# Life on the edge: Active microbial communities in the Kryos $MgCl_2$-brine basin at very low water activity

Lea Steinle[1,2,*], Katrin Knittel[3], Nicole Felber[1], Claudia Casalino[4], Gert de Lange[4], Chiara Tessarolo[5], Alina Stadnitskaia[6], Jaap S. Sinninghe Damsté[4,6], Jakob Zopfi[1], Moritz F. Lehmann[1], Tina Treude[7,8], Helge Niemann[1,6,9]

[1] Department of Environmental Sciences, University of Basel, Basel, Switzerland, Bernoullistr. 30, 4056 Basel, +41 62 207 35 96, lea.steinle@unibas.ch

[2] GEOMAR, Helmholtz Centre for Ocean Research, Kiel, Germany

[3] Max-Planck-Institute for Marine Microbiology, Bremen, Germany

[4] Faculty of Geosciences, Department of Earth Sciences, Utrecht University, Utrecht, Netherlands

[5] Department of Earth and Environmental Sciences, University of Milano-Bicocca, Milan, Italy

[6] Department of Marine Microbiology and Biogeochemistry, NIOZ Royal Netherlands Institute for Sea Research, and Utrecht University, Texel, Netherlands

[7] Department of Earth, Planetary and Space Sciences, University of Los Angeles, Los Angeles, California, USA

[8] Department of Atmospheric and Oceanic Sciences, University of Los Angeles, Los Angeles, California, USA

[9] CAGE – Centre for Arctic Gas Hydrate, Environment and Climate, Department of Geology, UiT the Arctic University of Norway, 9037 Tromsø, Norway

*Corresponding author

Running title: Active microbial communities in the Kryos brine

The authors declare no conflict of interest.

**The Kryos Basin is a deep-sea hypersaline anoxic basin (DHAB) located in the Eastern-Mediterranean Sea (34.98°N 22.04°E). It is filled with brine of re-dissolved Messinian evaporites and is nearly saturated with $MgCl_2$-equivalents, which makes this habitat extremely challenging for life. The strong density difference between the anoxic brine and the overlying oxic Mediterranean seawater impedes mixing, giving rise to a narrow chemocline. Here, we investigate the microbial community structure and activities across the seawater-brine interface using a combined biogeochemical, next-generation sequencing, and lipid biomarker approach. Within the interface, we detected fatty acids that were distinctly $^{13}C$-enriched when compared to other fatty acids. These likely originated from sulfide-oxidising bacteria that fix carbon via the reverse tricarboxylic acid cycle. In the lower part of the interface, we also measured elevated rates of methane oxidation, probably mediated by aerobic methanotrophs under micro-oxic conditions. Sulfate reduction rates increased across the interface and were highest within the brine, providing first evidence that sulfate reducers (likely *Desulfovermiculus* and *Desulfobacula*) thrive in the Kryos Basin at a water activity of only ~0.4 $A_w$. Our results demonstrate that a highly specialized microbial community in the Kryos Basin has adapted to the poly-extreme conditions of a DHAB with nearly saturated $MgCl_2$ brine, extending the known environmental range where microbial life can persist.**

## 1. Introduction

Environments characterized by salinities higher than 50 PSU are considered hypersaline (Capece et al, 2013). Such environments are challenging for life due to the high energetic costs for osmotic adaptation (Boetius & Joye, 2009) and the limitation of available water (Stevenson et al, 2015). Despite these constraints, microbial and eukaryotic life has been reported in many of these systems (Boetius & Joye, 2009, Oren, 2015). Hypersaline environments exist in terrestrial settings (e.g., lakes, salt flats, salterns), and marine environment (e.g., mud volcanoes, sea-ice brine channels or brine basins; Javor, 2012).

Furthermore, hypersaline settings were also discovered on extraterrestrial objects, for example on Mars, or on Saturn's moon Enceladus (Hansen et al, 2006; McEwen et al, 2014; Hsu et al, 2015; Martín-Torres et al, 2015). Hence, hypersaline environments on Earth may serve as analogues for potential niches for life in extraterrestrial environments (Preston and Dartnell, 2014). Marine brine basins have been discovered at the seafloor of the Gulf of Mexico, the Red Sea, the Black Sea, and the Eastern Mediterranean Sea (see Stock et al, 2013, for a review). The deep-sea hypersaline anoxic basins (DHABs) in the Mediterranean are located at the Mediterranean Ridge at water depths >3000 meters below sea level (mbsl). Mediterranean brines originate from the dissolution of evaporites deposited during the Messinian salinity crisis (5-6 million years ago; Hsü et al, 1973, Camerlenghi, 1990, Roveri et al, 2014). After sediment burial, tectonic activity mobilised relic brines and re-exposed some of these evaporite layers to seawater. Their exposure at the seafloor led to the formation of the present-day brine lakes (e.g., de Lange & ten Haven, 1983; Wallmann et al, 1997; Vengosh et al., 1998). As hypersaline solutions have a higher density than seawater, brines accumulate in seafloor depressions and form lake-like features, which can be several kilometres long and more than hundred meters deep (Camerlenghi, 1990, Stock et al, 2013). Even though many DHABs in the Mediterranean are located in close proximity to each other, their respective geochemical composition can differ quite strongly, depending on the source evaporite (Stock et al, 2013). The brines of most Mediterranean DHABs (l'Atalante, Bannock, Thetis, Tyro and Urania basins; van der Wielen et al, 2005; La Cono et al, 2011) are thalassohaline, i.e., the brine salts consist mainly of NaCl. In contrast, the Kryos and the Discovery Basin contain athalassohaline brines, dominated by $MgCl_2$ (Wallmann et al, 1997; Yakimov et al, 2015).

Vertical mixing across the extreme density gradients between brine and overlying seawater is extremely slow. Seawater and brines differ strongly in their solute composition (in particular, in the concentrations of key electron donors and acceptors), so that a narrow (1-3 m) chemocline forms between the two media (de Lange et al, 1990, Stock et al, 2013). In contrast to the overlying seawater, the brines are anoxic but electron acceptors other than oxygen are plentiful, most importantly sulfate (Stock et al, 2013). Hence, hotspots of biological activity were found at brine-seawater interfaces (e.g., Sass et al, 2001, van der Wielen et al, 2005, Daffonchio et al, 2006, Yakimov et al, 2007, Boetius & Joye, 2009, Pachiadaki et al, 2014, Yakimov et al, 2015). In addition to active microbial communities at the interface, previous studies have provided evidence for microbial activity (sulfate reduction, methanogenesis and heterotrophy) within thalassohaline brines (van der Wielen et al, 2005, Daffonchio et al, 2015, LaCono et al, 2011). Life in athalassohaline $MgCl_2$-rich brines, on the other hand, is considered much more challenging (van der Wielen et al, 2005, Hallsworth et al, 2007, Yakimov et al, 2015). In fact, microbial life was considered impossible in the Kryos brine basin due to its extremely high concentrations of $MgCl_2$ (Yakimov et al, 2015), and putative evidence for life in the nearby Discovery Basin (van der Wielen et al, 2005) has been questioned (Hallsworth et al, 2007, Oren, 2013). Major challenges for microbial life in $MgCl_2$-brines, in addition to osmotic stress, are chaotropicity (i.e., the disruption of hydrogen bonding network between water molecules causing denaturation of organic molecules; Stevenson et al, 2015, Cray et al, 2013) and exceptional low levels of water activity - $A_w$ ($A_w$: the vapour pressure of an aqueous solution relative to distilled water). $A_w$ is a key parameter used to determine the limits of life (Litchfield, 1998). It takes thermodynamically available water into account – in contrast to water content (percentage water) – and thus describes water availability on the organismic level due to binding effects promoted by ions (Grant, 2004). Cell division, for example, has only observed at $A_W \geq 0.605$ $A_w$ (Stevensson et al, 2015), much higher than the $A_w$ of ~0.4 that has been experimentally determined for the Kryos brine (Yakimov et al, 2015).

The main objective of this study is to determine whether the poly-extreme environmental conditions (anoxia, hypersalinity, chaotropicity) prevailing in the Kryos brine permit active microbial life. Towards this goal we use an interdisciplinary approach that combines geochemical measurements (i.e., major ions, methane), direct measurements of microbial activity (sulfate reduction and methane oxidation with radio-tracer assays), as well as lipid biomarker analyses and next-generation sequencing (NGS) of 16S rRNA genes to assess the microbial community structure.

## 2. Methods

### 2.1 Study site

The Kryos Basin (34.93°N 22.02°E – 35.02°N 22.05°E; Figure 1) is one of eight known DHABs located in the Eastern Mediterranean Sea (Stock et al, 2013, Yakimov et al, 2015; Figure 1), and is filled with brine originating from secondary late-stage evaporites, dominated by $MgCl_2$. Its composition is similar to that of the Discovery brine (Wallmann et al, 1997, 2002), but with even higher concentrations of $Na^+$ and $SO_4^{2-}$ (Yakimov et al, 2015). Samples presented in this study were collected on the "Ristretto e Lungo" Cruise (2010/2011) with the RV Meteor (Me83/3) within the framework of the "Moccha" and "Middle" projects (Eurodeep-Program of the European Science Foundation).

### 2.2 Sampling

Water samples were collected in January 2012 from the deepest part of the Kryos Basin (34.952°N 22.025°E; Figure 1) using a rosette sampler equipped with 12 × 10 l Niskin bottles and probes for continuous measurements of conductivity, temperature and density (CTD; Seabird SBE9). We sampled the water column just above the seawater-brine interface, within the interface, and in the brine. The position of the interface was detected with the conductivity sensor (mounted at the lower part of the rosette sampler frame) in real-time during the hydrocast (Daffonchio et al, 2006). For interface sampling, several Niskin bottles were closed in quick succession immediately after a conductivity increase was detected, while slowly lowering the sampler through the interface (de Lange et al, 1990). This way, each bottle contained sea-/brine water collected at slightly different depths within the interface (Figure 2). During recovery, the strong density gradient prevented vertical mixing within the bottle, preserving the in situ stratified conditions (Daffonchio et al, 2006). Upon retrieval, each bottle was sampled successively (at ~2 l batches, yielding a vertical resolution of ~20 cm). Distinct sampling within each batch was done following the same sequence: first for volatiles ($CH_4$, $HS^-$), dissolved $O_2$ and DIC, then for microbial rate measurements, and finally for the analysis of major elements, nutrients, and $SO_4^{2-}$. See supplements for details on standard geochemical analyses. The relative positions of the different Niskin bottles (Figure 2) were aligned using $Cl^-$ concentrations as a conservative tracer, as described previously (e.g., Yakimov et al, 2015). Separate Niskin bottles were taken for lipid biomarker and NGS analyses, just above the interface (3335.0 ± 0.5 meters below sealevel (mbsl)), in the upper (3335.8 ± 0.5 mbsl) and lower (3337.8 ± 0.5 mbsl) interface and in the brine (3344.6 ± 1 mbsl; Figure 2).

### 2.3 Methane oxidation and sulfate reduction rate measurements

Water samples for methane oxidation and sulfate reduction (SR) rate measurements were filled bubble-free into 20 mL glass vials, closed with bromobutyl stoppers (Niemann et al, 2015) and incubated in quadruplicates with $^{14}C$ and $^{35}S$ radiotracers, respectively, for 72 h at in-situ T in the dark (Jørgensen, 1977; Treude et al, 2003). Incubations were terminated, and samples fixed and stored, as described in Steinle et al (2016). For SR rates, one teaspoon of kaolin powder was added to samples to facilitate separation of $SO_4^{2-}$ and ZnS, and SR rates were then determined with the cold-chromium distillation method (Kallmeyer et al, 2004). MOx rates and the fraction of methane incorporated into biomass were assessed as described previously (Blees et al, 2014, Steinle et al, 2017).

All rate measurements were corrected for abiotic tracer turnover (<1% of live controls) in killed controls using the same matrix (i.e., seawater, interface water, or brine). We considered only rates that were at least as high as the mean tracer turnover in killed controls plus three standard deviations of the killed-control value (Grasshoff et al, 1999).

### 2.4 Biomarker analyses

For lipid biomarker analyses, 20 l of water/brine (combined from 2 - 3 Niskin bottles) from each layer (seawater, upper and lower interface, brine) was filtered on glass microfiber filters (GF/F, particle retention ~0.7 $\mu$m), and stored at -80 °C until extraction in the home laboratory. The largest portion (7/8th) of each filter (corresponding to ~17.5 l water/brine) was used for lipid extraction according to Elvert et al (2003), but we added an additional extraction step with methanol:$H_2O$ (1:3; v/v) to extract polar compounds. The resulting total lipid extract was further separated and analysed according to Elvert et al (2003) and Niemann et al (2005). Double-bond positions of monoenoic fatty acids were determined by analysing fatty acid dimethyl-disulfide derivatives (Nichols et al, 1986; Moss and Lambert-Fair, 1989). Identities, concentrations, and stable carbon isotope composition of individual compounds were determined with a gas chromatograph linked either to a quadrupole mass spectrometer, a flame-ionization detector, or an isotope ratio mass spectrometer (Blees et al, 2014).

### 2.5 Nucleic acid extraction and amplification of 16S rRNA genes

Nucleic acids were extracted from the remaining 1/8th of a GF/F filter (corresponding to 2.5 l water/brine) according to the method described by Zhou et al (1996). Prior to extraction, cells were removed from the filters by washing (Woebken et al, 2007) with 5 M NaCl to avoid DNA loss by binding to the glass fibre filters during the extraction process.

Bacterial 16S rRNA genes were amplified by PCR from extracted DNA using the primer pair Bakt_341F/Bakt_785R (Herlemann et al, 2011, Supplementary Table 1). Archaeal 16S rRNA genes were amplified using primer pair ARCH340F/ARCH1000R (Gantner et al, 2011; Supplementary Table 1). To allow the coverage of ANME-1 methanotrophic archaea and *Korarchaeota*, we added modified primers: ARCH340F-ANME-1, ARCH1000R-ANME1 and ARCH1000R-KOR (Supplementary Table 1). Forward primers ARCH340F and ARCH340F-ANME-1 were mixed in a molar ratio of 4:1; reverse primers ARCH1000R, ARCH1000R-ANME1, and ARCH1000R-KOR were mixed in a molar ratio of 8:1:1.

PCR reactions (20 $\mu$l volume) were performed using TaKaRa Taq polymerase (Germany) according to Supplementary Table 2. The resulting bacterial 450 bp-amplicons and archaeal 700 bp-amplicons were extracted from an agarose gel (1% w/v) and purified using the MinElute PCR Purification Kit (Qiagen) according to the manufacturer's recommendations.

### 2.6 Sequencing, sequence processing, and taxonomic analysis

Amplicons were analysed by massive parallel tag sequencing on a HiSeq 2500 sequencer (2x 250 bp; Illumina, San Diego, CA) at the Max Planck-Genome-Centre Cologne, Germany. Bacterial reads were quality-trimmed (trimq = 22, minlength = 238, homopolymers ≤8 nt) and merged (overlap >25) using the software package BBmap v4.3, and split using mothur v1.33.3 (Schloss et al, 2009). Archaeal forward and reverse reads were analysed separately because amplicons were too long to obtain an overlap of reads. Data shown here are based on forward reads. Settings for trimming of archaeal sequences were trimq = 25, homopolymers ≤8 nt. Archaeal and bacterial sequences were classified using the SILVAngs pipeline and database release 123.1, 03–2016 (Quast et al, 2013). Retrieved non-16S rRNA gene sequences were removed from the analysis. Similarly, from the bacterial sequence dataset, retrieved archaeal sequences were excluded, as they were unspecifically amplified during PCR. Raw reads were deposited at the EBI Short Read Archive (SRA), and can be accessed under the study accession number PRJEB24471.

## 3. Results and Discussion

### 3.1 Chemical stratification across the seawater-brine interface

The Kryos Basin is filled with athalassohaline brine, dominated by $MgCl_2$ equivalents at near-saturation, and with strongly elevated $SO_4^{2-}$-levels (~5-fold seawater concentration; Table 1). Accounting for $MgCl_2$ and $MgSO_4$ concentrations, density (1.31 kg $dm^{-3}$) and total dissolved solids (0.46 kg $dm^{-3}$), we calculated a water activity of 0.44 $A_w$ combining the Pitzer and Samapundo models (according to models by Pitzer, 1991 and Samapundo et al, 2010). This stands in relatively good agreement with a more realistic, direct measurement of an $A_w$-value of 0.4 for the Kryos brine, which was determined experimentally (Yakimov et al, 2015). Concentrations of $SO_4^{2-}$, $Cl^-$, and $Mg^{2+}$ increased sharply from seawater background values through the interface into the brine, to 0.144, 6.55, and 3.94 mol $kg^{-1}$, respectively (Figure 3a, b, Table 1), whereas $Na^+$ concentrations decreased from 0.510 to 0.075 mol $kg^{-1}$ (Figure 3b, Table 1).

Concentrations of the microbially relevant electron donors $CH_4$ and $H_2S_{tot}$ were low, or below detection limit, in the upper part of the interface, but the concentration of both species increased sharply in the lower interface to maximum concentrations of 20 and 150 $\mu$mol $kg^{-1}$, respectively (Figure 3c, d, Tab. 1). In contrast, $O_2$ sharply decreased to values below the detection limit (~1 $\mu$M) in the lower interface (Figure 3d). In the following, based on conductivity gradients and $O_2$ concentration levels, we will refer to the upper interface as the depth layer between 3335.75 - 3336.5 mbsl where $O_2$ was still detectable (3 - 193 $\mu$mol $kg^{-1}$), and no $H_2S_{tot}$ was measured. The lower interface refers to the depth layer between 3336.5 – 3337.5 mbsl, where $O_2$ concentrations were below the detection limit (<1 $\mu$M) and increasing levels of $H_2S_{tot}$ (0 – 64 $\mu$mol $kg^{-1}$) were observed. The uppermost samples (3335.5 – 3335.75; Figure 3) represent 'normal' seawater.

### 3.2 Stratification of microbial communities

Next-generation sequencing (NGS) analyses revealed distinct microbial communities in the seawater and the upper interface on the one hand, and within the lower interface and in brine samples on the other hand (Figure 4). In the seawater end-member above the interface, most sequences were affiliated with typical archaeal and bacterial planktonic groups, i.e., mostly *Thaumarchaeota*, *MG II*, *MG III*, *SAR202*, *SAR11*, and *Moraxella* (Figure 4). The bacterial and archaeal community composition of the upper interface was comparable to that of the seawater but low abundances of sequences of halophilic archaea were already present (e.g., MSBL1 and *Ca*. Halobonum sequences each made up 1% of all classified archaeal sequences). The community composition of the lower interface and the brine comprised a much higher percentage of sequences of known halophilic archaeal groups, such as *Halorhabdus*, *Halomicrobium*, and *Nanohaloarchaeota*, indicating the presence of a halophilic microbial community.

In the lower interface, 13% of the archaeal sequences fell into the candidate division MSBL1 (Mediterranean Sea Brine Lakes 1), previously found to be one of the key contributors to the halophilic communities in the athalassohaline Discovery brine (van der Wielen et al, 2005), as well as in most thalassohaline Mediterranean- and Red Sea brine basins (van der Wielen et al, 2005, Borin et al, 2009, Yakimov et al, 2013, Mwirichia et al, 2016). The most abundant archaeal group both in the lower interface and the brine (49% and 36% of all classified sequences, respectively) was "*Ca.* Nitrosopumilus". The presence of these ammonium-oxidising archaea (Könneke et al, 2005, Walker et al, 2010), abundant ambient $NH_4^+$ and potentially microoxic conditions (Coolen et al, 2007; Ngugi et al, 2015) suggests an ammonium-driven nitrogen cycle in the lower interface. In the lower interface and the brine, 9% of all bacterial sequences belonged to the candidate phylum *Acetothermia*, commonly reported from brine environments (e.g., Eder et al, 1999, van der Wielen et al, 2005, Daffonchio et al, 2006, Borin et al, 2009). This phylum includes previously used but now abandoned candidate divisions *Ca.* KB1, OP1, and MSBL6. Sequences classified as *Acetothermia* in the lower interface all grouped within the KB1 division, whereas a minor portion of the brine *Acetothermia* sequences (~0.2%) also fell into the group previously classified as MSBL6. Besides these known halophilic/halotolerant bacteria, most other bacterial sequences of the lower interface and the brine were related to sulfate-reducing and sulfur-oxidizing bacteria, as discussed in more detail below. We are aware that DNA of dead organisms may be preserved in anoxic brines, so that 16S rRNA-gene-sequence data can be ambiguous tracers of in-situ microbial life at a given depth within the interface and the brines (Fish et al, 2002, Orsi et al, 2013, Edgcomb et al, 2016). However, we observed a clear "stratification" of the microbial communities in the brine and lower interface, contrasting the upper interface and seawater (Fig. 4), which suggests an organized, and hence living, in-situ microbial community. Indeed, most sequences of halophiles found in the lower interface were not present at all or constituted only a minor fraction of the microbial community in the upper interface and the seawater. This precludes that these sequences represent preserved (i.e., nonliving) matter from overlying water layers. On the other hand, a small portion of sequences that were most abundant in the seawater and upper interface (e.g. SAR11) were also detected in the lower interface and the brine; these sequences may hence originate from the water layers above. Similarly, the intermixture of dead microbial cells from the lower interface into the brine cannot be ruled out completely (see below).

