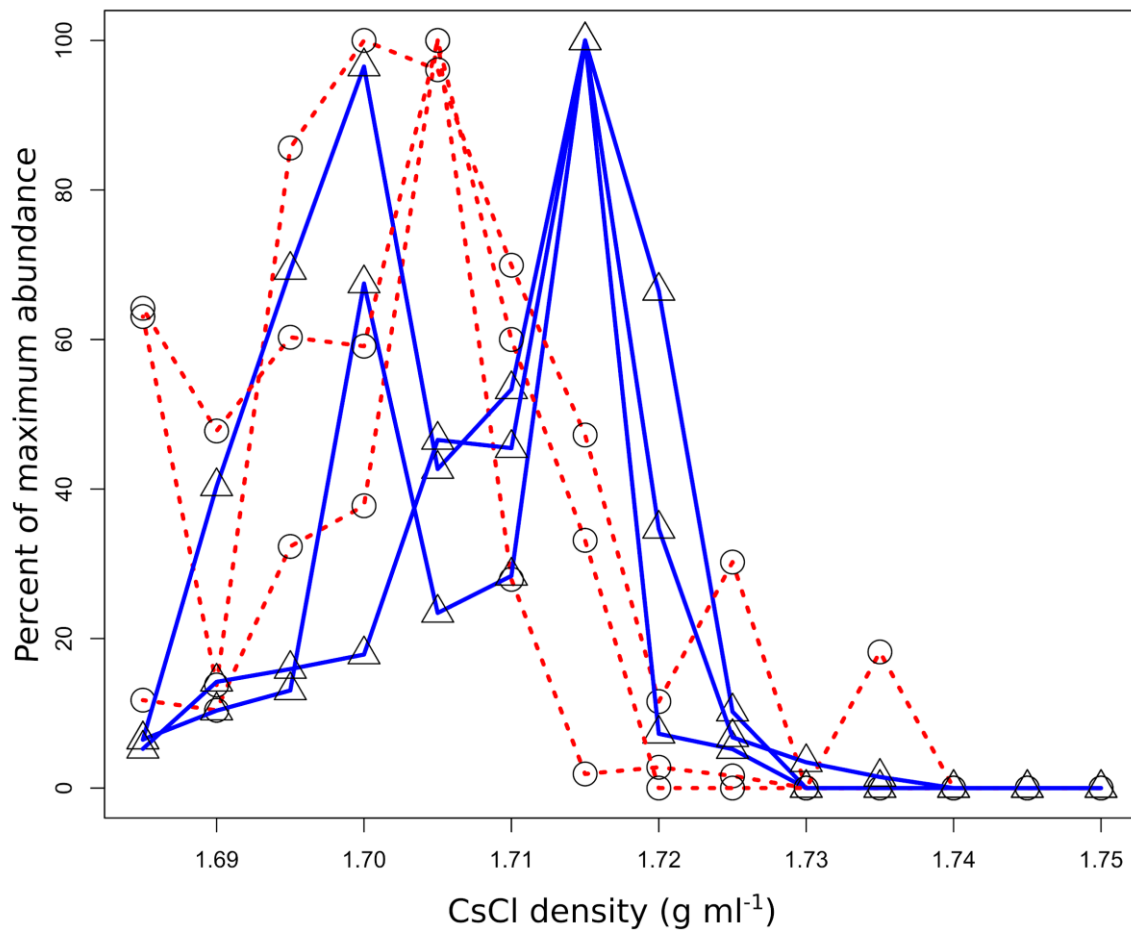
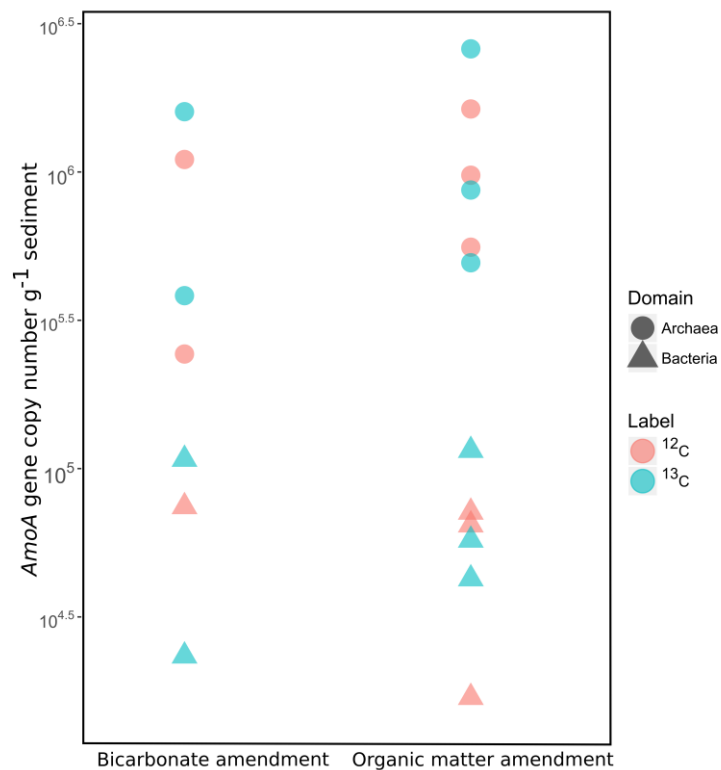


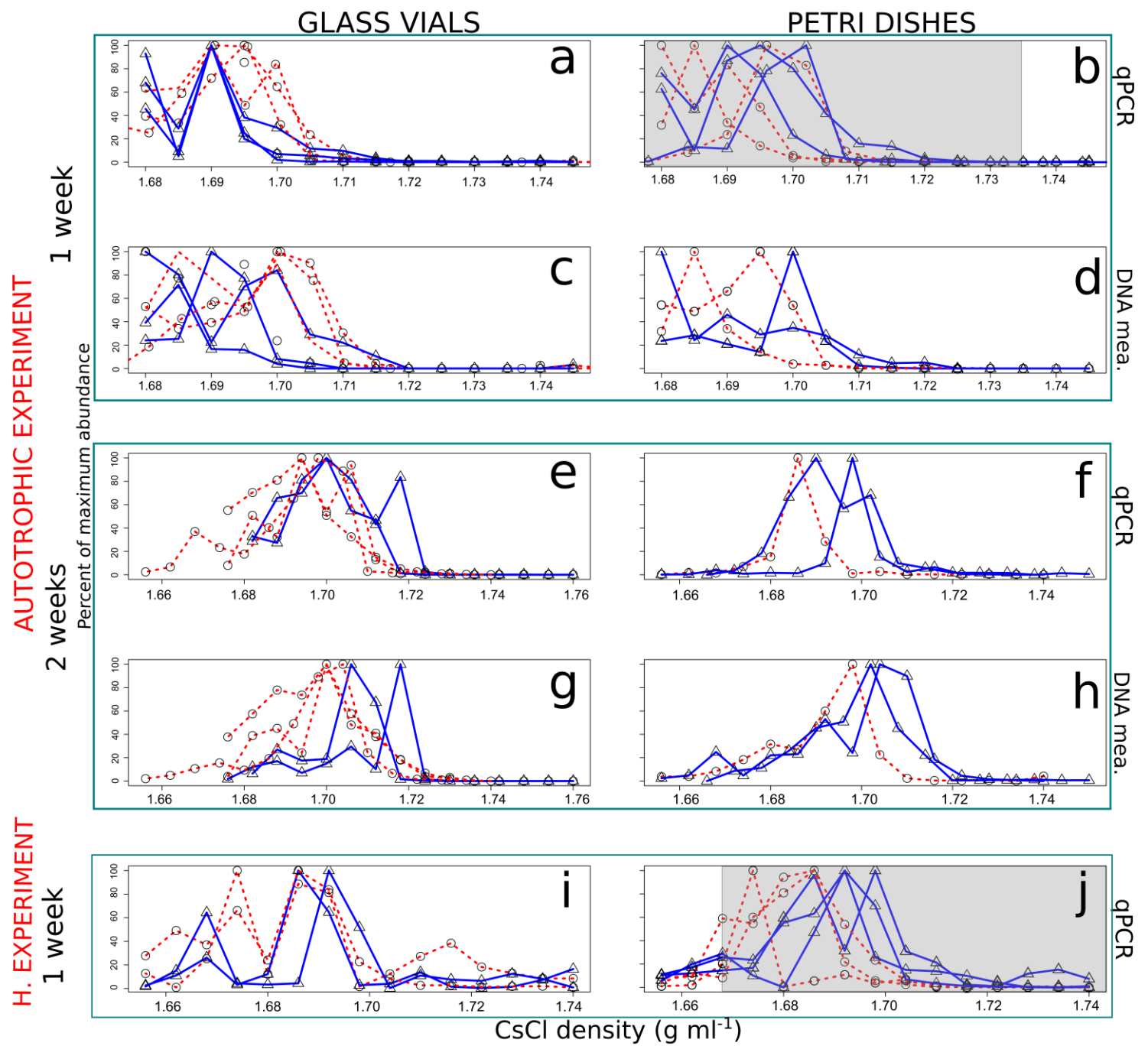
Density fractions for organic matter extraction



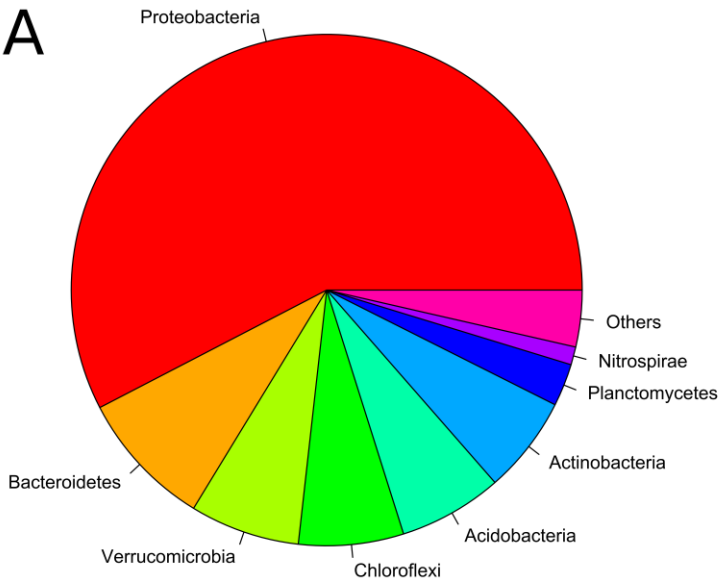
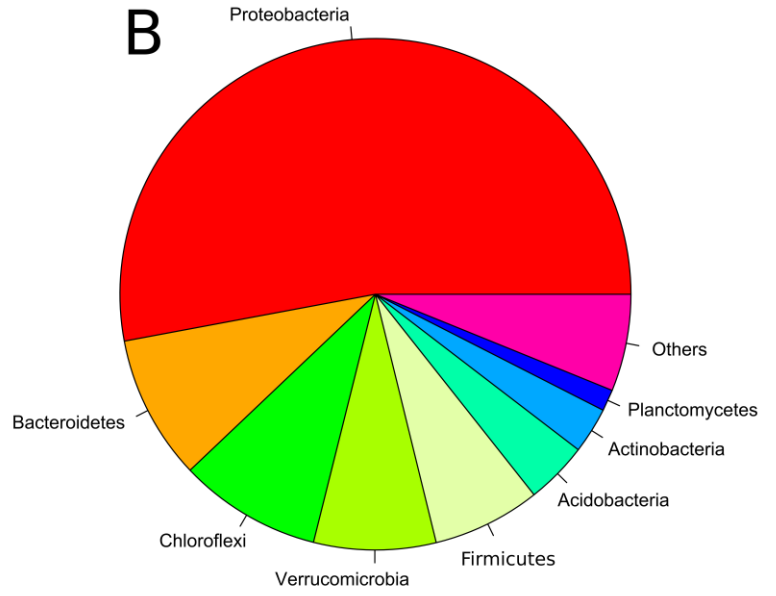
Supplementary Fig. 1. Plots representing the shifts in the BD of total DNA in each density fractions in glass vials