**Table S4** Microbial taxa detected in the Organic Lake water column profile.

|  |  |  |
| --- | --- | --- |
| **Phylum** | **Class** | **Genusa** |
| *Bacteroidetes* | *Flavobacteria* | *Psychroflexus*  unclassified *Flavobacteriales*  *Brumimicrobium*  *Owenweeksia*  *Stenothermobacter*  *Persicivirga* |
| *Sphingobacteria* | *Lewinella*  E6aC02  Ns11-12\_marine\_gp  WCHB1-69 |
| *Cytophagia* | Ml602j-37  unclassified *Cytophagales*  *Cyclobacterium*  *Marivirga* |
| VC2.1\_bac22 | VC2.1\_bac22 |
| SB-1 | SB-1 |
| *Proteobacteria* | *Gammaproteobacteria* | *Marinobacter*  unclassified Gammaproteobacteria unclassified Alteromonadales  *Saccharospirillim*  *Halomonas*  *Psychromonas*  *Glaciecola*  unclassified *Oceanospirillales Pseudomonas*  *Thiomicrospira*  *Thermomonas*  unclassified Enterobacteriales  Bps-ck174  *Modicisalibacter*  *Leucothrix*  *Thiorhodovibrio*  *Pseudospirillum* |
| *Alphaproteobacteria* | *Roseovarius*  unclassified *Rhodobacterales*  *Loktanella*  *Albimonas*  TK34  *Phaeobacter*  unclassified *Alphaproteobacteria* *Sphingomonas*  *Octadecabacter*  Db1-14  *Oceanicaulis*  *Sulfitobacter*  unclassified Rhodospirillales  *Roseibaca* |
| *Epsilonproteobacteria* | *Sulfurimonas*  *Sulfurospirillum*  *Arcobacter*  Br36 |
| *Deltaproteobacteria* | *Desulfotignum*  *Desulfopila*  unclassified *Bdellovibrionales*  *Peredibacter*  *Bacteriovorax*  *Desulfosalsimonas*  *Desulfobacterium*  *Desulfuromonas* |
| *Cyanobacteria* | Chloroplast | *Dunaliella* chloroplast  unclassified chloroplast  diatom chloroplast |
| *Cyanobacteria* | unclassified *Cyanobacteria* |
| *Actinobacteria* | *Actinobacteria* | “*Candidatus* Aquiluna”  unclassified Micrococcales  *Demequina* |
| *Firmicutes* | RF3 | FJ231138 Laguna Lejía  FM210971 Lake Shangmatala  AF142888 Ekho Lake  DQ909718 hydrothermal vent  HM973420 oil reservoir AB546068 oil well head  GU196243 anaerobic digester |
| *Clostridia* | *Halanaerobium*  unclassified *Clostridiales*  unclassified *Halanaerobiales*  *Fusibacter*  *Fastidiosipila* |
| *Bacilli* | unclassified *Bacillales*  *Paraliobacillus* |
| *Lentisphaerae* | *Lentisphaeria* | Wchb1-41  unclassified Victivallales  R76-b128 |
| *Spirochaetes* | *Spirochaetes* | *Spirochaeta*  unclassified *Spirochaetales* |
| *Verrucomicrobia* | *Verrucomicrobiae* | unclassified *Verrucomicrobiales*  *Rubritalea* |
| *Opitutae* | unclassified *Puniceicoccales*  marine *Puniceicoccales* |
| *Chlamydiae* | *Chlamydiae* | unclassified *Chlamydiales* |
| candidate divisions | OD1 | DQ521564 Lake Vida  JN454910 hypersaline mat  EU050865 Artic sediment JF743552 Marine sediments  GU197432 endosymbionts  JN408878 soil rhizosphere  JN440560 hypersaline mat  AY862782 Lake Tebenquiche  AF419697 hydrothermal sediment  HM481393 contaminated water  JN441150 hypersaline mat  JN447858 hypersaline mat |
| TM7 | TM7 |
| SR1 | SR1 |
| Bd1-5 | Bd1-5 |
| Bhi80-139 | Bhi80-139 |
| Euryarchaeota | *Halobacteria* | Deep\_sea\_hydrothermal\_vent\_gp\_6(dhveg-6) |
| Viridiplantae | *Chlorophyta* | unclassified *Chlorophyceae* unclassified *Chlorophyta*  *Dunaliella* |
| *Stramenopiles* | *Bacillariophyta* | *Cylindrotheca*  *Chaetoceros* |
| *Dictyochophyceae* | unclassified *Dictyochophyceae*  unclassified *Pedinellales* |
| unclassified *Stramenopiles* | unclassified *Stramenopiles* |
| *Metazoa* | *Arthropoda* | unclassified *Hexapoda* |
| *Fungi* | *Neocallimastigomycota* | *Neocallimastix*  unclassified *Neocallimatigomycetes* |
| *Dikarya* | unclassified *Ascomycota*  *Aspergillus*  *Aureobasidium*  *Cordyceps*  *Penicillum*  *Verticillum*  *Cryptococcus*  unclassified *Basidiomycota* |
| *Alveolata* | *Dinophyceae* | unclassified *Dinophyceae*  *Karlodinium*  unclassified *Gymnodiniales* |
| *Ciliophora* | *Euplotes*  *Tunicothrix* |
| *Choanoflagellida* | *Codonosigidae* | *Proterospongia*  unclassified *Choanoflagellida* |

Analysis of SSU gene sequences shown in phylum, class and genus ranks as defined by the SILVA taxonomy except RF3 which is placed with the *Firmicutes* according to Tajima *et al.* (1999).SSU gene sequences were classified to the genus level or to the lowest rank with bootstap confidence >85% (see materials and methods). The best BLAST matches to environmental SSU clone sequences are shown for the abundant candidate divisions RF3 and OD1.