### 3.3 Methanotrophy in the interface

The shape of the methane concentration profile across the interface, with abruptly decreasing methane concentrations in the lower interface (Figure 3e, Supplementary Figure 1a), indicates methane consumption in this water layer. Furthermore, $\delta^{13}$C- and $\delta$D-$CH_4$ values of the lowest interface sample are clearly enriched in $^{13}$C ($\Delta\delta^{13}C\text{-}CH_{4,\text{interface-brine}}$ = 5.2‰) and $^2$H ($\Delta\delta D\text{-}CH_{4,\text{interface-brine}}$ = 6.7‰) compared to methane in the brine (Figure 3f). This is consistent with methane oxidation occurring in the lower interface since methanotrophs preferentially use $^{12}$C-methane, and their activity enriches of the remaining methane in both $^{13}$C and $^2$H (Whiticar, 1999). Indeed, we measured elevated rates of microbial methane oxidation in the upper but also in the lower interface, where sulfide started to accumulate and oxygen concentrations were below detection limit (1-2 $\mu$M for Winkler titration; Figure 3). With specialised sensors, previous studies on methane oxidation at oxic/anoxic interfaces could demonstrate that oxygen is present at sub-micromolar levels even below an “apparent” oxicline (e.g., Blees et al, 2014). It is thus likely that traces of oxygen were also present in the lower interface at Kryos, serving as potential electron acceptors for methane oxidation besides sulfate. Hence, both aerobic and anaerobic modes of methane oxidation seem thermodynamically feasible. In order to distinguish between these modes of methane oxidation, supplementary information on the identity of present methanotrophs is needed.

Aerobic oxidation of methane (MOx) is mediated by aerobic methanotrophic bacteria (MOB), which belong to the *Gamma*- (Type I MOB) or *Alphaproteobacteria* (Type II MOB) Hanson and Hanson, 1996). In the lower interface, where we also measured highest methane oxidation rates (Figure 3h), we detected MOB-sequences belonging to the gammaproteobacterial *Methylococcales* and alphaproteobacterial *Methylobacterium* (although at a relatively low abundance levels of <0.1% of total bacterial sequences; Supplementary Table 3). The presence of MOB within the Kryos interface is also evident from lipid biomarker signatures. Membrane lipids depleted in $^{13}C$ relative to the $\delta^{13}C$-$CH_4$ can be diagnostic for MOB in aquatic environments (Hanson & Hanson, 1996; Summons et al, 1994; Hinrichs et al, 2003; Schubert et al, 2006; Elvert & Niemann, 2008; Blees et al, 2014). In the lower interface, we detected diplopterol and diploptene depleted in $^{13}C$ (-46.6‰ and -49.6‰, respectively; Supplementary Figure 2). Their $\delta^{13}C$-values are ~5‰ lower compared to ambient lower-interface methane (-42‰; Figure 3f). This observation is consistent with previous findings of slightly $^{13}C$-depleted MOB-biomarkers (diploptene, diplopterol) at the oxycline of the Black Sea (Wakeham et al, 2003; Schubert et al, 2006). We also measured traces of the fatty acid C16:1ω8, a diagnostic marker for type I MOB. Our DNA and biomarker data strongly suggest that lipids in the suspended particulate matter pool of the interface are partially comprised of MOB biomass, and that methane oxidation rates within the interface at oxygen concentrations below detection limit and highly elevated $MgCl_2$-concentrations are mediated by MOB. Several studies targeting oxic/anoxic interfaces in both marine (Schubert et al, 2006; Jakobs et al, 2013; Steinle et al, 2017) and lacustrine environments (Rudd et al, 1976; Blees et al, 2014a,b) reported MOx under micro-oxic conditions, providing evidence that at least some MOB are able to adapt to very low-oxygen conditions, though such conditions may not be optimal for growth (Steinle et al, 2017). At Kryos, the fraction of oxidised methane-carbon incorporated into biomass decreased from the upper to the lower interface (Figure 3i). Similar to findings from hypoxic Baltic Sea waters (Steinle et al, 2017), this suggests that MOB at Kryos live at the very edge of their habitable ecological niche. At the interface of thalassohaline brines, aerobic methanotrophy was already evidenced directly or indirectly (Schmidt et al, 2003; Abdallah et al, 2014; Wankel et al, 2010). With this study, we demonstrate for the first time that MOB can also adapt to micro-oxic conditions in an athalassohaline brine.

Although the environmental conditions within the lower interface would suggest that AOM is more important MOx, we could not find any indications for AOM. AOM with sulfate as the final electron acceptor is mediated by methanotrophic archaea (ANME), which are related to the order *Methanosarcinales* (Knittel & Boetius, 2007). We did not detect any sequences of ANMEs in the lower interface (Supplementary Table 5), even though we used a primer set specifically modified to target ANME-archaea, and we also did not detect any anaerobic methanotrophs using electron acceptors other than sulfate, i.e., nitrite, iron, or manganese (Raghoerbarsing et al 2006; Ettwig et al, 2008; Ettwig et al, 2016, Supplementary Table 3,5). Moreover, our rate measurements did not reveal any methanotrophic activity in the brine itself, despite high levels of methane and sulfate (Figure 3). Finally, our lipid biomarker analyses did not reveal any typical ANME signatures, such as strongly $^{13}$C-depleted archaeol and crocetane (Niemann & Elvert, 2008). Although both compounds were present in the lower interface and brine, their $\delta^{13}$C-values were relatively high (compared to the isotopic composition of the ambient methane and DIC (Table 1)), which argues against ANMEs as potential source organisms. Conclusively, our results suggest that ANME cannot thrive under the poly-extreme conditions of the Kryos brine (Joye et al, 2009; Maignien et al, 2013).

### 3.4 Methanogenesis in the interface and brine

The isoprenoid membrane-lipid archaeol is synthesized by a variety of archaea including methanogens (Koga & Morii, 2005). Crocetane in the marine environment is generally associated with ANMEs (Niemann & Elvert, 2008), but it was also detected in methanogenic sediments suggesting that it is synthesized by at least some methanogens too (Jahnke et al, 2008). Methanogens are hence possible source-organisms for the archaeol and crocetane with relatively high $\delta^{13}$C-values (see House et al, 2003). Indeed, our microbial diversity analyses provided evidence for the presence of methanogenic archaea within the interface and brine (Supplementary Tables 5-6): 0.5% of total archaeal sequences within the brine belonged to methanogenic archaea of the order Methanosarcinales, most importantly *Methanohalophilus*. Sporadically, sequences related to other methanogens (*Methanosaeta, Methanoregula,* *Methermicoccus, Methanobrevibacter, Methanoregula,* and *Methanolobus*) were also detected throughout the interface. As indicated by its isotopic composition ($\delta^{13}C$ = -47.1‰, $\delta D$ = -128.9‰; Whiticar, 1999) and its ratio relative to higher hydrocarbons ($CH_4$:$C_{2+}$ = 24; Bernard et al, 1978), methane in the Kryos Basin is dominantly of thermogenic origin. Yet, the admixture of biogenic methane is likely. The vertical profile of methane $\delta^{13}C$-values across the interface shows $^{12}C$-enriched methane in the upper interface when compared to the lower interface (Figure 3f). This observation cannot be explained by simple mixing with the overlying seawater, but indicates input of microbial methane within the upper interface (Whiticar, 1999). We found *Methanohalophilus* in the upper interface, but whether these methanogenic archaea are the source of the apparent methane input and can tolerate the oxic conditions prevailing in the upper interface remains questionable.

### 3.5 Sulfide oxidation within the interface: biomarker and molecular indication for thiotrophs potentially using the rTCA pathway for $CO_2$ fixation

Sulfide concentrations, similar to methane concentrations, sharply decreased to values below the detection limit at the boundary between the upper- and lower interface, indicating sulfide consumption mainly in the lower interface (Supplementary Figure 1b). Sulfide oxidation is mediated by a diversity of bacterial groups, typically by members of the Gamma- and Epsilonproteobacteria (for example, Yakimov et al, 2007, Borin et al, 2009, Hügler and Sievert, 2011, Pachiadaki et al, 2014). Indeed, we found abundant sequences related to sulfide-oxidising Epsilonproteobacteria in the lower interface and in the brine: *Sulfurimonas*- and *Sulfurovum*-related sequences accounted for 16% and 15%, respectively, of the total bacterial sequences in the lower interface, and 8% and 29%, respectively, in the brine (Figure 4). Moreover, gammaproteobacterial *Thiomicrospira*-related sequences constituted ~3% of all bacterial sequences both in the lower interface and the brine (Figure 4). In contrast, the abundance of these thiotrophs in the upper interface and the seawater was very low (<< 1%). Yakimov et al (2015) also detected one sequence of the *Sulfurovum* clade in the lower interface of the Kryos Brine, but did not find molecular evidence for *Sulfurimonas*. Similarly, thiotrophs are important parts of the microbial communities at other seawater-brine interfaces in the Mediterranean (e.g., Thetis brine: Pachiadaki et al, 2014, Urania brine: Borin et al, 2009, L'Atalante brine: Yakimov et al, 2007).

Within the lower interface and the brine, our lipid analysis revealed several fatty acids that were enriched in $^{13}$C (with $\delta^{13}$C-values up to -18‰; Figure 5) compared to the other fatty acids (concentration-weighted average: -28.6‰ – lower interface, -26.6‰ – brine). Similar to our findings, biomass at hydrothermal vents partitions into two isotopically distinct clusters (see Hügler & Sievert, 2011, for a review). The more strongly $^{13}$C-depleted values were explained by the large C-isotope fractionation during carbon fixation via the Calvin-Benson cycle (Hügler & Sievert, 2011), which is characterised by a C-isotope enrichment factor ($\Delta\delta^{13}$C) of 20-30‰ (Berg et al, 2010). This is the most common carbon fixation pathway in the bacterial realm. In contrast, the more $^{13}$C-enriched signatures often originate from other carbon fixation pathways, such as the reductive tricarboxylic acid cycle (rTCA), which is characterized by a comparatively low $\Delta\delta^{13}$C of only 2-12‰ (House et al, 2003, Berg et al, 2010). At Kryos, $CO_2$ would be more depleted than DIC ($\delta^{13}$C-DIC: -0.8 to 0.8‰; Mook et al, 1974). Together with $\delta^{13}$C-values of the fatty acids of about -18‰, the $\Delta\delta^{13}C_{\text{fatty acids-CO2}}$ would be <<18‰. Considering additional C-isotope fractionation during fatty acid synthesis of ~2-10‰ (Monson & Hayes, 1982; Hayes, 2001; Sakata et al, 2008), the $^{13}$C-enriched fatty acids may indeed originate from organisms utilising the rTCA cycle. Some of the $^{13}$C-enriched fatty acids (iC15:0, iC16:0 and iC17:0) are of bacterial origin (Kaneda 1991; Peters et al, 2007), but are not diagnostic for any specific phylogenetic group. The source organisms of the other two $^{13}$C-enriched fatty acids (17:1ω8 and 17:1ω11) remain unknown. Nevertheless, we suggest that the epsilonproteobacterial sulfide-oxidizers detected at Kryos (Figure 4) are the source organisms of the $^{13}$C-enriched fatty acids, likely fixing carbon via the rTCA (Hügler et al, 2005, Hügler & Sievert, 2011).

### 3.6 Sulfate reduction in the brine at nearly saturated $MgCl_2$ concentrations

SR rates reached maximum values of up to 460 $\mu$mol $kg^{-1}$ $d^{-1}$ (Figure 3g) within the brine at $MgCl_2$-equivalent concentrations of 3.9 mol $kg^{-1}$ (Figure 3b). These rates were ~5-20 times higher than the highest rates measured at most other Mediterranean brine basins (van der Wielen et al, 2005; Borin et al, 2009), but about 10 times lower than SR rates at the Bannock brine basin (Daffonchio et al, 2006). They were about three orders of magnitude higher than SR rates in brine systems in the Gulf of Mexico (Joye et al, 2009; Wankel et al, 2010) or at the Mercator mud volcano in the Gulf of Cadiz (Maignien et al, 2013). Evidence for potential candidates mediating SR at Kryos derives from our sequencing data and lipid biomarker analyses. In the brine and lower interface, bacterial sequences were mainly related to sulfate reducers typically detected in hypersaline environments (e.g. solar salterns (Dillon et al, 2013)) or Mediterranean DHABs (Borin et al, 2009; Yakimov et al, 2015): *Desulfovermiculus* of the family *Desulfohalobiacea* accounted for 25% and 20% of all bacterial sequences in the lower interface and the brine, respectively. Another potential candidate mediating SR in the lower interface and brine is *Desulfobacula* of the *Desulfobacteraceae,* constituting 1% (lower interface) and 3% (brine) of the total bacterial sequences in these layers. Finally, we detected high concentrations of the fatty acid 10MeC16:0, typical for *Desulfobacteraceae* and possibly originating from this group in these samples (Taylor & Parkes, 1983; Dowling et al, 1988; Frostegård et al, 1993; Rütters et al, 2002).

Several authors have argued against the possibility of microbial life in the Kryos brine (Hallsworth et al, 2007; Oren, 2013; Yakimov et al, 2015). The argumentation in these contributions was based on biophysical constraints of low water activity and chaotropicity, and on the absence of detectable mRNA of sulfate reducers and methanogenic archaea in the Discovery (Hallsworth et al, 2007) and the Kryos brines (Yakimov et al, 2015). However, our measurements now provide evidence for an active sulfate-reducing microbial community within the Kryos brine. Our results, together with previous findings of sulfate reduction (and methanogenesis) in the Discovery brine basin (van der Wielen et al, 2005), thus provide proof for microbial life at a water activity as low as 0.4 $A_w$ (Yakimov et al, 2015), in an environment that belongs to the most chaotropic systems on Earth (>300 kJ $kg^{-1}$).

### Concluding remarks

Combining geochemical analyses, rate measurements, lipid biomarker, and NGS analyses, we found active (micro-)aerobic methanotrophs, sulfide-oxidising bacteria (likely using the rTCA pathway for carbon fixation), and sulfate reducers living in close vicinity at the seawater-brine interface of the Kryos brine basin. Most intriguingly, we measured high sulfate reduction rates at nearly saturated $MgCl_2$-concentrations, providing evidence that microbes can likely be active at a high degree of chaotropicity, and very low water activity. The strong stratification of the detected bacterial community suggests that major phyla are autochthonous. Our results substantially broaden the known spectrum of poly-extreme environmental conditions supporting life on Earth and, potentially, beyond.

## Acknowledgements

We thank Captain Schneider, the crew and the scientific party of R/V Meteor for the excellent support at sea. Special thanks go to E. van Weerlee, K. Bakker, D. Gallego-Torres, C. Stalder, V. Darakchieva, R. Groenewegen, and to M. L. Goudeau for analytical support. Dagmar Woebken is thanked for help with DNA extraction from glass fibre filters, Kathrin Büttner for assistance with PCR, and Sebastian Miksch for sequence analysis. We also thank the anonymous reviewers for their helpful comments. This work received financial support through a D-A-CH project funded by the Swiss National Science Foundation and the German Research foundation (grant no. 200021L_138057, 200020_159878/1). Further support was provided through the EU COST Action PERGAMON (ESSEM 0902) and the Max Planck Society, Germany.

The authors declare no conflict of interest.

Supplementary information is available at ISME journal's website.

# References

Abdallah RZ, Adel M, Ouf A, Sayed A, Ghazy MA, Alam I, et al. (2014). Aerobic methanotrophic communities at the Red Sea brine-seawater interface. Front Microbiol 5: doi: 10.3389/fmicb.2014.00487.

Bazylinski DA, Williams TJ, Lefèvre CT, Berg RJ, Zhang CL, Bowser SS, et al. (2013). *Magnetococcus marinus* gen. nov., sp. nov., a marine, magnetotactic bacterium that represents a novel lineage (*Magnetococcaceae* fam. nov., *Magnetococcales* ord. nov.) at the base of the *Alphaproteobacteria*. Int J Syst Evol Microbiol 63:801-808.

Beal EJ, House CH, Orphan VJ. (2009). Manganese- and iron-dependent marine methane oxidation. Science 325:184-187.

Berg IA, Kochelkorn D, Ramos-Vera WH, Say RF, Zarzycki J, Hügler M et al., (2010). Autotrophic carbon fixation in archaea. Nature Rev Microbiol 8:447-460.

Bernard BB, Brooks JM, and Sackett WM. (1978). Light hydrocarbons in recent Texas continental shelf and slope sediments. J Geophy Res-Oceans 83:4053-4061.

Blees J, Niemann H, Wenk CB, Zopfi J, Schubert CJ, Jenzer JS, et al. (2014). Bacterial methanotrophs drive the formation of a seasonal anoxic benthic nepheloid layer in an alpine lake. Limnol Oceanogr 59:1410-1420.

Blees J, Niemann H, Wenk CB, Zopfi J, Schubert CJ, Kirf MK, et al. (2014). Micro-aerobic bacterial methane oxidation in the chemocline and anoxic water column of deep south-Alpine Lake Lugano (Switzerland). Limnol Oceanogr 59:311-324.

Blumenberg M, Seifert R, Michaelis W. (2007). Aerobic methanotrophy in the oxic-anoxic transition zone of the Black Sea water column. Org Geochem 38:84-91.

Boetius A, Joye SB. (2009). Thriving in salt. Science 324:1523-1525.

Boetius A, Ravenschlag K, Schubert CJ, Rickert D, Widdel F, Gieseke A, et al. (2000). A marine microbial consortium apparently mediating anaerobic oxidation of methane. Nature 407:623-626.

Borin S, Brusetti L, Mapelli F, D'Auria G, Brusa T, Marzorati M, et al. (2009). Sulfur cycling and methanogenesis primarily drive microbial colonization of the highly sulfidic Urania deep hypersaline basin. Proc Natl Acad Sci USA 106:9151-9156.

Camerlenghi A. (1990). Anoxic basins of the eastern Mediterranean:geological framework. Mar Chem 31:1-19.

Capece MC, Clark E, Saleh J, Halford D, Heinl N, Hoskins S, Rothschild LJ. (2013). Polyextremophiles and the constraints of terrestrial habitability. In: Polyextremophiles. Life under multiple forms of stress. Seckbach, J, Oren, A, and Stan-Lotter, H (eds). Dordrecht: Springer, pp. 3-60.

Cita MB. (2006). Exhumation of Messinian evaporites in the deep-sea and creation of deep anoxic brine-filled collapsed basins. Sediment Geol 188:357-378.

Coolen MJL, Abbas B, Van Bleijswijk J, Hopmans EC, Kuypers MMM, Wakeham SG. et al. (2007), Putative ammonia-oxidizing Crenarchaeota in suboxic waters of the Black Sea: a basin-wide ecological study using 16S ribosomal and functional genes and membrane lipids. Environ Microbiol 9:1001–1016. doi:10.1111/j.1462-2920.2006.01227.x.

Cypionka H. (2000). Oxygen respiration by *Desulfovibrio* species. Annu Rev Microbiol 54:827-848.

Daffonchio D, Borin S, Brusa T, Brusetti L, van der Wielen PW, Bolhuis H, et al. (2006). Stratified prokaryote network in the oxic-anoxic transition of a deep-sea halocline. Nature 440:203-207.