incubated with ¹³C-labeled bicarbonate for 2.5-month period. Red colored dashed lines with circles represent the control (¹²C-labeled fractions) and blue colored continuous lines with triangles represent the experiment (¹³C-labeled fractions). The x axis shows the CsCl density of all fractions and the y axis represents the relative abundances calculated from their maximal abundance. The two separate peaks in the ¹³C-labeled incubation likely derive from (1) unlabeled DNA from plants and detrital extracellular DNA (unlabeled peak to at ca. 1.70 g mL⁻¹) and (2) labeled DNA from actively growing microbes and their consumers (labeled peak at ca. 1.72 g mL⁻¹).



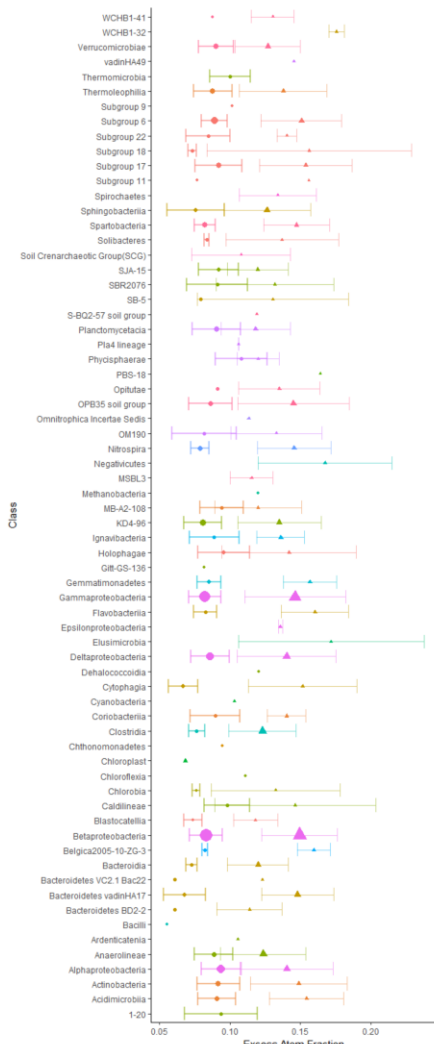
Supplementary Fig. 2. Archaeal and bacterial *amoA* gene copy numbers per gram sediment in labeled and unlabeled incubation settings. Note that archaeal *amoA* genes were more abundant than bacterial *amoA* genes in freshwater sediment with the average AOA:AOB ratio of ~15 in the incubation amended with ¹³C-labeled bicarbonate and ~19 in the incubation amended with ¹³C-enriched organic matter for 1 week period.



