

Supplementary Materials

Text S1: Redox state of sediment (EAC and EDC)

Total electron accepting (EAC) and donating capacities (EDC) of the sediment were determined by mediated electrochemical reduction and oxidation, respectively [1-3]. Samples were treated as for solid-phase Fe extraction and analyzed inside an anoxic glove box. Before measurement, each sample was diluted into a slurry by adding 2 ml of O₂-free Milli-Q water. Further details of the method used can be found in Fiskal, *et al.* [4].

Text S2: Nucleic acid extraction from sediment

Sediment samples from the syringes (surface sediments) and from cryovials (deeper sediment layers) were kept frozen for cutting and weighing. For the top layers, the frozen sediments were extruded from the syringes and cut in pieces of about 0.1 g, but not more than 0.2 g. This corresponded to a length of about 2mm and was consistent with the desired resolution in the higher layers: 1-3.5mm, 3.5-6mm, 6-8.5mm, 8.5-11mm, 14-16mm, 19-21mm, 24-26mm, 29-31mm and 34-36mm. For the deeper layers, the frozen sediments were taken out of the cryotubes and a portion of about the same weight as for the top layers was cut. Each slice of sediment was weighed and added to a 2 ml bead-beating tube filled to ~10% with 0.1mm zirconium beads. The simultaneous DNA/RNA extraction was performed following the protocol Lever, *et al.* [5]. Throughout the whole extraction, the sediments were kept on ice. To the bead-beating tubes containing the zirconium beads and the sediments, 100 µl of sodium hexametaphosphate solution (10mM, filtered twice and autoclaved) were added and samples were soaked by tapping. 500 µl of lysis solution I (30mM Tris-HCl, 30mM disodium EDTA, 0.5% Triton X-100 and 800mM guanidium hydrochloride, autoclaved twice and pH adjusted to 10.0 by adding NaOH) were then added and the content was homogenized by inverting/tapping. 500 µl of phenol-chloroformisoamylalcohol (25:24:1, 4_ C) were added and samples were vortexed. The tubes were bead-beat at 5000 shakings for 30 s (Precellys24, labgene scientific, CH). The samples were centrifuged (10000 x g, 4 °C, 10 min) and the supernatant was then transferred to clean 2 ml tubes. The samples were stored at -80 °C overnight. After thawing on ice, the samples were washed twice with 600 µl of chloroform-isoamyl alcohol (24:1, 4 °C) by vortexing the mixture and collecting the supernatant after spinning it down (10000 x g, 4 °C, 10 min). Linear polyacrylamide was added to a concentration of 20 µg ml⁻¹ as well as and 100 µl of sodium chloride (5M). Each tube was inverted three times for mixing. Additionally, 650 µl of isopropanol were mixed into the tubes to precipitate the samples at -20 °C for 2 h. The extracts were centrifuged (14000xg, 23 °C, 20 min) and the supernatant removed. The remaining pellet was washed twice with 800 µl 70% ethanol (14000 x g, 23 °C, 10 min between washings). The pellet was dried using a preheated SpeedVac (50 °C, 7 min, Savant SpeedVac SC100 Centrifugal Evaporator) and resuspended in 200 µl molecular grade water (thereafter referred as water) on ice. The extract was separated in two equal halves, one for

DNA and the other one for RNA. The DNA-extracts were purified using the CleanAll DNA/RNA Clean-Up and Concentration Micro Kit by Norgen Biotek (protocol A, chemicals provided by the kit were autoclaved before use).

For macrofauna DNA extraction only 50 µl of sodium hexametaphosphate (10 mM) solution were added. Mechanical lysis was performed using 0.1 mm Zirconium beads, bead beating was performed for 30 s (Labgene, Precellys 24, 5000 rpm).

Text S3: Methodology: reverse transcription and quantification of rRNA gene copies

For RNA, the extracts were first treated with 10 µl 10x Reaction Buffer and 2 µl Ambion® TURBO™ DNase (Life Technologies, US) in order to remove DNA. The reaction mix was incubated on a Thermomixer Confor (Eppendorf, DE) for 30 min at 300 rpm at 37°C. The products were cleaned using the CleanAll kit (procedure C but without β-mercaptoethanol). A quantitative polymerase chain reaction was carried out on those samples to evaluate the effectiveness of the DNase treatment. The samples were stored at -80 °C for further treatment. After thawing the extracts, the RNA was reverse transcribed into complementary DNA (cDNA) using the Omniscript RT Kit (Quiagen, NL), Random Hexamers (biomers.net, DE) as primers and Ambion® ANTI-RNase (Life Technologies, US) as RNase inhibitor. The master mix for one reaction (20 µl) was gained by mixing 2.05 µl buffer 10x RT, 2 µl dNTP Mix, 2 µl Random Hexamers, 0.5 µl RNase inhibitors (20 units µl⁻¹), 1 µl Omniscript Reverse Transcriptase and 10.45 µl RNase-free water. 2 µl of RNA template were mixed with 18 µl of master mix and incubated at 37°C for 60 min in a PCR cycler (Sensoquest Labcycler Basic). The samples were stored at -80°C.

Text S4 : Quantitative polymerase chain reaction (qPCR).

qPCR was performed using assays that target bacterial and archaeal 16S ribosomal RNA (16S rRNA) genes. Standards consisted of known concentrations of plasmids that were run in 10fold dilution series of approximately 10¹ to 10⁷ gene copies. For bacterial 16S rRNA the Bac 908F_mod (AAC TCA AAK GAA TTG ACG GG) [5] and Bac 1075R (CAC GAG CTG ACG ACA RCC) primers were used [6]. Standards were prepared from *Desulfotignum phosphitoxidans*. For archaeal 16S rRNA the Arc915F_mod (AAT TGG CGG GGG AGC AC) [7] and Arc1059R (GCC ATG CAC CWC CTC T) [8]. Standards were prepared from *Thermoplasma acidophilum*. All sample DNA extracts, extraction and qPCR negative controls, and standard dilutions were run in duplicate. For each qPCR reaction, 2 µl of DNA extract were mixed with 1 µl of molecular grade water, 1 µl of bovine serum albumin (10 mg/ml; New England Biolabs, USA), 0.5 µl each forward and reverse primers (10 µM), and 5 µl Syber Green Master Mix (2×concentrated, LightCycler 480 SYBR Green I Master (Roche, Switzerland). All standards and samples were kept on ice throughout the preparations and run in transparent 96-well plates on a Roche

LightCycler 480 immediately after preparation. The temperature protocol for gene quantification was as follows for bacterial/archaeal 16S rRNA: initial activation at 95°C (5min), followed by 40/45 cycles of: denaturation at 95°C (10s), annealing at 60/55°C (30s), polymerization at 72°C (15s), acquisition at 80/81°C (0.5s). Followed by denaturation at 95°C (01:15 min), acquisition from 60/55°C to 95°C and cooling at 4°C.

Text S5: *Next Generation Sequencing (NGS).*

Library preparation was performed using an initial booster PCR that was followed by a tail-PCR and subsequently an index PCR. Samples, extraction negative controls, and PCR negative controls were included in each sequencing run, and the products of each PCR were checked for correct length on a 1.5 % agarose gel using tris-acetate EDTA buffer. Negative controls that had no visible PCR products nonetheless proceeded to the next step. Booster PCRs were performed to increase gene copy numbers of different samples to roughly the same concentrations and ranged from 22-34 PCR cycles. The products of the booster PCR were next amplified by a tail-PCR using a mixture of equal amounts of 4 different forward and reverse primers (nex0-nex3) to introduce a tail to the region of interest using 10 cycles. The products of the tail PCR were cleaned using AMPure beads (Beckmann Coulter, ratio of 0.8) and PCR-amplified (8 cycles) using Illumina Index primers (Nextera XT Kit A and D, Illumina). Products were cleaned with AMPure beads (Beckmann, ratio of 0.8). After index PCR, DNA concentration was determined using a Qubit® Fluorometer (dsDNA BR assay kit, Thermo Fisher Scientific, invitrogen) and pooled adjusting the volumes to reach equimolar concentrations of each PCR product. The pooled mixture was then measured on a 2200 TapeStation System (Agilent Technologies, High Sensitivity D1000 Screen Tape) to assess average library size and pool concentration. Pooled DNA was then diluted to 10 pM and loaded onto a MiSeq (Illumina Inc., USA) using 10 % PhiX. For 16S, the universal prokaryotic 16S rRNA gene primer pair Univ519F (CAG CMG CCG CGG TAA) and Univ802R (TAC NVG GGT ATC TAA TCC) [9,10] was used.

Text S6: *Single burrow oxygen profiles*

In addition to vertical sediment O₂ profiles we measured O₂ gradients into chironomid larval and oligochaete burrows (Figure A5). O₂ concentrations measured in the tube structures of the chironomid larvae first decrease, however O₂ concentrations increase again between 8 and 1.2 mm sediment depth (Figure A5). This pattern of local subsurface maxima in O₂ concentrations can also be observed in profile b and c (measured into a burrow below the sediment water interface and between two burrows, respectively), however less pronounced. Similarly, O₂ concentrations are variable in the W treatments (Figure A5) lower panel), especially above the sediment water interface O₂ concentration are dynamic if measured close to active oligochaete worms (profiles a, b and c).

Text S7: Microbial community zonation across treatments

Bacteria

The bacterial community in the sediments consists of 54 different phyla. Due to the good agreement in microbial community structure based on 16S rRNA gene sequences and 16S rRNA sequences from transcribed RNA (cDNA) (Appendix B, Figure A14 and A15), we only focus on 16S rRNA gene sequences from now on. The most abundant phyla among all sampled depths are *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, *Planctomycetes*, *Verrucomicrobia*, *Chloroflexi*, *Omnitrophica*, *Cyanobacteria* and *Latescibacteria*.

While community profiles in controls are relatively stable over time and with increasing sediment depth, oxic treatments display gradual changes in bacterial communities in the top 2 cm over time (Table A1 with relative abundances on order level). These changes are driven by increases in α - (mostly *Caulobacteriales*), β - (mostly *Nitrosomonadales*, *Burkholderiales* and *Rhodocyclales*) and γ - (mostly *Methylococcales*, and *Cellvibrionales*) *Proteobacteria*, and *Nitrospirae* (*Nitrospira* and *Nitrospirales*). In addition, several groups decrease in surface sediments of oxic treatments. These include δ -*Proteobacteria* (mostly *Syntrophobacteriales*, *Syntrophobacteraceae*), *Actinobacteria* (mainly *Actinobacteria*, *Acidimicrobiia*, and *Thermoleophilia*), *Planctomycetes* (mainly *Planctomycetacia*), *Chloroflexi* (*Dehalococcoidia* and *Anaerolineae*), *Omnitrophica*, *Firmicutes* (mainly *Bacilli* and *Clostridia*), *Latescibacteria*, and *Cyanobacteria* (*Cyanobacteria* and *Chloroplast*). Only minimal changes through time or with sediment depth were present in *Verrucomicrobia* (mainly *Verrucomicrobiaceae*, OPB35_soil_group, *Opitutaceae*), and *Bacteroidetes*. Among the *Bacteroidetes*, there is, however a notable increase in *Sphingobacteriia* and *Cytophagia* and decrease in *Bacteroidia* in oxic cores.

Relative abundances of bacterial communities in tubes, feces, and faunal specimen are different from those in sediment (Appendix B, Figure A14, box). Relative abundances of β -, ϵ - and γ -*Proteobacteria* are clearly higher, whereas contributions of *Omnitrophica* and *Spirochaetes* are lower in tubes of larvae and worms compared to surface sediments. Worm and larval feces are similar to worm and larval tubes, respectively, but have higher fractions of ϵ -*Proteobacteria*. Whole worm or larval samples have very different, less diverse and more variable bacterial DNA sequences than the other sample categories. Whole worms mainly have α -, β -*Proteobacteria* and/or *Fusobacteria*, while whole larvae samples are dominated by α -, β - and/or γ -*Proteobacteria* or *Firmicutes*.

Archaea

The 13 identified archaeal phyla are dominated by *Pacearchaeota*, *Woesearchaeota*, *Diapherotrites* and *Euryarchaeota*. Overall archaeal RNA sequences are highly similar to archaeal DNA sequences (Appendix B, Figure A15). No major temporal or treatment-related trends are observed. Relative abundances of *Woesearchaeota* decrease slightly below 4 cm, whereas *Altiarchaeales* and *Euryarchaeota*

both increase with depth. *Pacearchaeota* show almost no depth- or treatment-related trends. Two uncharacterized phylum-level groups, which we call Unknown Asgardarchaeota Phylum III and *Woesearchaeota*-related phylum, have elevated abundances found in surface sediments.

