Figure S1. Bathymetry of Organic Lake 9 November 2008

Figure S2. Vertical profiles of physical and chemical parameters of Organic Lake taken *in situ* at the deepest point in the lake. σT (1000−density) was calculated from temperature and conductivity.

Figure 1. Vertical structure of Organic Lake. **A**. Parameters that varied unimodally with depth showed two zones: an aerobic mixed zone above 5.7 m and a dense suboxic deep zone below. σT (1000−density) was calculated from temperature and conductivity. **B**. Additional factors that revealed stratification within the deep zone. The peak in concentration at 6.5 m for ammonia was also observed for all other nutrients assayed except nitrate and nitrite (see Table 1). Abbreviations: cond, conductivity; turb, turbidity.

Figure S3. Epifluorescence microscopy images of Organic Lake microbiota filtered onto 0.01 µm 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 S4. PCA analysis of physico-chemical parameters and cell/VLP counts of Organic Lake profile. Data points are the sampling depths 1.7, 4.2, 5.7, 6.5 and 6.7 m. The overlaid vector diagram shows the relative contribution of the variables to explaining the difference between samples. PC1 explained 74.3% and PC2 14.7% of the variation between samples. Abbreviations: cond, conductivity; temp, temperature; turb, turbidity.

Figure 2. Diversity of (**A**) Bacteria and (**B**) Eucarya from each size fraction (0.1, 0.8 and 3.0 µm) at each sample depth (1.7–6.7m) or Organic Lake. The x-axis shows counts of SSU sequences normalized to the average number of reads acquired for each sample.

Figure 3. 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. SSU counts were normalized to the average number of reads from each sample and square root transformed. Taxa that comprised <2% of the sample were not included.

Figure 4. Genetic potential for carbon, nitrogen and sulfur in Organic Lake. The number of ORFs that matched to key KEGG orthologs in the C, N and S cycles from each sample was normalized across samples (100 000 reads) and plotted. The 3.0, 0.8 and 0.1 µm size fractions 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 (dddD\_tree). Phylogenetic tree of the amino acid sequence of dddD DMSP lyase homologs from Organic Lake and public databases with *E. coli* carnitine coenzyme A transferase of as an out-group. 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 (dddL\_tree). 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.