

SUPPLEMENTARY MATERIAL TABLES

Table S1. Preparation for the 2x AE buffer.

| Components | Concentration (in M) | Volume (in ml) |
|---------------|----------------------|----------------|
| EDTA | 0.5 | 20 |
| EGTA | 1.5 | 50 |
| NaCl | 1 | 40 |
| Tris (pH 8.0) | 1 | 40 |
| Milli-Q Water | --- | 50 |
| Total | | 200 |

Table S2. PCR primer pairs used for 16S/18S rRNA gene amplification.

| Domain | Primer | Sequence (5'-3') |
|-----------|--------|-----------------------|
| Bacteria | B341F | CCTACGGGAGGCAGCAG |
| | B785R | GACTACHVGGGTATCTAATCC |
| Eukaryote | A340F | CCCTACGGGGYGCASCAG |
| | A915R | GTGCTCCCCCGCCAATTCCT |
| Archaea | E960F | GGCTTAATTTGACTCAACRCG |
| | E1438R | GGGCATCACAGACCTGTTAT |

Table S3. PCR conditions used for 16S/18S rRNA gene amplification.

| Domain | | Denaturation | Annealing | Extension | Final extension |
|-----------|--------------|--------------|-----------|-------------|-----------------|
| Bacteria | Nb of cycles | | 35 | | 1 |
| | Time | 30 sec | 1 min | Time | 30 sec |
| | Temperature | 98°C | 57°C | Temperature | 98°C |
| Eukaryote | Nb of cycles | | 35 | | 1 |
| | Time | 30 sec | 30 sec | Time | 30 sec |
| | Temperature | 98°C | 61°C | Temperature | 98°C |
| Archaea | Nb of cycles | | 35 | | 1 |
| | Time | 30 sec | 30 sec | 1 min | 10 min |
| | Temperature | 98°C | 67°C | 72°C | 72°C |

Table S4. Primer pairs and probe used for the dPCR assays.

| Primer | Type | Sequence (5'-3') |
|--------|----------------|-----------------------|
| B341F | Forward primer | CCTACGGGAGGCAGCAG |
| B515 | Probe | GTGYCAGCMGCCGCGGTAA |
| B785R | Reverse primer | GACTACHVGGGTATCTAATCC |

Table S5. Conditions used for the dPCR assays.

| | Activation | Hybridization/Elongation | Denaturation | Final elongation |
|--------------|------------|--------------------------|--------------|------------------|
| Nb of cycles | 1 | 39 | | 1 |
| Time | 10 min | 3 min | 30 sec | 2 min |
| Temperature | 96°C | 56°C | 98°C | 56°C |

Table S6. Results of the Kruskal–Wallis tests between the rock properties of the 3 bioreactors. BR1, bioreactor 1; BR2, bioreactor 2; BR3, bioreactor 3.

| Parameter | | Z | p-value |
|----------------|---------|------------|-----------|
| Iron Oxide | | | |
| | BR1-BR2 | 0.7522085 | 0.9038514 |
| | BR1-BR3 | 1.6147739 | 0.3190790 |
| | BR2-BR3 | 0.7337965 | 0.4630727 |
| Quartz | | | |
| | BR1-BR2 | 0.3940416 | 0.6935503 |
| | BR1-BR3 | 1.3220515 | 0.5584530 |
| | BR2-BR3 | 0.8142107 | 0.8310485 |
| Red Feldspar | | | |
| | BR1-BR2 | 0.1711161 | 0.8641325 |
| | BR1-BR3 | -1.0413972 | 0.5953825 |
| | BR2-BR3 | -1.1046955 | 0.8078747 |
| White Feldspar | | | |
| | BR1-BR2 | -0.9125175 | 0.7229927 |
| | BR1-BR3 | -1.9410723 | 0.1567485 |
| | BR2-BR3 | -0.8740791 | 0.3820752 |
| Mica | | | |
| | BR1-BR2 | -0.5599539 | 1.0000000 |
| | BR1-BR3 | -0.3183535 | 1.0000000 |
| | BR2-BR3 | 0.2514474 | 0.8014682 |

Table S7. Results of Kruskal–Wallis tests between the geochemical property averages of the 3 bioreactors. BR1, bioreactor 1; BR2, bioreactor 2; BR3, bioreactor 3.

| Parameter | | Z | p-value |
|------------------------------|---------|------------|-----------|
| DIC | | | |
| | BR1-BR2 | -0.2286511 | 0.8191401 |
| | BR1-BR3 | -0.7240618 | 1.0000000 |
| | BR2-BR3 | -0.4954107 | 1.0000000 |
| DOC | | | |
| | BR1-BR2 | -1.5494015 | 0.2425704 |
| | BR1-BR3 | -1.6510017 | 0.2962147 |
| | BR2-BR3 | -0.1016001 | 0.9190741 |
| NO ₂ ⁻ | | | |
| | BR1-BR2 | -0.6454230 | 1.0000000 |
| | BR1-BR3 | -0.4388877 | 1.0000000 |
| | BR2-BR3 | 0.2065354 | 0.8363727 |
| NO ₃ ⁻ | | | |
| | BR1-BR2 | 1.1593176 | 0.4926535 |
| | BR1-BR3 | 1.3631536 | 0.5185023 |
| | BR2-BR3 | 0.2038361 | 0.8384816 |
| NH ₄ | | | |
| | BR1-BR2 | -0.5843306 | 1.0000000 |
| | BR1-BR3 | -0.8256845 | 1.0000000 |
| | BR2-BR3 | -0.2413539 | 0.8092808 |

Table S8. Rock-attached bacterial absolute abundance measured using digital PCR and expressed in gene copies per rock chip. BR, bioreactor.

| Sample | Abundance |
|---------------|------------------|
| BR1-1B | 1332608 |
| BR1-5B | 1649984 |
| BR1-7B | 818032 |
| BR1-8B | 729321 |
| BR1-1H | 928812 |
| BR1-3H | 67110.35 |
| BR1-6H | 1428149 |
| BR1-7H | 453429.5 |
| BR1-2M | 1132813 |
| BR1-3M | 476948.5 |
| BR1-4M | 809970 |
| BR1-6M | 2392239 |
| BR2-3B | 365066.5 |
| BR2-7B | 43592.8 |
| BR2-8B | 545134.8 |
| BR2-4H | 194.3 |
| BR2-6H | 453509.3 |
| BR2-3M | 141589.6 |
| BR2-7M | 652659.5 |
| BR2-8M | 553465 |
| BR3-1B | 1376036 |
| BR3-2B | 1506898 |
| BR3-5B | 1572235 |
| BR3-7B | 2386062 |
| BR3-4H | 748548 |
| BR3-5H | 446534.8 |
| BR3-8H | 1046161 |
| BR3-2M | 498009.8 |
| BR3-R3M | 463507 |
| BR3-6M | 142764.1 |

Table S9. Shared and unique genera between the sessile and planktonic communities of the Bacteria and Eukaryote domains.

| BACTERIA |
|---|
| Planktonic-Sessile shared |
| Gallionella;Gallionellaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Alkanindiges;Moraxellaceae;Pseudomonadales;Gammaproteobacteria;Proteobacteria |
| unclassified_Acetobacteraceae;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria |
| Collimonas;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Undibacterium;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Sideroxydans;Gallionellaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Herminiimonas;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Sulfurimonas;Sulfurimonadaceae;Campylobacteriales;Campylobacteria;Campylobacterota |
| Rhodoferrax;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Acidocella;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria |
| unclassified_Oxalobacteraceae;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Cupriavidus;Burkholderiaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Rhodoblastus;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria |
| unclassified_Hydrogenophilaceae;Hydrogenophilaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Methylothermus;Methylophilaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Afipia;Xanthobacteraceae;Rhizobiales;Alphaproteobacteria;Proteobacteria |
| unclassified_Acidimicrobiia;unclassified_Acidimicrobiia;unclassified_Acidimicrobiia;Acidimicrobiia;Actinobacteriota |
| Novosphingobium;Sphingomonadaceae;Sphingomonadales;Alphaproteobacteria;Proteobacteria |
| Rhodovastum;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria |
| Pseudomonas;Pseudomonadaceae;Pseudomonadales;Gammaproteobacteria;Proteobacteria |
| Candidatus Solibacter;Solibacteraceae;Solibacteriales;Acidobacteriae;Acidobacteriota |
| Burkholderia-Caballeronia-Paraburkholderia;Burkholderiaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Occallatibacter;Acidobacteriaceae (Subgroup 1);Acidobacteriales;Acidobacteriae;Acidobacteriota |
| Roseiarcus;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria |
| Variovorax;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| unclassified_Diplorickettsiaceae;Diplorickettsiaceae;Diplorickettsiales;Gammaproteobacteria;Proteobacteria |
| unclassified_Subgroup 2;unclassified_Subgroup 2;Subgroup 2;Acidobacteriae;Acidobacteriota |
| unclassified_Caulobacteraceae;Caulobacteraceae;Caulobacteriales;Alphaproteobacteria;Proteobacteria |
| Mucilaginibacter;Sphingobacteriaceae;Sphingobacteriales;Bacteroidia;Bacteroidota |
| unclassified_Gallionellaceae;Gallionellaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Candidatus Koribacter;Koribacteraceae;Acidobacteriales;Acidobacteriae;Acidobacteriota |
| unclassified_Acidobacteriales;unclassified_Acidobacteriales;Acidobacteriales;Acidobacteriae;Acidobacteriota |
| unclassified_Thermodesulfovibrionia;unclassified_Thermodesulfovibrionia;unclassified_Thermodesulfovibrionia;Thermodesulfovibrionia;Nitrospirota |
| Sediminibacterium;Chitinophagaceae;Chitinophagales;Bacteroidia;Bacteroidota |
| unclassified_Sutterellaceae;Sutterellaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Reyranella;Reyranellaceae;Reyranellales;Alphaproteobacteria;Proteobacteria |
| Glaciimonas;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| Bryobacter;Bryobacteraceae;Bryobacteriales;Acidobacteriae;Acidobacteriota |
| Pseudolabrys;Xanthobacteraceae;Rhizobiales;Alphaproteobacteria;Proteobacteria |
| unclassified_Micropepsaceae;Micropepsaceae;Micropepsales;Alphaproteobacteria;Proteobacteria |
| unclassified_Burkholderiales;unclassified_Burkholderiales;Burkholderiales;Gammaproteobacteria;Proteobacteria |
| unclassified_Alphaproteobacteria;unclassified_Alphaproteobacteria;unclassified_Alphaproteobacteria;Alphaproteobacteria;Proteobacteria |
| Granulicella;Acidobacteriaceae (Subgroup 1);Acidobacteriales;Acidobacteriae;Acidobacteriota |
| unclassified_Vermiphilaceae;Vermiphilaceae;Babeliales;Babeliae;Dependentiae |
| Methylorosula;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria |

