

Table S1. Number of reads, OTUs and indices of species hidden richness and evenness in the non-rarefied libraries of bacterial and archaeal 16S rRNA gene fragments (for a cluster distance of 0.03).

| | Sediment layers, cmblf | Reads Bacteria/Archaea | OTU_{0.03} Bacteria/Archaea | ACE Bacteria/Archaea | Chao1 Bacteria/Archaea | Shannon Bacteria/Archaea | Invers Simpso Bacteria/Archaea |
|----------------|-----------------------------------|-----------------------------------|--|---------------------------------|-----------------------------------|-------------------------------------|---|
| St6Grf4 | 0-5 | 1397/66385 | 454/316 | 808.2/356.7 | 738.5/373.2 | 5.39/2.22 | 96.67/4.58 |
| | 10-11 | 11820/49467 | 1022/273 | 1192.3/348.7 | 1190.3/336.7 | 5.72/2.11 | 110.83/4.31 |
| | 12-13_FeMn_L | 12683/63670 | 981/311 | 1174.6/135 | 1175.8/359.9 | 5.24/2.44 | 33.65/5.33 |
| | 22-23 | 14689/34121 | 886/275 | 1081.5/355.4 | 1089.4/310.7 | 5.07/2.51 | 49.17/3.75 |
| | 23-24_FeMn_L | 13921/33801 | 823/181 | 1032.8/306.9 | 1058/238.4 | 5.11/0.8 | 53.34/1.31 |
| | 24-25 | 13594/56584 | 686/257 | 777.4/210.8 | 805.2/288.3 | 4.99/2.91 | 45.90/9.54 |
| | 29-30 | 4104/48617 | 413/261 | 793.8/276.7 | 709.2/295.1 | 4.41/2.58 | 31.55/7.03 |
| St7Grf6 | 0-5 | 9084/35317 | 917/268 | 1020.4/316.6 | 1031.9/322.5 | 5.77/1.76 | 112.98/2.82 |
| | 6-7_FeMn_L | 5198/59369 | 813/260 | 1103.8/349.7 | 1054.8/422.2 | 5.65/2.04 | 110.58/4.04 |
| | 15-16 | 1525/15974 | 103/214 | 126.8/276.1 | 125.2/268.0 | 3.35/2.49 | 14.37/4.39 |
| | 19-20 | 23903/0 | 534/0 | 695.4/0 | 687.4/0 | 3.33/0 | 9.75/0 |
| | 20-21_FeMn_L | 26328/19215 | 452/274 | 631.9/300.6 | 658.9/299.4 | 3.65/3.01 | 15.73/7.31 |
| | 25-26 | 8910/9225 | 318/181 | 414.3/213.5 | 419.3/216.9 | 3.44/2.8 | 10.85/5.95 |

Table S2. General features of the of the 37 Lake Baikal MAGs.

| Phylum/class | GC Content (%) | Completeness | Contamination | ANI | Estimated genome size (Mp) | Taxonomic affiliation of MAGs (GTDB, referenced groups) | Origin of closest organism (source or reference) |
|-------------------------|----------------|--------------|---------------|-------|----------------------------|---|--|
| Actinobacteriota-c8 | 55.75 | 100 | 0 | 82.22 | 2.58 | Actinobacteria bacterium | Deep terrestrial subsurface fluid (GCA_003599235.1) |
| Actinobacteriota-c11 | 69.29 | 71.45 | 0.84 | - | 2.49 | <i>Actinobacteriota</i> | N/A ¹ |
| Gammaproteobacteria-c58 | 59.03 | 99.15 | 0.64 | 87.21 | 3.78 | <i>Azonexus</i> sp. | GCA_016705475.1 |
| Gammaproteobacteria-m2 | 56.16 | 75.06 | 0.43 | - | 2.23 | <i>Burkholderiales</i> | N/A |
| Gammaproteobacteria-m43 | 43.55 | 68.94 | 2.08 | 80.03 | 3.6 | <i>Methylothermus</i> sp. | Lake Baikal (GCA_009693255.1) |
| Gammaproteobacteria-m15 | 64.65 | 54.34 | 1.95 | 80.56 | 4.6 | Betaproteobacteria bacterium | Environmental aquatic freshwater lotic sediment (GCA_001771935.1) |
| Gammaproteobacteria-c3 | 62.92 | 53.03 | 9.32 | - | 4.73 | <i>Burkholderiales</i> | N/A |
| Gammaproteobacteria-c38 | 62.61 | 57.85 | 5.68 | 81.78 | 4.79 | <i>Rhodospirillum rubrum</i> | Sao Paulo Zoo's Lake water (GCF_006974105.1) |
| Desulfobacteriota-c66 | 54.35 | 91.98 | 7.89 | 79.96 | 5.28 | Desulfuromonadales bacterium | Siberian coastal permafrost (GCA_016650295.1) |
| Desulfobacteriota-m70 | 39.32 | 82.52 | 0.16 | - | 3.29 | <i>Desulfobacterota</i> | N/A |
| Desulfobacteriota-m4 | 56.04 | 74.6 | 1.52 | 82.9 | 3.33 | <i>Geobacter</i> sp. | Lake Hazen, Arctic (GCA_009886055.1) |
| Desulfobacteriota-c44 | 65.04 | 60.65 | 0.43 | 90.78 | 4.28 | Deltaproteobacteria bacterium | GCA_011391555.1 |
| Desulfobacteriota-m16 | 67.42 | 50.86 | 10.84 | 90.7 | 2.42 | Deltaproteobacteria bacterium | GCA_011391555.1 |
| Planctomycetota-m12 | 52.06 | 83.89 | 10.48 | 93.26 | 2.8 | Planctomycetes bacterium (<i>Brocadiales</i>) | Rifle well FP-101 under high O ₂ conditions (GCA_001828545.1) |
| Planctomycetota-c67 | 41.99 | 82.44 | 4.35 | 79.99 | 2.87 | Planctomycetes bacterium | Groundwater planktonic microbiome (GCA_016198835.1) |
| Nitrospirota-c4 | 61.35 | 70.85 | 8.23 | - | 9.54 | <i>Nitrospirales</i> | N/A |
| Nitrospirota-m35 | 63.26 | 63.3 | 8.62 | 91.95 | 5.53 | Nitrospirae bacterium | Soil sample from Angelo meadow plot 2; 20cm depth; 2 days after second rain event (91mm) (GCA_001914955.1) |
| Nitrospirota-m41 | 61.62 | 58.78 | 3.45 | 92.78 | 3.63 | Nitrospiraceae bacterium | Lake Baikal water (GCA_009692155.1) |
| Chloroflexota-c76 | 62.89 | 73.09 | 2.01 | 75.71 | 2.71 | Anaerolineae bacterium | Marine sediments (GCA_011192015.1) |
| Bacteroidota-m24 | 35 | 67.24 | 3.45 | - | 4.91 | <i>Bacteroidetes</i> | N/A |
| Bacteroidota-c69 | 38.91 | 58.8 | 0.51 | 88.65 | 3.88 | <i>Sediminibacterium</i> | Mine wastewater (GCA_002256765.1) |