In line with their low gene copy and read numbers, fauna, faunal tubes, and feces are dominated by few archaeal taxa. Larval and worm tubes and feces are somewhat similar to sediments and are dominated by *Diapherotrites*, *Pacearchaeota* and *Woesearchaeota*. Yet, major differences are again present between whole organisms and sediments. Archaeal communities of whole organisms are highly variable, but are typically dominated by *Diapherotrites*, *Pacearchaeota* and/or *Woesearchaeota* in worms or *Diapherotrites*, *Euryarchaeota*, *Pacearchaeota*, *Thaumarchaeota* or *Woesearchaeota* in larvae.

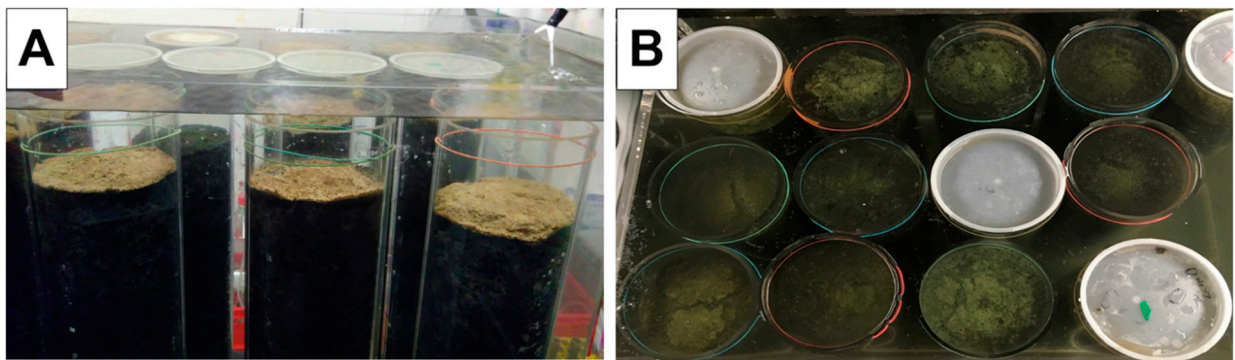


Figure S1: pictures of the sediment cores in the tank during the experiment. A: side view, B: top view. Sediment cores with lids are the hypoxic controls.

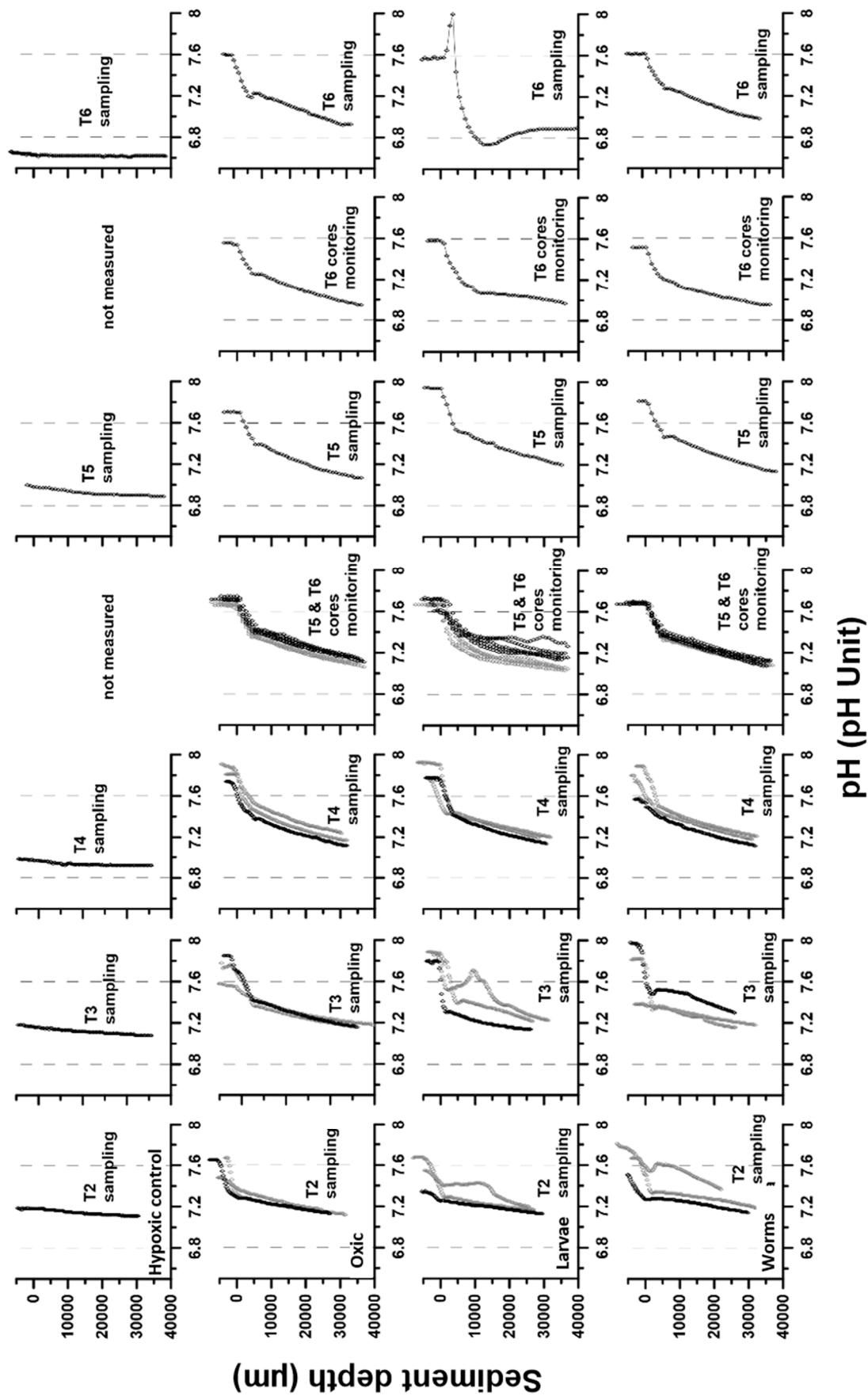


Figure S2: pH microsensor profiles during the course of the experiment, all profiles recorded on monitoring and sampling days are shown, cores to be sampled next are marked in black.

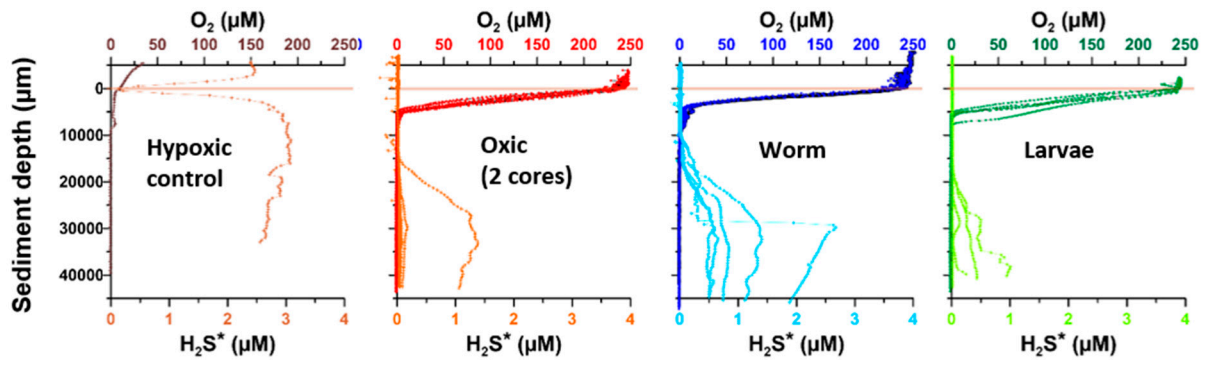


Figure S3: H_2S (lower x-axis) and O_2 (upper x-axis) microsensor profiles at T6 along sediment depth in micrometer (μm). In each core five profiles for O_2 and H_2S were measured except in the hypoxic controls where only one profile each was obtained. Please note for the oxic treatment two separate cores were measured (10 profiles of O_2 and H_2S). Please also note H_2S concentrations reflect H_2S and not total sulfide concentrations, as they were not corrected with pH.

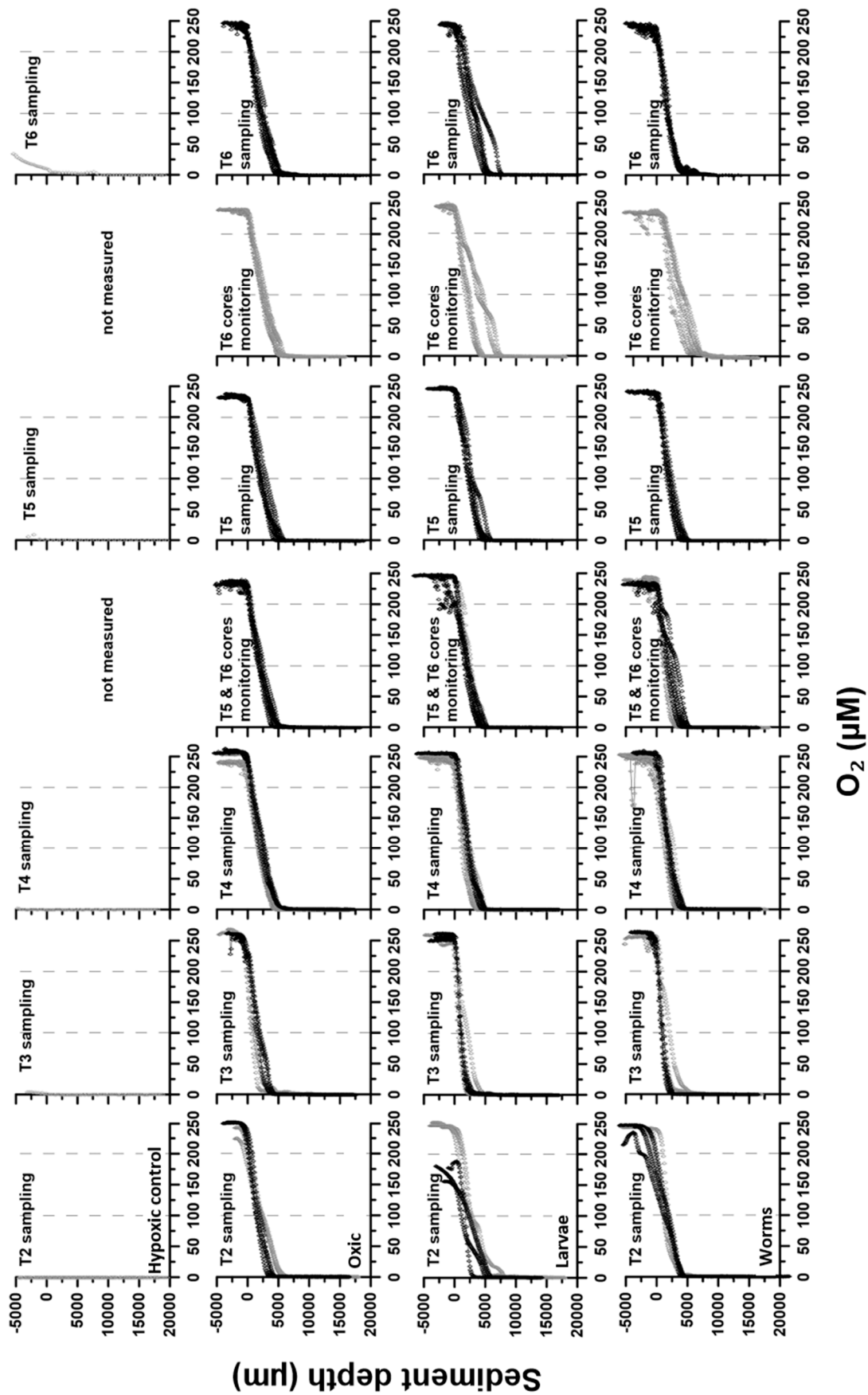


Figure S4: O₂ microsensor profiles during the course of the experiment, all profiles recorded on monitoring and sampling days are shown, cores to be sampled next are marked in black.