UTBCD1;Chitinophagaceae;Chitinophagales;Bacteroidia;Bacteroidota
unclassified_Xanthobacteraceae;Xanthobacteraceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
unclassified_Gemmatimonadaceae;Gemmatimonadaceae;Gemmatimonadales;Gemmatimonadetes;Gemmati-
monadota
BSV13;Prolixibacteraceae;Bacteroidales;Bacteroidia;Bacteroidota
unclassified_Lineage IV;unclassified_Lineage IV;Lineage IV;Elusimicrobia;Elusimicrobiota
unclassified_WD260;unclassified_WD260;WD260;Gammaproteobacteria;Proteobacteria
Cavicella;Moraxellaceae;Pseudomonadales;Gammaproteobacteria;Proteobacteria
Geothrix;Holophagaceae;Holophagales;Holophagae;Acidobacteriota
Edaphobaculum;Chitinophagaceae;Chitinophagales;Bacteroidia;Bacteroidota
Sulfuritalea;Rhodocyclaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Steroidobacteraceae;Steroidobacteraceae;Steroidobacterales;Gammaproteobacteria;Proteobacteria
unclassified_Desulfocapsaceae;Desulfocapsaceae;Desulfobulbales;Desulfobulbia;Desulfobacterota
Hyphomicrobium;Hyphomicrobiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
Legionella;Legionellaceae;Legionellales;Gammaproteobacteria;Proteobacteria
Candidatus Nitrotoga;Gallionellaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Beijerinckiaceae;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
unclassified_Chitinophagaceae;Chitinophagaceae;Chitinophagales;Bacteroidia;Bacteroidota
unclassified_Subgroup 7;unclassified_Subgroup 7;Subgroup 7;Holophagae;Acidobacteriota
unclassified_Rhodocyclaceae;Rhodocyclaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_UBA12409;UBA12409;Babeliales;Babeliae;Dependentiae
unclassified_4-29-1;unclassified_4-29-1;unclassified_4-29-1;4-29-1;Nitrospirota
Bradyrhizobium;Xanthobacteraceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
ADurb.Bin063-1;Pedosphaeraceae;Pedosphaerales;Verrucomicrobiae;Verrucomicrobiota
unclassified_Elsterales;unclassified_Elsterales;Elsterales;Alphaproteobacteria;Proteobacteria
Syntrophobacter;Syntrophobacteraceae;Syntrophobacterales;Syntrophobacteria;Desulfobacterota
Desulfobacca;Desulfobaccaceae;Desulfobaccales;Desulfobaccia;Desulfobacterota
Aquicella;Diplorickettsiaceae;Diplorickettsiales;Gammaproteobacteria;Proteobacteria
Janthinobacterium;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
Ferruginibacter;Chitinophagaceae;Chitinophagales;Bacteroidia;Bacteroidota
alphaI cluster;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
unclassified_Rhodospirillales;unclassified_Rhodospirillales;Rhodospirillales;Alphaproteobacteria;Proteobacteria
Sporichthya;Sporichthyaceae;Frankiales;Actinobacteria;Actinobacteriota
Puia;Chitinophagaceae;Chitinophagales;Bacteroidia;Bacteroidota
unclassified_Comamonadaceae;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Gammaproteobacteria;unclassified_Gammaproteobacteria;unclassified_Gammaproteobacteria;Gam-
maproteobacteria;Proteobacteria
unclassified_IMCC26256;unclassified_IMCC26256;IMCC26256;Acidimicrobiia;Actinobacteriota
unclassified_Subgroup 13;unclassified_Subgroup 13;Subgroup 13;Acidobacteriae;Acidobacteriota
unclassified_Holophagaceae;Holophagaceae;Holophagales;Holophagae;Acidobacteriota
unclassified_Babeliales;unclassified_Babeliales;Babeliales;Babeliae;Dependentiae
Paludibacterium;Chromobacteriaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Chlamydiales;unclassified_Chlamydiales;Chlamydiales;Chlamydiae;Verrucomicrobiota
unclassified_Geobacteraceae;Geobacteraceae;Geobacterales;Desulfuromonadia;Desulfobacterota
unclassified_Lineage IIa;unclassified_Lineage IIa;unclassified_Lineage IIa;Lineage IIa;Elusimicrobiota
Clostridium sensu stricto 9;Clostridiaceae;Clostridiales;Clostridia;Firmicutes
unclassified_BSV26;BSV26;Kryptoniales;Kryptonia;Bacteroidota
Inquilinus;Inquilinaceae;Azospirillales;Alphaproteobacteria;Proteobacteria
unclassified_MBNT15;unclassified_MBNT15;unclassified_MBNT15;unclassified_MBNT15;MBNT15
unclassified_Gaiellales;unclassified_Gaiellales;Gaiellales;Thermoleophilia;Actinobacteriota
unclassified_Holosporaceae;Holosporaceae;Holosporales;Alphaproteobacteria;Proteobacteria
unclassified_Microscillaceae;Microscillaceae;Cytophagales;Bacteroidia;Bacteroidota
Pajaroellobacter;Polyangiaceae;Polyangiales;Polyangia;Myxococcota
Neochlamydia;Parachlamydiaceae;Chlamydiales;Chlamydiae;Verrucomicrobiota