De Lange GJ, Catalano G, Klinkhammer GP, Luther GW. (1990). The interface between oxic seawater and the anoxic Bannock Brine; its sharpness and the consequences for the redox-related cycling of Mn and Ba. Mar Chem 31:205-217.

De Lange GJ, Ten Haven HL. (1983). Recent sapropel formation in the eastern Mediterranean. Nature 305:797-798.

Devlin SP, Saarenheimo J, Syväranta J, Jones RI. (2015). Top consumer abundance influences lake methane efflux. Nat Commun 6:8787.

Dillon JG, Carlin M, Gutierrez A, Nguyen V, McLain N. (2013). Patterns of microbial diversity along a salinity gradient in the Guerrero Negro solar saltern, Baja CA Sur, Mexico. Front Microbiol 4:399.

Dowling NJ, Nichols PD, White DC. (1988). Phospholipid fatty acid and infra-red spectroscopic analysis of a sulfate-reducing consortium. FEMS Microbiol Lett 53:325-333.

Edgcomb VP, Pachiadaki MP, Kormas KA, Paraskevi M, Bernhard JM, Leadbetter ER. (2016). Microbial activities in sediments below haloclines of thalassohaline and athalassohaline deep-sea brine lakes. ISME J 10:2643-2657.

Eder W, Jahnke LL, Schmidt M, Huber R. (2001). Microbial diversity of the brine-seawater interface of the Kebrit Deep, Red Sea, studied via 16S rRNA gene sequences and cultivation methods. Appl Environ Microbiol 67:3077-3085.

Egger M, Rasigraf O, Sapart CJ, Jilbert T, Jetten MS, Röckmann T, et al. (2015). Iron-mediated anaerobic oxidation of methane in brackish coastal sediments. Environ Sci Technol 49:277-283.

Elvert M, Niemann H. (2008). Occurrence of unusual steroids and hopanoids derived from aerobic methanotrophs at an active marine mud volcano. Org Geochem 39:167-177.

Elvert M, Boetius A, Knittel K, Jørgensen BB. (2003). Characterization of specific membrane fatty acids as chemotaxonomic markers for sulfate-reducing bacteria involved in anaerobic oxidation of methane. Geomicrobiol J 20:403-419.

Elvert M, Whiticar MJ, Suess E. (2001). Diploptene in varved sediments of Saanich Inlet: indicator of increasing bacterial activity under anaerobic conditions during the Holocene. Mar Geol 174:371-383.

Ettwig KF, Shima S, van de Pas-Schoonen KT, Kahnt J, Medema MH, op den Camp HJM et al. (2008). Denitrifying bacteria anaerobically oxidize methane in the absence of Archaea. Environ Microbiol 10:3164–3173.

Ettwig KF, Zhu B, Speth D, Keltjens JT, Jetten MSM, Kartal B. (2016). Archaea catalyze iron-dependent anaerobic oxidation of methane. Proc Natl Acad Sci USA 113:12792–12796, doi: 10.1073/pnas.1609534113

Fish, SA, Shepherd, TJ, McGenity, TJ, Grant WD. (2002). Recovery of 16S ribosomal RNA gene fragments from ancient halite. Nature 417:432-436.

Frostegård A, Tunlid A, Bååth E. (1993). Phospholipid fatty acid composition, biomass, and activity of microbial communities from two soil types experimentally exposed to different heavy metals. Appl Environ Microbiol 59:3605-3617.

Gantner S, Andersson AF, Alonso-Sáez L, Bertilsson S. (2011). Novel primers for 16S rRNA-based archaeal community analyses in environmental samples. J Microbiol. Methods 84:12-18.

Grasshoff K, Kremling K, Ehrhardt M. (1999). Methods of seawater analysis. Weinheim: Wiley-VCH.

Grant, W. D.: Life at low water activity, Philosophical Transactions of the Royal Society B: Biological Sciences, 359(1448), 1249–1267, doi:10.1098/rstb.2004.1502, 2004.

Glombitza C, Stockhecke M, Schubert CJ, Vetter A, Kallmeyer J. (2013). Sulfate reduction controlled by organic matter availability in deep sediment cores from the saline, alkaline Lake Van (Eastern Anatolia, Turkey). Front Microbiol 4:209.

Hallsworth JE, Yakimov MM, Golyshin PN, Gillion JL, D'Auria G, de Lima Alves F, et al. (2007). Limits of life in $MgCl_2$-containing environments: chaotropicity defines the window. Environ Microbiol 9:801-813.

Hansen CJ, Esposito L, Stewart AI, Colwell J, Hendrix A, Pryor W, et al. (2006). Enceladus' water vapor plume. Science 311:1422-1425.

Hanson RS, Hanson TE. (1996). Methanotrophic bacteria. Microbiol Rev 60:439-471.

Haroon MF, Hu S, Shi Y, Imelfort M, Keller J, Hugenholtz P, et al. (2013). Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. Nature 500:567-570.

Hayes, JM. (2001). Fractionation of carbon and hydrogen isotopes in biosynthetic processes. Stable Isot Geochem 43:225–277.

Herlemann DPR, Labrenz M, Jurgens K, Bertilsson S, Waniek JJ, Andersson AF. (2011) Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. ISME J 5:1571-1579.

Hinrichs KU, Hmelo LR, Sylva SP. (2003). Molecular fossil record of elevated methane levels in late Pleistocene coastal waters. Science 299:1214-1217.

House CH, Schopf JW, Stetter KO. (2003). Carbon isotopic fractionation by Archaeans and other thermophilic prokaryotes. Org Geochem 34:345-356.

Hsü KJ, Ryan WBF, Cita MB. (1973). Late Miocene desiccation of the Mediterranean. Nature 242:240-244.

Hügler M, Sievert SM. (2011). Beyond the Calvin cycle: autotrophic carbon fixation in the ocean. Annu Rev Mar Sci 3:261-289.

Iversen N, Blackburn TH. (1981). Seasonal Rates of Methane Oxidation in Anoxic Marine Sediments. Appl Environ Microbiol 41:1295-1300.

Jahnke LL, Orphan VJ, Embaye T, Turk KA, Kubo MD, Summons RE, Des Marais DJ. (2008). Lipid biomarker and phylogenetic analyses to reveal archaeal biodiversity and distribution in hypersaline microbial mat and underlying sediment. Geobiology 6:394-410.

Jakobs G, Rehder G, Jost G, Kießlich K, Labrenz M, Schmale O. (2013). Comparative studies of pelagic microbial methane oxidation within the redox zones of the Gotland Deep and Landsort Deep (central Baltic Sea). Biogeosciences 10:7863-7875.

Javor, B. (2012). Hypersaline environments: microbiology and biogeochemistry. Springer Science & Business Media.

Joye SB, Samarkin VA, MacDonald IR, Hinrichs K-U, Elvert M, Teske AP, et al. (2009). Metabolic variability in seafloor brines revealed by carbon and sulphur dynamics. Nat Geosci 2:349-354.

Jørgensen BB. (1977). The sulfur cycle of a coastal marine sediment (Limfjorden, Denmark). Limnol Oceanogr 22:814-832.

Jørgensen BB, Fenchel T. (1974). The sulfur cycle of a marine sediment model system. Marine Biology 24:189-201.

Kallmeyer J, Ferdelman TG, Weber A, Fossing H, Jørgensen BB. (2004). A cold chromium distillation procedure for radiolabeled sulfide applied to sulfate reduction measurements. Limnol Oceanogr-Meth 2:171-180.

Kaneda T. (1991). Iso- and anteiso-fatty acids in bacteria: biosynthesis, function, and taxonomic significance. Microbiol Rev 55(2):288-302.

Knittel K, Boetius A. (2009). Anaerobic oxidation of methane: Progress with an unknown process. Annu Rev Microbiol 63:311-334.

Koga, Y, Morii, H. (2005). Recent advances in structural research on ether lipids from archaea including comparative and physiological aspects. Biosci Biotechnol Biochem 69:2019-2034.

Könneke, M, Bernhard, AE, José, R, Walker, CB, Waterbury, JB, Stahl, DA. (2005). Isolation of an autotrophic ammonia-oxidizing marine archaeon. Nature 437:543-546.

Kool DM, Zhu B, Rijpstra WI, Jetten MS, Ettwig KF, Sinninghe Damsté JS. (2012). Rare branched fatty acids characterize the lipid composition of the intra-aerobic methane oxidizer "*Candidatus* Methylomirabilis oxyfera". Appl Environ Microbiol 78:8650-8656.

La Cono V, Smedile F, Bortoluzzi G, Arcadi E, Maimone G, Messina E, et al. (2011). Unveiling microbial life in new deep-sea hypersaline Lake Thetis. Part I: Prokaryotes and environmental settings. Environ Microbiol 13:2250-2268.

Litchfield CD. (1998). Survival strategies for microorganisms in hypersaline environments and their relevance to life on early Mars. Meteorit Planet Sci 33:813-819.

Luong J, Gras R, Cortes HJ, Shellie RA. (2013). Determination of trace ethylene glycol in industrial solvents and lubricants using phenyl boronic acid derivatization and multidimensional gas chromatography. Anal Chim Acta 805:101-106.

Madigan MT, Martinko JM, Bender KS, Buckley DH, Stahl DA. (2015). Brock Biology of Microorganisms. Pearson: Boston.

Maignien L, Parkes RJ, Cragg B, Niemann H, Knittel K, Coulon S, et al. (2013). Anaerobic oxidation of methane in hypersaline cold seep sediments. FEMS Microbiol Ecol 83:214-231.

Martín-Torres FJ, Zorzano M-P, Valentín-Serrano P, Harri A-M, Genzer M, Kemppinen O, et al. (2015). Transient liquid water and water activity at Gale crater on Mars. Nat Geosci 8:357–361.

McEwen AS, Dundas CM, Mattson SS, Toigo AD, Ojha L, Wray JJ, et al. (2014). Recurring slope lineae in equatorial regions of Mars. Nat Geosci 7:53-58.

Milucka J, Ferdelman TG, Polerecky L, Franzke D, Wegener G, Schmid M, et al. (2012). Zero-valent sulphur is a key intermediate in marine methane oxidation. Nature 491:541-546.

Monson KD, and Hayes JM. (1982). Carbon isotopic fractionation in the biosynthesis of bacterial fatty acids. Ozonolysis of unsaturated fatty acids as a means of determining the intramolecular distribution of carbon isotopes. Geochim Cosmochim Ac 46(2):139-149.

Mook WG, Bommerson JC, Staverman WH. (1974). Carbon isotope fractionation between dissolved bicarbonate and gaseous carbon dioxide. Earth Plan Sci Lett 22(2):169-176.

Moss CW, Lambert-Fair MA. (1989). Location of double bonds in monounsaturated fatty acids of Campylobacter cryaerophila with dimethyl disulfide derivatives and combined gas chromatography-mass spectrometry. J Clin Microbiol 27:1467-1470.s

Mwirichia R, Alam I, Rashid M, Vinu M, Ba-Alawi W, Kamau AA, Ngugi DK, Göker M, Klenk H-P, Bajic V, Stingl U. (2016). Metabolic traits of an uncultured archaeal lineage -MSBL1- from brine pools of the Red Sea. Sci Rep 6:19181. http: //doi.org/10.1038/srep19181.

Ngugi DK, Blom J, Alam I, Rashid M, Alawi W, Zhang G et al. (2015). Comparative genomics reveals adaptations of a halotolerant thaumarchaeon in the interfaces of brine pools in the Red Sea. ISME J 9:396–411.

Nichols PD, Guckert JB, White DC. (1986). Determination of monosaturated fatty acid double-bond position and geometry for microbial monocultures and complex consortia by capillary GC-MS of their dimethyl disulfide adducts. J Microbiol Meth 5:49-55.

Niemann H, Elvert M. (2008). Diagnostic lipid biomarker and stable carbon isotope signatures of microbial communities mediating the anaerobic oxidation of methane with sulfate. Org Geochem 39:1668-1677.

Niemann H, Elvert M, Hovland M, Orcutt B, Judd A, Suck I, et al. (2005). Methane emission and consumption at a North Sea gas seep (Tommeliten area). Biogeosciences 2:335-351.

Niemann H, Lösekann T, de Beer D, Elvert M, Nadalig T, Knittel K, et al. (2006). Novel microbial communities of the Haakon Mosby mud volcano and their role as a methane sink. Nature 443:854-858.

Niemann H, Steinle LI, Blees J, Krause S, Bussmann I, Treude T, et al. (2015). Toxic effects of butyl elastomers on aerobic methane oxidation. Limnol Oceanogr-Meth 13:40-52.

Ollivier B, Caumette P, Garcia J-L, Mah RA. (1994). Anaerobic bacteria from hypersaline environments. Microbiol Rev 58:27-38.

Oren A. (2015). Halophilic microbial communities and their environments. Curr Opin Biotechnol 33:119-124.

Oren A. (2013). Life in magnesium- and calcium-rich hypersaline environments: salt stress by chaotropic ions, In: Polyextremophiles. Life under multiple forms of stress. Seckbach J, Oren A, Stan-Lotter H. (eds). Dordrecht: Springer, pp. 215-232.

Orphan VJ, House CH, Hinrichs K-U, McKeegan KD, Delong EF. (2001). Methane-consuming archaea revealed by directly coupled isotopic and phylogenetic analysis. Science 293:484-487.

Orphan VJ, Jahnke LL, Embaye T, Turk KA, Pernthaler A, Summons RE, Des Marais DJ. (2008). Characterization and spatial distribution of methanogens and methanogenic biosignatures in hypersaline microbial mats of Baja California. Geobiol 6:376-393.

Pachiadaki MG, Yakimov MM, LaCono V, Leadbetter E, Edgcomb V. (2014). Unveiling microbial activities along the halocline of Thetis, a deep-sea hypersaline anoxic basin. ISME J 8:2478-2489.

Peters K, Walters C, Moldowan J. (2007). The Biomarker Guide: Biomarkers and isotopes in the environment and human history. Cambridge.

Pitzer, KS. (1991). Ion interaction approach: theory and data correlation. In: Pitzer, KS (ed). Activity coefficients in electrolyte solutions. CRC Press, Boca Raton: pp 75–153.

Preston LJ, Dartnell LR. (2014). Planetary habitability: lessons learned from terrestrial analogues. Int J Astrobiol 13:81-98.

Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P et al. (2013). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucl Acids Res 41:D590-D596.

Raghoebarsing AA, Pol A, van de Pas-Schoonen KT, Smolders AJP, Ettwig KF, Rijpstra WIC et al. (2006). A microbial consortium couples anaerobic methane oxidation to denitrification. Nature 440:918–921.

Roveri M, Flecker R, Krijgsman W, Lofi J, Lugli S, Manzi V et al. (2014). The Messinian Salinity Crisis: Past and future of a great challenge for marine sciences. Mar Geol 352:25–58.

Rudd JW, Furutani A, Flett RJ, Hamilton RD. (1976). Factors controlling methane oxidation in shield lakes: the role of nitrogen fixation and oxygen concentration. Limnol Oceanogr 21:357-364.

Rütters H, Sass H, Cypionka H, Rullkötter J. (2002). Phospholipid analysis as a tool to study complex microbial communities in marine sediments. J Microbiol Meth 48:149-160.

Sakata S, Hayes JM, Rohmer M, Hooper AB, Seemann M. (2008). Stable carbon-isotopic compositions of lipids isolated from the ammonia-oxidizing chemoautotroph Nitrosomonas europaea. Org Geochem 39(12):1725–1734. doi:10.1016/j.orggeochem.2008.08.005.

Samapundo S, Deschuyffeleer N, Van Laere D, De Leyn I, Devlieghere F. (2010). Effect of NaCl reduction and replacement on the growth of fungi important to the spoilage of bread. Food Microbiol 27(6):749-756. doi: 10.1016/j.fm.2010.03.009.

Sass AM, Sass H, Coolen MJ, Cypionka H, Overmann J. (2001). Microbial communities in the chemocline of a hypersaline deep-sea basin (Urania basin, Mediterranean Sea). Appl Environ Microbiol 67:5392-5402.

Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, et al. (2009). Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microbiol 75:7537-7541.

Schmidt M, Botz R, Faber E, Schmitt M, Poggenburg J, Garbe-Schönberg D, Stoffers P. (2003). High-resolution methane profiles across anoxic brine-seawater boundaries in the Atlantis-II, Discovery, and Kebrit Deeps (Red Sea). Chem Geol 200:359-375.

Schubert CJ, Coolen MJ, Neretin LN, Schippers A, Abbas B, Durisch-Kaiser E, et al. (2006). Aerobic and anaerobic methanotrophs in the Black Sea water column. Environ Microbiol 8:1844-1856.

Sivan O, Adler M, Pearson A, Gelman F, Bar-Or I, John SG, Eckert W. (2011). Geochemical evidence for iron-mediated anaerobic oxidation of methane. Limnol Oceanogr 56:1536-1544.

Steinle L, Schmidt M, Bryant L, Haeckel M, Linke P, Sommer S, et al. (2016). Linked sediment and water-column methanotrophy at a man-made gas blowout in the North Sea: Implications for methane budgeting in seasonally stratified shallow seas. Limnol Oceanogr 61:S367–S386. doi: 10.1002/lno.10388.

Steinle L, Maltby L, Engbersen N, Zopfi J, Bange HW, Lehmann MF, et al. (2017). Effects of low oxygen concentrations on aerobic methane oxidation in seasonally hypoxic coastal waters. Biogeosciences 14:1631–1645.

Stevenson A, Burkhardt J, Cockell CS, Cray JA, Dijksterhuis J, Fox-Powell M, et al. (2015). Multiplication of microbes below 0.690 water activity: implications for terrestrial and extraterrestrial life. Environ Microbiol 17:257-277.

Stock A, Filker S, Yakimov M, Stoeck T. (2013). Deep hypersaline anoxic basins as model systems for environmental selection of microbial plankton. In: Polyextremophiles. Life under multiple forms of stress. Seckbach J, Oren A, Stan-Lotter H (eds). Dordrecht: Springer, pp. 499-516.

Taylor J, Parkes RJ. (1983). The cellular fatty acids of the sulfate-reducing bacteria, *Desulfobacter* sp., *Desulfobulbus* sp. and *Desulfovibrio desulfuricans*. Microbiology 129:3303-3309.

Treude T, Boetius A, Knittel K, Wallmann K, Jørgensen BB. (2003). Anaerobic oxidation of methane above gas hydrates at Hydrate Ridge, NE Pacific Ocean. Mar Ecol-Prog Ser 264:1-14.

van der Wielen PW, Bolhuis H, Borin S, Daffonchio D, Corselli C, Giuliano L, et al. (2005). The enigma of prokaryotic life in deep hypersaline anoxic basins. Science 307:121-123.

Vengosh A, de Lange GJ, and Starinsky A. (1998). Boron isotope and geochemical evidence for the origin of Urania and Bannock brines at the eastern Mediterranean: Effect of water-rock interactions. Geochim Cosmochim Ac 62:3221-3228.

Wakeham SG, Lewis CM, Hopmans EC, Schouten S, Sinninghe Damsté JS. (2003). Archaea mediate anaerobic oxidation of methane in deep euxinic waters of the Black Sea. Geochim Cosmochim Acta 67:1359-1374.

Wallmann K, Aghib FS, Castradori D, Cita MB, Suess E, Greinert J, Rickert D. (2002). Sedimentation and formation of secondary minerals in the hypersaline Discovery Basin, eastern Mediterranean. Mar Geol 186:9-28.

Wallmann K, Suess E, Westbrook G, Winckler G, Cita M, the Medriff consortium. (1997). Salty brines on the mediterranean seafloor. Science 387:31-32.

Wankel SD, Joye SB, Samarkin VA, Shah SR, Friederich G, Melas-Kyriazi J, Girguis PR. (2010). New constraints on methane fluxes and rates of anaerobic methane oxidation in a Gulf of Mexico brine pool via in situ mass spectrometry. Deep Sea Res Pt II 57:2022-2029.

Whiticar MJ. (1999). Carbon and hydrogen isotope systematics of bacterial formation and oxidation of methane. Chem Geol 161:291-314.

Woebken D, Teeling H, Wecker P, Dumitriu A, Kostadinov I, DeLong EF, et al. (2007). Fosmids of novel marine Planctomycetes from the Namibian and Oregon coast upwelling systems and their cross-comparison with planctomycete genomes. ISME J 1:419-435.

