Figure. Bathymetry of Organic Lake 9 November 2008

Figure . Vertical profiles of physical and chemical parameters of Organic Lake taken *in situ* on 9 November 2008 at the deepest point in the lake. (YSI sonde V6600 used record conductivity, turbidity, depth, pH, dissolved oxygen. Temperature recorded with a min/max thermometer. Salinity calculated from temperature and conductivity.

Figure. PCA analysis of physico-chemical parameters and cell and VLP counts from Organic Lake depth profile. Data points are the sampling depths 1.7, 4.2, 5.7, 6.5 and 6.7 m. Overlaid vector diagram shows the relative contribution of the variables to explaining the difference between samples.

Figure. Vertical profiles of Organic Lake nutrients from samples taken on 9 November 2008. Red dots are measurements from unfiltered water, blue dots are from water filtered (< 0.1 µm).

Figure. Epifluorescence microscopy images of Organic Lake microbiota. Lake water was filtered onto 0.01 um polycarbonate membrane and stained with SYBR Gold. From top to bottom, 1.7, 4.2, 5.7, 6.5 and 6.7 m sample depths.

Figure. Heatmap and biclustering plot of the SSU composition of size fractionated (3.0, 0.8 and 0.1 µm ) samples from a depth profile (1.7, 4.2, 5.7, 6.5 and 6.7 m) of Organic Lake. SSU were classified to the taxonomic rank that gave bootstrap confidence > 85% to the genus level.

Figure. Genetic potential for elemental cycles in Organic Lake. The number of ORFs that matched to key KEGG orthologs in the carbon, nitrogen and sulfur cycles from each sample was normalized across samples (100 000 reads) and plotted. The 3.0, 0.8 and 0.1 µm filters are shown as green, red and blue respectively. The relative counts for genes that map to each process are proportional to the arrow size shown on a log10 scale. **A**. Carbon cycle KEGG orthologs are: aerobic carbon fixation (), aerobic carbon fixation(), CO oxidation(), methane oxidation(), anaerobic carbon fixation(), fermentation () and methanogenesis. **B**. Nitrogen cycle KEGG orthologs are: nitrogen assimilation (), mineralization (), nitrogen fixation (), denitrification (), ammonification () and nitrification (). **C**. Sulfur cycle KEGG orthorlogs are: assimilatory sulfate reduction (), mineralization (), dissimilatory sulfate reduction and sulfur oxidiation.

Figure. Phylogenetic tree of the amino acid sequence of dddD DMSP lyase homologs from Organic Lake and public databases with *E. coli* carnitine CoA transferase of as an outgroup. The tree was computed from a 75 residue region within the conserved amino-terminal class III coenzyme A domain (CaiB) using the neighbor-joining algorithm. Bootstrap values are shown at the nodes. Organic Lake sequences from this study are marked with an asterisk (\*). Numbers in parentheses are counts of sequences which clustered with the Organic Lake homolog shown in the tree with 90% amino acid identity. Sequences with confirmed DMSP lyase activity are shown in bold. Accession numbers from top to bottom are: EBA01716.1, AEV37420.1, ACY01992.1, ADZ91595.1, EAQ63474.1, ABR72937.1, ACV84065.1, ACY02894.1, ABI89851.1, YP\_002822700.1, EEE36156.1, ABV95365.1, AAV94987.1 and EGB36199.1.

Figure. Phylogenetic tree of the amino acid sequence of dddL DMSP lyase homologs from Organic Lake and public databases. The tree was computed from an 84 residue N-terminal region using the neighbor-joining algorithm. Bootstrap values are shown at the nodes. Organic Lake sequences from this study are marked with an asterisk (\*). Numbers in parentheses are counts of sequences which clustered with the Organic Lake homolog shown in the tree with 90% amino acid identity. Sequences with confirmed DMSP lyase activity are shown in bold. Accession numbers from top to bottom are: EEB86351.1, ADK55772.1, EAQ07081.1, EEE47811.1, EAV43167.1, EAU41122.1, EAQ10619.1, ABV95046.1, EAQ04071.1, ABA77574.1 and EHJ04839.1.