| | | | | | | | |
|-----------------------|-------|-------|-------|-------|------|---|--|
| Methylomirabilota-m34 | 69.83 | 93.97 | 5.9 | 81.93 | 2.45 | Candidate division NC10 bacterium | Groundwater sites across Northern California (GCA_016180705.1) |
| Methylomirabilota-m11 | 60.01 | 81.27 | 0.16 | 87.39 | 4.08 | <i>Ca. Methylomirabilis limnetica</i> | Bioreactor (GCF_003044035.1) |
| Methylomirabilota-m8 | 66.06 | 71.47 | 0 | 84.45 | 3.58 | <i>Ca. Rokubacteria bacterium</i> | Groundwater planktonic microbiome (GCA_016201645.1) |
| Methylomirabilota-m62 | 65.35 | 71.42 | 2.62 | 84.79 | 5.84 | Candidate division NC10 bacterium | Hydrothermal vent sediments and freshwater spring sediments (GCA_011054645.1) |
| Methylomirabilota-c71 | 62.7 | 62.9 | 5.33 | - | 5.87 | <i>Methylomirabilota</i> | N/A |
| Methylomirabilota-c9 | 68.39 | 58.14 | 4.98 | 89.41 | 4.8 | <i>Ca. Rokubacteria bacterium</i> | Sediment at 5m depth (GCA_001443385.1) |
| Deinococcota-m54 | 62.33 | 63.13 | 10.14 | - | 5.73 | <i>Deinococcota</i> | N/A |
| Elusimicrobiota-c55 | 64.2 | 94.83 | 0 | 84.74 | 4.37 | Elusimicrobia bacterium | Groundwater sites across Northern California (GCA_016182905.1) |
| Patescibacteria-c49 | 40.99 | 63.87 | 0.69 | - | 3.33 | <i>Curtissbacterales</i> | N/A |
| Acidobacteriota-m10 | 55.32 | 80.37 | 5.16 | 79.32 | 5.53 | <i>Chloracidobacterium</i> sp. | GCA_002427845.1 |
| Acidobacteriota-m40 | 65.26 | 62.08 | 8.36 | 76.97 | 3.51 | Acidobacteria bacterium | Soil samples from a meadow in the Angelo Coastal Range Reserve, CA (GCA_003222385.1) |
| Bacteria-c16 | 56.5 | 69.36 | 5.49 | 76.57 | 8.62 | - ² | Freshwater recirculating aquaculture system biofilter (GCF_001458735.1) |
| Bacteria-m33 | 44.2 | 53.61 | 1.88 | - | 4.86 | - | N/A |
| Crenarchaeota-m3 | 34.6 | 90.93 | 3.44 | 79.02 | 1.54 | Thaumarchaeota archaeon (<i>Nitrosopumilaceae</i>) | Sediment at 5m depth (GCA_001443365.1) |
| Halobacterota-c31 | 45.38 | 89.16 | 1.6 | 96.51 | 2.27 | <i>Ca. Methanoperedens</i> sp | GCA_902386255.1 |
| Thermoplasmatota-c23 | 55.38 | 99.07 | 3.5 | 79.93 | 2.07 | Thermoplasmatota archaeon | Crystalline bedrock of the Fennoscandian Shield (GCA_001800815.1) |

¹ N/A – not classified

² - – not data