Yakimov MM, La Cono V, Denaro R, D'Auria G, Decembrini F, Timmis KN, et al. (2007). Primary producing prokaryotic communities of brine, interface and seawater above the halocline of deep anoxic lake L'Atalante, Eastern Mediterranean Sea. ISME J 1:743-755.

Yakimov MM, La Cono V, Spada GL, Bortoluzzi G, Messina E, Smedile F, et al. (2015). Microbial community of the deep-sea brine Lake Kryos seawater-brine interface is active below the chaotropicity limit of life as revealed by recovery of mRNA. Environ Microbiol 17:364-382.

## Titles and legends to figures

Table 1. Geochemical parameters and rate measurements within the Kryos brine basin and across the seawater-brine interface. For the upper and lower interface, the value on the left represents the value for the deepest sample, the value on the right the value for the shallowest sample. *ns*: not sampled. *bd*: below detection. C2+ denotes hydrocarbons with two and more carbon atoms. For rates of methane oxidation (MOx) and sulfate reduction (SR) standard deviation is indicated if applicable.

Figure 1. **(a)** Overview map of DHABs in the Eastern Mediterranean. The position of the Kryos Basin is indicated with a red star, the other basins with green dots. **(b)** Bathymetry of the Kryos Basin and the adjacent sea floor (resolution = 30 m). The extent of the Kryos brine basin is delimited with a dark orange line, and the depth of the basin is indicated by the coloured scale bar.

Figure 2. Scheme for high-resolution sampling across the seawater-brine interface with Niskin Bottles. Interface sampling was conducted during very calm weather conditions with minimal pitch/roll of the ship, preventing erratic up and down movement of the water sampler. The strong density difference impeded mixing of seawater and brine in the closed Niskin bottles during recovery. Immediately upon recovery, each Niskin bottle was sampled repeatedly (5 – 7 cycles) for different parameters resulting in a vertical resolution of the water column of ~20 cm. Vertical depth profiles were aligned based on chlorinity. Separate bottles were taken for 16S rRNA- and biomarker analyses.

Figure 3. Geochemical profiles and rate measurements across the seawater-brine interface. Concentrations of **(a)** chloride (filled symbols) and sulfate (open symbols), **(b)** magnesium (filled symbols) and sodium (open symbols), **(c)** oxygen, **(d)** ammonium (filled symbols) and sulfide (open symbols), and **(e)** methane. **(f)** Isotopic composition of methane - δD (filled

symbols) and $\delta^{13}$C (open symbols). Rates of **(g)** sulfate reduction (SR), and (**h**) methane oxidation (MOx). **(i)** Fraction of oxidised methane-C incorporated into biomass. Values in (**a**) – (**f**) represent single measurements. Error bars in (**g**) – (**i**) represent standard deviations of quadruplicates. The dashed horizontal line indicates the border between upper and lower interface, and the continuous horizontal line the beginning of the brine. Note the different depth scales for the interface and brine. We vertically resolved the interface with four, substantially overlapping Niskin bottle samplings (represented by different symbols: circle, square, upward- and downward triangle). The profiles from these bottles were aligned based on chlorinity.

Figure 4. Relative abundances of bacterial and archaeal genera and unclassified clades in the Kryos brine and interface based on sequencing of 16S RNA genes (V3-V4 region for *Bacteria*, V3-V6 region for *Archaea*). Taxonomy is based on SILVAngs, release 123.1. Sequence abundances are given in per cent of total classified *Bacteria* and *Archaea*, respectively. Only taxa that made up >1% of total archaeal or bacterial sequences in any given sample are shown. Archaeal sequence abundances shown in this figure are based on unassembled reverse sequence reads. Forward reads showed a nearly congruent community composition.

Figure 5. Fatty-acid fingerprints across the seawater-brine interface. Fractional abundance (black bars) and compound-specific $\delta^{13}$C-values (diamonds, grey line) of fatty acids (C14 - C22) from **(a)** the seawater, **(b)** the upper interface, **(c)** the lower interface, and **(d)** the brine. The fingerprint comprised fatty acids with methyl groups at the iso (i) or anteiso (ai) position, or at carbon atom position 10 (10Me). In several cases, we could not determine the position of the methyl branch in the alkyl chain. Chain isomerism was then denoted by sequential numbers in parentheses (e.g. MeC14:0(1) and MeC14:0(2)). Mass traces of C16:1ω8 were detected as DMDS-derivate in interface and brine samples. Concentration-weighted averages

of bulk fatty acid $\delta^{13}$C-values are -28.9‰ (seawater), -29‰ (upper interface), -28.6‰ (lower interface), -26.6‰ (brine).

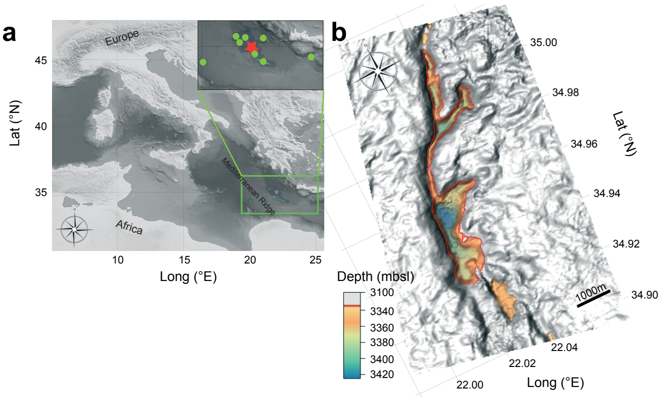

a
Europe
Africa
Mediterranean Ridge
Lat (°N)
45
40
35
Long (°E)
10
15
20
25
b
35.00
34.98
34.96
34.94
34.92
34.90
Lat (°N)
22.00
22.02
22.04
Long (°E)
1000m
Depth (mbsl)
3100
3340
3360
3380
3400
3420

Figure 1

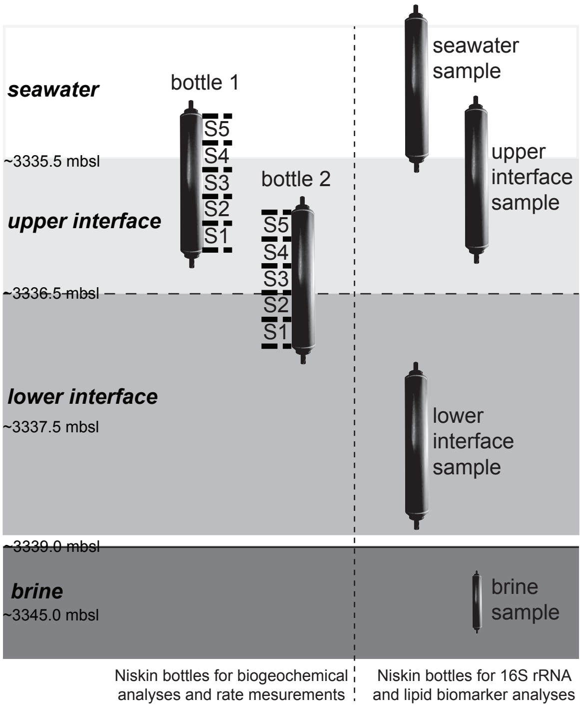
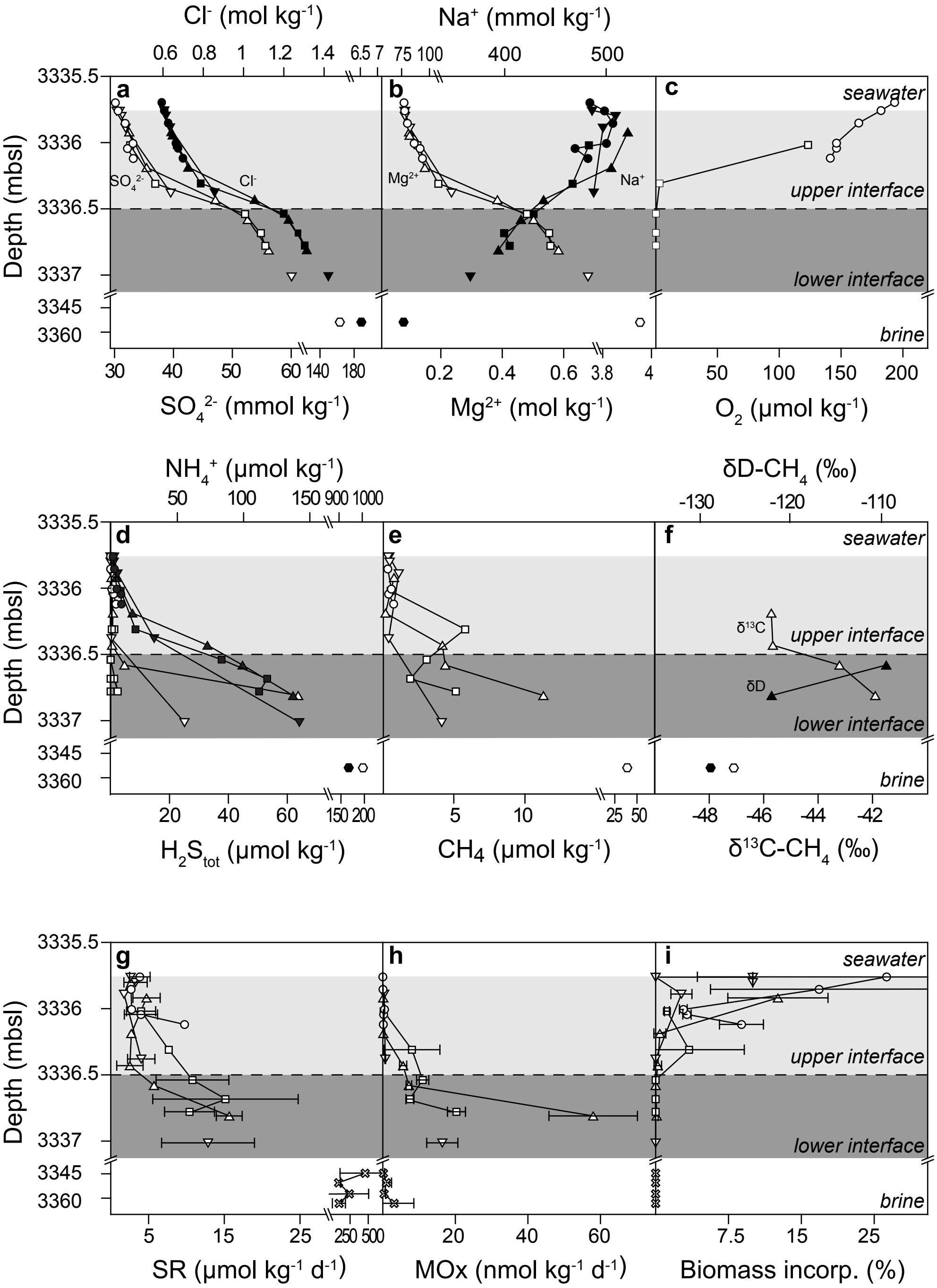
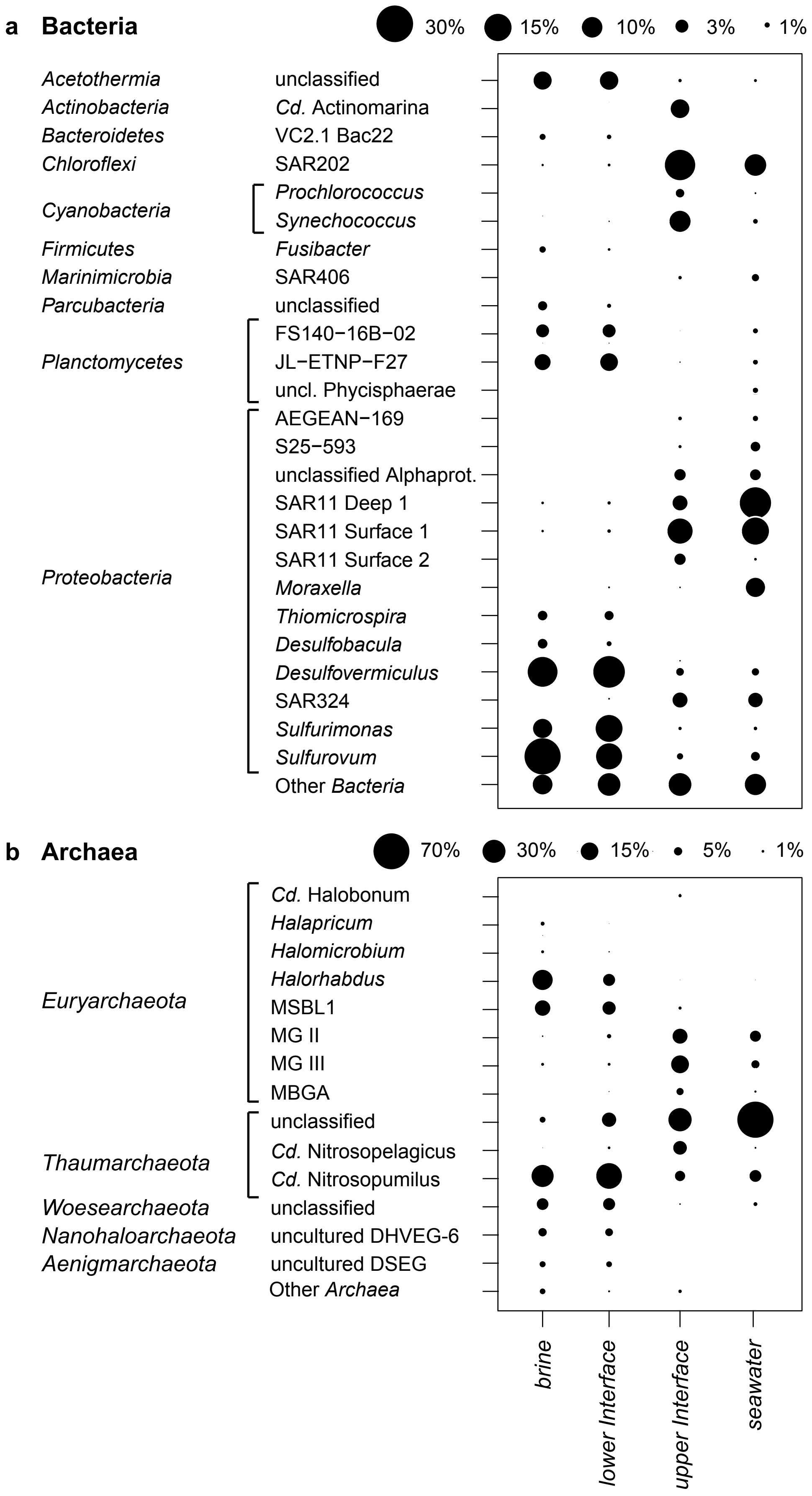
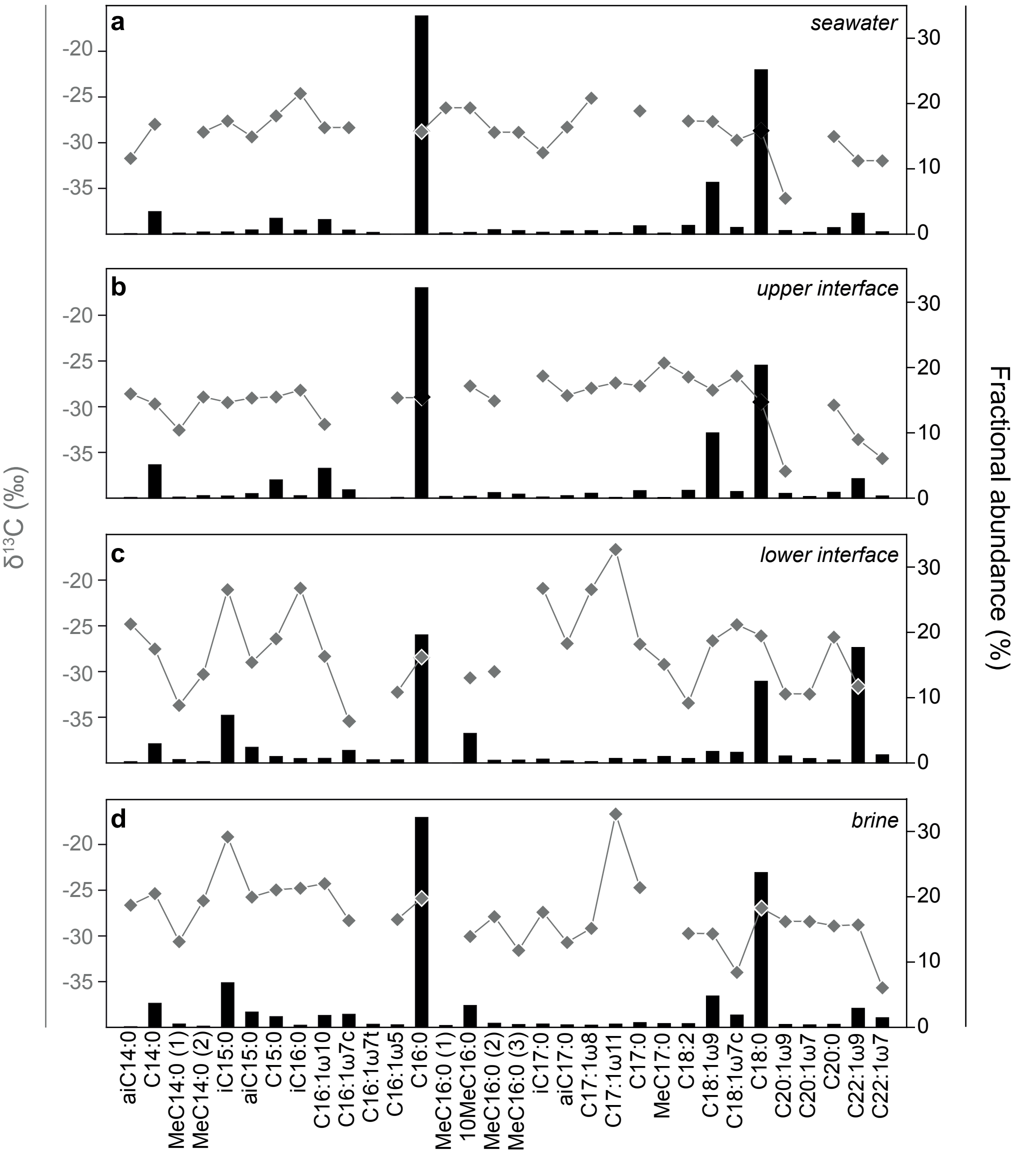

seawater
bottle 1
S5
S4
S3
S2
S1
~3335.5 mbsl
upper interface
bottle 2
S5
S4
S3
S2
S1
~3336.5 mbsl
lower interface
~3337.5 mbsl
~3339.0 mbsl
brine
~3345.0 mbsl
seawater sample
upper interface sample
lower interface sample
brine sample
Niskin bottles for biogeochemical analyses and rate mesurements
Niskin bottles for 16S rRNA and lipid biomarker analyses

Figure 2


Cl- (mol kg-1)
0.6 0.8 1 1.2 1.4 6.5 7
Na+ (mmol kg-1)
75 100 400 500
a
b
c
seawater
upper interface
lower interface
brine
SO4 2-
Cl-
Mg2+
Na+
Depth (mbsl)
3335.5 3336 3336.5 3337 3345 3360
30 40 50 60 140 180
SO4 2- (mmol kg-1)
0.2 0.4 0.6 3.8 4
Mg2+ (mol kg-1)
50 100 150 200
O2 (µmol kg-1)
NH4+ (µmol kg-1)
50 100 150 900 1000
δD-CH4 (‰)
-130 -120 -110
d
e
f
δ13C
δD
20 40 60 150 200
H2Stot (µmol kg-1)
5 10 25 50
CH4 (µmol kg-1)
-48 -46 -44 -42
δ13C-CH4 (‰)
g
h
i
5 15 25 250 500
SR (µmol kg-1 d-1)
20 40 60
MOx (nmol kg-1 d-1)
7.5 15 25
Biomass incorp. (%)


a Bacteria
30%
15%
10%
3%
1%
Acetothermia
unclassified
Actinobacteria
Cd. Actinomarina
Bacteroidetes
VC2.1 Bac22
Chloroflexi
SAR202
Cyanobacteria
Prochlorococcus
Synechococcus
Firmicutes
Fusibacter
Marinimicrobia
SAR406
Parcubacteria
unclassified
Planctomycetes
FS140−16B−02
JL−ETNP−F27
uncl. Phycisphaerae
Proteobacteria
AEGEAN−169
S25−593
unclassified Alphaprot.
SAR11 Deep 1
SAR11 Surface 1
SAR11 Surface 2
Moraxella
Thiomicrospira
Desulfobacula
Desulfovermiculus
SAR324
Sulfurimonas
Sulfurovum
Other Bacteria
b Archaea
70%
30%
15%
5%
1%
Euryarchaeota
Cd. Halobonum
Halapricum
Halomicrobium
Halorhabdus
MSBL1
MG II
MG III
MBGA
Thaumarchaeota
unclassified
Cd. Nitrosopelagicus
Cd. Nitrosopumilus
Woesearchaeota
unclassified
Nanohaloarchaeota
uncultured DHVEG-6
Aenigmarchaeota
uncultured DSEG
Other Archaea
brine
lower Interface
upper Interface
seawater


a
seawater
b
upper interface
c
lower interface
d
brine
δ13C (‰)
-20
-25
-30
-35
Fractional abundance (%)
30
20
10
0
aiC14:0
C14:0
MeC14:0 (1)
MeC14:0 (2)
iC15:0
aiC15:0
C15:0
iC16:0
C16:1ω10
C16:1ω7c
C16:1ω7t
C16:1ω5
C16:0
MeC16:0 (1)
10MeC16:0
MeC16:0 (2)
MeC16:0 (3)
iC17:0
aiC17:0
C17:1ω8
C17:1ω11
C17:0
MeC17:0
C18:2
C18:1ω9
C18:1ω7c
C18:0
C20:1ω9
C20:1ω7
C20:0
C22:1ω9
C22:1ω7

## Supplementary methods

### 1 Bathymetric mapping

Morphobathymetric data were collected with the Simrad EM122 Multibeam Echosounder (12kHz) onboard R/V Meteor. Due to its low frequency, the EM122 allows for a vertical resolution of ~0.4% of the investigated depths (i.e., <12m at >3000 m water depth). The acquisition was performed in geographic coordinates (Lat/Long, datum WGS84) with the support of the SIS Navigation System. Data processing and export of the base Digital Terrain Model (XYZ data grid, with a 30m cell size resolution) was realized with the CARIS HIPS and SIPS software, and subsequently mapped with Surfer® and Global Mapper. All data were projected in UTM (WGS84, 34N) coordinate system.