Acidothermus; Acidothermaceae; Frankiales; Actinobacteria; Actinobacteriota
unclassified_Simkaniaceae; Simkaniaceae; Chlamydiales; Chlamydiae; Verrucomicrobiota
unclassified_JG36-TzT-191; unclassified_JG36-TzT-191; JG36-TzT-191; Gammaproteobacteria; Proteobacteria
Heliomonas; Chitinophagaceae; Chitinophagales; Bacteroidia; Bacteroidota
Geobacter; Geobacteraceae; Geobacterales; Desulfuromonadia; Desulfobacterota
Rhodopila; Acetobacteraceae; Acetobacterales; Alphaproteobacteria; Proteobacteria
unclassified_Paludibaculum; unclassified_Paludibaculum; Paludibaculum; Acidobacteriae; Acidobacteriota
Ferroplasma; Ferroplasmaceae; Burkholderiales; Gammaproteobacteria; Proteobacteria
unclassified_Desulfobulbales; unclassified_Desulfobulbales; Desulfobulbales; Desulfobulbia; Desulfobacterota
Desulfomonile; Desulfomonilaceae; Desulfomonilales; Desulfomonilia; Desulfobacterota
Pandora; Burkholderiaceae; Burkholderiales; Gammaproteobacteria; Proteobacteria
unclassified_vadinBA26; unclassified_vadinBA26; vadinBA26; Dehalococcoidia; Chloroflexi
unclassified_Solirubrobacteraceae; Solirubrobacteraceae; Solirubrobacterales; Thermoleophilia; Actinobacteriota
Coxiella; Coxiellaceae; Coxiellales; Gammaproteobacteria; Proteobacteria
unclassified_Bacteria; unclassified_Bacteria; unclassified_Bacteria; unclassified_Bacteria; unclassified_Bacteria
unclassified_cvE6; cvE6; Chlamydiales; Chlamydiae; Verrucomicrobiota
Sterolibacterium; Rhodocyclaceae; Burkholderiales; Gammaproteobacteria; Proteobacteria
unclassified_0319-6G20; unclassified_0319-6G20; 0319-6G20; Oligoflexia; Bdellovibrionota
Mycobacterium; Mycobacteriaceae; Corynebacteriales; Actinobacteria; Actinobacteriota
Desulfosporosinus; Desulfotuberculiaceae; Desulfotuberculiales; Desulfotuberculia; Firmicutes
unclassified_Babeliaceae; Babeliaceae; Babeliales; Babelia; Dependitiae
Paludibacter; Paludibacteraceae; Bacteroidales; Bacteroidia; Bacteroidota
Acidisphaera; Acetobacteraceae; Acetobacterales; Alphaproteobacteria; Proteobacteria
unclassified_Acidobacteriaceae (Subgroup 1); Acidobacteriaceae (Subgroup 1); Acidobacteriales; Acidobacteriae; Acidobacteriota
Candidatus Omnitrophus; Omnitrophaceae; Omnitrophales; Omnitrophia; Verrucomicrobiota
unclassified_Pedospaeraceae; Pedospaeraceae; Pedospaerales; Verrucomicrobiae; Verrucomicrobiota
Bdellovibrio; Bdellovibrionaceae; Bdellovibrionales; Bdellovibrionia; Bdellovibrionota
unclassified_Syntrophobacteraceae; Syntrophobacteraceae; Syntrophobacterales; Syntrophobacteria; Desulfobacterota
Rhodanobacter; Rhodanobacteraceae; Xanthomonadales; Gammaproteobacteria; Proteobacteria
unclassified_CWT CU03-E12; CWT CU03-E12; Sphingobacteriales; Bacteroidia; Bacteroidota
unclassified_Bacteroidetes vadinHA17; Bacteroidetes vadinHA17; Bacteroidales; Bacteroidia; Bacteroidota
unclassified_Neisseriaceae; Neisseriaceae; Burkholderiales; Gammaproteobacteria; Proteobacteria
Candidatus Paracaedibacter; Paracaedibacteraceae; Paracaedibacterales; Alphaproteobacteria; Proteobacteria
unclassified_Paludibacteraceae; Paludibacteraceae; Bacteroidales; Bacteroidia; Bacteroidota
unclassified_Sva0485; unclassified_Sva0485; unclassified_Sva0485; unclassified_Sva0485; Sva0485
Telmatobacter; Acidobacteriaceae (Subgroup 1); Acidobacteriales; Acidobacteriae; Acidobacteriota
Telmatospirillum; Magnetospirillaceae; Rhodospirillales; Alphaproteobacteria; Proteobacteria
Ga0074140; Simkaniaceae; Chlamydiales; Chlamydiae; Verrucomicrobiota
unclassified_Magnetospirillaceae; Magnetospirillaceae; Rhodospirillales; Alphaproteobacteria; Proteobacteria
unclassified_Ignavibacteriales; unclassified_Ignavibacteriales; Ignavibacteriales; Ignavibacteria; Bacteroidota
Candidatus Berkiella; Unknown Family; Gammaproteobacteria Incertae Sedis; Gammaproteobacteria; Proteobacteria
Citri fermentans; Geobacteraceae; Geobacterales; Desulfuromonadia; Desulfobacterota
unclassified_SC-I-84; SC-I-84; Burkholderiales; Gammaproteobacteria; Proteobacteria
unclassified_WOR-1; unclassified_WOR-1; unclassified_WOR-1; unclassified_WOR-1; WOR-1
Azovibrio; Rhodocyclaceae; Burkholderiales; Gammaproteobacteria; Proteobacteria
Sphingomonas; Sphingomonadaceae; Sphingomonadales; Alphaproteobacteria; Proteobacteria
unclassified_Elusimicrobiota; unclassified_Elusimicrobiota; unclassified_Elusimicrobiota; unclassified_Elusimicrobiota; Elusimicrobiota
unclassified_Syntrophobacterales; unclassified_Syntrophobacterales; Syntrophobacterales; Syntrophobacteria; Desulfobacterota
Syntrophorhabdus; Syntrophorhabdaceae; Syntrophorhabdales; Syntrophorhabdia; Desulfobacterota
unclassified_Rhodospirillaceae; Rhodospirillaceae; Rhodospirillales; Alphaproteobacteria; Proteobacteria
unclassified_Lentimicrobiaceae; Lentimicrobiaceae; Sphingobacteriales; Bacteroidia; Bacteroidota

Aliidongia;Elsteraceae;Elsterales;Alphaproteobacteria;Proteobacteria

unclassified_RCP2-54;unclassified_RCP2-54;unclassified_RCP2-54;unclassified_RCP2-54;RCP2-54

unclassified_Moraxellaceae;Moraxellaceae;Pseudomonadales;Gammaproteobacteria;Proteobacteria

unclassified_Parachlamydiaceae;Parachlamydiaceae;Chlamydiales;Chlamydiae;Verrucomicrobiota

s3t2d-1089;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria

Paraherbaspirillum;Oxalobacteraceae;Burkholderiales;Gammaproteobacteria;Proteobacteria

unclassified_S15A-MN91;S15A-MN91;Sphingobacteriales;Bacteroidia;Bacteroidota

unclassified_Kapabacteriales;unclassified_Kapabacteriales;Kapabacteriales;Kapabacteria;Bacteroidota

Minicystis;Polyangiaceae;Polyangiales;Polyangia;Myxococcota

unclassified_Clostridia;unclassified_Clostridia;unclassified_Clostridia;Clostridia;Firmicutes

unclassified_Myxococcota;unclassified_Myxococcota;unclassified_Myxococcota;unclassified_Myxococcota;Myxococcota

unclassified_CHAB-XI-27;unclassified_CHAB-XI-27;CHAB-XI-27;Gammaproteobacteria;Proteobacteria

unclassified_661239;unclassified_661239;661239;Dehalococcoidia;Chloroflexi

unclassified_Candidatus Protistobacter;Candidatus Protistobacter;Burkholderiales;Gammaproteobacteria;Proteobacteria

unclassified_Acidobacteriales;unclassified_Acidobacteriales;unclassified_Acidobacteriales;Acidobacteriales;Acidobacteriales

Acidicapsa;Acidobacteriaceae (Subgroup 1);Acidobacteriales;Acidobacteriae;Acidobacteriota

Acidisoma;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria

unclassified Rickettsiales;unclassified Rickettsiales;Rickettsiales;Alphaproteobacteria;Proteobacteria

Rhodomicrobium;Rhodomicrobiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria

Thermoanaerobacterium;Family III;Thermoanaerobacterales;Thermoanaerobacteria;Firmicutes

unclassified Sulfuricellaceae;Sulfuricellaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria

Terracidiphilus;Acidobacteriaceae (Subgroup 1);Acidobacteriales;Acidobacteriae;Acidobacteriota

unclassified_Fimbriimonadaceae:Fimbriimonadaceae:Fimbriimonadales:Fimbriimonadia:Armatimonadota

Chungangia;Planococcaceae;Bacillales;Bacilli;Firmicutes

unclassified 37-13;37-13;Chitinophagales;Bacteroidia;Bacteroidota

Herbaspirillum:Oxalobacteraceae:Burkholderiales:Gammaproteobacteria:Proteobacteria

Bifidobacterium:Bifidobacteriaceae:Bifidobacteriales:Actinobacteria:Actinobacteriota

