar *et al.*, 2008; Harshvardhan and Jha, 2013; Paço *et al.*, 2017; Syranidou, Karkanorachaki, Amorotti, Repouskou, *et al.*, 2017).

It is still unclear whether bacteria metabolizing LDPE-originating carbon compounds can completely breakdown the polymer into the final oxidized plastic products (biomass, CO₂, H₂O and/or CH₄; Amaral-Zettler *et al.*, 2020). It is possible that they metabolize leaching compounds associated to the plastic (Chapter IV), for example, additives, without degrading the stable polymeric chain. Methane and ethylene have been shown to be produced when LDPE is exposed to solar radiation (Royer *et al.*, 2018), which can also be utilized by bacteria. Nevertheless, changes in the weight and chemistry of LDPE when incubated with a microbial consortium that can utilize LDPE as carbon source (Chapter III; Syranidou, Karkanorachaki, Amorotti, Repouskou, *et al.*, 2017) imply that regardless of what these bacteria are degrading, their action results in changes of the plastic surface. The ubiquitous presence of some of these bacteria on the biofilm of plastics collected at the ocean surface in different water masses (Chapter II) suggests that they might play a role in the fate of the plastic floating at the ocean surface.

Enzymes related to alkane degradation are the main candidates for PE degradation (Syranidou, Karkanorachaki, Amorotti, Repouskou, *et al.*, 2017; Chapter III). This is supported by an enrichment of bacteria closely related to known alkane degraders such as those related to *Alcanivorax* and *Ketobacter* species and of bacteria with genes related to alkane

degradation in their genomes in incubations where LDPE was the sole carbon source (Chapter III). Also, one of the only identified complete metabolic pathways that increased in relative abundance over time in the same incubations was fatty acid beta-oxidation. Alkane-derived carbon is incorporated into the cells through the fatty-acid beta-oxidation pathway (Rojo, 2009). This further strengthens the hypothesis that alkane degraders can metabolize LDPE-related carbon compounds through alkane degradation pathways. Nevertheless, the potential pathways and enzymes related to LDPE degradation in the ocean are only poorly studied with most studies so far mainly focusing on the *alkB* gene (Yoon *et al.*, 2012). The *alkB* gene encodes for an alkane monooxygenase that catalyzes the hydroxylation of n-alkanes and fatty acids and is one of the key enzymes in alkane degradation pathways in several bacteria (Vomberg and Klinner, 2000). A correlation between the development of bacterial consortiums capable of surviving with LDPE as sole carbon source and an increase in the relative abundance of the *alkB* gene in the same incubations (Yoon *et al.*, 2012; Syranidou, Karkanorachaki, Amorotti, Repouskou, *et al.*, 2017; Chapter III) have been reported. However, other alkane hydroxylases, like for example, a cytochrome P450 CYP153 alkane hydroxylase, a putative FAD-binding monooxygenase and a long-chain alkane monooxygenase encoded by the genes CYP153, *AlmA* and *LadA*, respectively, are possible candidates to substitute the *alkB*-encoded alkane monooxygenase in the initial oxidation step of LDPE (Chapter III). Several bacteria with these alkane oxidases in their genomes also have genes encoding for alkane transporters and surfactant producing proteins (Chapter III). Surfactants decrease the hydrophobicity of compounds and might facilitate the oxidation of the long polymer chains and play an important role in facilitating the potential degradation of LDPE and associated compounds (Noordman *et al.*, 2002) especially in dark conditions, where photo-oxidations is absent.

Bacteria classified as *Rhodobacteraceae*, found to be ubiquitous in plastic biofilms and to also thrive in incubations where LDPE was the sole carbon source (Chapter II) also discriminated for LDPE over PP and glass (Chapter II) in early stages of biofilm development. Interestingly, *Rhodobacteraceae* species that increased in relative abundance in incubations where LDPE was the sole carbon source harbor several genes related to alkane degradation, including the *alkB* gene (Chapter III). *Rhodobacteraceae* are commonly abundant on biofilms, including PE biofilms (Oberbeckmann and Labrenz, 2019). Therefore, if some of the *Rhodobacteraceae* species that are common in PE biofilms can degrade the PE polymer or

associated compounds, they could have a significant impact on the life cycle of these plastics in the ocean.

It is, however, unclear if putative LDPE degraders would degrade the polymer and associated compounds in the environment where other carbon sources are available. Biofilms provide a variety of different organic compounds (Dobretsov, 2010) probably more easily metabolized than a polymer like PE. Therefore, even if some of the bacteria on the biofilm would have the genetic potential to degrade PE, it is possible they would not do it if they could access other carbon sources. Furthermore, the relatively slow weight loss of PE pieces incubated with communities tailored to utilize LDPE-derived carbon (Chapter III) suggests that even if a small component of the plastic biofilm community would degrade PE in the ocean, it would probably occur at very slow rates. On the other hand, in natural environments plastics are also subjected to environmental degradation, especially at the ocean surface where photo-oxidation is strong which might facilitate subsequent microbial action (Esmaeili *et al.*, 2013).