### 2 Geochemical analyses

$CH_4$, dissolved total sulfide ($H_2S_{tot} = H_2S + HS^- + S_2^-$, hereafter 'sulfide'), dissolved inorganic carbon (DIC) and concentrations of $CH_4$, higher hydrocarbons, dissolved $O_2$ and $NH_4^+$ were measured onboard, whereas $SO_4^{2-}$ concentration, major elements, and stable isotope measurements ($\delta^{13}C$-$CH_4$, $\delta D$-$CH_4$, $\delta^{13}C$-DIC) were conducted onshore. Concentrations of $CH_4$ and higher hydrocarbons were determined with a headspace technique and gas chromatography with flame ionization detection (Mastalerz et al. 2009). Sulfide, $NH_4^+$ and DIC were quantified using a TRAACS800 continuous flow analyser according to Grasshoff et al. (1999; sulfide, $NH_4^+$) and Stoll et al. (2001; DIC). Oxygen concentrations were measured by Winkler titration (Grasshoff et al. 1999). All measurements were carried out in technical triplicates, yielding analytical errors (standard deviation) of <0.5% for $O_2$ and DIC and <2% for $NH_4^+$ and sulfide. Water samples for $SO_4^{2-}$-measurements were acidified onboard and subsequently purged with $N_2$-gas inside an anoxic glovebox in order to remove all sulfide. Total $SO_4^{2-}$ was then measured onshore using an ICP-AES (Stefansson et al. 2007). Major elements were diluted to fall in the range of ~3.5 mg $L^{-1}$ and concentrations determined with an ICP-AES (Stefansson et al. 2007). The stable carbon and hydrogen isotope composition of $CH_4$ was analysed onshore using a gas chromatograph coupled to an isotope ratio mass spectrometer (GC–IRMS; Agilent HP 6890 GC connected to a Finnigan Deltaplus XP IRMS; Luong et al., 2013). Gaseous compounds were separated on a HPPLOT column (D: 32 m, 0.32 mm i.d. 10 $\mu$m d.f.), using the following temperature program: 2 min hold time at 40 °C, followed by a temperature ramp (12 °C $min^{-1}$ to 140 °C), and a final hold time of 3 min (after Mastalerz et al. 2009). $\delta^{13}C$ and $\delta D$ values are reported as ‰-deviation relative to the VPDB and SMOW standards, respectively. $\delta^{13}C$-DIC values were measured using an elemental analyser-continuous flow isotope ratio-mass spectrometry setup (St-Jean 2003) with a Fisons 1500 NCS elemental analyser coupled to a Finnigan Mat Delta Plus mass spectrometer. Analytical precision based on routine analysis of internal laboratory reference material was ±0.15 ‰.

In brine systems, $Cl^-$ can be used as a conservative tracer for mixing of the brine and seawater (de Lange et al. 1990; van der Wielen et al. 2005). The exact depths of the samples from the different Niskin bottles taken along the seawater-brine interface were aligned considering the respective Cl- concentrations.

## 3 Radio-tracer amounts used for ex-situ incubations

For methane oxidation rate measurements, 10 µl of $^{14}$C-labelled aqueous methane solution (4 kBq, ~150 nmol $CH_4$, American Radiolabeled Chemicals, USA) were injected in each incubation vial. For sulfate reduction rate measurements, 25 µl of $^{35}$S-labelled aqueous sulfate solution (20 kBq, American Radiolabeled Chemicals, USA) were injected in each incubation vial.

## 4 Incorporation of $CH_4$-carbon into biomass

Incorporation of $CH_4$-carbon into biomass was determined as described previously (Blees et al. 2014, Steinle et al. 2016). In brief, methane oxidation rate incubations were stopped by fixing the samples in butyl rubber sealed glass bottles with 1 g of solid NaOH, and bottles were stored at room temperature until determination of $CH_4$-oxidation rates onshore. First, $^{14}CH_4$ was combusted (Treude et al. 2005), followed by $^{14}CO_2$-acidification and determination of residual activity in the remaining sample (Blees et al. 2014). $CH_4$-oxidation rates were assessed by combustion of unreacted $^{14}CH_4$ (Treude et al. 2005), followed by quantification of produced $^{14}CO_2$ by acidification, and determination of residual activity in the remaining sample (Blees et al. 2014). Activities were determined by liquid scintillation and corrected for (insubstantial) fractional turnover (~0.1 – 0.01%) in killed controls (addition of 100 µl saturated $HgCl_2$ solution). The first-order rate constant (k) was calculated from the fractional tracer turnover with consideration of $^{14}$C-label transfer into biomass:

$$k_{MOx} = \frac{(A_{CO_2} + A_R)}{(A_{CO_2} + A_R + A_{CH_4})} \times \frac{1}{t}$$

where $A_{CH_4}$ is the activity of remaining $^{14}C\text{-}CH_4$ after incubation, $A_{CO_2}$ is the activity of the generated $CO_2$, $A_R$ is the rest activity (biomass and potentially non-carbonate intermediates), and t is the incubation time. The MOx rates ($r_{MOx}$) were then calculated assuming first order kinetics:

$$r_{MOx} = k \times [CH_4]_{initial}$$

where $[CH_4]_{initial}$ is the methane concentration at the beginning of the incubation. Methane-carbon incorporated into biomass was calculated from $A_R$ and $A_{CO_2}$ as described in Blees et al. (2014) and Steinle et al. (2017):

$$Biomass\_incorp.(\%) = \frac{A_R}{(A_{CO_2} + A_R)}$$

The values shown in Fig. 3i is hence the fraction of $^{14}$C-carbon incorporated into biomass compared to the total. $^{14}C\text{-}CH_4$ turned over.

## 5 Biomarker analyses

Lipid extraction was done according to Elvert et al. (2003). In short, we obtained a total lipid extract (TLE) by ultrasonication of the filters with solvents in decreasing polarity: (1) dichloromethane (DCM):methanol (MeOH) 1:2; (2) DCM:MeOH 2:1; and (3, 4) DCM. We added an additional ultrasonication step with MeOH:$H_2O$ 1:3 to extract water-soluble compounds. The TLE was further separated into a hydrocarbon, keton, alcohol, and polar fatty acid (FA) fractions. FA (comprising lipid-derived and free fatty acids) and alcohols were derivatised into FA methyl esters with

methanolic $BF_3$ and trimethylsilyl ethers with bis(trimethylsilyl)trifluoracetamide using the methods described previously (Elvert et al. 2003, Niemann et al. 2005). The positions of FA methyl ester double bonds were determined through analysis of their dimethyl–disulfide adducts (Nichols et al. 1986, Moss and Lambert-Fair 1989).
These fractions were then analyzed with a gas chromatograph (GC) linked either to a mass spectrometer, a flame-ionization detector, or an isotope ratio mass spectrometer, as described in Blees et al. (2014). The abundance of different compounds was determined with a GC (Trace GC Ultra, Thermo Scientific equipped with a split-splitless injector operated in splitless mode at 300°C, capillary column (Rxi®-5 ms, 60 m × 0.25 mm inner diameter × 0.25 μm film thickness), constant helium flow of 1 mL $min^{-1}$) linked to a flame ionization detector. The following temperature program was used: initial oven temperature 50°C, held for 2 min, increased to 140°C at a rate of 10°C $min^{-1}$, then to 300°C at 4°C $min^{-1}$, held at 300°C for 63 min. Internal standards were used to calculate concentrations and concentrations were corrected for the introduction of carbon atoms. Compounds were identified by GC-mass spectrometry with electron ionization (Thermo Scientific DSQII Dual Stage Quadrupole). Finally, compound-specific stable carbon isotope ratios were determined using a GC-IRMS (Delta V Advantage, Thermo Scientific). $\delta^{13}C$-values were corrected for the introduction of carbon atoms (Blees et al. 2014).

## Supplementary References

Blees J, Niemann H, Wenk CB, Zopfi J, Schubert CJ, Kirf MK, et al. Micro-aerobic bacterial methane oxidation in the chemocline and anoxic water column of deep south-Alpine Lake Lugano (Switzerland). Limnol Oceanogr. 2014;59:311-324.

De Lange GJ, Catalano G, Klinkhammer GP, Luther GW. The interface between oxic seawater and the anoxic Bannock Brine; its sharpness and the consequences for the redox-related cycling of Mn and Ba. Mar Chem. 1990;31:205-217.

Elvert M, Boetius A, Knittel K, Jørgensen BB. Characterization of specific membrane fatty acids as chemotaxonomic markers for sulfate-reducing bacteria involved in anaerobic oxidation of methane. Geomicrobiol J. 2003;20:403-419.

Grasshoff K, Kremling K, Ehrhardt M. Methods of seawater analysis. Weinheim: Wiley-VCH. 1999.

Luong J, Gras R, Cortes HJ, Shellie RA. Determination of trace ethylene glycol in industrial solvents and lubricants using phenyl boronic acid derivatization and multidimensional gas chromatography. Anal Chim Ac. 2013;805:101-106.

Mastalerz V, de Lange GJ, Dählmann A. Differential aerobic and anaerobic oxidation of hydrocarbon gases discharged at mud volcanoes in the Nile deep-sea fan. Geochim Cosmochim Ac. 2009;73: 3849-3863.

Niemann H, Elvert M, Hovland M, Orcutt B, Judd A, Suck I, et al. Methane emission and consumption at a North Sea gas seep (Tommeliten area). Biogeosciences. 2005;2:335-351.

Stefansson A, Gunnarsson I, Giroud N. New methods for the direct determination of dissolved inorganic, organic and total carbon in natural waters by reagent-free ion chromatography and inductively coupled plasma atomic emission spectrometry. Anal Chim Ac. 2007;582: 69-74.

Stoll MH, Bakker K, Nobbe GH, Haese RR. Continuous-flow analysis of dissolved inorganic carbon content in seawater. Anal Chem. 2001;73: 4111-4116.

Steinle L, Schmidt M, Bryant L, Haeckel M, Linke P, Sommer S, et al. Linked sediment and water-column methanotrophy at a man-made gas blowout in the North Sea: Implications for methane budgeting in seasonally stratified shallow seas. Limnol Oceanogr. 2016;61:S367–S386. doi: 10.1002/lno.10388.

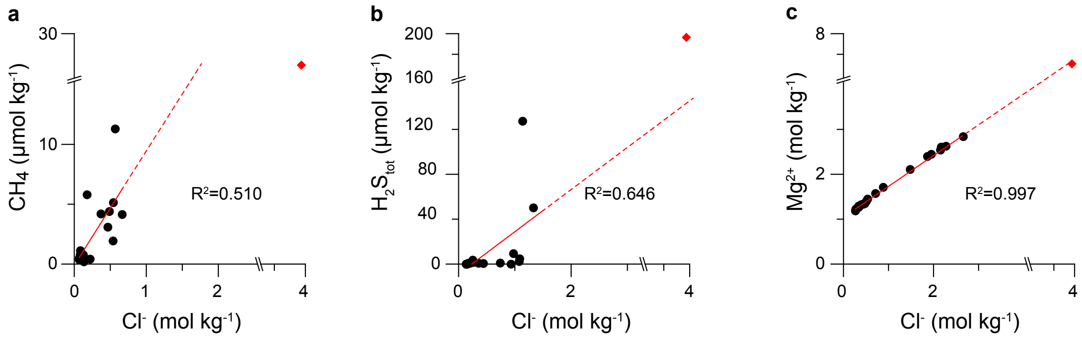
Steinle L, Maltby L, Engbersen N, Zopfi J, Bange HW, Lehmann MF, et al. Effects of low oxygen concentrations on aerobic methane oxidation in seasonally hypoxic coastal waters. Biogeosciences 2017;14:1631–1645.

St-Jean, G. Automated quantitative and isotopic (13C) analysis of dissolved inorganic carbon and dissolved organic carbon in continuous-flow using a total organic carbon analyser. Rapid Commun Mass Spectrom. 2003;17:419–428. doi:10.1002/rcm.926.

Treude T, Boetius A, Knittel K, Wallmann K, Jørgensen BB. Anaerobic oxidation of methane above gas hydrates at Hydrate Ridge, NE Pacific Ocean. Mar Ecol-Prog Ser. 2003;264:1-14.

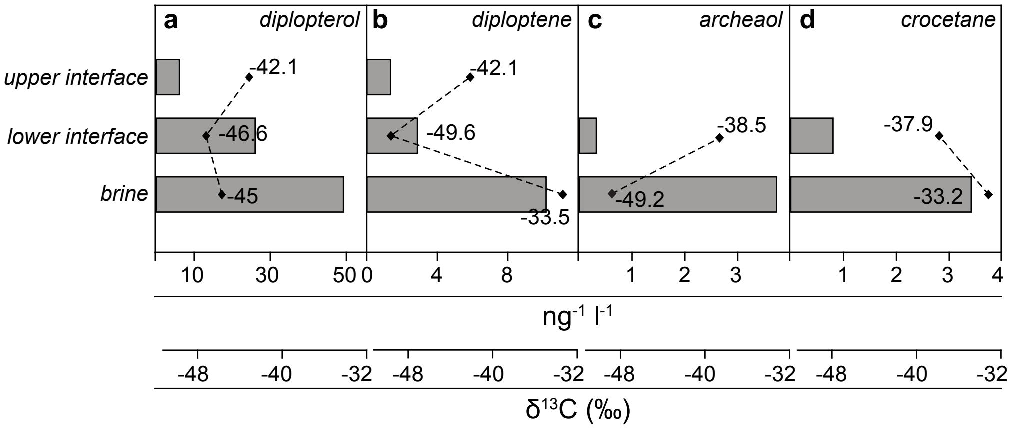
van der Wielen PW, Bolhuis H, Borin S, Daffonchio D, Corselli C, Giuliano L, et al. The enigma of prokaryotic life in deep hypersaline anoxic basins. Science. 2005;307: 121-123.

# Supplementary Figure 1



**Linear correlation of $CH_4$, $H_2S$, and $Mg^{2+}$ with $Cl^-$.** Non-conservative mixing behaviour (i.e., sources or sinks) of a given solute in a seawater-brine interface can be evidenced as a deviation from a linear correlation of solute and chloride concentrations. Black dots denote discrete samples recovered from the seawater-brine interface, red diamonds represent brine samples. Red lines show the linear correlation of solute and $Cl^-$ in the seawater brine interface, and red dashed lines the interpolation of the linear correlation towards the brine values. a) $CH_4$ vs. $Cl^-$ concentrations and b) $H_2S_{tot}$ vs. $Cl^-$ concentration show a strong deviation from a linear relationship, which suggests net $CH_4$ and $H_2S_{tot}$ removal within the interface. c) For $Mg^{2+}$ vs. $Cl^-$, a clear linear relationship is observed ($R^2 = 0.997$), highlighting the conservative mixing character of $Mg^{2+}$.

## Supplementary Figure 2



Concentrations and stable carbon isotope ratios of specific lipid biomarkers across the seawater-brine interface. **(a)** Diplopterol, **(b)** diploptene, **(c)** archaeol, **(d)** crocetane. In the seawater fraction, only traces of diplopterol and diploptene were detected, but none of the other compounds was present. $\delta^{13}C$-values are indicated.