Thiomonas;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
Conexibacter;Solirubrobacteraceae;Solirubrobacterales;Thermoleophilia;Actinobacteriota
Anoxybacillus;Bacillaceae;Bacillales;Bacilli;Firmicutes
unclassified_Criblamydiaceae;Criblamydiaceae;Chlamydiales;Chlamydiae;Verrucomicrobiota
Arthrobacter;Micrococcaceae;Micrococcales;Actinobacteria;Actinobacteriota
Pedosphaera;Pedosphaeraceae;Pedosphaerales;Verrucomicrobiae;Verrucomicrobiota
Rhizobacter;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
1174-901-12;Beijerinckiacaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
Leptothrix;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Subgroup 15;unclassified_Subgroup 15;Subgroup 15;Acidobacteriae;Acidobacteriota
unclassified_BD72BR169;unclassified_BD72BR169;BD72BR169;Gammaproteobacteria;Proteobacteria
Brevinema;Brevinemataceae;Brevinematales;Brevinematia;Spirochaetota
Fonticella;Caloramatoraceae;Clostridiales;Clostridia;Firmicutes
Geobacillus;Bacillaceae;Bacillales;Bacilli;Firmicutes
unclassified_Sphingobacteriales;unclassified_Sphingobacteriales;Sphingobacteriales;Bacteroidia;Bacteroidota
unclassified_Candidatus Jidaibacter;Candidatus Jidaibacter;Rickettsiales;Alphaproteobacteria;Proteobacteria
unclassified_Subgroup 5;unclassified_Subgroup 5;unclassified_Subgroup 5;Subgroup 5;Acidobacteriota
unclassified_env.OPS 17;env.OPS 17;Sphingobacteriales;Bacteroidia;Bacteroidota
Holophaga;Holophagaceae;Holophagales;Holophagae;Acidobacteriota
Bauldia;Rhizobiales Incertae Sedis;Rhizobiales;Alphaproteobacteria;Proteobacteria
P3OB-42;Myxococcaceae;Myxococcales;Myxococcia;Myxococcota
unclassified_UBA12411;UBA12411;Babeliales;Babeliae;Dependentiae
Candidatus Ovatusbacter;Unknown Family;Gammaproteobacteria Incertae Sedis;Gammaproteobacteria;Proteobacteria
unclassified_AB1;AB1;Rickettsiales;Alphaproteobacteria;Proteobacteria
Myroides;Flavobacteriaceae;Flavobacteriales;Bacteroidia;Bacteroidota
unclassified_EC3;unclassified_EC3;EC3;Gammaproteobacteria;Proteobacteria
unclassified_KD3-93;KD3-93;Sphingobacteriales;Bacteroidia;Bacteroidota
Paenibacillus;Paenibacillaceae;Paenibacillales;Bacilli;Firmicutes
Thermoanaerobaculum;Thermoanaerobaculaceae;Thermoanaerobaculales;Thermoanaerobaculia;Acidobacteriota
GOUTA6;Nitrosomonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
Rhodococcus;Nocardiaceae;Corynebacteriales;Actinobacteria;Actinobacteriota
Dysgonomonas;Dysgonomonadaceae;Bacteroidales;Bacteroidia;Bacteroidota
unclassified_Subgroup 12;unclassified_Subgroup 12;Subgroup 12;Acidobacteriae;Acidobacteriota
Parablastomonas;Sphingomonadaceae;Sphingomonadales;Alphaproteobacteria;Proteobacteria
Desulfatirhabdium;Desulfosarcinaceae;Desulfobacterales;Desulfobacteria;Desulfobacterota
unclassified_AKIW659;unclassified_AKIW659;AKIW659;Acidobacteriae;Acidobacteriota
unclassified_Unknown Family;Unknown Family;Gammaproteobacteria Incertae Sedis;Gammaproteobacteria;Proteobacteria
FCPS473;Ktedonobacteraceae;Ktedonobacterales;Ktedonobacteria;Chloroflexi
Acidibacter;Unknown Family;Gammaproteobacteria Incertae Sedis;Gammaproteobacteria;Proteobacteria
Nocardioides;Nocardiodaceae;Propionibacteriales;Actinobacteria;Actinobacteriota
unclassified_Weeksellaceae;Weeksellaceae;Flavobacteriales;Bacteroidia;Bacteroidota
Paucibacter;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_mle1-27;unclassified_mle1-27;mle1-27;Polyangia;Myxococcota
unclassified_Bacteroidales;unclassified_Bacteroidales;Bacteroidales;Bacteroidia;Bacteroidota
Desulfobulbus;Desulfobulbaceae;Desulfobulbales;Desulfobulbia;Desulfobacterota
unclassified_A21b;A21b;Burkholderiales;Gammaproteobacteria;Proteobacteria
Asticcacaulis;Caulobacteraceae;Caulobacterales;Alphaproteobacteria;Proteobacteria
unclassified_SJA-28;unclassified_SJA-28;SJA-28;Ignavibacteria;Bacteroidota
unclassified_Pleomorphomonadaceae;Pleomorphomonadaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
Ellin516;Pedosphaeraceae;Pedosphaerales;Verrucomicrobiae;Verrucomicrobiota
Plot4-2H12;Sphingomonadaceae;Sphingomonadales;Alphaproteobacteria;Proteobacteria
Flavobacterium;Flavobacteriaceae;Flavobacteriales;Bacteroidia;Bacteroidota

unclassified_Micrococcaceae;Micrococcaceae;Micrococcales;Actinobacteria;Actinobacteriota
Actinospica;Actinospicaceae;Catenulisporales;Actinobacteria;Actinobacteriota
Nguyenibacter;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria
unclassified_B122;B122;Fibrobacterales;Fibrobacteria;Fibrobacterota
Spirochaeta 2;Spirochaetaceae;Spirochaetales;Spirochaetia;Spirochaetota
Nevskia;Solimonadaceae;Salinisphaerales;Gammaproteobacteria;Proteobacteria
unclassified_Aminicenantales;unclassified_Aminicenantales;Aminicenantales;Aminicenantia;Acidobacteriota
Peredibacter;Bacteriovoraceae;Bacteriovoracales;Bdellovibrionia;Bdellovibrionota
unclassified_Parcubacteria;unclassified_Parcubacteria;unclassified_Parcubacteria;Parcubacteria;Patescibacteria
Buttiauxella;Enterobacteriaceae;Enterobacteriales;Gammaproteobacteria;Proteobacteria
unclassified_GIF3;unclassified_GIF3;GIF3;Dehalococcoidia;Chloroflexi
DEV008;Pedosphaeraceae;Pedosphaerales;Verrucomicrobiae;Verrucomicrobiota
Frateuria;Rhodanobacteraceae;Xanthomonadales;Gammaproteobacteria;Proteobacteria
Weeksellia;Weeksellaceae;Flavobacteriales;Bacteroidia;Bacteroidota

Planktonic unique

Polynucleobacter;Burkholderiaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Pectobacteriaceae;Pectobacteriaceae;Enterobacteriales;Gammaproteobacteria;Proteobacteria
unclassified_Bdellovibrionota;unclassified_Bdellovibrionota;unclassified_Bdellovibrionota;unclassified_Bdel-
lovibrionota;Bdellovibrionota
Endomicrobium;Endomicrobiaceae;Endomicrobiales;Endomicrobia;Elusimicrobiota
unclassified_MSBL5;unclassified_MSBL5;MSBL5;Dehalococcoidia;Chloroflexi
Gluconacetobacter;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria
unclassified_RBG-13-46-9;unclassified_RBG-13-46-9;RBG-13-46-9;Dehalococcoidia;Chloroflexi
Aquabacterium;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Campylobacteriales;unclassified_Campylobacteriales;Campylobacteriales;Campylobacteria;Campylo-
bacterota
Clostridium sensu stricto 1;Clostridiaceae;Clostridiales;Clostridia;Firmicutes
unclassified_SAR202 clade;unclassified_SAR202 clade;SAR202 clade;Dehalococcoidia;Chloroflexi
unclassified_Berkelbacteria;unclassified_Berkelbacteria;unclassified_Berkelbacteria;Berkelbacteria;Patescibacteria
unclassified_Dehalococcoidales;unclassified_Dehalococcoidales;Dehalococcoidales;Dehalococcoidia;Chloroflexi
unclassified_Sporichthyaceae;Sporichthyaceae;Frankiales;Actinobacteria;Actinobacteriota
Polaromonas;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
Methylocystis;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
unclassified_Methylacidiphilaceae;Methylacidiphilaceae;Methylacidiphilales;Verrucomicrobiae;Verrucomicrobiota
Phaselicystis;Phaselicystidaceae;Polyangiales;Polyangia;Myxococcota
unclassified_SAR324 clade(Marine group B);unclassified_SAR324 clade(Marine group B);unclassified_SAR324
clade(Marine group B);unclassified_SAR324 clade(Marine group B);SAR324 clade(Marine group B)
E1B-B3-114;Streptomycetaceae;Streptomycetales;Actinobacteria;Actinobacteriota
unclassified_Fibrobacteraceae;Fibrobacteraceae;Fibrobacterales;Fibrobacteria;Fibrobacterota
unclassified_Methylophilaceae;Methylophilaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
Methylovirgula;Beijerinckiaceae;Rhizobiales;Alphaproteobacteria;Proteobacteria
Candidatus Renichlamydia;Simkaniaceae;Chlamydiales;Chlamydiae;Verrucomicrobiota
unclassified_SJA-15;unclassified_SJA-15;SJA-15;Anaerolineae;Chloroflexi
unclassified_Proteobacteria;unclassified_Proteobacteria;unclassified_Proteobacteria;unclassified_Proteobacte-
ria;Proteobacteria
Staphylococcus;Staphylococcaceae;Staphylococcales;Bacilli;Firmicutes
Annwodia;Hydrogenophilaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_NKB15;unclassified_NKB15;unclassified_NKB15;unclassified_NKB15;NKB15
Pelosinus;Sporomusaceae;Veillonellales-Selenomonadales;Negativicutes;Firmicutes
unclassified_bacteriap25;unclassified_bacteriap25;unclassified_bacteriap25;bacteriap25;Myxococcota
unclassified_Syntrophales;unclassified_Syntrophales;Syntrophales;Syntrophia;Desulfobacterota
unclassified_Cardiobacteriales;unclassified_Cardiobacteriales;Cardiobacteriales;Gammaproteobacteria;Proteobac-
teria
unclassified_Firmicutes;unclassified_Firmicutes;unclassified_Firmicutes;unclassified_Firmicutes;Firmicutes