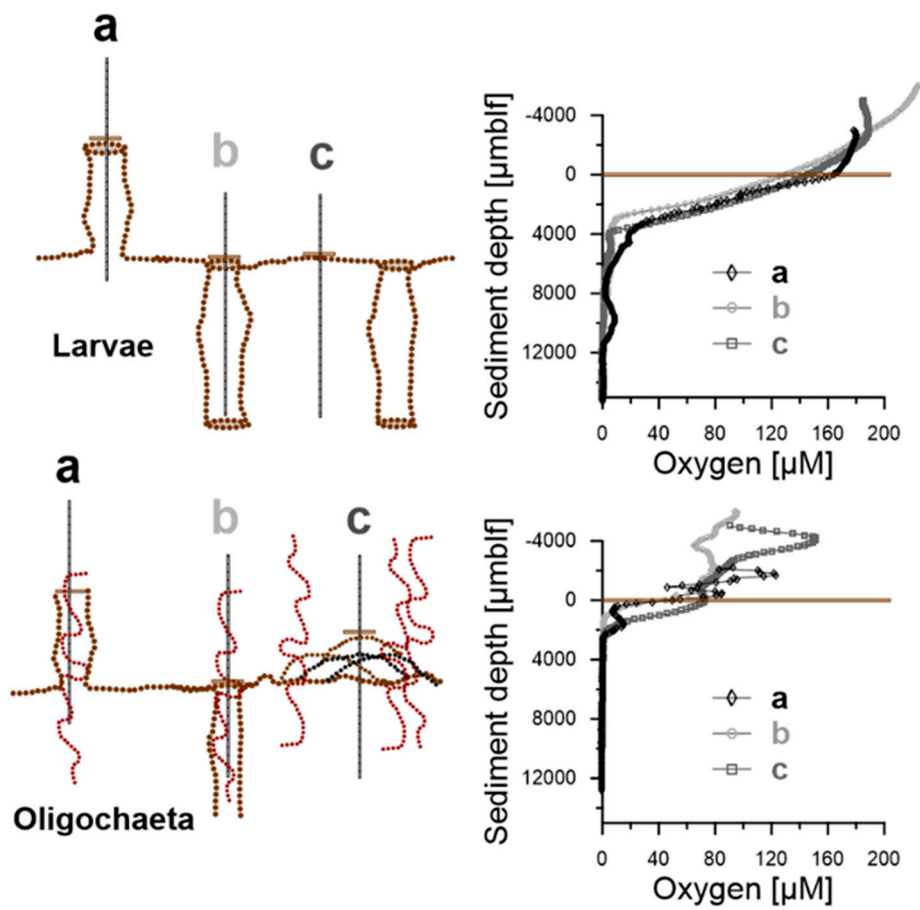


Figure S5: representative single burrow O₂ gradients measured in L (upper panel) and W (lower panel) treatments at different points in the core (profiles a-c), measured at T2.

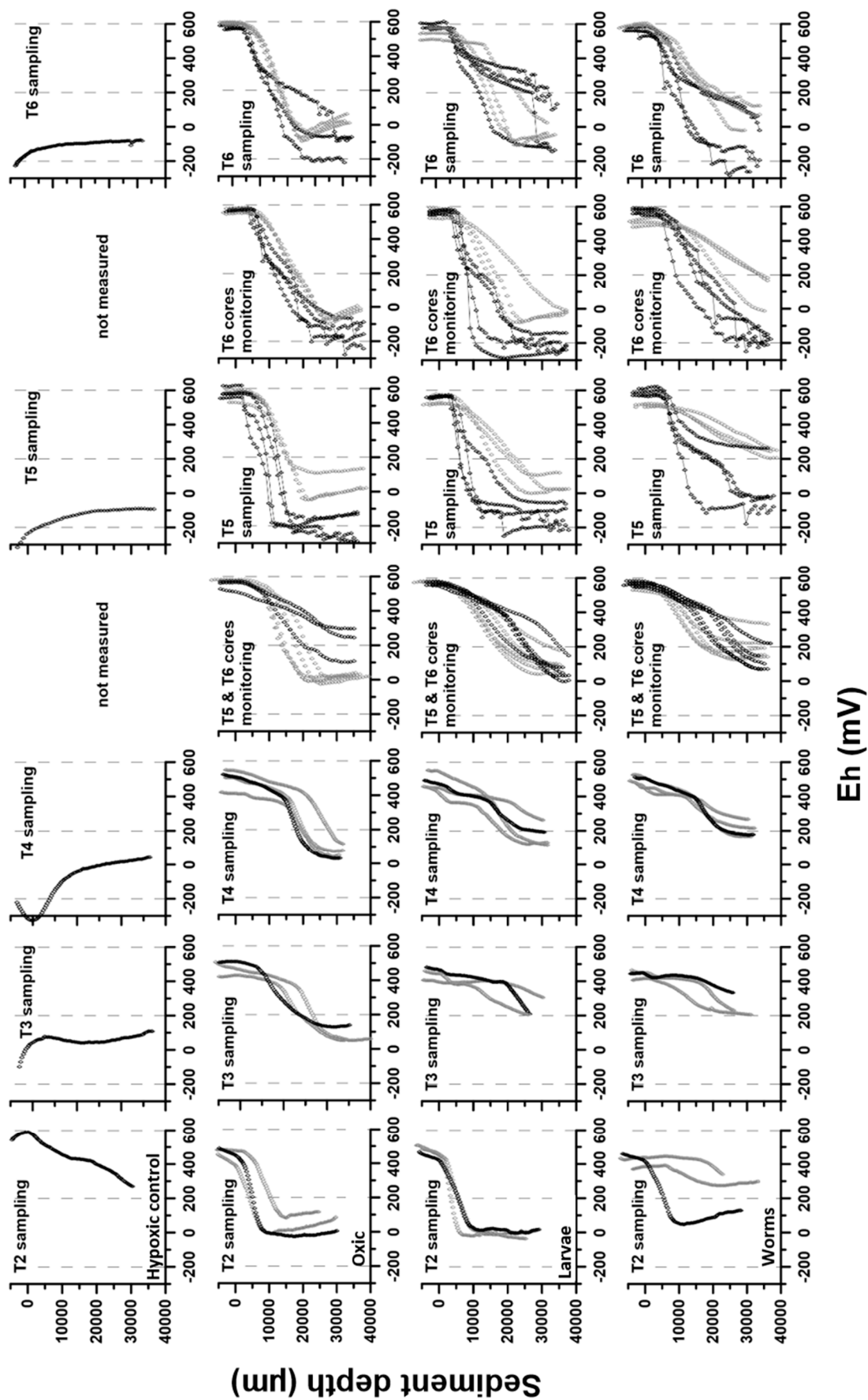


Figure S6: Redox potential (Eh) profiles during the experiment. Cores to be samples next are marked in black, whereas monitoring profiles are marked in grey lines.

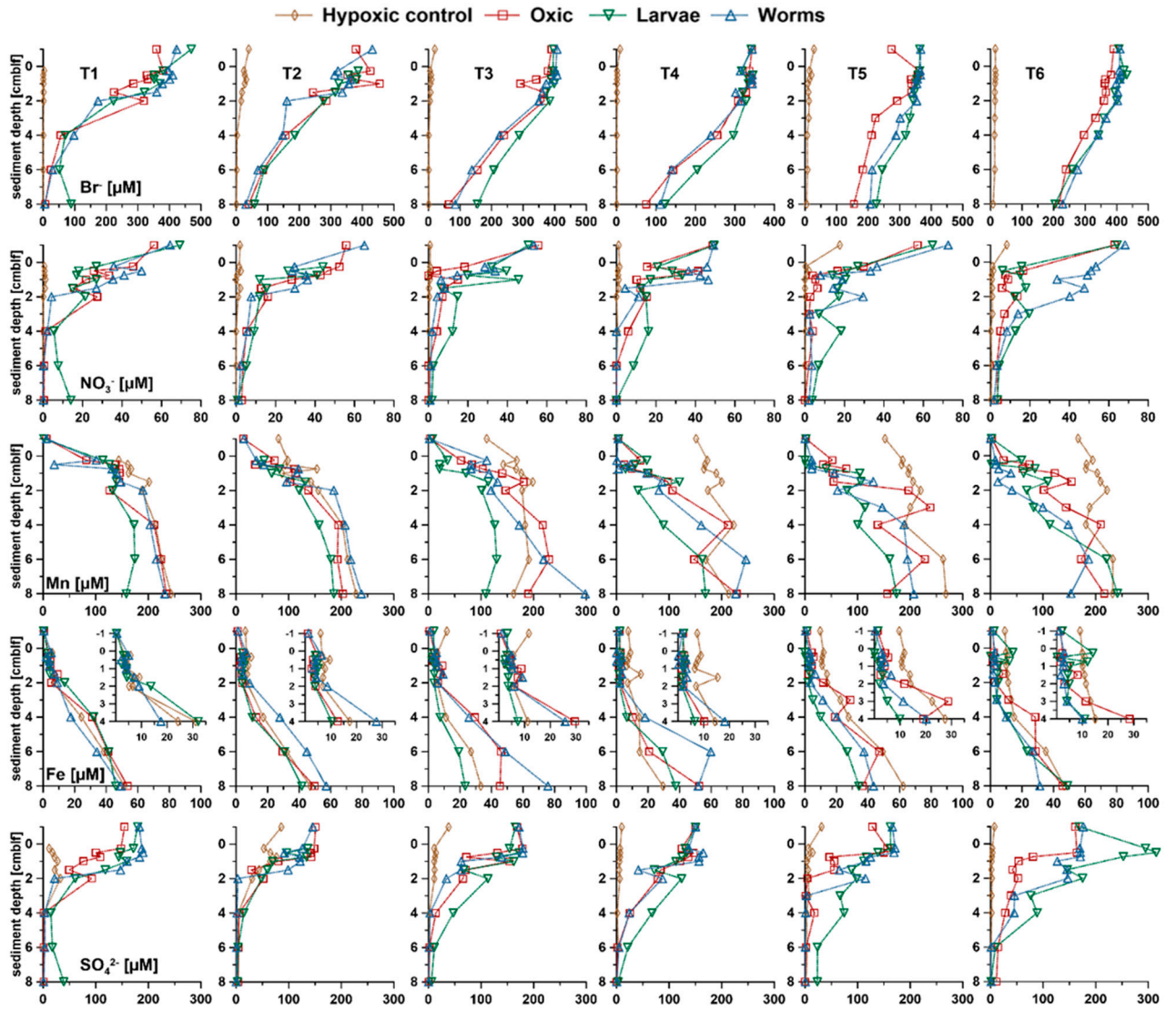


Figure S7: Porewater profiles of all measured anions and cations at all timepoints. Please note concentration ranges on x-axis differ between different analytes.

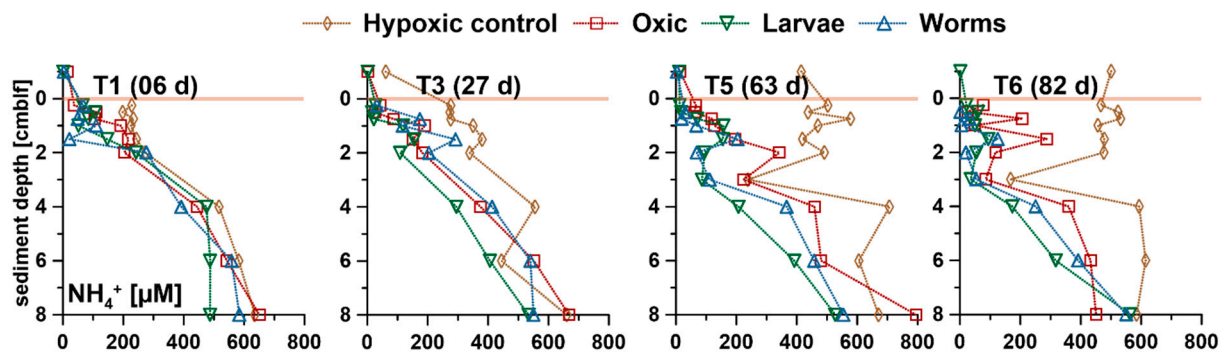


Figure S8: Concentration profiles of NH_4^+ . The sediment-water interface is indicated with a horizontal line.

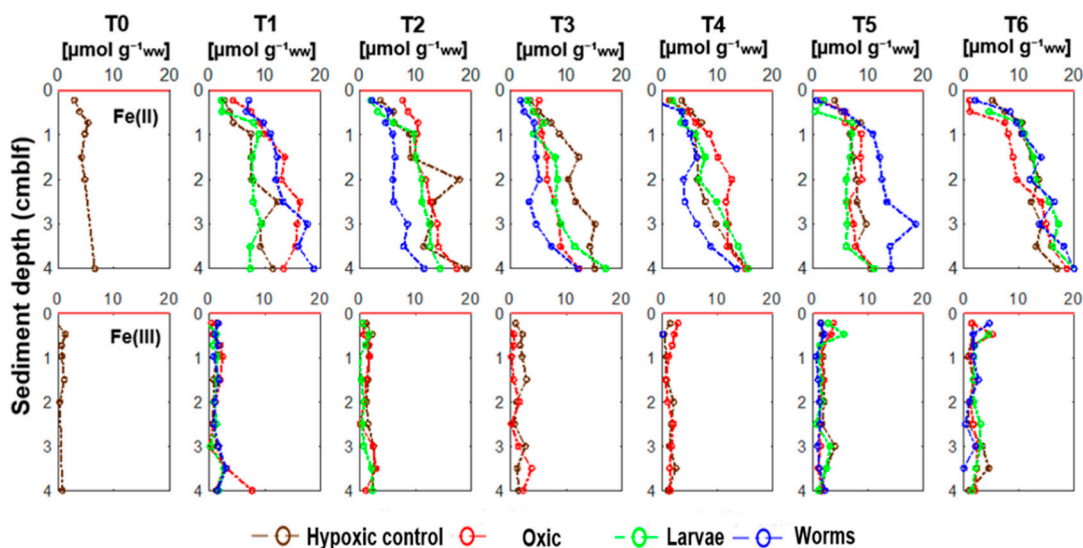


Figure S9: Bioavailable Fe(II) and Fe(III) concentrations in $\mu\text{mol g}^{-1}\text{ww}$ in the upper 4 cm of the sediment, extractions were performed with 0.5 M HCl.