## Supplementary Table 1

PCR primers used for amplification of 16S rRNA genes.

| Primer | Sequence |
|---|---|
| Bakt_341F | 5’ CCTACGGGNGGCWGCAG 3’ |
| Bakt_785R | 5’ GACTACHVGGGTATCTAATCC 3’ |
| ARCH340F | 5’ CCTAYGGGGYGCASCAG 3’ |
| ARCH1000R | 5’ GGCCATGCACYWCYTCTC 3’ |
| ARCH340F-ANME-1 | 5’ CCTACGGGACGCATCAG 3’ |
| ARCH1000R-ANME1 | 5’ GGCCATGCGCCACCTCTC 3’ |
| ARCH1000R-KOR | 5’ GGCCATGCACCACCCCTC 3’ |

## Supplementary Table 2

PCR conditions used in this study. a) Composition of PCR mix. b) PCR programm.

a)

| Compound | Amount for one PCR reaction |
|---|---|
| DNA | ca. 1 ng |
| PCR buffer | 1x |
| dNTPs (each) | 200 µM |
| Primer forward | 0.5 µM |
| Primer reverse | 0.5 µM |
| Taq polymerase (TaKaRa, Germany) | 1.5 U |

b)

| Step | Temperature | Time | |
|---|---|---|---|
| initial denaturation | 95°C | 2 min | |
| denaturation | 94°C | 1 min | 39 cycles |
| annealing | 55°C | 1 min | |
| elongation | 72°C | 2 min | |
| final elongation | 74°C | 10 min | |

**Supplementary Table 3**

Classification of archaeal partial 16S rRNA gene sequences according to SILVAngs (release 128, Sept. 2016). Given are the total number of sequences assigned to each taxonomic clade.

| Genus | **Brine** | **Lower interface** |
|---|---|---|
| Bacteria;Acetothermia;unclassified;unclassified;unclassified;unclassified | 3953 | 2402 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 11;unclassified;unclassified | 0 | 0 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 13;unclassified;unclassified | 0 | 0 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 21;unclassified;unclassified | 2 | 4 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 3;PAUC26f;unclassified | 0 | 1 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 5;unclassified;unclassified | 0 | 0 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 6;unclassified;unclassified | 3 | 12 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 9;unclassified;unclassified | 0 | 0 |
| Bacteria;Acidobacteria;Subgroup 26;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Acidimicrobiaceae;uncultured | 0 | 2 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;OM1 clade;unclassified | 53 | 21 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;OM1 clade;Candidatus Actinomarina | 30 | 27 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Sva0996 marine group;unclassified | 107 | 107 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;uncultured;unclassified | 36 | 32 |
| Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces | 0 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;unclassified | 2 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;Corynebacterium 1 | 2 | 2 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;uncultured | 0 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Mycobacteriaceae;Mycobacterium | 3 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Frankiales;Geodermatophilaceae;Blastococcus | 0 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Dermabacteraceae;Brachybacterium | 0 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Leifsonia | 0 | 2 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Lysinimonas | 0 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Microbacterium | 1 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Micrococcus | 2 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Rothia | 2 | 1 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Yaniella | 0 | 3 |
| Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Nocardioidaceae;Aeromicrobium | 0 | 0 |
| Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Propionibacteriaceae;Propionibacterium | 72 | 68 |
| Bacteria;Actinobacteria;OPB41;unclassified;unclassified;unclassified | 1 | 0 |
| Bacteria;Actinobacteria;Thermoleophilia;Gaiellales;uncultured;unclassified | 0 | 1 |
| Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;480-2;unclassified | 0 | 2 |
| Bacteria;Aerophobetes;unclassified;unclassified;unclassified;unclassified | 5 | 0 |
| Bacteria;Aminicenantes;unclassified;unclassified;unclassified;unclassified | 1 | 0 |
| Bacteria;Armatimonadetes;unclassified;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Atribacteria;unclassified;unclassified;unclassified;unclassified | 18 | 4 |
| Bacteria;Bacteroidetes;Bacteroidetes BD2-2;unclassified;unclassified;unclassified | 20 | 11 |
| Bacteria;Bacteroidetes;Bacteroidetes VC2.1 Bac22;unclassified;unclassified;unclassified | 603 | 229 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Marinifilum | 0 | 0 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured | 117 | 73 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Petrimonas | 0 | 7 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Alloprevotella | 0 | 3 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidia Incertae Sedis;Draconibacteriaceae;Tangfeifania | 11 | 2 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidia Incertae Sedis;Prolixibacteraceae;Prolixibacter | 2 | 0 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Hymenobacter | 0 | 1 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Candidatus Amoebophilus | 0 | 0 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Ekhidna | 0 | 1 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Fabibacter | 0 | 3 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Marinoscillum | 2 | 9 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Rapidithrix | 0 | 1 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Reichenbachiella | 1 | 0 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;uncultured | 11 | 10 |
| Bacteria;Bacteroidetes;Cytophagia;Order III;Unknown Family;Balneola | 0 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Crocinitomix | 3 | 2 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Fluviicola | 3 | 9 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;NS10 marine group | 1 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Owenweeksia | 1 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Salinirepens | 0 | 5 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;uncultured | 24 | 54 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Aquibacter | 11 | 22 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Aureicoccus | 1 | 2 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Chryseobacterium | 1 | 8 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Elizabethkingia | 0 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Flavobacterium | 5 | 1 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Gilvibacter | 1 | 4 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Gramella | 0 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Leeuwenhoekiella | 0 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Lutibacter | 2 | 5 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Lutimonas | 1 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;NS2b marine group | 1 | 4 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;NS4 marine group | 1 | 3 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;NS5 marine group | 2 | 0 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Polaribacter | 40 | 101 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Pseudofulvibacter | 6 | 4 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Psychroserpens | 0 | 3 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Sufflavibacter | 16 | 67 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Tenacibaculum | 19 | 73 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Wenyingzhuangia | 15 | 40 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;uncultured | 2 | 6 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;NS7 marine group;unclassified | 3 | 4 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;NS9 marine group;unclassified | 6 | 8 |
| Bacteria;Bacteroidetes;SB-5;unclassified;unclassified;unclassified | 1 | 1 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;B01R012;unclassified | 4 | 6 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;Hydrotalea | 0 | 0 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;Sediminibacterium | 0 | 3 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;uncultured | 0 | 0 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;E6aC02;unclassified | 47 | 21 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;KD1-131;unclassified | 3 | 2 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;NS11-12 marine group;unclassified | 5 | 2 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;ST-12K33;unclassified | 1 | 0 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Saprospiraceae;uncultured | 3 | 9 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;uncultured | 1 | 0 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;WCHB1-69;unclassified | 27 | 11 |
| Bacteria;Candidate division OP3;unclassified;unclassified;unclassified;unclassified | 16 | 8 |
| Bacteria;Candidate division SR1;unclassified;unclassified;unclassified;unclassified | 375 | 166 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Chlamydiaceae;unclassified | 1 | 0 |

| | | |
|---|---|---|
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Chlamydiales Incertae Sedis;unclassified | 0 | 0 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Parachlamydia | 1 | 3 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus Fritschea | 2 | 3 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus Renichlamydia | 0 | 1 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Simkania | 1 | 2 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;uncultured | 2 | 2 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;cvE6;unclassified | 0 | 1 |
| Bacteria;Chlorobi;Chlorobia;Chlorobiales;Chlorobiaceae;Chlorobium | 2 | 2 |
| Bacteria;Chlorobi;Ignavibacteria;Ignavibacteriales;PHOS-HE36;unclassified | 0 | 0 |
| Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermomarinilinea | 4 | 0 |
| Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured | 0 | 1 |
| Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured | 0 | 0 |
| Bacteria;Chloroflexi;Dehalococcoidia;FW22;unclassified;unclassified | 1 | 0 |
| Bacteria;Chloroflexi;Dehalococcoidia;GIF3;unclassified;unclassified | 1 | 1 |
| Bacteria;Chloroflexi;Dehalococcoidia;GIF9;unclassified;unclassified | 5 | 2 |
| Bacteria;Chloroflexi;Dehalococcoidia;MSBL5;unclassified;unclassified | 76 | 31 |
| Bacteria;Chloroflexi;JG30-KF-CM66;unclassified;unclassified;unclassified | 4 | 4 |
| Bacteria;Chloroflexi;KD4-96;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Chloroflexi;S085;unclassified;unclassified;unclassified | 2 | 4 |
| Bacteria;Chloroflexi;SAR202 clade;unclassified;unclassified;unclassified | 165 | 123 |
| Bacteria;Chloroflexi;TK10;unclassified;unclassified;unclassified | 0 | 3 |
| Bacteria;Chloroflexi;uncultured;unclassified;unclassified;unclassified | 3 | 1 |
| Bacteria;Cloacimonetes;MSBL2;unclassified;unclassified;unclassified | 125 | 9 |
| Bacteria;Cloacimonetes;MSBL8;unclassified;unclassified;unclassified | 131 | 30 |
| Bacteria;Cyanobacteria;Chloroplast;unclassified;unclassified;unclassified | 8 | 17 |
| Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI; | 0 | 1 |
| Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI;Prochlorococcus | 13 | 10 |
| Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI;Synechococcus | 64 | 58 |
| Bacteria;Cyanobacteria;ML635J-21;unclassified;unclassified;unclassified | 3 | 1 |
| Bacteria;Cyanobacteria;Melainabacteria;Caenarcaniphilales;unclassified;unclassified | 2 | 0 |
| Bacteria;Cyanobacteria;Melainabacteria;Obscuribacterales;unclassified;unclassified | 0 | 1 |
| Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Trueperaceae;Truepera | 0 | 0 |
| Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter | 0 | 0 |
| Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;uncultured | 1 | 3 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus | 1 | 0 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Family XI;Gemella | 1 | 0 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus | 0 | 0 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus | 4 | 5 |
| Bacteria;Firmicutes;Bacilli;Lactobacillales;P5D1-392;unclassified | 0 | 0 |
| Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae 1;Fonticella | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Family XI;Finegoldia | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Family XI;Peptoniphilus | 0 | 1 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Family XII;Fusibacter | 663 | 114 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-004 | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-008 | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;uncultured | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Halanaerobiales;64K2;unclassified | 19 | 6 |
| Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halanaerobiaceae;Halanaerobium | 5 | 0 |
| Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halanaerobiaceae;Halocella | 1 | 0 |
| Bacteria;Firmicutes;Clostridia;Natranaerobiales;Natranaerobiaceae;uncultured | 3 | 0 |
| Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Pelosinus | 0 | 0 |
| Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Veillonella | 0 | 0 |
| Bacteria;Firmicutes;OPB54;unclassified;unclassified;unclassified | 1 | 1 |
| Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Fusobacterium | 0 | 0 |
| Bacteria;Gemmatimonadetes;Gemmatimonadetes;BD2-11 terrestrial group;unclassified;unclassified | 3 | 0 |
| Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas | 0 | 0 |
| Bacteria;Gemmatimonadetes;Gemmatimonadetes;PAUC43f marine benthic group;unclassified;unclassified | 1 | 0 |
| Bacteria;Gracilibacteria;unclassified;unclassified;unclassified;unclassified | 28 | 34 |
| Bacteria;Hyd24-12;unclassified;unclassified;unclassified;unclassified | 57 | 23 |
| Bacteria;Hydrogenedentes;unclassified;unclassified;unclassified;unclassified | 0 | 1 |
| Bacteria;LCP-89;unclassified;unclassified;unclassified;unclassified | 3 | 4 |
| Bacteria;Latescibacteria;unclassified;unclassified;unclassified;unclassified | 70 | 78 |
| Bacteria;Lentisphaerae;BS5;unclassified;unclassified;unclassified | 1 | 0 |
| Bacteria;Lentisphaerae;LD1-PA26;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Lentisphaerae;LD1-PB3;unclassified;unclassified;unclassified | 47 | 53 |
| Bacteria;Lentisphaerae;Lentisphaeria;Lentisphaerales;Lentisphaeraceae;Lentisphaera | 297 | 259 |
| Bacteria;Lentisphaerae;Oligosphaeria;unclassified;unclassified;unclassified | 9 | 8 |
| Bacteria;Lentisphaerae;Oligosphaeria;Oligosphaerales;unclassified;unclassified | 4 | 0 |
| Bacteria;Lentisphaerae;R76-B128;unclassified;unclassified;unclassified | 16 | 1 |
| Bacteria;Lentisphaerae;WCHB1-41;unclassified;unclassified;unclassified | 2 | 1 |
| Bacteria;Marinimicrobia (SAR406 clade);unclassified;unclassified;unclassified;unclassified | 54 | 43 |
| Bacteria;Microgenomates;unclassified;unclassified;unclassified;unclassified | 21 | 6 |
| Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Leptospirillum | 0 | 0 |
| Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira | 3 | 1 |
| Bacteria;Omnitrophica;NPL-UPA2;unclassified;unclassified;unclassified | 2 | 0 |
| Bacteria;PAUC34f;unclassified;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Parcubacteria;unclassified;unclassified;unclassified;unclassified | 1196 | 201 |
| Bacteria;Parcubacteria;Parcubacteria Incertae Sedis;Unknown Order;Unknown Family;Candidatus Paceibacter | 107 | 2 |
| Bacteria;Planctomycetes;028H05-P-BN-P5;unclassified;unclassified;unclassified | 0 | 2 |
| Bacteria;Planctomycetes;BD7-11;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Planctomycetes;C47;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Planctomycetes;MBMPE71;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Planctomycetes;OM190;unclassified;unclassified;unclassified | 71 | 169 |
| Bacteria;Planctomycetes;Phycisphaerae;C86;unclassified;unclassified | 0 | 0 |
| Bacteria;Planctomycetes;Phycisphaerae;MSBL9;unclassified;unclassified | 31 | 9 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;08D2Z94 hypersaline microbial mat group;unclassified | 0 | 1 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;AKAU3564 sediment group;unclassified | 0 | 1 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;ODP1230B30.02 sediment group;unclassified | 2 | 1 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;CL500-3 | 3 | 10 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;FS140-16B-02 marine group | 1697 | 1291 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;I-8 | 60 | 65 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;JL-ETNP-F27 | 3162 | 2235 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Phycisphaera | 2 | 0 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;SM1A02 | 1 | 3 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Urania-1B-19 marine sediment group | 196 | 260 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;uncultured | 13 | 10 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;SBYZ-1154;unclassified | 0 | 1 |
| Bacteria;Planctomycetes;Phycisphaerae;Pla1 lineage;unclassified;unclassified | 0 | 0 |

| | | |
|---|---|---|
| Bacteria;Planctomycetes;Phycisphaerae;SHA-43;unclassified;unclassified | 2 | 7 |
| Bacteria;Planctomycetes;Pla3 lineage;unclassified;unclassified;unclassified | 3 | 8 |
| Bacteria;Planctomycetes;Pla4 lineage;unclassified;unclassified;unclassified | 3 | 1 |
| Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae;Candidatus Scalindua | 1 | 0 |
| Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae;PB79 | 0 | 1 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula | 1 | 1 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Bythopirellula | 0 | 0 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata | 0 | 0 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir4 lineage | 10 | 19 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces | 398 | 204 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Rhodopirellula | 27 | 48 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured | 51 | 33 |
| Bacteria;Planctomycetes;SGST604;unclassified;unclassified;unclassified | 3 | 0 |
| Bacteria;Proteobacteria;AEGEAN-245;unclassified;unclassified;unclassified | 1 | 4 |
| Bacteria;Proteobacteria;ARKICE-90;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas | 0 | 2 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;Hyphomonas | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;uncultured | 2 | 4 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Kordiimonadales;Kordiimonadaceae;Kordiimonas | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Magnetococcales;Magnetococcaceae;Magnetococcus | 4 | 3 |
| Bacteria;Proteobacteria;Alphaproteobacteria;OCS116 clade;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Parvularculales;Parvularculaceae;Parvularcula | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;A0839;unclassified | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Aurantimonadaceae;Aurantimonas | 5 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Chelatococcus | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bosea | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bradyrhizobium | 4 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Hyphomicrobium | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;KF-JG30-B3;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae;Meganema | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae;Methylobacterium | 5 | 12 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Ahrensia | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Cohaesibacter | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Mesorhizobium | 2 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Nitratireductor | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rhizobium | 4 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales Incertae Sedis;Nordella | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales Incertae Sedis;Phreatobacter | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Anderseniella | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Rhodobium | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Variibacter | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;uncultured;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Amylibacter | 2 | 9 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Ascidiaceihabitans | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Defluviimonas | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Gemmobacter | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Jannaschia | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Nautella | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus | 3 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseobacter clade NAC11-7 lineage | 26 | 15 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseovarius | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rubellimicrobium | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Shimia | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Sulfitobacter | 2 | 2 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Thalassobius | 4 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Tropicibacter | 2 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;uncultured | 374 | 124 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AT-s3-44;unclassified | 2 | 3 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;DA111;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;AEGEAN-169 marine group | 13 | 11 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Defluviicoccus | 4 | 5 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Magnetospira | 1 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;OM75 clade | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Thalassospira | 0 | 4 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Tistrella | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;uncultured | 8 | 8 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillales Incertae Sedis;Candidatus Alysiosphaera | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillales Incertae Sedis;Reyranella | 2 | 4 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Holosporaceae;Holospora | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;LWSR-14;unclassified | 5 | 3 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Mitochondria;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;uncultured | 6 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiales Incertae Sedis;Candidatus Lariskella | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;S25-593;unclassified | 19 | 19 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;SAR116 clade;unclassified | 2 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;SAR116 clade;Candidatus Puniceispirillum | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;SHWN-night2;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;unclassified;unclassified | 38 | 25 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Deep 1;unclassified | 192 | 147 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 1;unclassified | 180 | 161 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 1;Candidatus Pelagibacter | 0 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 2;unclassified | 16 | 9 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 3;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 4;unclassified | 2 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SB1-18;unclassified;unclassified | 1 | 2 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sneathiellales;Sneathiellaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter | 1 | 0 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter | 8 | 1 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium | 0 | 3 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium | 0 | 2 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas | 11 | 28 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis | 2 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Achromobacter | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;MWH-UniP1 aquatic group | 0 | 0 |

| | | |
|---|---|---|
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus | 126 | 83 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Limnobacter | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia | 0 | 2 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax | 34 | 12 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium | 5 | 17 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Methylibium | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Piscinibacter | 0 | 1 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas | 0 | 1 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pseudorhodoferax | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Simplicispira | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xylophilus | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured | 2 | 2 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Candidatus Profftella | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia | 0 | 4 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Paucimonas | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;OM43 clade | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Neisseria | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas | 0 | 1 |
| Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azoarcus | 1 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira | 1 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Thauera | 1 | 0 |
| Bacteria;Proteobacteria;Betaproteobacteria;oca12;unclassified;unclassified | 0 | 1 |
| Bacteria;Proteobacteria;Deltaproteobacteria;43F-1404R;unclassified;unclassified | 0 | 3 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Halobacteriovorax | 1 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Peredibacter | 0 | 3 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;uncultured | 2 | 1 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;OM27 clade | 28 | 58 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfatiglans | 9 | 5 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;unclassified | 1 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacterium | 2 | 1 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacula | 1305 | 262 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfocella | 3 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum | 3 | 2 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;SEEP-SRB1 | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;uncultured | 111 | 18 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopila | 1 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;MSBL7 | 43 | 8 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;uncultured | 25 | 11 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;Candidatus Entotheonella | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;Nitrospina | 1 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfohalobiaceae;Desulfovermiculus | 9020 | 6600 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfurellales;Desulfurellaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas | 1 | 1 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;GR-WP33-58;unclassified | 18 | 33 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Sva1033;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;GR-WP33-30;unclassified;unclassified | 5 | 6 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;BIrii41;unclassified | 0 | 1 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Blfdi19;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Eel-36e1D6;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;MidBa8;unclassified | 1 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;P3OB-42;unclassified | 2 | 2 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Chondromyces | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;bacteriap25;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;unclassified;unclassified | 2 | 0 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;Oligoflexaceae;unclassified | 0 | 2 |
| Bacteria;Proteobacteria;Deltaproteobacteria;SAR324 clade(Marine group B);unclassified;unclassified | 64 | 70 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Sh765B-TzT-29;unclassified;unclassified | 32 | 10 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Sva0485;unclassified;unclassified | 17 | 3 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella | 0 | 0 |
| Bacteria;Proteobacteria;Elev-16S-509;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;BR36;unclassified;unclassified | 44 | 40 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter | 169 | 107 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas | 3710 | 4312 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurovum | 13265 | 4047 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;R103-B63;unclassified;unclassified | 121 | 44 |
| Bacteria;Proteobacteria;Gammaproteobacteria;1013-28-CG33;unclassified;unclassified | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Oceanimonas | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Aliiglaciecola | 0 | 4 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Alteromonas | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Paraglaciecola | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Salinimonas | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;uncultured | 2 | 12 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Colwelliaceae;Colwellia | 6 | 13 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Colwelliaceae;Thalassotalea | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Idiomarinaceae;Idiomarina | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Moritellaceae;Moritella | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Algicola | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Pseudoalteromonas | 9 | 13 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Psychromonadaceae;Psychromonas | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;Psychrobium | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;Shewanella | 0 | 7 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Arenicellales;Arenicellaceae;Arenicella | 0 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;B38;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Maricurvus | 1 | 3 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Pseudomaricurvus | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Simiduia | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Umboniibacter | 2 | 9 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;uncultured | 1 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Haliea | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;OM60(NOR5) clade | 2 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;C1-B045 | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;Porticoccus | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;SAR92 clade | 0 | 2 |