unclassified_Pseudomonadaceae;Pseudomonadaceae;Pseudomonadales;Gammaproteobacteria;Proteobacteria
unclassified_LWQ8;LWQ8;Saccharimonadales;Saccharimonadia;Patescibacteria
unclassified_Gracilibacteria;unclassified_Gracilibacteria;unclassified_Gracilibacteria;Gracilibacteria;Patescibacteria
Sphingobacterium;Sphingobacteriaceae;Sphingobacteriales;Bacteroidia;Bacteroidota
TPD-58;Thermoanaerobaculaceae;Thermoanaerobaculales;Thermoanaerobaculia;Acidobacteriota
unclassified_Desulfarculaceae;Desulfarculaceae;Desulfarculales;Desulfarculia;Desulfobacterota
unclassified_Candidatus Peribacteria;unclassified_Candidatus Peribacteria;Candidatus Peribacteria;Gracilibacte-
ria;Patescibacteria
Acidicaldus;Acetobacteraceae;Acetobacterales;Alphaproteobacteria;Proteobacteria
Candidatus Symbiobacter;Comamonadaceae;Burkholderiales;Gammaproteobacteria;Proteobacteria
unclassified_Lineage IIb;unclassified_Lineage IIb;unclassified_Lineage IIb;Lineage IIb;Elusimicrobiota
unclassified_KF-JG30-C25;unclassified_KF-JG30-C25;KF-JG30-C25;Gammaproteobacteria;Proteobacteria
Abditibacterium;Abitibacteriaceae;Abitibacteriales;Abitibacteria;Abitibacteriota
unclassified_Bacteroidota;unclassified_Bacteroidota;unclassified_Bacteroidota;unclassified_Bacteroidota;Bacteroi-
dota
unclassified_Micavibrionaceae;Micavibrionaceae;Micavibrionales;Alphaproteobacteria;Proteobacteria
Candidatus Endoecksteinascidia;Piscirickettsiaceae;Piscirickettsiales;Gammaproteobacteria;Proteobacteria
unclassified_WCHB1-41;unclassified_WCHB1-41;WCHB1-41;Kiritimatiellae;Verrucomicrobiota
unclassified_Lineage IIc;unclassified_Lineage IIc;unclassified_Lineage IIc;Lineage IIc;Elusimicrobiota
unclassified_Sphingomonadaceae;Sphingomonadaceae;Sphingomonadales;Alphaproteobacteria;Proteobacteria

EUKARYOTE

Planktonic-Sessile shared

Apoikiales;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Synurales;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Glissomonadida;Filosa-Sarcomonadea;Cercozoa;Rhizaria;TSAR
Unclassified_Eukaryota;Unclassified_Eukaryota;Unclassified_Eukaryota;Unclassified_Eukaryota;Unclassified_Eu-
karyota
Peritrichia_2;Oligohymenophorea;Ciliophora;Alveolata;TSAR
Unclassified_Chrysophyceae;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Pezizomycotina;Ascomycota;Fungi;Opisthokonta;Obazoa
Unclassified_Amoebzoa;Unclassified_Amoebzoa;Unclassified_Amoebzoa;Unclassified_Amoebzoa;Amoebzoa
Rozellomycota_X;Rozellomycota;Fungi;Opisthokonta;Obazoa
Choanoflagellata_X;Choanoflagellata;Choanoflagellata;Opisthokonta;Obazoa
Tetramitida_III;Heterolobosea;Discoba_X;Discoba;Excavata
Cercomonadida;Filosa-Sarcomonadea;Cercozoa;Rhizaria;TSAR
Unclassified_Opisthokonta;Unclassified_Opisthokonta;Unclassified_Opisthokonta;Opisthokonta;Obazoa
Unclassified_Ciliophora;Unclassified_Ciliophora;Ciliophora;Alveolata;TSAR
Saccharomycotina;Ascomycota;Fungi;Opisthokonta;Obazoa
Turbellaria;Platyhelminthes;Metazoa;Opisthokonta;Obazoa
Agaricomycotina;Basidiomycota;Fungi;Opisthokonta;Obazoa
Eimeriida;Coccidiomorphea;Apicomplexa;Alveolata;TSAR
Microsporidia;Opisthosporidia;Fungi;Opisthokonta;Obazoa
Hypotrichia;Spirotrichea;Ciliophora;Alveolata;TSAR
Cryptomonadales;Cryptophyceae;Cryptophyta_X;Cryptophyta;Cryptista
Unclassified_Metazoa;Unclassified_Metazoa;Metazoa;Opisthokonta;Obazoa
Chrysophyceae_X;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Ochromonadales;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Flamellidae;Variosea;Evosea_X;Evosea;Amoebzoa
Neobodonida;Kinetoplastea;Euglenozoa;Discoba;Excavata
Thaumatomonadida;Filosa-Imbricatea;Cercozoa;Rhizaria;TSAR
Unclassified_Fungi;Unclassified_Fungi;Fungi;Opisthokonta;Obazoa
Embryophyceae_X;Embryophyceae;Streptophyta_X;Streptophyta;Archaeplastida

Gastrotricha_X;Gastrotricha;Metazoa;Opisthokonta;Obazoa
Colpodellida;Colpodellidea;Chrompodellids;Alveolata;TSAR
Unclassified_Cercozoa;Unclassified_Cercozoa;Cercozoa;Rhizaria;TSAR
Mortierellaceae;Mucoromycota;Fungi;Opisthokonta;Obazoa
Himatismenida;Centramoebia;Discosea_X;Discosea;Amoebozoa
Unclassified_Alveolata;Unclassified_Alveolata;Unclassified_Alveolata;Alveolata;TSAR
Nucleariida;Nucleariidea;Rotosphaerida;Opisthokonta;Obazoa
Unclassified_TSAR;Unclassified_TSAR;Unclassified_TSAR;Unclassified_TSAR;TSAR
Chromadorea;Nematoda;Metazoa;Opisthokonta;Obazoa
Armophorea_X;Armophorea;Ciliophora;Alveolata;TSAR
Craniata_X;Craniata;Metazoa;Opisthokonta;Obazoa
CONTH_2_X;CONTH_2;Ciliophora;Alveolata;TSAR
Litostomatea_X;Litostomatea;Ciliophora;Alveolata;TSAR
Pucciniomycotina;Basidiomycota;Fungi;Opisthokonta;Obazoa
Annelida_X;Annelida;Metazoa;Opisthokonta;Obazoa
Rotifera_X;Rotifera;Metazoa;Opisthokonta;Obazoa
Neogregarinorida;Gregarinomorphea;Apicomplexa;Alveolata;TSAR
Flabellinia_X;Flabellinia;Discosea_X;Discosea;Amoebozoa
Scuticociliatia_2;Oligohymenophorea;Ciliophora;Alveolata;TSAR
Unclassified_Mucoromycota;Mucoromycota;Fungi;Opisthokonta;Obazoa
Blastocladiomycotina;Blastocladiomycota;Fungi;Opisthokonta;Obazoa
Unclassified_Gyrista;Unclassified_Gyrista;Gyrista;Stramenopiles;TSAR
Haptoria_6;Litostomatea;Ciliophora;Alveolata;TSAR
Novel-clade-10;Novel-clade-10-12;Cercozoa;Rhizaria;TSAR
Paracercomonadida;Filosa-Imbricatea;Cercozoa;Rhizaria;TSAR
Unclassified_Choanoflagellata;Choanoflagellata;Choanoflagellata;Opisthokonta;Obazoa
Labyrinthulomycetes;Sagenista;Bigyra;Stramenopiles;TSAR
Enoplea;Nematoda;Metazoa;Opisthokonta;Obazoa
Pseudodendromonadales;Bicoecia;Bigyra;Stramenopiles;TSAR
Opalozoa_X;Opalozoa;Bigyra;Stramenopiles;TSAR
Unclassified_Litostomatea;Litostomatea;Ciliophora;Alveolata;TSAR
Unclassified_Kinetoplastea;Kinetoplastea;Euglenozoa;Discoba;Excavata
Chytridiales;Chytridiomycota;Fungi;Opisthokonta;Obazoa
Chlamydomonadales;Chlorophyceae;Chlorophyta_X;Chlorophyta;Archaeplastida

Sessile unique

Tetramitia_I;Heterolobosea;Discoba_X;Discoba;Excavata
Chrysophyceae_Cluster-II;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Mastigamoebida;Archamoebae;Evosea_X;Evosea;Amoebozoa
Arcellinida;Elardia;Tubulinea_X;Tubulinea;Amoebozoa
Acanthoecida;Choanoflagellata;Choanoflagellata;Opisthokonta;Obazoa
Dactylopodida;Flabellinia;Discosea_X;Discosea;Amoebozoa
Ustilaginomycotina;Basidiomycota;Fungi;Opisthokonta;Obazoa
Crustacea;Arthropoda;Metazoa;Opisthokonta;Obazoa
Lobulomycetales;Chytridiomycota;Fungi;Opisthokonta;Obazoa

Planktonic unique

Mucoromycotina;Mucoromycota;Fungi;Opisthokonta;Obazoa
Rigifilida_XXX;Rigifilida_XX;Rigifilida_X;Rigifilida;CRuMs
Bicoecales;Bicoecia;Bigyra;Stramenopiles;TSAR
Colpodea_X;Colpodea;Ciliophora;Alveolata;TSAR
Rotosphaerida_XX;Rotosphaerida_X;Rotosphaerida;Opisthokonta;Obazoa
Unclassified_Filosa-Imbricatea;Filosa-Imbricatea;Cercozoa;Rhizaria;TSAR
Eugregarinorida;Gregarinomorphea;Apicomplexa;Alveolata;TSAR
Chelicerata;Arthropoda;Metazoa;Opisthokonta;Obazoa
Ancyromonadida_XXX;Ancyromonadida_XX;Ancyromonadida_X;Ancyromonadida;Eukaryota_X