The presence of bacteria with the potential to metabolize PE and associated compounds both in the seawater and on PE biofilms, altering the plastic surface (Chapter III) and influencing the DOC pool (Chapter IV) in the ocean, reveals that there are several aspects to the microbes-plastics interaction in the ocean that might have important environmental impacts. Determining the processes through which PE, one of the main plastics produced worldwide, can be altered by microbial communities is an essential step in determining the fate of plastics in the environment.

References

- Amaral-Zettler, L.A., Zettler, E.R., and Mincer, T.J. (2020) Ecology of the plastisphere. *Nat Rev Microbiol* 1–13.
- Amaral-Zettler, L.A., Zettler, E.R., Slikas, B., Boyd, G.D., Melvin, D.W., Morrall, C.E., et al. (2015) The biogeography of the Plastisphere: implications for policy. *Front Ecol Environ* 13: 541–546.
- Bardají, D.K.R., Moretto, J.A.S., Furlan, J.P.R., and Stehling, E.G. (2020) A mini-review: current advances in polyethylene biodegradation. *World J Microbiol Biotechnol* 36: 32.
- Cherif Lahimer, M., Ayed, N., Horriche, J., and Belgaied, S. (2017) Characterization of plastic packaging additives: Food contact, stability and toxicity. *Arab J Chem* 10: S1938–S1954.
- Da Costa, J.P., Nunes, A.R., Santos, P.S.M., Girão, A. V, Duarte, A.C., and Rocha-Santos, T. (2018) Degradation of polyethylene microplastics in seawater: Insights into the environmental degradation of polymers. *J Environ Sci Heal Part A* 53: 866–875.
- Das, M. and Kumar, S. (2014) An approach to low-density polyethylene biodegradation by *Bacillus amyloliquefaciens*. 3 *Biotech* 1–6.
- Dobretsov, S. (2010) Marine biofilms. *Biofouling* 123–136.
- Dudek, K.L., Cruz, B.N., Polidoro, B., and Neuer, S. (2020) Microbial colonization of microplastics in the Caribbean Sea. *Limnol Oceanogr Lett* 5–17.
- Eriksen, M., Lebreton, L., Carson, H., Thiel, M., Moore, C., Borerro, J., et al. (2014) Plastic Pollution in the World's Oceans: More than 5 Trillion Plastic Pieces Weighing over 250,000 Tons Afloat at Sea. *PLoS One* 9: e111913.
- Esmaeili, A., Pourbabaee, A.A., Alikhani, H.A., Shabani, F., and Esmaeili, E. (2013) Biodegradation of low-density polyethylene (LDPE) by mixed culture of *Lysinibacillus xylanilyticus* and *Aspergillus niger* in soil. *PLoS One* 8: e71720.
- Harshvardhan, K. and Jha, B. (2013) Biodegradation of low-density polyethylene by marine bacteria from pelagic waters, Arabian Sea, India. *Mar Pollut Bull* 77: 100–106.
- Hermabessiere, L., Dehaut, A., Paul-Pont, I., Lacroix, C., Jezequel, R., Soudant, P., and Duflos, G. (2017) Occurrence and effects of plastic additives on marine environments and organisms: A review. *Chemosphere* 182: 781–793.
- Hunt, A.P. and Parry, J.D. (1998) The effect of substratum roughness and river flow rate on the development of a freshwater biofilm community. *Biofouling* 12: 287–303.
- Kirstein, I.V., Wichels, A., Gullans, E., Krohne, G., and Gerdt, G. (2019) The Plastisphere – Uncovering tightly attached plastic “specific” microorganisms. *PLoS One* 14: e0215859.
- Krause, S., Molari, M., Gorb, E. V, Gorb, S.N., Kossel, E., and Haeckel, M. (2020) Persistence of plastic debris and its colonization by bacterial communities after two decades on the abyssal seafloor. *Sci Rep* 10: 1–15.
- Min, K., Cuiffi, J.D., and Mathers, R.T. (2020) Ranking environmental degradation trends of plastic marine debris based on physical properties and molecular structure. *Nat Commun* 11: 727.
- Muhonja, C.N., Makonde, H., Magoma, G., and Imbuga, M. (2018) Biodegradability of polyethylene by bacteria and fungi from Dandora dumpsite Nairobi-Kenya. *PLoS One* 13: e0198446.
- Myint, A.A., Lee, W., Mun, S., Ahn, C.H., Lee, S., and Yoon, J. (2010) Influence of membrane surface properties on the behavior of initial bacterial adhesion and biofilm development onto nanofiltration membranes. *Biofouling* 26: 313–321.
- Noordman, W.H., Wachter, J.H.J., De Boer, G.J., and Janssen, D.B. (2002) The enhancement by surfactants of hexadecane degradation by *Pseudomonas aeruginosa* varies with substrate availability. *J Biotechnol* 94: 195–212.
- Oberbeckmann, S., Kreikemeyer, B., and Labrenz, M. (2018) Environmental Factors Support the