| | | |
|---|---|---|
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;BD1-7 clade | 2 | 10 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;Dasania | 0 | 7 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Nitrosococcus | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiohalobacter | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiorhodospira | 1 | 8 |
| Bacteria;Proteobacteria;Gammaproteobacteria;E01-9C-26 marine group;unclassified;unclassified | 16 | 16 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Citrobacter | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella | 4 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis;Unknown Family;Sedimenticola | 13 | 11 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis;Unknown Family;Thiohalomonas | 1 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;HOC36;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;KI89A clade;unclassified;unclassified | 0 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Coxiella | 7 | 11 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;uncultured | 29 | 12 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;ET-SHO;unclassified | 1 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;IheB2-23;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Marine Methylotrophic Group 2;unclassified | 8 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylococcus | 0 | 3 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Milano-WF1B-03;unclassified | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;NKB5;unclassified;unclassified | 9 | 7 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;CrystalBog021C3;unclassified | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;GSP65;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;JL-ETNP-Y6;unclassified | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Litoricolaceae;Litoricola | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;OM182 clade;unclassified | 1 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;ORI-860-26;unclassified | 4 | 4 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;unclassified | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Marinomonas | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Neptunomonas | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Oceanospirillum | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Pseudospirillum | 2 | 6 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oleiphilaceae;Oleiphilus | 0 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SAR86 clade;unclassified | 9 | 6 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SS1-B-06-26;unclassified | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SUP05 cluster;unclassified | 7 | 6 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;V1F82b;unclassified | 7 | 5 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;ZD0405;unclassified | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Order Incertae Sedis;Family Incertae Sedis;Marinicella | 0 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;PYR10d3;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Haemophilus | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter | 15 | 15 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Moraxella | 60 | 77 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter | 1 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas | 4 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Salinisphaerales;Salinisphaeraceae;ZD0417 marine group | 5 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;unclassified;unclassified | 1 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Cycloclasticus | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Galenea | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Hydrogenovibrio | 2 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Thiomicrospira | 1275 | 692 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;endosymbionts | 9 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;uncultured | 7 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thiothrix | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;uncultured | 4 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichales Incertae Sedis;Caedibacter | 2 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichales Incertae Sedis;Candidatus Endoecteinascidia | 2 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Aliivibrio | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Catenococcus | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Enterovibrio | 1 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Photobacterium | 1 | 2 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio | 8 | 15 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;uncultured | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;JTB255 marine benthic group;unclassified | 12 | 13 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Solimonadaceae;uncultured | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter | 0 | 0 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas | 0 | 4 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;uncultured | 0 | 1 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;uncultured;unclassified | 5 | 2 |
| Bacteria;Proteobacteria;JTB23;unclassified;unclassified;unclassified | 5 | 7 |
| Bacteria;Proteobacteria;Proteobacteria Incertae Sedis;Unknown Order;Unknown Family;Candidatus Thiobios | 0 | 0 |
| Bacteria;Proteobacteria;SC3-20;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Proteobacteria;SPOTSOCT00m83;unclassified;unclassified;unclassified | 3 | 5 |
| Bacteria;Proteobacteria;TA18;unclassified;unclassified;unclassified | 1 | 4 |
| Bacteria;Proteobacteria;Zetaproteobacteria;Mariprofundales;Mariprofundaceae;Mariprofundus | 0 | 0 |
| Bacteria;Saccharibacteria;unclassified;unclassified;unclassified;unclassified | 0 | 0 |
| Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta 2 | 1 | 2 |
| Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured | 1 | 0 |
| Bacteria;TA06;unclassified;unclassified;unclassified;unclassified | 1 | 0 |
| Bacteria;TM6;unclassified;unclassified;unclassified;unclassified | 7 | 3 |
| Bacteria;Tenericutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;Mycoplasma | 3 | 4 |
| Bacteria;Tenericutes;Mollicutes;NB1-n;unclassified;unclassified | 2 | 0 |
| Bacteria;Verrucomicrobia;Arctic97B-4 marine group;unclassified;unclassified;unclassified | 0 | 3 |
| Bacteria;Verrucomicrobia;OPB35 soil group;unclassified;unclassified;unclassified | 0 | 1 |
| Bacteria;Verrucomicrobia;Opitutae;A714019;unclassified;unclassified | 0 | 0 |
| Bacteria;Verrucomicrobia;Opitutae;MB11C04 marine group;unclassified;unclassified | 1 | 1 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Cerasicoccus | 0 | 0 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Coraliomargarita | 1 | 5 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Lentimonas | 0 | 0 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Pelagicoccus | 0 | 0 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;marine group | 4 | 2 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;uncultured | 0 | 0 |
| Bacteria;Verrucomicrobia;Opitutae;RS-B22;unclassified;unclassified | 0 | 0 |
| Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;unclassified | 0 | 0 |
| Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Roseibacillus | 1 | 0 |
| No Relative (according to SILVA ngs classification) | 2217 | 529 |

| | | |
|---|---|---|
| Total sequences | 47646 | 27231 |
| **Total sequences excluding "No relative"** | **45429** | **26702** |

**Supplementary Table 4**

Classification of bacterial partial 16S rRNA gene sequences according to SILVAngs (release 128, Sept. 2016). Given is the relative contribution of each taxonomic clade to total sequences. Sequences classified as "no relatives" were excluded from the analysis.

| | **Brine** | **Lower interface** |
|---|---|---|
| Bacteria;Acetothermia;unclassified;unclassified;unclassified;unclassified | 8.701 | 8.996 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 11;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 13;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 21;unclassified;unclassified | 0.004 | 0.015 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 3;PAUC26f;unclassified | 0.000 | 0.004 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 5;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 6;unclassified;unclassified | 0.007 | 0.045 |
| Bacteria;Acidobacteria;Acidobacteria;Subgroup 9;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Acidobacteria;Subgroup 26;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Acidimicrobiaceae;uncultured | 0.000 | 0.007 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;OM1 clade;unclassified | 0.117 | 0.079 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;OM1 clade;Candidatus Actinomarina | 0.066 | 0.101 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Sva0996 marine group;unclassified | 0.236 | 0.401 |
| Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;uncultured;unclassified | 0.079 | 0.120 |
| Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;unclassified | 0.004 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;Corynebacterium 1 | 0.004 | 0.007 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Mycobacteriaceae;Mycobacterium | 0.007 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Frankiales;Geodermatophilaceae;Blastococcus | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Dermabacteraceae;Brachybacterium | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Leifsonia | 0.000 | 0.007 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Lysinimonas | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Microbacterium | 0.002 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Micrococcus | 0.004 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Rothia | 0.004 | 0.004 |
| Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Yaniella | 0.000 | 0.011 |
| Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Nocardioidaceae;Aeromicrobium | 0.000 | 0.000 |
| Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Propionibacteriaceae;Propionibacterium | 0.158 | 0.255 |
| Bacteria;Actinobacteria;OPB41;unclassified;unclassified;unclassified | 0.002 | 0.000 |
| Bacteria;Actinobacteria;Thermoleophilia;Gaiellales;uncultured;unclassified | 0.000 | 0.004 |
| Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;480-2;unclassified | 0.000 | 0.007 |
| Bacteria;Aerophobetes;unclassified;unclassified;unclassified;unclassified | 0.011 | 0.000 |
| Bacteria;Aminicenantes;unclassified;unclassified;unclassified;unclassified | 0.002 | 0.000 |
| Bacteria;Armatimonadetes;unclassified;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Atribacteria;unclassified;unclassified;unclassified;unclassified | 0.040 | 0.015 |
| Bacteria;Bacteroidetes;Bacteroidetes BD2-2;unclassified;unclassified;unclassified | 0.044 | 0.041 |
| Bacteria;Bacteroidetes;Bacteroidetes VC2.1 Bac22;unclassified;unclassified;unclassified | 1.327 | 0.858 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Marinifilum | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured | 0.258 | 0.273 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Petrimonas | 0.000 | 0.026 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Alloprevotella | 0.000 | 0.011 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidia Incertae Sedis;Draconibacteriaceae;Tangfeifania | 0.024 | 0.007 |
| Bacteria;Bacteroidetes;Bacteroidia;Bacteroidia Incertae Sedis;Prolixibacteraceae;Prolixibacter | 0.004 | 0.000 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Hymenobacter | 0.000 | 0.004 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Candidatus Amoebophilus | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Ekhidna | 0.000 | 0.004 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Fabibacter | 0.000 | 0.011 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Marinoscillum | 0.004 | 0.034 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Rapidithrix | 0.000 | 0.004 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Reichenbachiella | 0.002 | 0.000 |
| Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;uncultured | 0.024 | 0.037 |
| Bacteria;Bacteroidetes;Cytophagia;Order III;Unknown Family;Balneola | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Crocinitomix | 0.007 | 0.007 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Fluviicola | 0.007 | 0.034 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;NS10 marine group | 0.002 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Owenweeksia | 0.002 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;Salinirepens | 0.000 | 0.019 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;uncultured | 0.053 | 0.202 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Aquibacter | 0.024 | 0.082 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Aureicoccus | 0.002 | 0.007 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Chryseobacterium | 0.002 | 0.030 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Elizabethkingia | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Flavobacterium | 0.011 | 0.004 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Gilvibacter | 0.002 | 0.015 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Gramella | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Leeuwenhoekiella | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Lutibacter | 0.004 | 0.019 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Lutimonas | 0.002 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;NS2b marine group | 0.002 | 0.015 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;NS4 marine group | 0.002 | 0.011 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;NS5 marine group | 0.004 | 0.000 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Polaribacter | 0.088 | 0.378 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Pseudofulvibacter | 0.013 | 0.015 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Psychroserpens | 0.000 | 0.011 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Sufflavibacter | 0.035 | 0.251 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Tenacibaculum | 0.042 | 0.273 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Wenyingzhuangia | 0.033 | 0.150 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;uncultured | 0.004 | 0.022 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;NS7 marine group;unclassified | 0.007 | 0.015 |
| Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;NS9 marine group;unclassified | 0.013 | 0.030 |
| Bacteria;Bacteroidetes;SB-5;unclassified;unclassified;unclassified | 0.002 | 0.004 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;B01R012;unclassified | 0.009 | 0.022 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;Hydrotalea | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;Sediminibacterium | 0.000 | 0.011 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;E6aC02;unclassified | 0.103 | 0.079 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;KD1-131;unclassified | 0.007 | 0.007 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;NS11-12 marine group;unclassified | 0.011 | 0.007 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;ST-12K33;unclassified | 0.002 | 0.000 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Saprospiraceae;uncultured | 0.007 | 0.034 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;uncultured | 0.002 | 0.000 |
| Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;WCHB1-69;unclassified | 0.059 | 0.041 |
| Bacteria;Candidate division OP3;unclassified;unclassified;unclassified;unclassified | 0.035 | 0.030 |
| Bacteria;Candidate division SR1;unclassified;unclassified;unclassified;unclassified | 0.825 | 0.622 |

| | | |
|---|---|---|
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Chlamydiaceae;unclassified | 0.002 | 0.000 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Chlamydiales Incertae Sedis;unclassified | 0.000 | 0.000 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Parachlamydia | 0.002 | 0.011 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus Fritschea | 0.004 | 0.011 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus Renichlamydia | 0.000 | 0.004 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Simkania | 0.002 | 0.007 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;uncultured | 0.004 | 0.007 |
| Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;cvE6;unclassified | 0.000 | 0.004 |
| Bacteria;Chlorobi;Chlorobia;Chlorobiales;Chlorobiaceae;Chlorobium | 0.004 | 0.007 |
| Bacteria;Chlorobi;Ignavibacteria;Ignavibacteriales;PHOS-HE36;unclassified | 0.000 | 0.000 |
| Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermomarinilinea | 0.009 | 0.000 |
| Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured | 0.000 | 0.004 |
| Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Chloroflexi;Dehalococcoidia;FW22;unclassified;unclassified | 0.002 | 0.000 |
| Bacteria;Chloroflexi;Dehalococcoidia;GIF3;unclassified;unclassified | 0.002 | 0.004 |
| Bacteria;Chloroflexi;Dehalococcoidia;GIF9;unclassified;unclassified | 0.011 | 0.007 |
| Bacteria;Chloroflexi;Dehalococcoidia;MSBL5;unclassified;unclassified | 0.167 | 0.116 |
| Bacteria;Chloroflexi;JG30-KF-CM66;unclassified;unclassified;unclassified | 0.009 | 0.015 |
| Bacteria;Chloroflexi;KD4-96;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Chloroflexi;S085;unclassified;unclassified;unclassified | 0.004 | 0.015 |
| Bacteria;Chloroflexi;SAR202 clade;unclassified;unclassified;unclassified | 0.363 | 0.461 |
| Bacteria;Chloroflexi;TK10;unclassified;unclassified;unclassified | 0.000 | 0.011 |
| Bacteria;Chloroflexi;uncultured;unclassified;unclassified;unclassified | 0.007 | 0.004 |
| Bacteria;Cloacimonetes;MSBL2;unclassified;unclassified;unclassified | 0.275 | 0.034 |
| Bacteria;Cloacimonetes;MSBL8;unclassified;unclassified;unclassified | 0.288 | 0.112 |
| Bacteria;Cyanobacteria;Chloroplast;unclassified;unclassified;unclassified | 0.018 | 0.064 |
| Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI; | 0.000 | 0.004 |
| Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI;Prochlorococcus | 0.029 | 0.037 |
| Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI;Synechococcus | 0.141 | 0.217 |
| Bacteria;Cyanobacteria;ML635J-21;unclassified;unclassified;unclassified | 0.007 | 0.004 |
| Bacteria;Cyanobacteria;Melainabacteria;Caenarcaniphilales;unclassified;unclassified | 0.004 | 0.000 |
| Bacteria;Cyanobacteria;Melainabacteria;Obscuribacterales;unclassified;unclassified | 0.000 | 0.004 |
| Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Trueperaceae;Truepera | 0.000 | 0.000 |
| Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter | 0.000 | 0.000 |
| Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;uncultured | 0.002 | 0.011 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus | 0.002 | 0.000 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Family XI;Gemella | 0.002 | 0.000 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus | 0.000 | 0.000 |
| Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus | 0.009 | 0.019 |
| Bacteria;Firmicutes;Bacilli;Lactobacillales;P5D1-392;unclassified | 0.000 | 0.000 |
| Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae 1;Fonticella | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Family XI;Finegoldia | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Family XI;Peptoniphilus | 0.000 | 0.004 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Family XII;Fusibacter | 1.459 | 0.427 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-004 | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-008 | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;uncultured | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Halanaerobiales;64K2;unclassified | 0.042 | 0.022 |
| Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halanaerobiaceae;Halanaerobium | 0.011 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halanaerobiaceae;Halocella | 0.002 | 0.000 |
| Bacteria;Firmicutes;Clostridia;Natranaerobiales;Natranaerobiaceae;uncultured | 0.007 | 0.000 |
| Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Pelosinus | 0.000 | 0.000 |
| Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Veillonella | 0.000 | 0.000 |
| Bacteria;Firmicutes;OPB54;unclassified;unclassified;unclassified | 0.002 | 0.004 |
| Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Fusobacterium | 0.000 | 0.000 |
| Bacteria;Gemmatimonadetes;Gemmatimonadetes;BD2-11 terrestrial group;unclassified;unclassified | 0.007 | 0.000 |
| Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas | 0.000 | 0.000 |
| Bacteria;Gemmatimonadetes;Gemmatimonadetes;PAUC43f marine benthic group;unclassified;unclassified | 0.002 | 0.000 |
| Bacteria;Gracilibacteria;unclassified;unclassified;unclassified;unclassified | 0.062 | 0.127 |
| Bacteria;Hyd24-12;unclassified;unclassified;unclassified;unclassified | 0.125 | 0.086 |
| Bacteria;Hydrogenedentes;unclassified;unclassified;unclassified;unclassified | 0.000 | 0.004 |
| Bacteria;LCP-89;unclassified;unclassified;unclassified;unclassified | 0.007 | 0.015 |
| Bacteria;Latescibacteria;unclassified;unclassified;unclassified;unclassified | 0.154 | 0.292 |
| Bacteria;Lentisphaerae;BS5;unclassified;unclassified;unclassified | 0.002 | 0.000 |
| Bacteria;Lentisphaerae;LD1-PA26;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Lentisphaerae;LD1-PB3;unclassified;unclassified;unclassified | 0.103 | 0.198 |
| Bacteria;Lentisphaerae;Lentisphaeria;Lentisphaerales;Lentisphaeraceae;Lentisphaera | 0.654 | 0.970 |
| Bacteria;Lentisphaerae;Oligosphaeria;unclassified;unclassified;unclassified | 0.020 | 0.030 |
| Bacteria;Lentisphaerae;Oligosphaeria;Oligosphaerales;unclassified;unclassified | 0.009 | 0.000 |
| Bacteria;Lentisphaerae;R76-B128;unclassified;unclassified;unclassified | 0.035 | 0.004 |
| Bacteria;Lentisphaerae;WCHB1-41;unclassified;unclassified;unclassified | 0.004 | 0.004 |
| Bacteria;Marinimicrobia (SAR406 clade);unclassified;unclassified;unclassified;unclassified | 0.119 | 0.161 |
| Bacteria;Microgenomates;unclassified;unclassified;unclassified;unclassified | 0.046 | 0.022 |
| Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Leptospirillum | 0.000 | 0.000 |
| Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira | 0.007 | 0.004 |
| Bacteria;Omnitrophica;NPL-UPA2;unclassified;unclassified;unclassified | 0.004 | 0.000 |
| Bacteria;PAUC34f;unclassified;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Parcubacteria;unclassified;unclassified;unclassified;unclassified | 2.633 | 0.753 |
| Bacteria;Parcubacteria;Parcubacteria Incertae Sedis;Unknown Order;Unknown Family;Candidatus Paceibacter | 0.236 | 0.007 |
| Bacteria;Planctomycetes;028H05-P-BN-P5;unclassified;unclassified;unclassified | 0.000 | 0.007 |
| Bacteria;Planctomycetes;BD7-11;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Planctomycetes;C47;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Planctomycetes;MBMPE71;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Planctomycetes;OM190;unclassified;unclassified;unclassified | 0.156 | 0.633 |
| Bacteria;Planctomycetes;Phycisphaerae;C86;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Planctomycetes;Phycisphaerae;MSBL9;unclassified;unclassified | 0.068 | 0.034 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;08D2Z94 hypersaline microbial mat group;unclassified | 0.000 | 0.004 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;AKAU3564 sediment group;unclassified | 0.000 | 0.004 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;ODP1230B30.02 sediment group;unclassified | 0.004 | 0.004 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;CL500-3 | 0.007 | 0.037 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;FS140-16B-02 marine group | 3.735 | 4.835 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;I-8 | 0.132 | 0.243 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;JL-ETNP-F27 | 6.960 | 8.370 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Phycisphaera | 0.004 | 0.000 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;SM1A02 | 0.002 | 0.011 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Urania-1B-19 marine sediment group | 0.431 | 0.974 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;uncultured | 0.029 | 0.037 |
| Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;SBYZ-1154;unclassified | 0.000 | 0.004 |

| | | |
|---|---|---|
| Bacteria;Planctomycetes;Phycisphaerae;Pla1 lineage;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Planctomycetes;Phycisphaerae;SHA-43;unclassified;unclassified | 0.004 | 0.026 |
| Bacteria;Planctomycetes;Pla3 lineage;unclassified;unclassified;unclassified | 0.007 | 0.030 |
| Bacteria;Planctomycetes;Pla4 lineage;unclassified;unclassified;unclassified | 0.007 | 0.004 |
| Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae;Candidatus Scalindua | 0.002 | 0.000 |
| Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae;PB79 | 0.000 | 0.004 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula | 0.002 | 0.004 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Bythopirellula | 0.000 | 0.000 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata | 0.000 | 0.000 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir4 lineage | 0.022 | 0.071 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces | 0.876 | 0.764 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Rhodopirellula | 0.059 | 0.180 |
| Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured | 0.112 | 0.124 |
| Bacteria;Planctomycetes;SGST604;unclassified;unclassified;unclassified | 0.007 | 0.000 |
| Bacteria;Proteobacteria;AEGEAN-245;unclassified;unclassified;unclassified | 0.002 | 0.015 |
| Bacteria;Proteobacteria;ARKICE-90;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;Hyphomonas | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;uncultured | 0.004 | 0.015 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Kordiimonadales;Kordiimonadaceae;Kordiimonas | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Magnetococcales;Magnetococcaceae;Magnetococcus | 0.009 | 0.011 |
| Bacteria;Proteobacteria;Alphaproteobacteria;OCS116 clade;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Parvularculales;Parvularculaceae;Parvularcula | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;A0839;unclassified | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Aurantimonadaceae;Aurantimonas | 0.011 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Chelatococcus | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bosea | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bradyrhizobium | 0.009 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Hyphomicrobium | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;KF-JG30-B3;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae;Meganema | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae;Methylobacterium | 0.011 | 0.045 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Ahrensia | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Cohaesibacter | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Mesorhizobium | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Nitratireductor | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rhizobium | 0.009 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales Incertae Sedis;Nordella | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales Incertae Sedis;Phreatobacter | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Anderseniella | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Rhodobium | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Variibacter | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;uncultured;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Amylibacter | 0.004 | 0.034 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Ascidiaceihabitans | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Defluviimonas | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Gemmobacter | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Jannaschia | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Nautella | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracocccus | 0.007 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseobacter clade NAC11-7 lineage | 0.057 | 0.056 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseovarius | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rubellimicrobium | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Shimia | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Sulfitobacter | 0.004 | 0.007 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Thalassobius | 0.009 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Tropicibacter | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;uncultured | 0.823 | 0.464 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AT-s3-44;unclassified | 0.004 | 0.011 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;DA111;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;AEGEAN-169 marine group | 0.029 | 0.041 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Defluviicoccus | 0.009 | 0.019 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Magnetospira | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;OM75 clade | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Thalassospira | 0.000 | 0.015 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Tistrella | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;uncultured | 0.018 | 0.030 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillales Incertae Sedis;Candidatus Alysiosphaera | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillales Incertae Sedis;Reyranella | 0.004 | 0.015 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Holosporaceae;Holospora | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;LWSR-14;unclassified | 0.011 | 0.011 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Mitochondria;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;uncultured | 0.013 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiales Incertae Sedis;Candidatus Lariskella | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;S25-593;unclassified | 0.042 | 0.071 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;SAR116 clade;unclassified | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;SAR116 clade;Candidatus Puniceispirillum | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;SHWN-night2;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;unclassified;unclassified | 0.084 | 0.094 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Deep 1;unclassified | 0.423 | 0.551 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 1;unclassified | 0.396 | 0.603 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 1;Candidatus Pelagibacter | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 2;unclassified | 0.035 | 0.034 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 3;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 4;unclassified | 0.004 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;SB1-18;unclassified;unclassified | 0.002 | 0.007 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sneathiellales;Sneathiellaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter | 0.018 | 0.004 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium | 0.000 | 0.011 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas | 0.024 | 0.105 |
| Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Achromobacter | 0.000 | 0.000 |