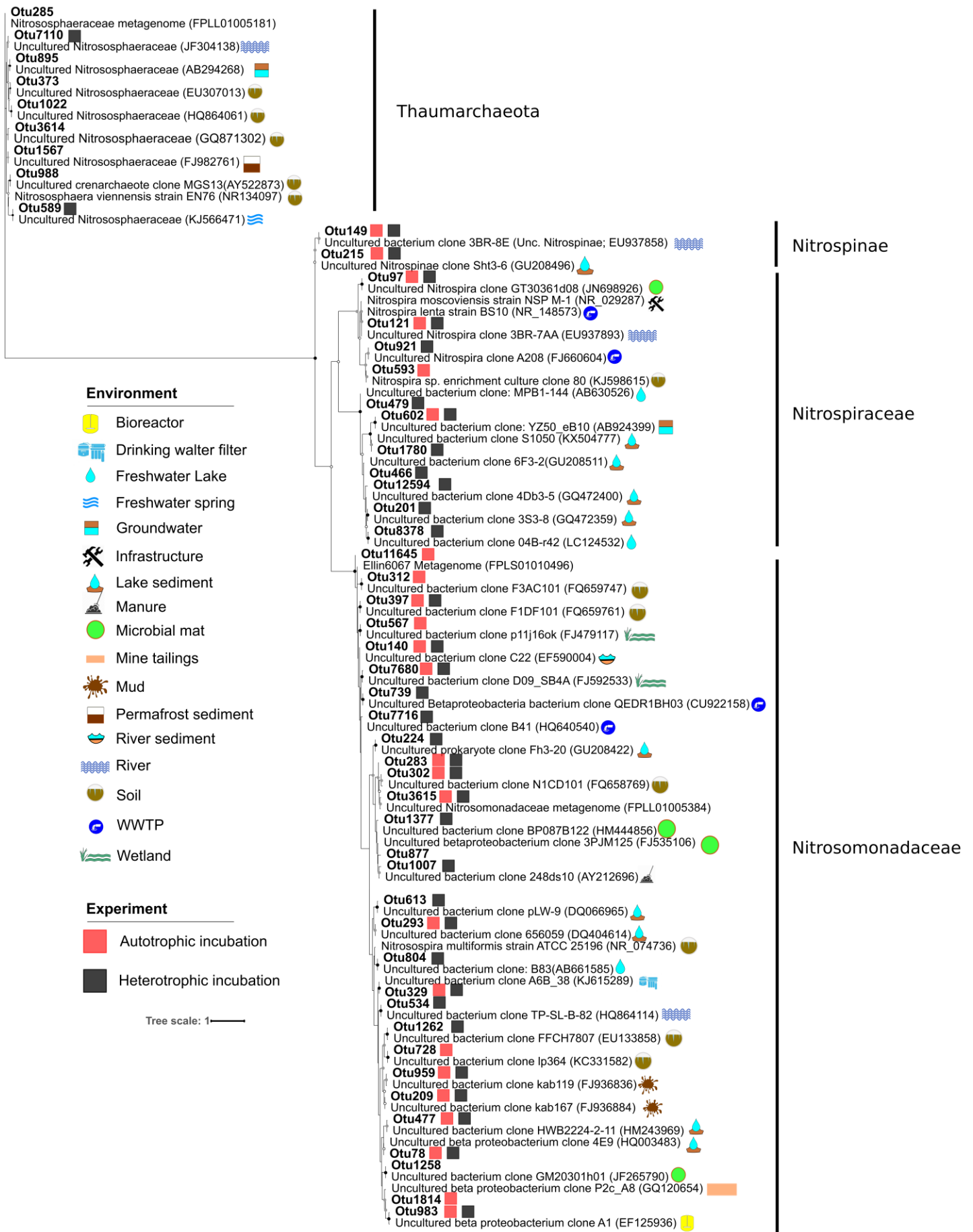
Supplementary Fig. 3. Plots representing the shifts in the BD of density fractions in glass vials and petri dishes. Red colored dashed lines with circles represent the control (^{12}C -labeled fractions) and Blue colored continuous lines with triangles represent the experiment (^{13}C -labeled fractions). The x axis shows the CsCl density of all fractions and the y axis represents the relative abundances calculated from their maximal abundance. Gray shading and symbols filled with black color indicate the fractions used for sequencing. Abbreviations: BD, buoyant density, DNA mea., lines plotted based on DNA measurements, qPCR, lines plotted based on quantitative PCR, H., Heterotrophic.