- Formation of Specific Bacterial Assemblages on Microplastics. *Front Microbiol* **8**: 2709.
- Oberbeckmann, S. and Labrenz, M. (2019) Marine Microbial Assemblages on Microplastics: Diversity, Adaptation, and Role in Degradation. *Ann Rev Mar Sci*.
- Oberbeckmann, S., Löder, M.G.J., and Labrenz, M. (2015) Marine microplastic-associated biofilms—a review. *Environ Chem* **12**: 551–562.
- Oberbeckmann, S., Osborn, A.M., and Duhaime, M.B. (2016) Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. *PLoS One* **11**: e0159289.
- Orr, I.G., Hadar, Y., and Sivan, A. (2004) Colonization, biofilm formation and biodegradation of polyethylene by a strain of *Rhodococcus ruber*. *Appl Microbiol Biotechnol* **65**: 97–104.
- Ostle, C., Thompson, R.C., Broughton, D., Gregory, L., Wootton, M., and Johns, D.G. (2019) The rise in ocean plastics evidenced from a 60-year time series. *Nat Commun* **10**: 1622.
- Paço, A., Duarte, K., da Costa, J.P., Santos, P.S.M., Pereira, R., Pereira, M.E., et al. (2017) Biodegradation of polyethylene microplastics by the marine fungus *Zalerion maritimum*. *Sci Total Environ* **586**: 10–15.
- PlasticsEurope (2019). Plastics - the Facts 2019
- Roager, L. and Sonnenschein, E.C. (2019) Bacterial Candidates for Colonization and Degradation of Marine Plastic Debris. *Environ Sci Technol* **53**: 11636–11643.
- Rojo, F. (2009) Degradation of alkanes by bacteria. *Environ Microbiol* **11**: 2477–2490.
- Royer, S.-J., Ferrón, S., Wilson, S.T., and Karl, D.M. (2018) Production of methane and ethylene from plastic in the environment. *PLoS One* **13**: e0200574.
- Seeley, M.E., Song, B., Passie, R., and Hale, R.C. (2020) Microplastics affect sedimentary microbial communities and nitrogen cycling. *Nat Commun* **11**: 1–10.
- Sudhakar, M., Doble, M., Murthy, P.S., and Venkatesan, R. (2008) Marine microbe-mediated biodegradation of low- and high-density polyethylenes. *Int Biodeterior Biodegradation* **61**: 203–213.
- Suhrhoff, T.J. and Scholz-Böttcher, B.M. (2016) Qualitative impact of salinity, UV radiation and turbulence on leaching of organic plastic additives from four common plastics — A lab experiment. *Mar Pollut Bull* **102**: 84–94.
- Syranidou, E., Karkanorachaki, K., Amorotti, F., Franchini, M., Repouskou, E., Kaliva, M., et al. (2017) Biodegradation of weathered polystyrene films in seawater microcosms. *Sci Rep* **7**: 1–12.
- Syranidou, E., Karkanorachaki, K., Amorotti, F., Repouskou, E., Kroll, K., Kolvenbach, B., et al. (2017) Development of tailored indigenous marine consortia for the degradation of naturally weathered polyethylene films. *PLoS One* **12**: e0183984.
- Tetu, S.G., Sarker, I., and Moore, L.R. (2020) How will marine plastic pollution affect bacterial primary producers? *Commun Biol* **3**: 1–4.
- Tetu, S.G., Sarker, I., Schrammeyer, V., Pickford, R., Elbourne, L.D.H., Moore, L.R., and Paulsen, I.T. (2019) Plastic leachates impair growth and oxygen production in *Prochlorococcus*, the ocean's most abundant photosynthetic bacteria. *Commun Biol* **2**: 184.
- Teughels, W., Van Assche, N., Sliepen, I., and Quirynen, M. (2006) Effect of material characteristics and/or surface topography on biofilm development. *Clin Oral Implants Res* **17**: 68–81.
- Vomberg, A. and Klinner, U. (2000) Distribution of alkB genes within n-alkane-degrading bacteria. *J Appl Microbiol* **89**: 339–348.
- Wright, R.J., Bosch, R., Gibson, M.I., and Christie-Oleza, J.A. (2020) Plasticizer Degradation by Marine Bacterial Isolates: A Proteogenomic and Metabolomic Characterization. *Environ Sci Technol* **54**: 2244–2256.
- Yoon, M., Jeon, H., and Kim, M. (2012) Biodegradation of polyethylene by a soil bacterium and AlkB cloned recombinant cell. *J Bioremed Biodegrad* **3**: 1–8.

- Yoshida, S., Hiraga, K., Takehana, T., Taniguchi, I., Yamaji, H., Maeda, Y., et al. (2016) A bacterium that degrades and assimilates poly(ethylene terephthalate). *Science* **351**: 1196–1199.
- Zettler, E.R., Mincer, T.J., and Amaral-Zettler, L. (2013) Life in the “plastisphere”: Microbial communities on plastic marine debris. *Environ Sci Technol* **47**: 7137–7146.