Unclassified_Oligohymenophorea;Oligohymenophorea;Ciliophora;Alveolata;TSAR
Vampyrellida;Endomyxa;Cercozoa;Rhizaria;TSAR
Euplotia;Spirotrichea;Ciliophora;Alveolata;TSAR
Pterocystida_X;Pterocystida;Centroplasthelida_X;Centroplasthelida;Haptista
Oligohymenophorea_X;Oligohymenophorea;Ciliophora;Alveolata;TSAR
Nassophorea_X;Nassophorea;Ciliophora;Alveolata;TSAR
Gregarinomorphea_X_GRE7;Gregarinomorphea;Apicomplexa;Alveolata;TSAR
Ascomycota_X;Ascomycota;Fungi;Opisthokonta;Obazoa
Peronosporomycetes_X;Peronosporomycetes;Gyrista;Stramenopiles;TSAR
Craspedida;Choanoflagellata;Choanoflagellata;Opisthokonta;Obazoa
Zygnemophyceae_X;Zygnemophyceae;Streptophyta_X;Streptophyta;Archaeplastida
Unclassified_Dinophyceae;Dinophyceae;Dinoflagellata;Alveolata;TSAR
Limnofilida;Filosa-Granofilosea;Cercozoa;Rhizaria;TSAR
Unclassified_Chytridiomycota;Chytridiomycota;Fungi;Opisthokonta;Obazoa
Chromulinales;Chrysophyceae;Gyrista;Stramenopiles;TSAR
Unclassified_Spirotrichea;Spirotrichea;Ciliophora;Alveolata;TSAR
Unclassified_Pterocystida;Pterocystida;Centroplasthelida_X;Centroplasthelida;Haptista
Cryomonadida;Filosa-Thecofilosea;Cercozoa;Rhizaria;TSAR
Unclassified_Gregarinomorphea;Gregarinomorphea;Apicomplexa;Alveolata;TSAR
Unclassified_Obazoa;Unclassified_Obazoa;Unclassified_Obazoa;Unclassified_Obazoa;Obazoa
Spizellomycetales;Chytridiomycota;Fungi;Opisthokonta;Obazoa
Pterista;Pterocystida;Centroplasthelida_X;Centroplasthelida;Haptista
Hyphochytriales;Hyphochytriomyceta;Gyrista;Stramenopiles;TSAR
Unclassified_Apicomplexa;Unclassified_Apicomplexa;Apicomplexa;Alveolata;TSAR
Euamoebida;Elardia;Tubulinea_X;Tubulinea;Amoebozoa
Prorodontida;Prostomatea;Ciliophora;Alveolata;TSAR
Plasmodiophorida;Endomyxa-Phytomyxea;Cercozoa;Rhizaria;TSAR
Unclassified_Bicoecia;Bicoecia;Bigyra;Stramenopiles;TSAR
Watanabea-Clade;Trebouxiophyceae;Chlorophyta_X;Chlorophyta;Archaeplastida
Unclassified_Centroplasthelida_X;Unclassified_Centroplasthelida_X;Centroplasthelida_X;Centroplasthelida;Haptista
Acanthopodida;Centramoebia;Discosea_X;Discosea;Amoebozoa

Table S10. Results of the Kruskal–Wallis comparisons of the Shannon diversity indices, for the Bacteria, Eukaryote, and Archaea domains.

| Domain | Comparison | P-value |
|-----------|--------------------|-------------|
| Bacteria | Sessile-Planktonic | 0.01109 |
| | Sessile BR1-BR2 | 0.157025695 |
| | Sessile BR1-BR3 | 0.004941286 |
| | Sessile BR2-BR2 | 0.192582241 |
| | Planktonic BR1-BR2 | 0.9190651 |
| | Planktonic BR1-BR3 | 0.5493827 |
| | Planktonic BR2-BR2 | 0.6975113 |
| Eukaryote | Sessile-Planktonic | 0.9901 |
| | Sessile BR1-BR2 | 0.1039152 |
| | Sessile BR1-BR3 | 0.1706923 |
| | Sessile BR2-BR2 | 0.5918819 |
| | Planktonic BR1-BR2 | 0.6366212 |
| | Planktonic BR1-BR3 | 0.2238265 |
| | Planktonic BR2-BR2 | 0.2425647 |
| Archaea | Planktonic BR1-BR2 | 0.8722325 |
| | Planktonic BR1-BR3 | 0.7316842 |
| | Planktonic BR2-BR2 | 0.8214565 |

Table S11. Distance-based RDA (db-RDA) analyses between bacterial, eukaryotic, and archaeal planktonic or sessile community compositions (beta diversity) and environmental conditions (geochemical variables for the planktonic communities, and mineral compositions for the sessile communities).

| Domain | Environmental variable | Parameters | Df | SumofSqs | F | P-value |
|-----------|------------------------|-----------------|----|----------|--------|---------|
| Bacteria | Mineralogy | Iron oxide | 1 | 0.06620 | 0.9739 | 0.434 |
| | | Quartz | 1 | 0.13037 | 1.9181 | 0.019 |
| | | Red feldspar | 1 | 0.05730 | 0.8430 | 0.640 |
| | | White feldspar | 1 | 0.11697 | 1.7210 | 0.041 |
| | | Mica | 1 | 0.06743 | 0.9921 | 0.395 |
| | | Abundance | 1 | 0.11523 | 1.6954 | 0.05 |
| | | Residual | 23 | 1.56323 | | |
| | Geochemical | DIC | 1 | 0.56073 | 5.7929 | 0.001 |
| | | DOC | 1 | 0.08467 | 0.8747 | 0.480 |
| | | NO ₂ | 1 | 0.15501 | 1.6014 | 0.130 |
| | | NH ₄ | 1 | 0.11580 | 1.1963 | 0.259 |
| | | NO ₃ | 1 | 0.03562 | 0.3680 | 0.958 |
| | | Residual | 18 | 1.74232 | | |
| Eukaryote | Mineralogy | Iron oxide | 1 | 0.11800 | 0.9989 | 0.382 |
| | | Quartz | 1 | 0.08928 | 0.7559 | 0.648 |
| | | Red feldspar | 1 | 0.05422 | 0.4590 | 0.971 |
| | | White feldspar | 1 | 0.10517 | 0.8903 | 0.523 |
| | | Mica | 1 | 0.08088 | 0.6847 | 0.750 |
| | | Residual | 10 | 1.18121 | | |
| | Geochemical | DIC | 1 | 0.40914 | 3.8334 | 0.002 |
| | | DOC | 1 | 0.07352 | 0.6888 | 0.674 |
| | | NO ₂ | 1 | 0.20912 | 1.9593 | 0.067 |
| | | NH ₄ | 1 | 0.16871 | 1.5806 | 0.121 |
| | | NO ₃ | 1 | 0.10307 | 0.9657 | 0.427 |
| | | Residual | 12 | 1.28078 | | |
| Archaea | Geochemical | DIC | 1 | 0.35129 | 3.7454 | 0.002 |
| | | DOC | 1 | 0.33469 | 3.5684 | 0.018 |
| | | NO ₂ | 1 | 0.09278 | 0.9892 | 0.357 |
| | | NH ₄ | 1 | 0.10305 | 1.0987 | 0.192 |
| | | NO ₃ | 1 | 0.06748 | 0.7195 | 0.458 |
| | | Residual | 10 | 0.93792 | | |

Table S12. Differential abundance of genera between the planktonic and sessile communities for the Bacteria and Eukaryote domains, determined using LEfSe. Sess, sessile; Plank, planktonic.

| Bacteria | | |
|----------------------------------|------------|---------|
| Genus | Class | LDA |
| Gallionella | Sessile | 4.6056 |
| Alkanindiges | Sessile | 4.4707 |
| Rhodoferrax | Sessile | 4.06278 |
| Undibacterium | Sessile | 3.83441 |
| Methylotenera | Sessile | 3.78551 |
| Sideroxydans | Sessile | 3.78457 |
| Rhodovastum | Sessile | 3.76878 |
| Acidocella | Sessile | 3.76845 |
| unclassified_Hydrogenophilaceae | Sessile | 3.63885 |
| Afipia | Sessile | 3.58337 |
| Variovorax | Sessile | 3.49629 |
| Candidatus Solibacter | Sessile | 3.4484 |
| Roseiarcus | Sessile | 3.3668 |
| Novosphingobium | Sessile | 3.36282 |
| Occallatibacter | Sessile | 3.31293 |
| unclassified_Diplorickettsiaceae | Sessile | 3.26281 |
| unclassified_Caulobacteraceae | Sessile | 3.22162 |
| unclassified_Gallionellaceae | Sessile | 3.19045 |
| unclassified_Subgroup 2 | Sessile | 3.13244 |
| Mucilaginibacter | Sessile | 3.12509 |
| Reyranella | Sessile | 3.12131 |
| unclassified_Sutterellaceae | Sessile | 3.11448 |
| Sediminibacterium | Sessile | 3.09439 |
| unclassified_Acidobacteriales | Sessile | 3.0157 |
| Bryobacter | Sessile | 2.98229 |
| Candidatus Koribacter | Sessile | 2.96664 |
| Bacillus | Sessile | 2.93043 |
| Glaciimonas | Sessile | 2.91003 |
| unclassified_Vermiphilaceae | Sessile | 2.90501 |
| unclassified_Gemmatimonadaceae | Sessile | 2.89698 |
| Methylorosula | Sessile | 2.87912 |
| unclassified_Alphaproteobacteria | Sessile | 2.86912 |
| Legionella | Sessile | 2.86797 |
| Edaphobaculum | Sessile | 2.81654 |
| UTBCD1 | Sessile | 2.74502 |
| Janthinobacterium | Sessile | 2.62749 |
| Geothrix | Sessile | 2.61135 |
| Sulfurimonas | Planktonic | 4.87653 |
| Collimonas | Planktonic | 4.64423 |