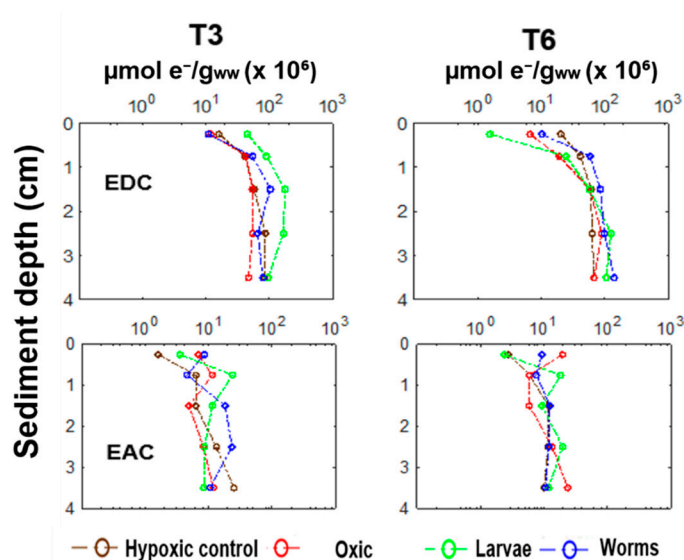


Figure S10: EAC and EDC measurements from mediated electrochemical analysis (MER and MEO) in number (nb) electrons (e^-).

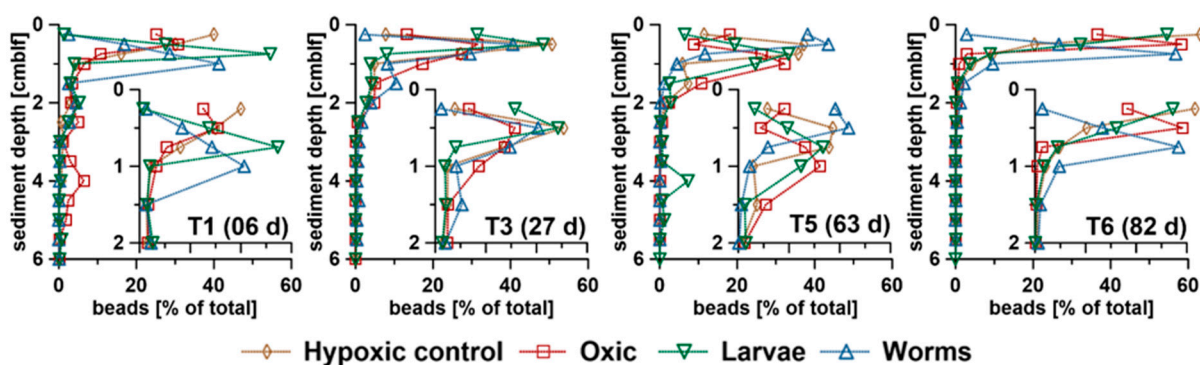


Figure S11: Luminophore bead counts at T1 (06d), T3 (27d), T5 (63d) and T6 (82d). Displayed as % of total (sum of the whole profile) for each treatment. Subplots show zoom in on the upper 2 cm of the core.

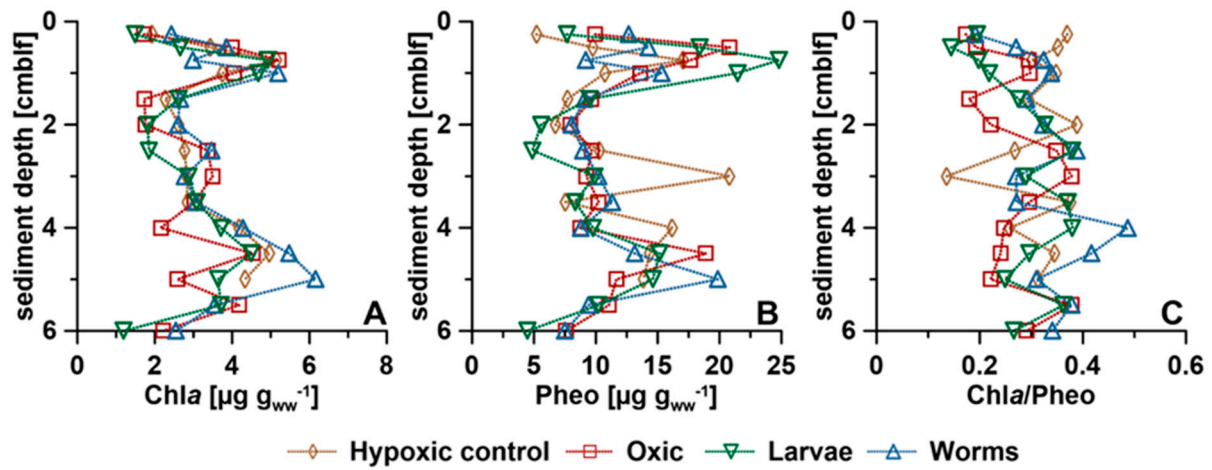


Figure S12: Chlorophyll *a* (Chla) (A) and Pheopigments (Pheo) (B) in $\mu\text{g g}_{\text{ww}}^{-1}$ as well as the ratio of Chla to Pheo (C) at T6 (82 d) for all treatments vs. sediment depth (cmblf).

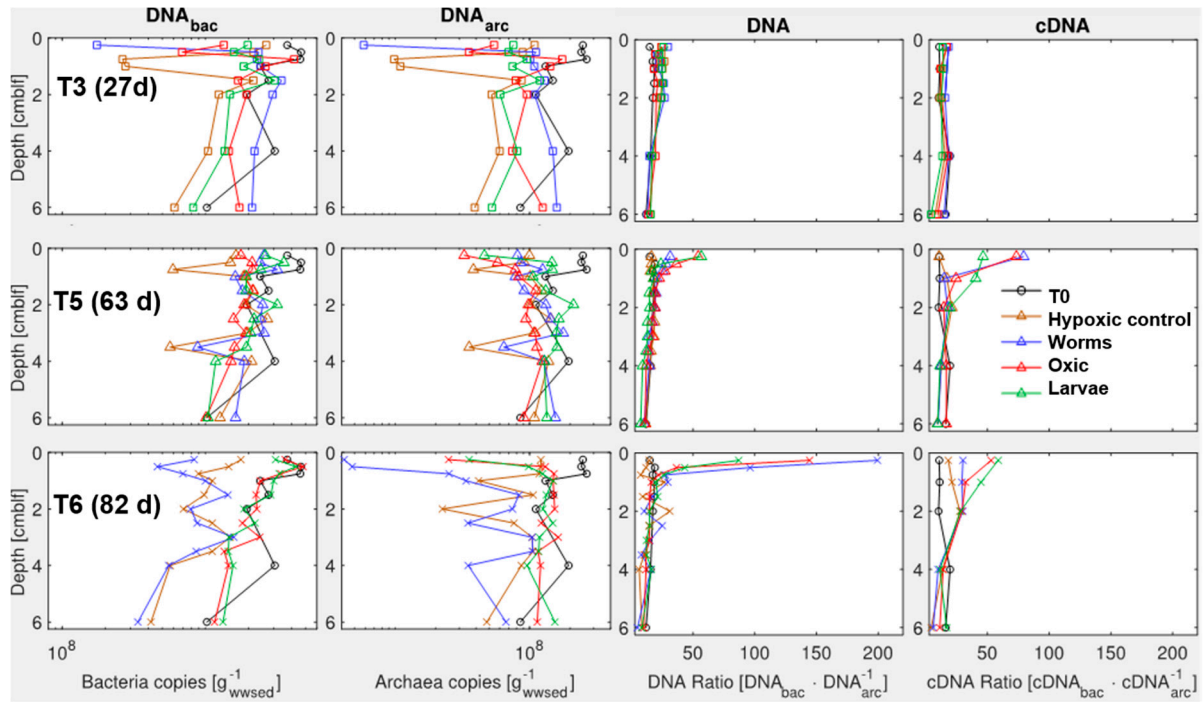


Figure S13: Left: bacterial (DNA_{bac}), and right: archaeal (DNA_{arc}) copy numbers and Bacteria to Archaea ratios (BARs) plotted against sediment depth. Left: BAR calculated from DNA, right: BAR calculated from cDNA. Each row corresponds to one different time-point (T3 (27d), T5 (63d) and T6 (82d)) with t0 as common reference line (same data).

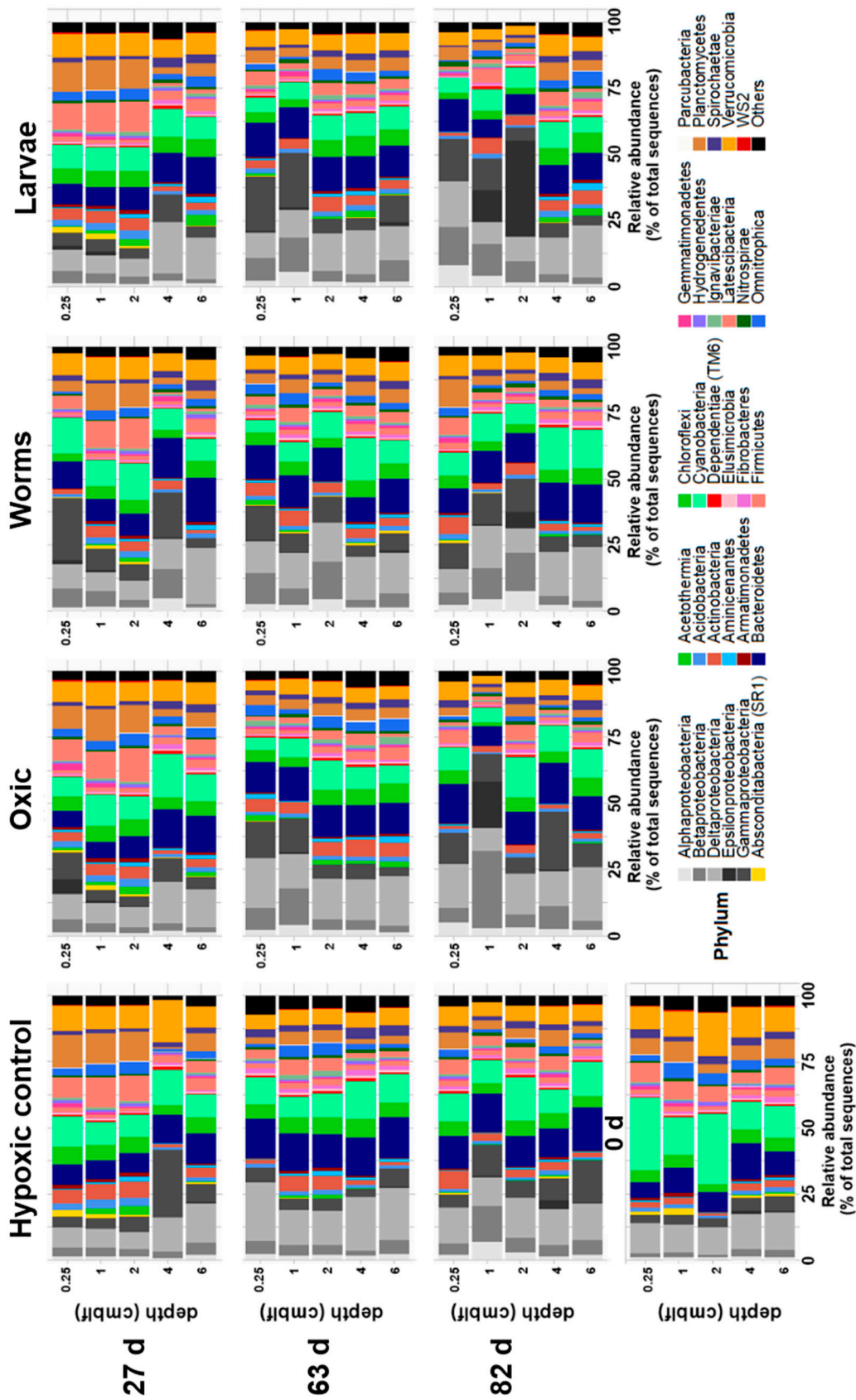


Figure S14: Relative abundances of Bacteria based on RNA extracts on the phylum level vs. sediment depth (cmblf). Columns show different treatments (C, O, W, L), rows show timepoints (T3 (27d), T5 (63d), T6 (82d)).

