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 denser 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 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) of Organic Lake. The x-axis shows counts of SSU sequences normalized to the average number of reads acquired for each sample. Taxa that belong to the same phylum or higher rank are shown grouped with a square bracket in the legend. Taxa are numbered in the plot where they are highly abundant with corresponding numbered boxes in the legend.

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 cycling in Organic Lake. The number of matches from each sample to KEGG orthologs (KOs) of marker genes involved in C, N and S cycles 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 sum of matches from the whole lake to each process is shown proportional to the arrow size (log10 scale). (**A**) Carbon cycle. Aerobic carbon fixation = (K00855 + K01602)/2, aerobic respiration = (K02256 + K02262 + K02274 + K02276)/4, CO oxidation = (K03518 + K03519 + K03520)/3, methane oxidation = K08684, methanogenesis = (K00401 + K00400)/2, fermentation = K00016 + (K00169 + K00170)/2 and anaerobic carbon fixation = (K01648 + K00174 + K00175 + K00244)/4 + (K00194 + K00197)/2. Carbon cycle marker genes: phosphoribulokinase (K00855), RuBisCO small chain (K01602), cytochrome C oxidase subunit I (*coxI*) (K02256), cytochrome C oxidase subunit III (*coxIII*) (K02262), cytochrome C oxidase subunit I (*coxA*) (K02274), cytochrome C oxidase subunit III (*coxC*) (K02276), carbon monoxide dehydrogenase small subunit (*coxS*)(K03518), carbon monoxide dehydrogenase medium subunit (*coxM*) (K03519), carbon monoxide dehydrogenase large subunit (*coxL*) (K03520), soluble methane monooxygenase (K08684), coenzyme M methyl reductase beta subunit (*mcrB*) (K00401), methyl coenzyme M reductase system, component A2 (K00400), L-lactate dehydrogenase (K00016), pyruvate:ferredoxin oxidoreductase alpha subunit (K00169), pyruvate:ferredoxin oxidoreductase beta subunit (K00170), ATP citrate lyase (K01648), 2-oxoglutarate:ferredoxin oxidoreductase subunit alpha (K00174), 2-oxoglutarate:ferredoxin oxidoreductase subunit beta (K00175), fumarate reductase flavoprotein subunit (K00244), CO dehydrogenase subunit delta (K00194) and CO dehydrogenase subunit gamma (K00197). Note that methane monooxygenase (K08684) orthologs may also hydrolyze other hydrocarbons. (**B**) Nitrogen cycle. Nitrogen assimilation (K00360 + K00367)/2 + (K01915 + K00265 + K00284)/3, mineralization = K00260 + K00261 + K00262, nitrogen fixation = (K00531 + K02586 + K02588 + K02591)/4, denitrification = (K02305 +K04561+ K00376)/3, ammonification = K05904 + K03385, nitrification (K10944 + K10945 + K10946)/3 and Anammox = K10535. Nitrogen cycle marker genes: assimilatory nitrate reductase (K00360), assimilatory nitrate reductase (K00367), glutamine synthetase (*glnA*) (K01915), glutamate synthase (NADPH/NADH) large chain (*gltB*) (K00265), glutamate synthase (ferredoxin-dependent) (*gltS*) (K00284), glutamate dehydrogenase (K00260, K00261, K00262), nitrogenase (K00531), nitrogenase molybdenum-iron protein alpha chain (*nifD*) (K02586), nitrogenase iron protein (*nifH*) (K02588), nitrogenase molybdenum-iron protein beta chain (*nifK*) (K02591), nitric-oxide reductase (*norC*) (K02305), nitric-oxide reductase (*norB*) (K04561), nitrous oxide reductase (*nosZ*) (K00376), Cytochrome c nitrite reductase (*nrfA*) (K05904), formate-dependent nitrite reductase periplasmic cytochrome c552 subunit (*nrfA*) (K03385), ammonia monooxygenase subunit A (*amoA*) (K10944), ammonia monooxygenase subunit B (*amoB*) (K10945), ammonia monooxygenase subunit C (*amoC*) (K10946) and hydroxilamine oxidase (*hao*) (K10535). (**C**) Sulfur cycle. Assimilatory sulfate reduction (K00860 + K00956 + K00957)/3, mineralization = K00456 + K01011 and dissimilatory sulfate reduction/sulfur oxidiation = (K00394 + K00395 + K00396)/3. Dissimilatory sulfate reduction and sulfur oxidation utilize orthologous genes and were distinguished based on the phylogenetic affiliation of the gene match. Sulfur cycle marker genes: adenylyl sulfate kinase (*cysC*) (K00860), sulfate adenylyltransferase subunit 1 (*cysN*) (K00956), sulfate adenylyltransferase subunit 1 (*cysD*) (K00957), cysteine dioxygenase (K00456), 3-mercaptopyruvate sulfurtransferase (K01011), adenylylsulfate reductase subunit A (*aprA*) (K00394), adenylylsulfate reductase subunit B (*aprB*) (K00395) and sulfite reductase (*dsrA*) (K00396).

Figure S1. Map of the Vestfold Hills and location of Organic Lake.

Figure S2. Bathymetry of Organic Lake 9 November 2008

Figure S3. 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 S4. 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 S5. 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 S6. Phylogenetic tree of dddD DMSP lyase homologs. *E. coli* carnitine coenzyme A transferase was used as an out-group. The tree was computed from a 75 amino acid 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 S7. Phylogenetic tree of dddL DMSP lyase homologs from Organic Lake and public databases. The tree was computed from an 84 amino acid 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.

Figure S8. Phylogenetic tree of rhodopsin homologs including proteorhodopsin, bacteriorhodopsin, actinorhodopsin and xanthorhodopsin. The *Halobacterim salinarum* R1 halorhodopsin was used as an out-group. The tree was computed from a 78 amino acid region spanning the motif involved in ‘spectral tuning’ using the neighbor-joining algorithm. 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 light-dependent growth are shown in bold. Accession numbers from top to bottom are: EAZ99241.1, EDP63929.1, EGF32634.1, ZP\_09955974.1, AEG32267.1, EDY76405.1, EDY88259.1, YP\_445623.1, ACN42850.1, EIC91904.1, AAZ21446.1, AAT38609.1, AEE49633.1, EAS71907.1, John Bowman personal correspondence, EAQ40507.1, EAQ40925.1, EAR12394.1, EHQ04368.1, EAZ94876.1, EIA08356.1, AEE20201.1, EEG43331.1, ZP\_09501337.1 and YP\_001689404.1