| | | |
|---|---|---|
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;MWH-UniP1 aquatic group | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus | 0.277 | 0.311 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Limnobacter | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax | 0.075 | 0.045 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium | 0.011 | 0.064 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Methylibium | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Piscinibacter | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pseudorhodoferax | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Simplicispira | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xylophilus | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured | 0.004 | 0.007 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Candidatus Profftella | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia | 0.000 | 0.015 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Paucimonas | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;OM43 clade | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Neisseria | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azoarcus | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Thauera | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Betaproteobacteria;oca12;unclassified;unclassified | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Deltaproteobacteria;43F-1404R;unclassified;unclassified | 0.000 | 0.011 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Halobacteriovorax | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Peredibacter | 0.000 | 0.011 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;uncultured | 0.004 | 0.004 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;OM27 clade | 0.062 | 0.217 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfatiglans | 0.020 | 0.019 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;unclassified | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacterium | 0.004 | 0.004 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacula | 2.873 | 0.981 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfocella | 0.007 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum | 0.007 | 0.007 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;SEEP-SRB1 | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;uncultured | 0.244 | 0.067 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopila | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;MSBL7 | 0.095 | 0.030 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;uncultured | 0.055 | 0.041 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;Candidatus Entotheonella | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;Nitrospina | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfohalobiaceae;Desulfovermiculus | 19.855 | 24.717 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfurellales;Desulfurellaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;GR-WP33-58;unclassified | 0.040 | 0.124 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Sva1033;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;GR-WP33-30;unclassified;unclassified | 0.011 | 0.022 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;BIrii41;unclassified | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Blfdi19;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Eel-36e1D6;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;MidBa8;unclassified | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;P3OB-42;unclassified | 0.004 | 0.007 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Chondromyces | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;bacteriap25;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;unclassified;unclassified | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;Oligoflexaceae;unclassified | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Deltaproteobacteria;SAR324 clade(Marine group B);unclassified;unclassified | 0.141 | 0.262 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Sh765B-TzT-29;unclassified;unclassified | 0.070 | 0.037 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Sva0485;unclassified;unclassified | 0.037 | 0.011 |
| Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Elev-16S-509;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;BR36;unclassified;unclassified | 0.097 | 0.150 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter | 0.372 | 0.401 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas | 8.167 | 16.149 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurovum | 29.199 | 15.156 |
| Bacteria;Proteobacteria;Epsilonproteobacteria;R103-B63;unclassified;unclassified | 0.266 | 0.165 |
| Bacteria;Proteobacteria;Gammaproteobacteria;1013-28-CG33;unclassified;unclassified | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Oceanimonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Aliiglaciecola | 0.000 | 0.015 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Alteromonas | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Paraglaciecola | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Salinimonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;uncultured | 0.004 | 0.045 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Colwelliaceae;Colwellia | 0.013 | 0.049 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Colwelliaceae;Thalassotalea | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Idiomarinaceae;Idiomarina | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Moritellaceae;Moritella | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Algicola | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Pseudoalteromonas | 0.020 | 0.049 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Psychromonadaceae;Psychromonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;Psychrobium | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;Shewanella | 0.000 | 0.026 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Arenicellales;Arenicellaceae;Arenicella | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;B38;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Maricurvus | 0.002 | 0.011 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Pseudomaricurvus | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Simiduia | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Umboniibacter | 0.004 | 0.034 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;uncultured | 0.002 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Haliea | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;OM60(NOR5) clade | 0.004 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;C1-B045 | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;Porticoccus | 0.000 | 0.000 |

| | | |
|---|---|---|
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;SAR92 clade | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;BD1-7 clade | 0.004 | 0.037 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;Dasania | 0.000 | 0.026 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Nitrosococcus | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiohalobacter | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiorhodospira | 0.002 | 0.030 |
| Bacteria;Proteobacteria;Gammaproteobacteria;E01-9C-26 marine group;unclassified;unclassified | 0.035 | 0.060 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Citrobacter | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella | 0.009 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis;Unknown Family;Sedimenticola | 0.029 | 0.041 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis;Unknown Family;Thiohalomonas | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;HOC36;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;KI89A clade;unclassified;unclassified | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Coxiella | 0.015 | 0.041 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;uncultured | 0.064 | 0.045 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;ET-SHO;unclassified | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;IheB2-23;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Marine Methylotrophic Group 2;unclassified | 0.018 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylococcus | 0.000 | 0.011 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Milano-WF1B-03;unclassified | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;NKB5;unclassified;unclassified | 0.020 | 0.026 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;CrystalBog021C3;unclassified | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;GSP65;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;JL-ETNP-Y6;unclassified | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Litoricolaceae;Litoricola | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;OM182 clade;unclassified | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;ORI-860-26;unclassified | 0.009 | 0.015 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;unclassified | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Marinomonas | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Neptunomonas | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Oceanospirillum | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Pseudospirillum | 0.004 | 0.022 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oleiphilaceae;Oleiphilus | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SAR86 clade;unclassified | 0.020 | 0.022 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SS1-B-06-26;unclassified | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SUP05 cluster;unclassified | 0.015 | 0.022 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;V1F82b;unclassified | 0.015 | 0.019 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;ZD0405;unclassified | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Order Incertae Sedis;Family Incertae Sedis;Marinicella | 0.000 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;PYR10d3;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Haemophilus | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter | 0.033 | 0.056 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Moraxella | 0.132 | 0.288 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas | 0.009 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Salinisphaerales;Salinisphaeraceae;ZD0417 marine group | 0.011 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;unclassified;unclassified | 0.002 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Cycloclasticus | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Galenea | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Hydrogenovibrio | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Thiomicrospira | 2.807 | 2.592 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;endosymbionts | 0.020 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;uncultured | 0.015 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thiothrix | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;uncultured | 0.009 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichales Incertae Sedis;Caedibacter | 0.004 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichales Incertae Sedis;Candidatus Endoecteinascidia | 0.004 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Aliivibrio | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Catenococcus | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Enterovibrio | 0.002 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Photobacterium | 0.002 | 0.007 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio | 0.018 | 0.056 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;uncultured | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;JTB255 marine benthic group;unclassified | 0.026 | 0.049 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Solimonadaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter | 0.000 | 0.000 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas | 0.000 | 0.015 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;uncultured | 0.000 | 0.004 |
| Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;uncultured;unclassified | 0.011 | 0.007 |
| Bacteria;Proteobacteria;JTB23;unclassified;unclassified;unclassified | 0.011 | 0.026 |
| Bacteria;Proteobacteria;Proteobacteria Incertae Sedis;Unknown Order;Unknown Family;Candidatus Thiobios | 0.000 | 0.000 |
| Bacteria;Proteobacteria;SC3-20;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Proteobacteria;SPOTSOCT00m83;unclassified;unclassified;unclassified | 0.007 | 0.019 |
| Bacteria;Proteobacteria;TA18;unclassified;unclassified;unclassified | 0.002 | 0.015 |
| Bacteria;Proteobacteria;Zetaproteobacteria;Mariprofundales;Mariprofundaceae;Mariprofundus | 0.000 | 0.000 |
| Bacteria;Saccharibacteria;unclassified;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta 2 | 0.002 | 0.007 |
| Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured | 0.002 | 0.000 |
| Bacteria;TA06;unclassified;unclassified;unclassified;unclassified | 0.002 | 0.000 |
| Bacteria;TM6;unclassified;unclassified;unclassified;unclassified | 0.015 | 0.011 |
| Bacteria;Tenericutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;Mycoplasma | 0.007 | 0.015 |
| Bacteria;Tenericutes;Mollicutes;NB1-n;unclassified;unclassified | 0.004 | 0.000 |
| Bacteria;Verrucomicrobia;Arctic97B-4 marine group;unclassified;unclassified;unclassified | 0.000 | 0.011 |
| Bacteria;Verrucomicrobia;OPB35 soil group;unclassified;unclassified;unclassified | 0.000 | 0.004 |
| Bacteria;Verrucomicrobia;Opitutae;A714019;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Opitutae;MB11C04 marine group;unclassified;unclassified | 0.002 | 0.004 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Cerasicoccus | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Coraliomargarita | 0.002 | 0.019 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Lentimonas | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Pelagicoccus | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;marine group | 0.009 | 0.007 |
| Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;uncultured | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Opitutae;RS-B22;unclassified;unclassified | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;unclassified | 0.000 | 0.000 |
| Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Roseibacillus | 0.002 | 0.000 |

| | | |
|---|---|---|
| **Sum [%]** | 100 | 100 |

**Supplementary Table 5**

Classification of archaeal partial 16S rRNA gene sequences according to SILVAngs (release 128, Sept. 2016). Given are the total number of sequences assigned to each taxonomic clade.

| | **Brine** | **Lower interface** |
|---|---|---|
| Archaea;Aenigmarchaeota;Deep Sea Euryarchaeotic Group(DSEG);unclassified;unclassified;unclassified | 990 | 1319 |
| Archaea;Aigarchaeota;Terrestrial Hot Spring Gp(THSCG);unclassified;unclassified;unclassified | 2 | 2 |
| Archaea;Diapherotrites;unclassified;unclassified;unclassified;unclassified | 4 | 6 |
| Archaea;Diapherotrites;Diapherotrites Incertae Sedis;Unknown Order;Unknown Family;Candidatus Iainarchaeum | 1 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;unclassified | 8 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Candidatus Halobonum | 9 | 7 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halapricum | 531 | 128 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halarchaeum | 1 | 1 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloarcula | 85 | 34 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halobacterium | 3 | 4 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halobaculum | 3 | 1 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halobellus | 0 | 3 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halococcus | 2 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halomicroarcula | 16 | 4 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halomicrobium | 360 | 225 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halopelagius | 1 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halopiger | 1 | 1 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloplanus | 1 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloquadratum | 1 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorhabdus | 7926 | 4410 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorientalis | 1 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorubellus | 0 | 1 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorubrum | 4 | 2 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halosimplex | 1 | 20 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloterrigena | 0 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halovenus | 16 | 6 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halovivax | 4 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronoarchaeum | 0 | 1 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronobacterium | 1 | 2 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronomonas | 0 | 7 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronorubrum | 1 | 0 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Salinarchaeum | 1 | 10 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;uncultured | 11 | 9 |
| Archaea;Euryarchaeota;Methanobacteria;Methanobacteriales;Methanobacteriaceae;Methanosphaera | 1 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;ANME-1;unclassified;unclassified | 0 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiales Incertae Sedis;Methanocalculus | 0 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanolinea | 0 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;GOM Arc I;unclassified | 0 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;GOM Arc I;Candidatus Methanoperedens | 1 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanohalophilus | 154 | 3 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina | 1 | 0 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methermicoccaceae;Methermicoccus | 0 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Kazan-3A-21;unclassified;unclassified | 1 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;MSBL1;unclassified;unclassified | 4861 | 5222 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;unclassified;unclassified | 2 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;20c-4;unclassified | 1 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;AMOS1A-4113-D04;unclassified | 1 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;ANT06-05;unclassified | 6 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;ASC21;unclassified | 0 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;CCA47;unclassified | 26 | 99 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;KTK 4A;unclassified | 6 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;unclassified | 0 | 0 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group II;unclassified | 176 | 837 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group III;unclassified | 353 | 497 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Thermoplasmatales Incertae Sedis;unclassified | 4 | 0 |
| Archaea;Marine Hydrothermal Vent Group(MHVG);unclassified;unclassified;unclassified;unclassified | 0 | 0 |
| Archaea;Miscellaneous Crenarchaeotic Group;unclassified;unclassified;unclassified;unclassified | 6 | 0 |
| Archaea;Miscellaneous Euryarchaeotic Group(MEG);unclassified;unclassified;unclassified;unclassified | 0 | 1 |
| Archaea;Nanohaloarchaeota;unclassified;unclassified;unclassified;unclassified | 1148 | 1422 |
| Archaea;Thaumarchaeota;AK59;unclassified;unclassified;unclassified | 2 | 0 |
| Archaea;Thaumarchaeota;F9P122000-Arc-2-E02;unclassified;unclassified;unclassified | 0 | 1 |
| Archaea;Thaumarchaeota;Marine Benthic Group A;unclassified;unclassified;unclassified | 12 | 21 |
| Archaea;Thaumarchaeota;Marine Benthic Group B;unclassified;unclassified;unclassified | 0 | 1 |
| Archaea;Thaumarchaeota;Marine Group I;unclassified;unclassified;unclassified | 948 | 5951 |
| Archaea;Thaumarchaeota;Marine Group I;Cenarchaeales;Cenarchaeaceae;Cenarchaeum | 3 | 3 |
| Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosoarchaeum | 149 | 92 |
| Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopelagicus | 92 | 452 |
| Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus | 9358 | 17581 |
| Archaea;Thaumarchaeota;Soil Crenarchaeotic Group(SCG);unclassified;unclassified;unclassified | 1 | 0 |
| Archaea;Thaumarchaeota;South African Gold Mine Gp 1(SAGMCG-1);unclassified;unclassified;unclassified | 0 | 0 |
| Archaea;Thaumarchaeota;South African Gold Mine Gp 1(SAGMCG-1);Unknown Order;Unknown Family;Candidatus Nitrosotalea | 1 | 0 |
| Archaea;Thaumarchaeota;pSL12;unclassified;unclassified;unclassified | 0 | 2 |
| Archaea;Woesearchaeota (DHVEG-6);unclassified;unclassified;unclassified;unclassified | 2960 | 4417 |
| No Relative (according to SILVAngs classification) | 3009 | 3938 |
| Total sequences | 33268 | 46743 |
| **Total sequences excluding "No relative"** | **30259** | **42805** |

**Supplementary Table 6**

Classification of bacterial partial 16S rRNA gene sequences according to SILVAngs (release 128, Sept. 2016). Given is the relative contribution of each taxonomic clade to total sequences. Sequences classified as "no relatives" were excluded from the analysis.

| | **Brine** | **Lower interface** |
|---|---|---|
| Archaea;Aenigmarchaeota;Deep Sea Euryarchaeotic Group(DSEG);unclassified;unclassified;unclassified | 3.272 | 3.081 |
| Archaea;Aigarchaeota;Terrestrial Hot Spring Gp(THSCG);unclassified;unclassified;unclassified | 0.007 | 0.005 |
| Archaea;Diapherotrites;unclassified;unclassified;unclassified;unclassified | 0.013 | 0.014 |
| Archaea;Diapherotrites;Diapherotrites Incertae Sedis;Unknown Order;Unknown Family;Candidatus Iainarchaeum | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;unclassified | 0.026 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Candidatus Halobonum | 0.030 | 0.016 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halapricum | 1.755 | 0.299 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halarchaeum | 0.003 | 0.002 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloarcula | 0.281 | 0.079 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halobacterium | 0.010 | 0.009 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halobaculum | 0.010 | 0.002 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halobellus | 0.000 | 0.007 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halococcus | 0.007 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halomicroarcula | 0.053 | 0.009 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halomicrobium | 1.190 | 0.526 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halopelagius | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halopiger | 0.003 | 0.002 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloplanus | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloquadratum | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorhabdus | 26.194 | 10.303 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorientalis | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorubellus | 0.000 | 0.002 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halorubrum | 0.013 | 0.005 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halosimplex | 0.003 | 0.047 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Haloterrigena | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halovenus | 0.053 | 0.014 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halovivax | 0.013 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronoarchaeum | 0.000 | 0.002 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronobacterium | 0.003 | 0.005 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronomonas | 0.000 | 0.016 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Natronorubrum | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Salinarchaeum | 0.003 | 0.023 |
| Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;uncultured | 0.036 | 0.021 |
| Archaea;Euryarchaeota;Methanobacteria;Methanobacteriales;Methanobacteriaceae;Methanosphaera | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;ANME-1;unclassified;unclassified | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiales Incertae Sedis;Methanocalculus | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanolinea | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;GOM Arc I;unclassified | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;GOM Arc I;Candidatus Methanoperedens | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanohalophilus | 0.509 | 0.007 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methermicoccaceae;Methermicoccus | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Kazan-3A-21;unclassified;unclassified | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;MSBL1;unclassified;unclassified | 16.065 | 12.200 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;unclassified;unclassified | 0.007 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;20c-4;unclassified | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;AMOS1A-4113-D04;unclassified | 0.003 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;ANT06-05;unclassified | 0.020 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;ASC21;unclassified | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;CCA47;unclassified | 0.086 | 0.231 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;KTK 4A;unclassified | 0.020 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;unclassified | 0.000 | 0.000 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group II;unclassified | 0.582 | 1.955 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group III;unclassified | 1.167 | 1.161 |
| Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Thermoplasmatales Incertae Sedis;unclassified | 0.013 | 0.000 |
| Archaea;Marine Hydrothermal Vent Group(MHVG);unclassified;unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Archaea;Miscellaneous Crenarchaeotic Group;unclassified;unclassified;unclassified;unclassified | 0.020 | 0.000 |
| Archaea;Miscellaneous Euryarchaeotic Group(MEG);unclassified;unclassified;unclassified;unclassified | 0.000 | 0.002 |
| Archaea;Nanohaloarchaeota;unclassified;unclassified;unclassified;unclassified | 3.794 | 3.322 |
| Archaea;Thaumarchaeota;AK59;unclassified;unclassified;unclassified | 0.007 | 0.000 |
| Archaea;Thaumarchaeota;F9P122000-Arc-2-E02;unclassified;unclassified;unclassified | 0.000 | 0.002 |
| Archaea;Thaumarchaeota;Marine Benthic Group A;unclassified;unclassified;unclassified | 0.040 | 0.049 |
| Archaea;Thaumarchaeota;Marine Benthic Group B;unclassified;unclassified;unclassified | 0.000 | 0.002 |
| Archaea;Thaumarchaeota;Marine Group I;unclassified;unclassified;unclassified | 3.133 | 13.903 |
| Archaea;Thaumarchaeota;Marine Group I;Cenarchaeales;Cenarchaeaceae;Cenarchaeum | 0.010 | 0.007 |
| Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosoarchaeum | 0.492 | 0.215 |
| Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopelagicus | 0.304 | 1.056 |
| Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus | 30.926 | 41.072 |
| Archaea;Thaumarchaeota;Soil Crenarchaeotic Group(SCG);unclassified;unclassified;unclassified | 0.003 | 0.000 |
| Archaea;Thaumarchaeota;South African Gold Mine Gp 1(SAGMCG-1);unclassified;unclassified;unclassified | 0.000 | 0.000 |
| Archaea;Thaumarchaeota;South African Gold Mine Gp 1(SAGMCG-1);Unknown Order;Unknown Family;Candidatus Nitrosotalea | 0.003 | 0.000 |
| Archaea;Thaumarchaeota;pSL12;unclassified;unclassified;unclassified | 0.000 | 0.005 |
| Archaea;Woesearchaeota (DHVEG-6);unclassified;unclassified;unclassified;unclassified | 9.782 | 10.319 |
| | | |
| **Sum [%]** | 100 | 100 |