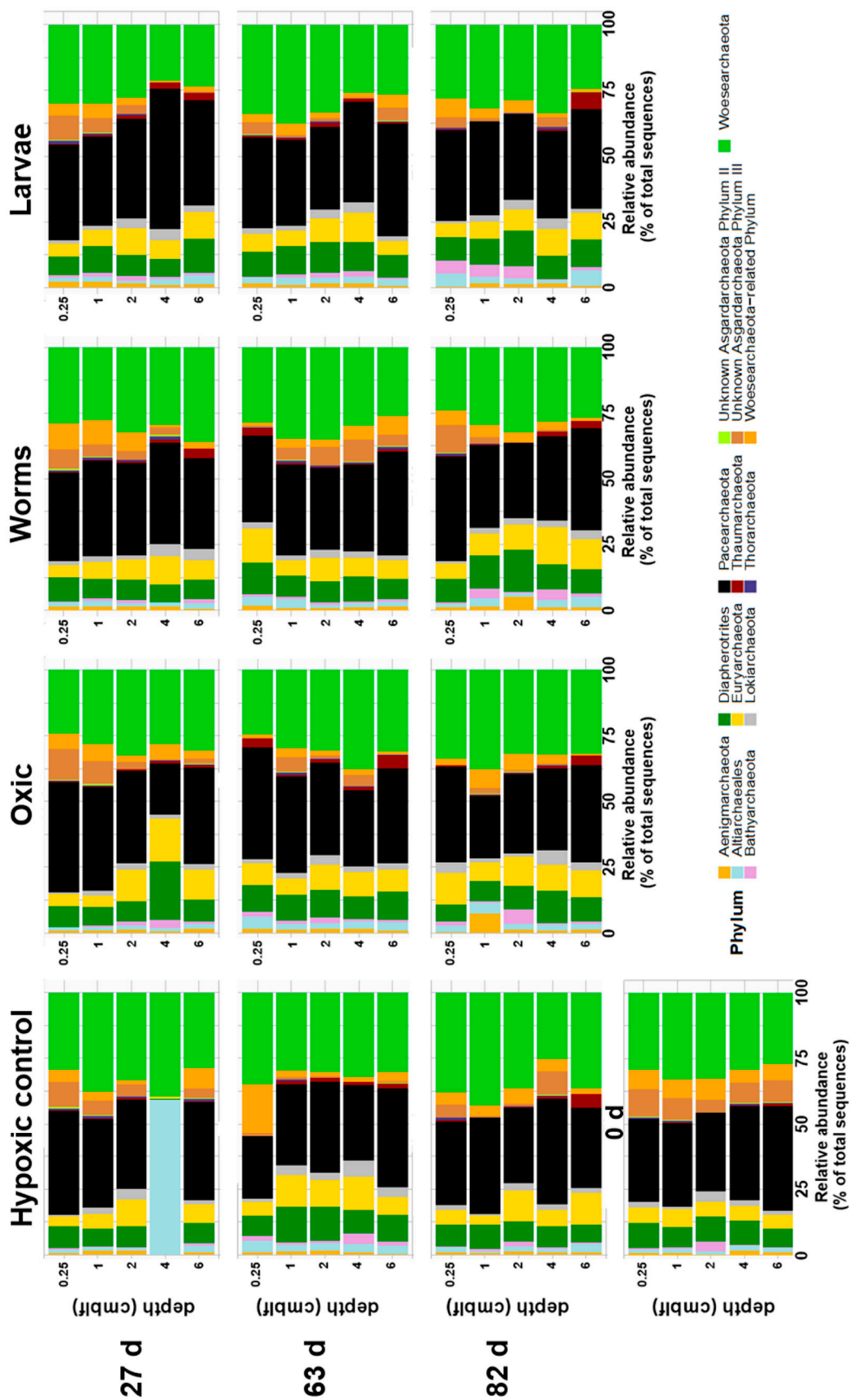


Figure S15: Relative abundances of Archaea based on RNA extracts on the phylum level vs. sediment depth (cmblf). Columns show different treatments (C, O, W, L), rows show timepoints (T3 (27d), T5 (63d), T6 (82d)).

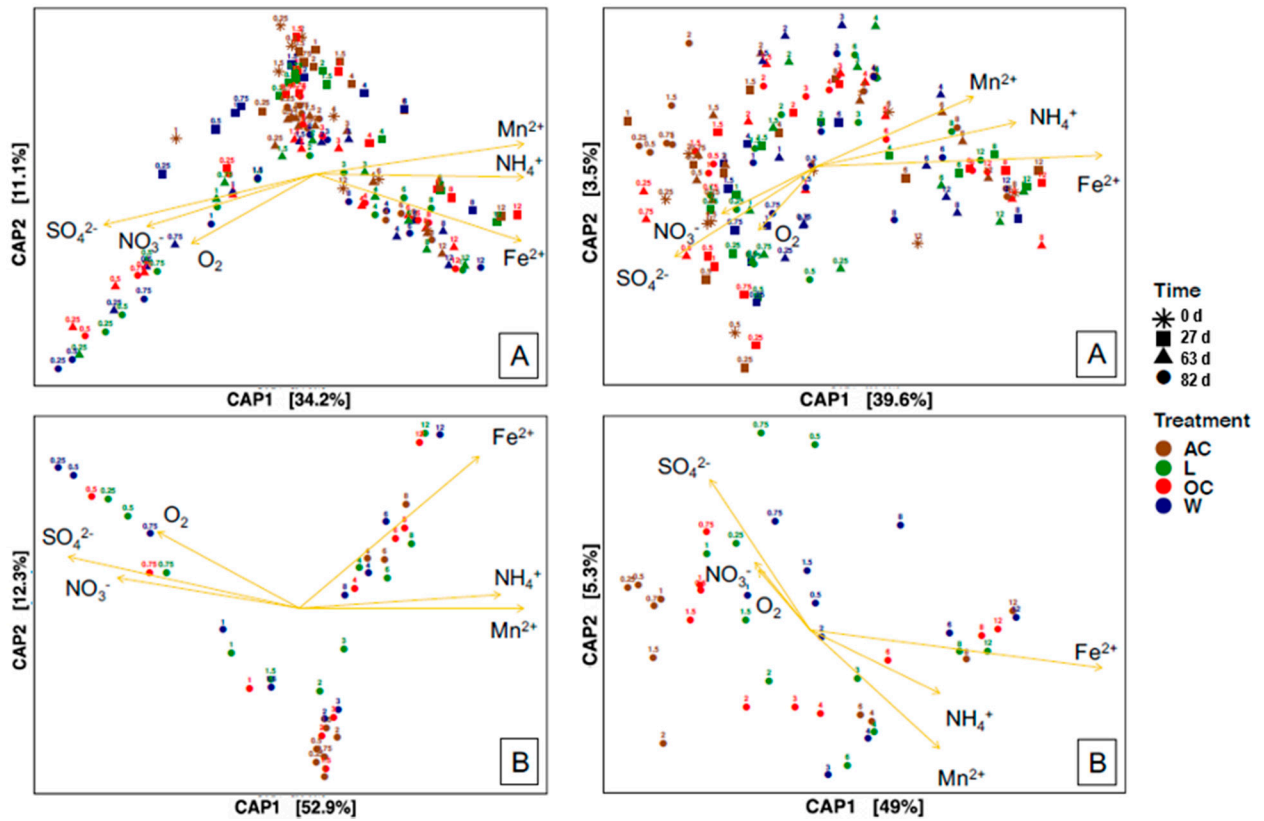


Figure S16. Left: CAP plots on bacterial phylum-level based on weighted-UniFrac: A) samples from all time points and all treatments, B) T6 samples from all treatments. Right: CAP plots on archaeal phylum-level based on weighted-UniFrac: A) samples from all time points and all treatments, B) T6 samples from all treatments.

Table S1: Bacteria to Archaea ratios (BARs) calculated from qPCR and from reads obtained from NGS with standard deviations and bacterial and archaeal read numbers according to sample type. Number of values for each category can be found in parenthesis.

Sample type	Bacterial reads (NGS)	Archaeal reads (NGS)	Bacterial zOTU numbers	Archaeal zOTU numbers
Sediment	15,470,600	712,090	4938	442
Worm tubes	1,015,312	2,427	1948	64
Larval tubes	762,976	8,969	3354	208
Worm feces	1,274,047	2,481	1323	27
Larval feces	200,664	397	1562	39
Whole worms	350,269	866	306	12
Whole larvae	814,195	97	220	4

Table S2: Table of relative abundance on the Phylum, Class and Order level for Archaea and Bacteria, with mean relative abundance (mra), maximum (Max) and the overall maximum (Overall), all T6 (82d).

nra	Max	Phyla	C						O						W						L						
			0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	
Overall	58.89	22.85	22.44	21.74	22.34	22.98	22.94	55.20	57.32	31.19	23.14	22.62	22.21	58.89	55.56	35.73	23.34	21.23	24.34	52.47	49.79	34.70	23.65	23.22	21.30		
Proteobacteria	10.12	12.41	16.89	9.86	11.09	10.53	9.84	11.61	9.50	12.23	9.48	11.04	10.66	11.74	9.68	10.58	12.10	11.76	10.51	12.41	8.84	11.49	11.76	10.90	12.30	11.26	10.15
Bacteroidetes	7.03	11.60	11.72	10.81	9.82	11.60	10.82	7.38	8.13	4.58	5.17	8.17	10.47	7.57	7.15	5.23	5.10	8.87	10.99	7.30	7.15	5.41	6.12	9.07	9.97	7.72	7.39
Actinobacteria	6.78	7.69	12.04	7.33	6.75	7.69	6.91	5.00	5.48	4.19	3.48	6.08	7.09	5.14	5.83	3.79	3.74	5.63	7.24	4.66	5.28	4.82	4.55	6.02	6.31	5.49	5.98
Planctomycetes	6.22	7.54	11.58	7.43	7.53	6.80	6.21	5.41	4.98	6.84	5.21	7.17	6.75	5.77	4.86	1.67	6.16	6.36	7.54	5.62	4.52	5.91	5.69	6.40	6.60	5.63	5.82
Chloroflexi	6.01	7.45	9.22	5.27	5.62	5.09	4.92	7.36	7.42	1.71	2.22	4.74	5.33	7.32	7.45	6.26	2.30	4.57	5.93	6.40	6.90	2.75	3.47	4.79	5.66	7.14	6.91
Onnitrophica	5.02	9.15	9.15	3.95	4.90	5.35	5.40	7.26	7.84	0.40	1.03	4.21	5.60	7.09	6.56	0.53	0.86	3.71	4.24	6.64	6.98	1.42	1.78	3.93	5.03	6.90	9.15
Cyanobacteria	4.98	7.59	24.28	7.59	6.16	5.43	4.95	2.48	2.51	4.69	4.62	4.87	4.98	4.82	2.53	3.35	3.16	4.26	4.91	3.01	2.75	3.43	3.61	4.31	4.45	3.34	2.51
Latesebacteria	4.58	7.37	10.63	4.62	4.93	5.97	7.37	2.32	1.95	1.34	1.97	4.91	6.37	1.87	2.08	0.23	0.81	2.65	4.82	2.73	2.28	1.60	1.98	3.70	4.67	2.05	1.90
Actinothermia	2.76	6.07	15.05	0.35	0.34	0.42	1.11	4.08	3.18	0.03	0.03	0.12	0.80	3.69	6.07	0.13	0.18	0.43	1.08	5.33	4.77	0.16	0.16	0.38	1.98	4.44	3.32
Firmicutes	2.72	4.79	6.42	3.63	3.21	2.68	2.83	3.40	3.67	0.56	1.32	2.40	2.53	2.94	4.79	0.63	0.59	1.93	3.01	3.69	3.66	0.94	1.10	2.16	2.60	3.48	2.88
Globobacteria	2.05	2.25	6.15	1.42	1.48	1.42	1.48	2.25	1.78	1.44	1.13	1.68	1.88	1.96	1.60	1.79	1.83	1.84	1.87	1.96	1.80	1.71	1.66	1.76	2.18	1.88	1.55
Ignavibacteriae	1.95	3.71	3.92	1.38	1.42	1.58	1.44	3.27	3.71	0.48	0.61	1.25	1.73	2.98	3.40	0.57	0.82	1.36	1.94	3.35	3.40	0.74	0.85	1.30	2.22	2.66	3.68
Armanicantes	1.83	3.95	5.92	0.73	0.80	0.74	1.43	2.95	3.31	0.08	0.17	0.43	0.82	1.91	2.96	0.08	0.18	0.61	1.14	2.77	3.37	0.22	0.26	0.56	1.25	2.11	3.95
Spirochaetae	1.69	2.52	6.15	1.76	1.82	1.92	1.38	1.77	2.14	0.45	0.88	1.65	1.56	1.93	1.80	0.16	0.34	1.20	1.45	1.89	2.52	0.59	0.79	1.46	1.57	1.49	2.06
Gemmatimonadetes	1.19	3.16	3.16	2.17	2.21	1.46	1.27	1.25	1.25	2.72	1.71	2.00	1.08	0.85	0.78	3.16	2.95	1.68	1.01	0.74	0.72	2.21	1.84	1.60	0.97	0.93	0.89
Armatimonadetes	1.07	1.65	2.47	0.72	0.60	0.64	0.67	1.27	1.29	0.14	0.19	0.42	0.64	1.13	1.55	0.13	0.14	0.48	0.99	1.39	1.65	0.24	0.23	0.40	0.65	1.20	1.41
Nitrospirae	0.69	1.67	1.67	0.40	0.49	0.54	0.57	0.58	0.48	1.09	0.56	0.80	0.68	0.73	0.57	1.67	1.47	0.83	0.74	0.52	0.60	0.95	0.90	0.79	0.71	0.53	0.47
Others	7.12	8.67	9.69	7.75	8.38	8.38	8.06	7.88	8.44	1.83	2.90	6.86	7.87	7.93	8.13	1.12	1.70	6.08	7.26	1.70	8.45	2.94	3.45	7.25	8.54	8.67	