| | | |
|-------------------------------------|------------|---------|
| Pseudomonas | Planktonic | 4.38598 |
| unclassified_Thermodesulfovibrionia | Planktonic | 3.33477 |
| Candidatus Nitrotoga | Planktonic | 3.261 |
| Paludibacterium | Planktonic | 3.16971 |
| Ferrovum | Planktonic | 3.12539 |
| unclassified_Paludibacteraceae | Planktonic | 3.11066 |
| unclassified_vadinBA26 | Planktonic | 3.00766 |
| Clostridium sensu stricto 9 | Planktonic | 2.93816 |
| Sulfuritalea | Planktonic | 2.93522 |
| Massilia | Planktonic | 2.91059 |
| alphaI cluster | Planktonic | 2.88715 |
| Aureimonas | Planktonic | 2.79982 |

Eukaryote

| Genus | Class | LDA |
|-------------------------------|------------|---------|
| Glissomonadida | Sessile | 4.85406 |
| Apoikiales | Sessile | 4.71073 |
| Unclassified_Amoebzoa | Sessile | 4.37756 |
| Peritrichia_2 | Sessile | 3.96559 |
| Rhynchostomatia | Sessile | 3.72376 |
| Unclassified_Alveolata | Sessile | 3.52328 |
| Unclassified_TSAR | Sessile | 2.70175 |
| Eimeriida | Planktonic | 4.37059 |
| Saccharomycotina | Planktonic | 3.86954 |
| Choanoflagellata_X | Planktonic | 3.45973 |
| Rozellomycota_X | Planktonic | 3.45774 |
| Hypotrichia | Planktonic | 3.31657 |
| Euplotia | Planktonic | 2.7649 |
| Scuticociliatia_2 | Planktonic | 2.64061 |
| Pseudodendromonadales | Planktonic | 2.56439 |
| Armophorea_X | Planktonic | 2.5614 |
| Microsporida | Planktonic | 2.48486 |
| Colpodellida | Planktonic | 2.39229 |
| Chlorellales | Planktonic | 2.38696 |
| Oligohymenophorea_X | Planktonic | 2.37171 |
| Unclassified_Cercozoa | Planktonic | 2.34252 |
| Unclassified_Choanoflagellata | Planktonic | 2.30172 |

Table S13. Differential abundance of genera between the sessile communities in the 3 different bio-reactors (BR1, BR2, and BR3), for the Bacteria and Eukaryote domains, determined using LEfSe.

| Bacteria | | |
|--|-------|---------|
| Genus | Class | LDA |
| unclassified_Hydrogenophilaceae | BR1 | 3.90529 |
| Rhodoferrax | BR1 | 3.84376 |
| Burkholderia-Caballeronia-Paraburkholderia | BR1 | 3.67421 |
| unclassified_Paludibacteraceae | BR1 | 3.55818 |
| Undibacterium | BR2 | 4.30134 |
| Methylothera | BR2 | 3.97546 |
| Occallatibacter | BR2 | 3.8264 |
| Cupriavidus | BR2 | 3.7613 |
| Collimonas | BR2 | 3.8276 |
| Variovorax | BR2 | 3.66914 |
| Rhodoblastus | BR3 | 4.27024 |
| Sulfurimonas | BR3 | 4.05471 |
| Novosphingobium | BR3 | 3.72718 |
| Acidocella | BR3 | 3.64668 |
| Eukaryote | | |
| Genus | Class | LDA |
| Synurales | BR1 | 4.84436 |
| Peritrichia_2 | BR1 | 4.3308 |

Table S14. Differential abundance of genera between the planktonic communities during the different incubation time groups, for the Bacteria, Eukaryote, and Archaea domains, determined using LEfSe.

| Bacteria | | |
|--------------------------------|------------|---------|
| Genus | Class | LDA |
| Sulfurimonas | Day 2 | 4.9588 |
| unclassified_Acidimicrobiia | Day 2 | 3.59462 |
| Collimonas | Days 4-12 | 4.74936 |
| Undibacterium | Days 4-12 | 4.29444 |
| Sideroxydans | Days 4-12 | 3.76162 |
| Gallionella | Days 14-22 | 4.75134 |
| unclassified_Acetobacteraceae | Days 14-22 | 4.53353 |
| Alkanindiges | Days 14-22 | 4.10762 |
| Eukaryote | | |
| Genus | Class | LDA |
| Pezizomycotina | Days 2-4 | 5.32844 |
| Saccharomycotina | Days 2-4 | 4.29346 |
| Embryophyceae_X | Days 2-4 | 3.87508 |
| Synurales | Days 6-12 | 5.34312 |
| Apoikiales | Days 14-22 | 5.34256 |
| Archaea | | |
| Genus | Class | LDA |
| Unclassified_Bathyarchaeia | Days 2-8 | 4.4431 |
| Unclassified_SCGC AAA011_D5 | Days 18-20 | 4.65894 |
| Unclassified_GW2011_GWC1_47_15 | Days 18-20 | 4.07171 |
| Unclassified_Woesearchaeales | Days 18-20 | 3.99404 |
| Unclassified_CG1_02_32_21 | Days 18-20 | 3.94348 |

SUPPLEMENTARY MATERIAL FIGURE LEGENDS

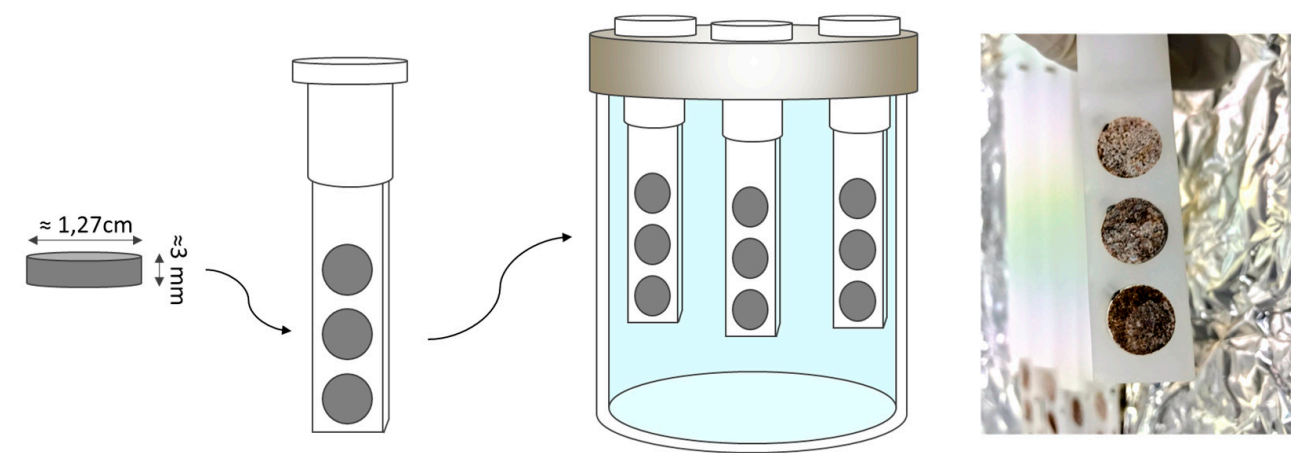


Figure S1. Diagram of the rock pellets and a bioreactor containing columns with the pellets.

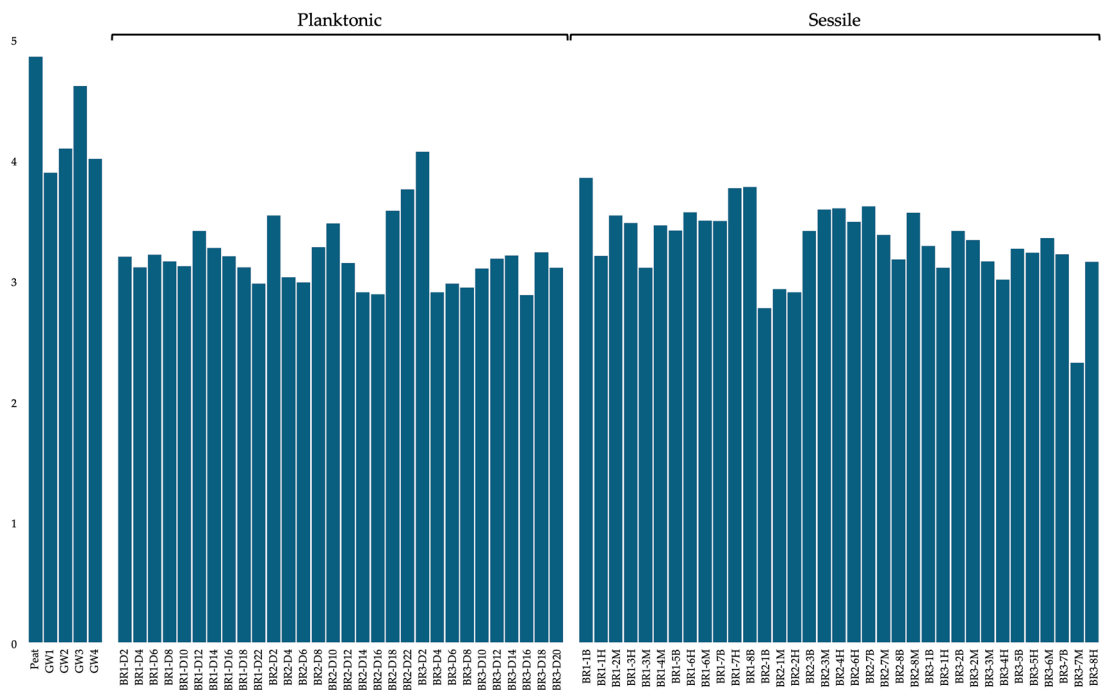


Figure S2. Shannon diversity indices for the *in-situ* peat bog water and groundwater samples, and the sessile and planktonic communities, for the Bacteria domain. GW, groundwater; BR, bioreactor; D, day.

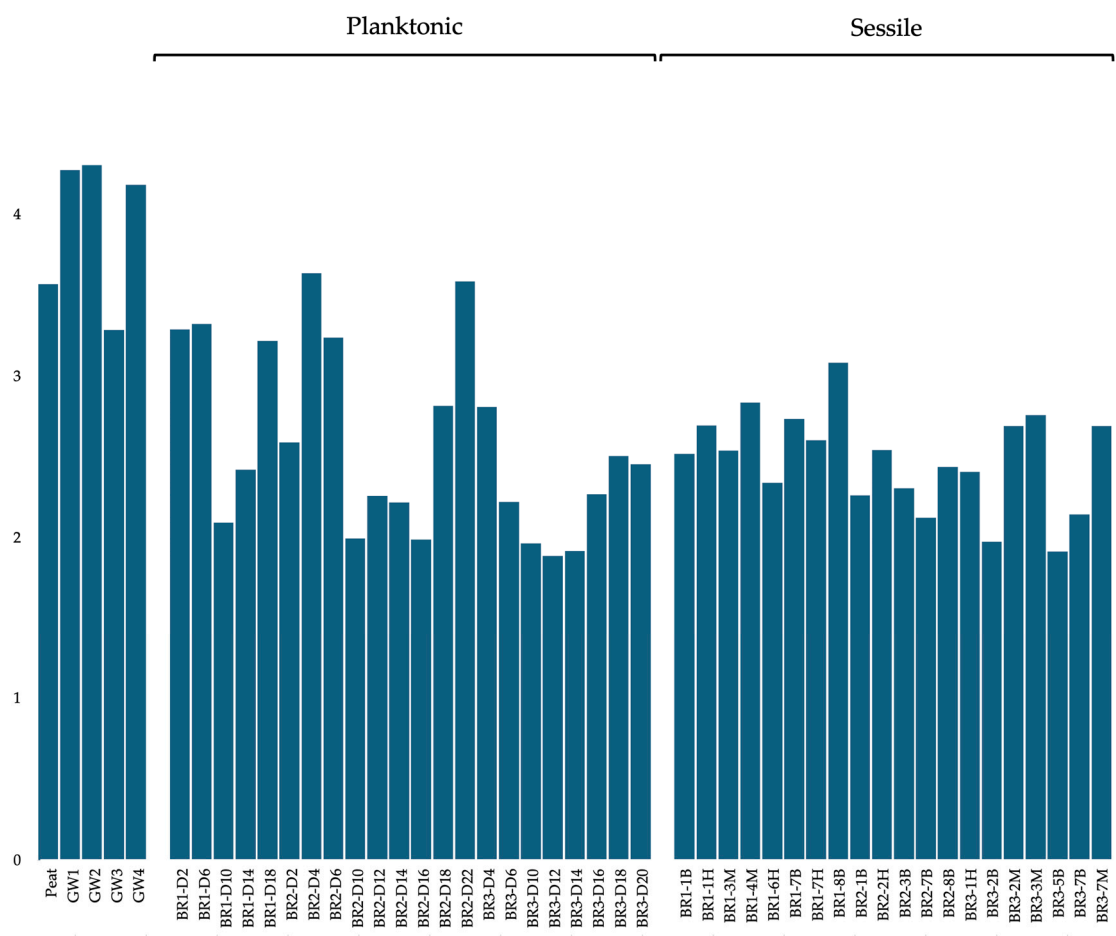


Figure S3. Shannon diversity indices for the *in-situ* peat bog water and groundwater samples, and the sessile and planktonic communities, for the Eukaryote domain. GW, groundwater; BR, bioreactor; D, day.

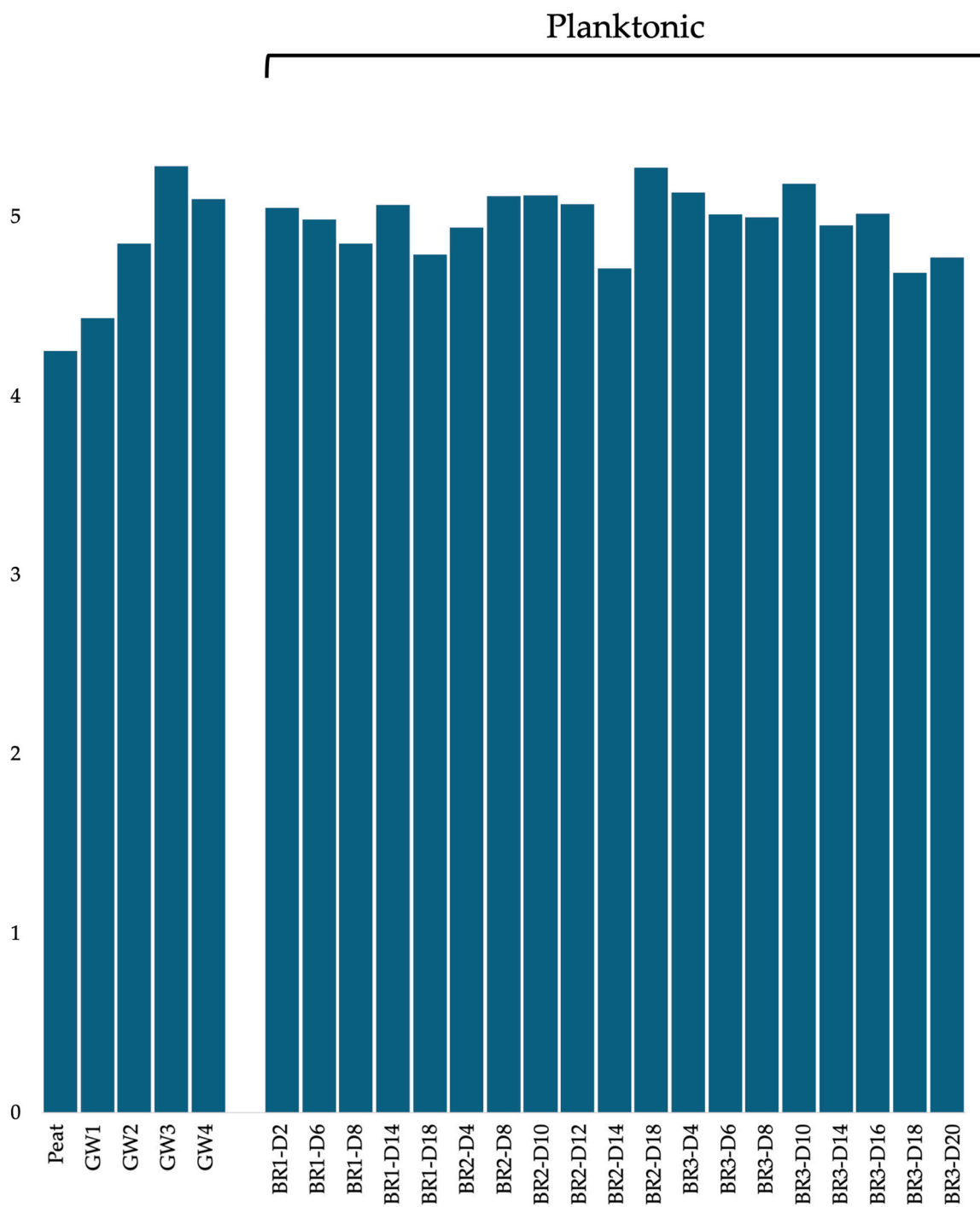


Figure S4. Shannon diversity indices for the *in-situ* peat bog water and groundwater samples, and the planktonic community, for the Archaea domain. GW, groundwater; BR, bioreactor; D, day.