nra	Max	Overall	C						O						W						L						
			0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	
Betaproteobacteria	6.44	30.49	30.49	4.97	5.23	4.44	4.60	3.44	2.53	20.92	30.49	8.73	4.90	3.61	2.60	16.99	19.27	13.20	5.20	3.10	3.29	21.05	20.95	12.15	5.29	3.32	2.42
Gammaproteobacteria	6.74	26.83	26.83	5.37	5.67	6.39	6.42	4.49	3.67	17.10	15.66	8.45	6.82	4.87	3.63	26.83	23.41	9.93	6.64	4.36	3.65	15.14	13.67	9.51	6.47	4.34	3.32
Deltaproteobacteria	12.66	18.17	20.85	12.73	12.00	11.53	12.30	15.49	17.56	6.54	7.33	12.98	11.84	14.35	16.41	5.00	5.87	10.61	11.68	14.52	18.17	9.40	10.25	11.54	11.79	15.56	16.40
Alphaproteobacteria	2.32	11.53	11.53	2.19	2.30	2.38	2.50	1.59	1.21	11.53	5.76	3.62	2.70	1.55	1.54	9.04	7.37	3.62	2.17	1.39	1.23	8.37	6.67	3.83	2.24	1.79	1.09
Sphingobacteria	3.43	8.18	8.18	3.84	4.27	3.94	3.88	3.03	2.30	8.18	4.40	4.53	4.50	3.35	2.49	7.19	7.68	4.98	3.51	3.28	2.26	6.65	6.33	4.49	4.57	2.95	2.70
Chloroplast	2.86	5.68	24.80	5.68	4.29	3.39	2.87	1.12	0.80	3.46	3.67	2.86	2.61	1.96	1.14	2.32	2.21	2.32	2.45	1.34	0.89	2.20	2.26	2.44	2.38	1.15	1.00
Acidimicrobia	2.19	5.29	5.29	4.87	4.60	5.29	4.32	1.92	2.05	1.64	2.17	3.56	4.18	2.16	2.07	1.40	1.38	2.80	3.72	1.50	1.74	1.85	2.36	3.53	3.26	1.88	2.13
Planctomycetia	3.17	4.67	6.85	4.67	3.81	4.45	3.66	1.69	1.67	2.64	2.05	3.43	3.93	1.88	1.79	2.63	2.27	3.11	3.74	1.94	1.47	3.33	2.94	3.67	3.43	2.21	1.84
Thermopicrophilia	3.16	5.22	5.65	3.44	3.15	4.24	4.83	3.74	4.06	0.90	1.38	2.84	4.27	3.43	3.11	1.30	1.51	3.56	5.22	4.32	3.40	1.48	1.82	3.24	4.66	3.89	3.55
Gemmatimonadetes	1.26	3.19	3.45	2.38	2.47	1.66	1.42	0.75	1.24	2.78	1.77	2.21	1.20	0.82	0.73	3.19	3.01	1.78	1.06	0.72	0.64	0.78	1.92	1.72	1.02	0.90	0.88
Chlorisidia	2.10	3.15	4.58	2.94	2.82	2.13	2.10	2.76	2.59	0.39	1.02	2.11	1.97	2.30	3.15	0.35	0.39	1.40	2.32	3.01	2.81	0.71	0.83	1.79	2.02	2.54	2.26
Dehalococcidia	1.89	2.85	3.51	2.21	2.85	2.37	1.79	1.54	2.49	0.26	0.73	2.39	1.99	1.85	2.00	0.09	0.41	1.42	1.49	1.63	1.71	0.75	1.01	1.50	1.62	2.16	1.74
OPDPB35 soil group	2.10	2.77	2.83	2.16	2.20	2.47	2.35	2.25	1.77	2.77	1.85	2.04	2.26	2.21	1.69	2.24	2.36	2.34	2.43	2.40	1.80	2.31	2.09	2.35	2.17	1.94	1.90
uncultured bacterium	2.90	5.55	5.60	2.03	2.63	2.87	3.04	4.36	4.64	0.18	0.52	2.21	3.19	4.37	3.91	0.22	0.40	2.00	2.53	4.28	4.30	0.70	0.95	2.30	3.12	4.42	5.55
Bacteroidia	1.59	2.62	2.62	2.36	2.62	2.20	1.77	1.46	1.18	0.51	1.01	2.07	1.73	1.55	1.19	0.29	0.70	1.76	1.73	1.81	0.95	1.07	1.41	1.81	2.16	1.40	0.92
Bacteroidetes vadinHA17	4.01	6.41	7.78	1.94	2.57	3.00	3.50	6.41	5.02	1.40	1.40	2.60	3.58	5.59	4.96	0.37	0.97	3.29	4.16	6.13	4.08	1.28	1.83	3.22	4.97	5.87	5.78
Cyanobacteria	2.54	3.06	10.83	2.48	2.16	2.48	2.65	1.45	1.59	1.25	0.91	2.23	2.72	3.06	1.30	1.04	0.95	2.06	2.79	1.84	1.94	1.30	1.45	2.21	2.39	1.56	1.66
Actinobacteria	1.78	2.90	3.20	2.44	2.36	2.90	2.70	1.71	1.93	2.00	1.51	2.02	2.74	1.89	1.73	2.44	2.13	2.52	2.56	1.53	1.68	1.95	1.80	2.46	2.45	1.79	1.64
Phycisphaerae	3.24	3.90	6.86	2.12	2.39	2.98	3.00	2.85	3.56	0.44	0.75	2.12	2.86	2.85	3.83	0.24	0.45	1.88	2.97	2.45	3.38	0.74	0.93	1.81	2.52	2.93	3.90
Cytophaga	0.38	2.27	2.72	0.74	0.79	0.46	0.28	0.09	0.10	2.27	0.97	0.93	0.38	0.16	0.08	1.90	1.65	0.62	0.29	0.13	0.07	1.50	1.13	0.62	0.23	0.12	0.06
Anaerolineae	2.61	4.08	4.26	2.11	2.13	1.94	2.15	4.08	3.17	0.58	0.75	1.62	2.24	3.61	3.64	0.40	0.76	1.74	2.74	3.12	3.13	0.90	1.22	1.94	2.51	3.45	3.42
Spirochaetes	1.81	2.67	7.02	1.91	2.03	2.16	1.56	1.84	2.27	0.44	0.90	1.81	1.74	2.04	1.92	0.16	0.34	1.27	1.58	2.04	2.67	0.61	0.81	1.56	1.70	1.57	2.23
Verucomicrobiae	1.55	2.08	3.33	1.90	1.83	1.63	1.22	0.92	1.44	2.00	1.44	2.02	1.56	0.80	1.06	1.69	1.66	1.40	2.08	0.85	0.64	1.35	1.38	1.44	1.64	0.80	1.82
WCBB1-41	1.13	1.75	1.88	1.55	1.75	1.17	1.45	1.23	1.01	1.20	0.53	1.38	1.68	1.55	1.26	0.15	0.27	1.12	1.25	1.37	1.15	0.48	0.56	1.11	1.28	1.10	1.15
Nitrospira	0.76	1.69	1.69	0.45	0.56	0.62	0.67	0.64	0.52	1.11	0.58	0.90	0.77	0.80	0.62	1.69	1.50	0.90	0.83	0.58	0.65	0.99	0.95	0.87	0.79	0.58	0.52
Flavobacteriia	0.61	1.11	1.40	0.84	0.88	1.11	0.90	0.23	0.26	0.54	0.54	0.94	0.79	0.35	0.30	0.71	0.88	0.90	0.75	0.34	0.18	0.58	0.66	0.70	0.55	0.24	0.22
Others	0.62	1.68	1.68	0.77	0.53	0.64	0.87	0.72	1.11	0.27	0.14	0.25	0.37	0.65	0.66	1.68	0.23	0.16	0.52	0.79	0.74	0.93	0.19	0.23	0.41	0.66	

Order	mm	C						O						W						L									
		Max	Overall	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm		
Methylococcales	2.09	16.90	16.90	0.88	0.83	0.91	0.91	0.83	0.46	4.92	9.37	2.56	1.07	1.06	0.57	16.90	15.98	3.82	1.55	0.86	0.53	7.44	6.03	3.59	1.36	0.84	0.48		
Sphingobacteriales	3.94	9.23	9.23	4.46	4.91	4.51	4.34	3.51	2.66	9.23	5.70	5.13	5.20	4.13	2.90	7.91	8.49	5.69	3.86	3.83	2.62	7.60	7.23	5.16	5.10	3.38	3.16		
Burkholderiales	2.37	8.34	9.62	2.66	2.86	1.88	2.06	1.08	0.77	7.92	8.34	3.35	2.18	1.21	0.87	6.86	5.82	4.01	1.86	1.03	1.21	5.41	6.08	3.89	2.07	1.47	0.65		
Rhodocyclales	1.34	7.48	7.48	0.74	0.82	0.93	0.87	1.05	0.54	3.44	7.48	1.38	0.91	0.99	0.56	2.07	3.75	2.82	1.14	0.76	0.65	4.63	4.86	2.92	1.18	0.67	0.57		
Nitrosomonadales	1.20	7.01	8.21	0.65	0.70	0.66	0.75	0.68	0.58	4.77	7.01	1.39	0.79	0.78	0.60	4.08	4.73	2.34	0.94	0.67	0.70	5.16	4.59	2.22	1.05	0.58	0.58		
Syntrophobacteriales	5.28	7.32	8.44	6.70	5.75	5.44	6.04	6.17	7.15	0.79	2.21	4.60	5.38	5.60	6.69	0.58	0.99	3.92	5.01	6.00	7.32	1.73	2.00	4.13	5.05	6.13	6.50		
Acidimicrobiales	2.57	6.16	6.16	5.70	5.33	6.16	5.05	2.26	2.38	1.86	2.59	4.07	4.87	2.53	2.42	1.54	1.53	3.24	4.33	4.34	3.83	1.77	2.02	2.12	2.72	4.11	3.84	2.19	2.51
Planctomycetales	3.73	5.47	7.99	5.47	4.42	5.18	4.27	1.98	1.93	2.99	2.43	3.92	4.59	2.20	2.08	2.90	2.52	3.59	4.34	2.28	1.71	3.83	3.39	4.27	4.03	2.56	2.15		
Mycococcales	2.01	4.78	11.92	2.40	2.24	1.56	1.48	2.78	2.89	3.49	2.45	2.08	1.72	2.26	2.20	2.52	2.49	1.84	1.91	2.20	2.52	4.46	4.78	2.89	1.74	2.84	2.54		
Caulobacteriales	0.36	4.60	4.60	0.17	0.23	0.19	0.21	0.07	0.04	4.60	2.63	0.82	0.24	0.09	0.05	1.82	1.50	0.53	0.13	0.05	0.02	2.29	1.85	0.72	0.15	0.11	0.04		
HTA4	0.08	4.44	4.44	0.01	0.01	0.01	0.01	0.00	0.00	4.44	2.18	0.53	0.05	0.00	0.00	0.62	0.26	0.14	0.01	0.01	0.00	0.30	0.45	0.11	0.01	0.05	0.00		
Xanthomonadales	2.26	3.72	3.72	1.94	2.21	2.54	2.78	2.20	2.04	2.67	1.73	2.45	2.87	2.14	1.93	3.72	3.09	2.92	2.72	2.07	2.13	2.42	2.56	2.70	2.62	1.91	1.77		
Gemmatimonadales	1.47	3.52	3.91	2.79	2.86	1.93	1.66	0.88	1.44	3.15	2.11	2.52	1.40	0.97	0.85	3.52	3.34	2.05	1.24	0.85	0.75	2.63	2.21	2.00	1.20	1.05	1.03		
Clostridiales	2.28	3.51	5.04	3.23	3.09	2.35	2.37	3.05	2.90	0.42	1.15	2.29	2.16	2.53	3.51	0.35	0.41	1.52	2.58	3.33	3.10	0.75	0.89	1.98	2.26	2.82	2.53		
Cellvibrionales	1.09	2.92	2.92	0.85	1.01	1.25	1.30	0.87	0.68	2.50	1.69	1.32	1.30	1.03	0.63	2.92	2.25	1.45	1.23	0.80	0.69	1.76	1.89	1.45	1.28	0.81	0.65		
GIF9	0.97	2.71	2.98	2.03	2.71	1.72	1.04	0.34	0.40	0.21	0.73	1.98	1.31	0.37	0.45	0.07	0.26	0.92	0.47	0.32	0.32	0.65	0.88	1.15	0.71	0.30	0.34		
Rhizobiales	0.96	2.68	2.68	0.97	0.85	0.97	1.03	0.98	0.85	2.63	1.39	1.00	1.11	0.77	1.19	2.68	2.20	1.27	1.04	0.89	0.84	2.14	1.99	1.34	1.09	0.77	0.69		
Methylophilales	0.41	2.59	4.32	0.25	0.26	0.21	0.20	0.12	0.05	2.20	2.22	0.60	0.21	0.15	0.06	2.54	2.59	0.69	0.21	0.08	0.05	1.67	1.30	0.71	0.17	0.14	0.06		
Cytophagales	0.44	2.56	2.56	0.86	0.92	0.53	0.32	0.10	0.11	2.56	1.16	1.07	0.45	0.19	0.10	2.10	1.83	0.72	0.34	0.16	0.08	1.72	1.31	0.72	0.28	0.14	0.07		
Anaerolineales	3.06	4.79	4.94	2.48	2.47	2.26	2.52	4.79	3.69	0.65	0.90	1.85	2.61	4.24	4.26	0.44	0.85	2.01	3.19	3.67	3.64	1.04	1.41	2.25	2.96	4.01	4.02		
Gastellales	2.72	4.55	5.33	2.44	2.37	2.95	3.69	3.67	3.56	0.68	1.04	2.10	3.50	3.38	2.62	1.08	1.26	2.90	4.55	4.19	3.05	1.22	1.49	2.57	4.02	3.57	3.06		
Subsection I	2.60	3.39	10.22	2.36	2.05	2.67	2.65	1.52	1.59	1.12	0.75	2.07	2.81	3.39	1.40	1.03	0.89	2.02	3.01	1.96	2.10	1.16	1.33	2.06	2.53	2.50	1.65		
Spirochaetales	2.11	3.09	8.16	2.20	2.31	2.47	1.82	2.16	2.64	0.49	1.06	2.06	2.02	2.37	2.24	0.18	0.38	1.47	1.82	2.38	3.09	0.70	0.93	1.80	1.99	1.83	2.61		
Verrucomicrobiales	1.83	2.43	4.01	2.23	2.12	1.90	1.43	1.08	1.68	2.27	1.72	2.31	1.83	0.93	1.23	1.87	1.84	1.61	2.43	1.00	0.74	1.55	1.59	1.67	1.93	0.94	2.14		
Rhodobacterales	0.39	2.19	2.19	0.44	0.45	0.50	0.42	0.12	0.08	2.19	1.01	0.82	0.47	0.15	0.12	1.61	1.24	0.74	0.33	0.16	0.09	1.42	0.91	0.71	0.32	0.19	0.12		
Bacteroidales	1.22	2.08	2.08	2.04	2.08	1.47	1.32	1.17	1.07	0.27	0.72	1.36	1.29	1.32	1.07	0.07	0.40	1.24	1.30	1.48	0.85	0.80	1.00	1.25	1.62	1.18	0.88		
Nitrospirales	0.89	1.87	1.87	0.53	0.65	0.72	0.78	0.75	0.61	1.26	0.69	1.03	0.90	0.94	0.73	1.87	1.66	1.03	0.96	0.68	0.75	1.14	1.09	1.01	0.93	0.67	0.61		
Desulfobacterales	1.18	2.04	2.04	1.10	1.00	1.24	1.06	1.22	1.06	0.37	1.00	2.04	1.07	1.16	1.06	0.42	0.51	1.43	1.06	1.07	1.24	1.35	1.70	1.87	1.46	0.98	0.85		
Flavobacteriales	0.72	1.29	1.64	0.98	1.02	1.29	1.05	0.27	0.30	0.61	0.64	1.07	0.93	0.42	0.35	0.79	0.98	1.04	0.87	0.39	0.21	0.67	0.76	0.82	0.65	0.27	0.26		
Rhodospirillales	0.55	2.07	2.07	0.45	0.59	0.58	0.80	0.42	0.22	1.44	0.73	0.66	0.81	0.57	0.24	1.40	1.28	0.84	0.63	0.32	0.28	2.07	1.80	1.02	0.65	0.54	0.22		
Others	47.87	40.89	68.13	39.97	40.89	43.04	45.77	53.89	55.64	23.86	25.17	39.55	43.98	52.15	57.04	23.52	24.64	40.14	44.94	54.75	56.67	28.17	28.98	36.89	45.74	54.59	57.24		

Phyla	C										O										W										L									
	Overall					C					O					W					L																			
	max	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm											
Paecearchaeota	36.45	41.37	52.76	31.04	32.16	33.26	27.98	35.30	35.82	34.02	34.17	34.21	31.29	36.02	38.06	32.31	38.98	36.37	37.25	34.31	41.37	35.55	39.88	34.41	33.38	34.05	34.05													
Woesearchaeota	28.74	39.23	50.00	37.42	36.96	37.32	39.21	26.93	29.70	35.06	36.56	33.33	33.75	30.10	27.55	39.23	29.40	31.99	27.36	27.49	23.79	30.37	26.11	31.62	32.61	27.99	30.57													
Diapherotrites	10.54	13.33	18.25	8.29	8.90	8.64	8.54	11.42	11.54	11.20	11.75	11.45	12.31	10.68	12.14	6.15	8.46	10.04	9.57	13.33	9.62	11.36	11.81	10.40	12.68	12.48	11.68													
Euryarchaeota	8.35	13.40	50.00	6.04	5.36	5.35	8.68	13.40	8.82	4.56	4.13	4.59	8.13	8.76	10.00	8.02	6.04	10.98	10.82	9.99	6.07	5.42	4.04	6.82	10.73	8.49														
Unk. Asgardarchaeota Phylum III	3.33	7.99	13.71	6.60	6.02	5.67	5.25	0.74	0.19	5.19	5.98	5.43	3.48	1.14	0.14	1.54	3.79	5.05	3.01	0.52	0.03	7.99	6.66	6.69	6.57	0.79	0.17													
Altiarchaeates	2.87	4.69	8.72	1.58	1.78	1.83	2.64	2.00	3.14	2.28	1.63	2.76	3.06	2.50	2.97	0.77	1.56	2.01	1.69	3.20	4.69	2.02	3.11	2.72	2.88	2.79	2.89													
Woesearchaeota-related phylum	2.83	4.45	9.14	4.30	4.32	3.06	2.67	0.80	1.25	2.28	1.09	4.18	2.60	1.71	1.19	1.54	1.11	2.27	2.70	1.77	1.04	3.15	2.22	4.45	2.64	1.23	0.96													
Lokiarchaeota	2.27	4.43	4.60	1.72	1.89	1.89	1.78	3.61	2.05	3.11	2.18	0.88	1.02	4.43	2.16	3.85	3.12	1.82	3.04	2.87	3.81	1.01	1.51	1.54	2.25	3.27	2.57													
Thaumarchaeota	1.68	6.81	7.45	0.33	0.39	0.57	0.83	3.41	5.74	0.00	0.54	0.42	1.06	1.52	4.65	0.77	1.78	1.28	1.47	2.77	3.17	0.67	0.80	0.59	0.70	4.29	6.81													
Aenigmarchaeota	1.25	3.85	3.85	1.19	0.72	1.09	1.39	1.32	0.65	0.62	0.87	1.04	1.10	1.41	1.32	3.85	1.34	1.31	1.57	1.84	1.09	0.67	0.71	1.51	1.37	1.18	0.69													
Bathyarchaeota	0.99	1.41	3.86	0.06	0.15	0.17	0.68	0.90	0.99	0.00	0.22	0.04	0.96	0.79	0.87	0.00	0.22	0.45	0.50	0.89	1.41	0.45	0.89	0.70	0.98	1.02	1.04													
Thorarchaeota	0.56	1.78	1.78	1.03	0.85	1.00	0.30	0.16	0.11	1.66	0.65	1.59	1.04	0.22	0.19	0.00	1.78	1.28	0.78	0.14	0.00	0.56	0.53	1.10	0.98	0.18	0.07													
Unk. Asgardarchaeota Phylum II	0.12	0.50	0.55	0.42	0.50	0.14	0.06	0.00	0.00	0.00	0.22	0.08	0.20	0.05	0.00	0.00	0.45	0.10	0.06	0.05	0.00	0.11	0.36	0.22	0.14	0.00	0.00													

Classes	mra	Max	0.25cm						0.5cm						1cm						2cm						4cm						6cm																							
			Overall	36.45	41.37	52.76	31.04	32.16	33.26	27.98	35.30	35.82	34.02	34.17	34.21	31.29	36.02	38.06	32.31	38.98	36.37	37.25	34.31	41.37	35.55	39.88	34.41	33.38	34.05	34.05	36.45	41.37	52.76	31.04	32.16	33.26	27.98	35.30	35.82	34.02	34.17	34.21	31.29	36.02	38.06	32.31	38.98	36.37	37.25	34.31	41.37	35.55	39.88	34.41	33.38	34.05
Unc. Pacarachaota	36.45	41.37	52.76	31.04	32.16	33.26	27.98	35.30	35.82	34.02	34.17	34.21	31.29	36.02	38.06	32.31	38.98	36.37	37.25	34.31	41.37	35.55	39.88	34.41	33.38	34.05	34.05	36.45	41.37	52.76	31.04	32.16	33.26	27.98	35.30	35.82	34.02	34.17	34.21	31.29	36.02	38.06	32.31	38.98	36.37	37.25	34.31	41.37	35.55	39.88	34.41	33.38	34.05	34.05		
Unc. Woesearchaota	28.74	39.23	50.00	37.42	36.96	37.32	39.21	26.93	29.70	35.06	36.56	33.33	33.75	30.10	27.55	39.23	29.40	31.99	27.36	27.49	23.79	30.37	26.11	31.62	32.61	27.99	30.57	28.74	39.23	50.00	37.42	36.96	37.32	39.21	26.93	29.70	35.06	36.56	33.33	33.75	30.10	27.55	39.23	29.40	31.99	27.36	27.49	23.79	30.37	26.11	31.62	32.61	27.99	30.57		
Micrarchaea	6.55	8.96	12.75	5.18	5.32	4.84	4.95	8.25	7.47	8.09	6.86	5.93	6.12	7.55	7.27	5.38	6.46	7.48	6.50	8.18	5.03	5.40	5.42	5.77	8.96	8.78	7.26	6.55	8.96	12.75	5.18	5.32	4.84	4.95	8.25	7.47	8.09	6.86	5.93	6.12	7.55	7.27	5.38	6.46	7.48	6.50	8.18	5.03	5.40	5.42	5.77	8.96	8.78	7.26		
Thermoplasmata	5.46	9.13	25.00	5.49	4.84	4.87	6.99	6.61	4.90	3.53	3.70	3.80	6.41	5.22	5.27	6.15	5.12	4.70	9.13	5.67	6.42	5.51	5.24	3.38	4.71	5.63	3.98	5.46	9.13	25.00	5.49	4.84	4.87	6.99	6.61	4.90	3.53	3.70	3.80	6.41	5.22	5.27	6.15	5.12	4.70	9.13	5.67	6.42	5.51	5.24	3.38	4.71	5.63	3.98		
Iainarchaea	4.00	6.39	12.16	3.10	3.58	3.81	3.59	3.17	4.07	3.11	4.90	5.51	6.18	3.12	4.87	0.77	2.00	2.56	3.07	5.15	4.58	5.96	6.39	4.63	3.72	3.70	4.42	4.00	6.39	12.16	3.10	3.58	3.81	3.59	3.17	4.07	3.11	4.90	5.51	6.18	3.12	4.87	0.77	2.00	2.56	3.07	5.15	4.58	5.96	6.39	4.63	3.72	3.70	4.42		
Unc. Asgardarc. Phylum III	3.33	7.99	13.71	6.60	6.02	5.67	5.25	0.74	1.19	5.19	5.98	5.43	3.48	1.14	0.14	1.54	3.79	5.05	3.01	0.52	0.03	7.99	6.66	6.69	2.57	0.79	0.17	3.33	7.99	13.71	6.60	6.02	5.67	5.25	0.74	1.19	5.19	5.98	5.43	3.48	1.14	0.14	1.54	3.79	5.05	3.01	0.52	0.03	7.99	6.66	6.69	2.57	0.79	0.17		
Unc. Woesearchaota-rel.	2.83	4.45	9.14	4.30	4.32	3.06	2.67	0.80	1.25	2.28	1.09	4.18	2.60	1.71	1.19	1.54	1.11	2.27	2.70	1.77	1.04	3.15	2.22	4.45	2.64	1.23	0.96	2.83	4.45	9.14	4.30	4.32	3.06	2.67	0.80	1.25	2.28	1.09	4.18	2.60	1.71	1.19	1.54	1.11	2.27	2.70	1.77	1.04	3.15	2.22	4.45	2.64	1.23	0.96		
Lokiarchaeota Beta Subgroup	2.19	4.13	4.58	1.72	1.85	1.89	1.75	3.59	1.88	3.11	2.07	0.88	1.00	4.13	2.08	3.85	2.44	1.76	2.95	2.82	3.81	1.01	1.51	2.22	4.45	2.64	1.23	2.19	4.13	4.58	1.72	1.85	1.89	1.75	3.59	1.88	3.11	2.07	0.88	1.00	4.13	2.08	3.85	2.44	1.76	2.95	2.82	3.81	1.01	1.51	2.22	4.45	2.64	1.23	0.96	
Alii-2	2.14	3.94	8.16	1.33	1.45	1.46	1.39	1.58	2.62	1.87	1.41	2.34	1.98	1.58	2.14	0.00	1.34	1.41	1.10	2.52	3.94	1.57	2.31	1.95	1.44	1.75	2.49	2.14	3.94	8.16	1.33	1.45	1.46	1.39	1.58	2.62	1.87	1.41	2.34	1.98	1.58	2.14	0.00	1.34	1.41	1.10	2.52	3.94	1.57	2.31	1.95	1.44	1.75	2.49		
Unc. Freshwater Euryarc. Class I	1.79	5.35	5.65	0.25	0.04	0.03	1.33	5.35	3.23	0.62	0.11	0.38	1.26	3.64	2.81	3.08	2.67	1.15	1.63	4.15	2.18	0.45	0.09	0.55	1.69	4.33	3.46	1.79	5.35	5.65	0.25	0.04	0.03	1.33	5.35	3.23	0.62	0.11	0.38	1.26	3.64	2.81	3.08	2.67	1.15	1.63	4.15	2.18	0.45	0.09	0.55	1.69	4.33	3.46		
Nitrososphacteria	1.52	6.67	7.26	0.11	0.26	0.40	0.47	3.09	4.96	0.00	0.33	0.29	0.86	1.33	4.43	0.77	1.78	0.93	1.26	2.73	3.09	0.34	0.44	0.48	0.60	4.06	6.67	1.52	6.67	7.26	0.11	0.26	0.40	0.47	3.09	4.96	0.00	0.33	0.29	0.86	1.33	4.43	0.77	1.78	0.93	1.26	2.73	3.09	0.34	0.44	0.48	0.60	4.06	6.67		
Aenignnarchaeota Group II	0.96	1.54	2.47	0.80	0.59	1.03	1.16	1.00	0.51	0.41	0.44	1.00	0.98	0.76	1.00	1.54	0.89	0.96	0.91	1.06	0.64	0.45	0.62	1.12	0.88	0.52	0.96	1.54	2.47	0.80	0.59	1.03	1.16	1.00	0.51	0.41	0.44	1.00	0.98	0.76	1.00	1.54	0.89	0.96	0.91	1.06	0.64	0.45	0.62	1.12	0.88	0.52				
Unc. Freshwater Euryarc. Class II	0.77	1.24	25.00	0.17	0.20	0.17	0.27	1.24	0.27	0.41	0.33	0.25	0.10	0.43	0.30	0.77	0.00	0.06	0.16	0.73	0.88	0.11	0.00	0.00	0.21	0.45	0.67	0.77	1.24	25.00	0.17	0.20	0.17	0.27	1.24	0.27	0.41	0.33	0.25	0.10	0.43	0.30	0.77	0.00	0.06	0.16	0.73	0.88	0.11	0.00	0.00	0.21	0.45	0.67		
Unc. Altiiarchaeales	0.74	1.44	2.44	0.25	0.33	0.37	1.24	0.42	0.53	0.41	0.22	0.42	1.08	0.92	0.84	0.77	0.22	0.61	0.60	0.68	0.75	0.45	0.80	0.77	1.44	1.04	0.40	0.74	1.44	2.44	0.25	0.33	0.37	1.24	0.42	0.53	0.41	0.22	0.42	1.08	0.92	0.84	0.77	0.22	0.61	0.60	0.68	0.75	0.45	0.80	0.77	1.44	1.04	0.40		
MCG-6	0.66	0.90	3.83	0.03	0.15	0.17	0.56	0.20	0.38	0.00	0.22	0.04	0.90	0.27	0.43	0.00	0.00	0.38	0.19	0.27	0.37	0.45	0.62	0.70	0.81	0.34	0.54	0.66	0.90	3.83	0.03	0.15	0.17	0.56	0.20	0.38	0.00	0.22	0.04	0.90	0.27	0.43	0.00	0.00	0.38	0.19	0.27	0.37	0.45	0.62	0.70	0.81	0.34	0.54		
Others	1.85	3.79	3.79	2.22	1.93	1.66	1.61	1.19	1.72	2.24	1.87	1.63	2.01	2.00	2.06	1.62	2.31	3.79	2.33	2.20	1.95	2.08	1.22	1.69	2.17	1.90	1.70	1.41	1.85	3.79	3.79	2.22	1.93	1.66	1.61	1.19	1.72	2.24	1.87	1.63	2.01	2.00	2.06	1.62	2.31	3.79	2.33	2.20	1.95	2.08	1.22	1.69	2.17	1.90	1.70	1.41

Orders	C					O					W					L											
	<i>nra</i>	Max	Overall	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm	0.25cm	0.5cm	1cm	2cm	4cm	6cm						
Unc. Pacarchaeota	36.45	41.37	52.76	31.04	32.16	33.26	27.98	35.30	35.82	34.02	34.17	34.21	31.29	36.02	38.06	32.31	38.98	36.37	37.25	34.31	41.37	35.55	39.88	34.41	33.38	34.05	34.05
Unc. Woesearchaeota	28.74	39.23	50.00	37.42	36.96	37.32	39.21	26.93	29.70	35.06	36.56	33.33	33.75	30.10	27.55	39.23	29.40	31.99	27.36	27.49	23.79	30.37	26.11	31.62	32.61	27.99	30.57
Unc. Micrarchaeia	6.55	8.96	12.75	5.18	5.32	4.84	4.95	8.25	7.47	8.09	6.86	5.93	6.12	7.55	7.27	5.38	6.46	7.48	6.50	8.18	5.03	5.40	5.42	5.77	8.96	8.78	7.26
Thermoplasmatales	4.09	8.03	9.96	3.74	3.78	3.15	4.83	5.37	3.55	2.90	2.94	2.72	4.38	4.46	4.35	3.85	3.79	3.26	8.03	4.66	5.38	2.36	2.31	2.21	3.37	4.54	2.79
Unc. Iainarchaeia	4.00	6.39	12.16	3.10	3.58	3.81	3.59	3.17	4.07	3.11	4.90	5.51	6.18	3.12	4.87	0.77	2.00	2.56	3.07	5.15	4.58	5.96	6.39	4.63	3.72	3.70	4.42
Unc. Asgardarchaeota Phylum III	3.33	7.99	13.71	6.60	6.02	5.67	5.25	0.74	0.19	5.19	5.98	5.43	3.48	1.14	0.14	1.54	3.79	5.05	3.01	0.52	0.03	7.99	6.66	6.69	2.57	0.79	0.17
Unc. Woesearchaeota-rel.	2.83	4.45	9.14	4.30	4.32	3.06	2.67	0.80	1.25	2.28	1.09	4.18	2.60	1.71	1.19	1.54	1.11	2.27	2.70	1.77	1.04	3.15	2.22	4.45	2.64	1.23	0.96
Unc. Lokiarchaeota Beta Subgroup	2.19	4.13	4.58	1.72	1.85	1.89	1.75	3.59	1.88	3.11	2.07	0.88	1.00	4.13	2.08	3.85	2.45	1.76	2.95	2.82	3.81	1.01	1.51	1.40	2.21	3.27	2.44
Unc. Alti-2	2.14	3.94	8.16	1.33	1.45	1.46	1.39	1.58	2.62	1.87	1.41	2.34	1.98	1.58	2.14	3.08	2.67	1.15	1.63	4.15	2.18	0.45	0.09	0.55	1.69	4.33	3.46
Unc. Freshwater Euryarc. Class I	1.79	5.35	5.65	0.25	0.04	0.03	1.33	5.35	3.23	0.62	0.11	0.38	1.26	3.64	2.81	3.08	2.67	1.15	1.63	4.15	2.18	0.45	0.09	0.55	1.69	4.33	3.46
MBG-D	1.37	3.15	25.00	1.75	1.06	1.72	2.16	1.24	1.35	0.62	0.76	1.09	2.02	0.76	0.92	2.31	1.34	1.44	1.10	1.01	1.04	3.15	2.93	1.18	1.34	1.09	1.19
Aenigmarc. Group II Unc. Subgroup	0.96	1.54	2.47	0.80	0.59	1.03	1.16	1.00	0.51	0.41	0.44	1.00	0.98	0.76	1.00	1.54	0.89	0.96	0.91	1.06	0.64	0.45	0.62	1.03	1.12	0.88	0.52
Nitrososphaeria Subgroup III	0.80	3.70	4.88	0.03	0.04	0.14	0.21	1.08	2.36	0.00	0.00	0.08	0.48	0.57	2.00	0.77	0.22	0.35	0.66	1.39	1.28	0.00	0.18	0.15	0.11	2.31	3.70
Unc. Altiarchaeales	0.74	1.44	2.44	0.25	0.33	0.37	1.24	0.42	0.53	0.41	0.22	0.42	1.08	0.92	0.84	0.77	0.22	0.61	0.60	0.68	0.75	0.45	0.80	0.77	1.44	1.04	0.40
Unc. MCG-6	0.66	0.90	3.83	0.03	0.15	0.17	0.56	0.20	0.38	0.00	0.22	0.04	0.90	0.27	0.43	0.00	0.00	0.38	0.19	0.27	0.37	0.45	0.62	0.70	0.81	0.34	0.54
Unc. Thorarchaeota	0.56	1.78	1.78	1.03	0.85	1.00	0.30	0.16	0.11	1.66	0.65	1.59	1.04	0.22	0.19	0.00	1.78	1.28	0.78	0.14	0.00	0.56	0.53	1.10	0.98	0.18	0.07
Nitrososphaeria Subgroup IV	0.43	2.62	2.90	0.03	0.00	0.00	0.03	1.82	2.32	0.00	0.00	0.00	0.00	0.60	2.19	0.00	0.00	0.00	0.25	0.86	1.73	0.00	0.00	0.07	0.04	1.47	2.62
Unc. C3	0.32	1.04	2.10	0.03	0.00	0.00	0.12	0.70	0.61	0.00	0.00	0.00	0.06	0.52	0.43	0.00	0.22	0.06	0.31	0.62	1.04	0.00	0.27	0.00	0.18	0.68	0.49
Methanobacteriales	0.32	0.51	1.47	0.14	0.28	0.29	0.09	0.20	0.42	0.00	0.00	0.17	0.36	0.14	0.38	0.00	0.22	0.13	0.06	0.27	0.51	0.00	0.09	0.11	0.21	0.32	0.40
Nitrososphaerales	0.29	1.56	1.56	0.06	0.22	0.26	0.24	0.18	0.27	0.00	0.33	0.21	0.38	0.16	0.24	0.00	1.56	0.58	0.35	0.48	0.08	0.34	0.27	0.26	0.46	0.27	0.35
Nitrosopumilales	0.16	0.78	0.78	0.22	0.13	0.17	0.36	0.32	0.78	0.00	0.22	0.13	0.20	0.19	0.22	0.00	0.00	0.35	0.22	0.05	0.08	0.34	0.36	0.11	0.11	0.23	0.15
Others	1.27	3.08	25.00	0.97	0.87	0.37	0.59	1.58	0.59	0.62	1.09	0.38	0.44	1.44	0.70	3.08	1.56	0.58	0.97	1.60	1.33	0.45	0.44	0.85	0.63	0.75	0.96

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