A**B**

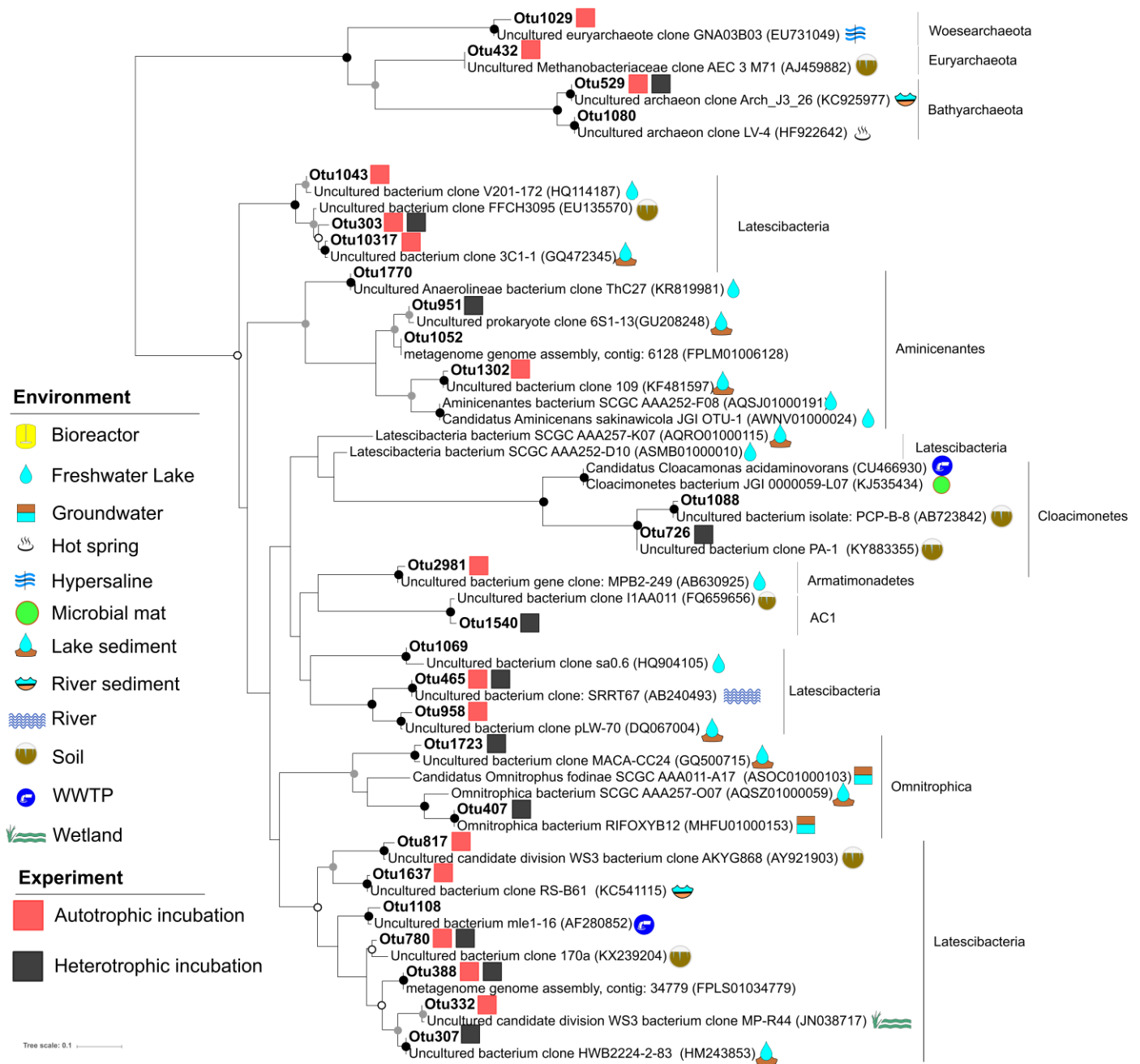
Supplementary Fig. 4. Pie charts representing the total bacterial community of the density fractions regardless of assimilation of the ^{13}C -labeled bicarbonate (A) and HMW organic matter (B).



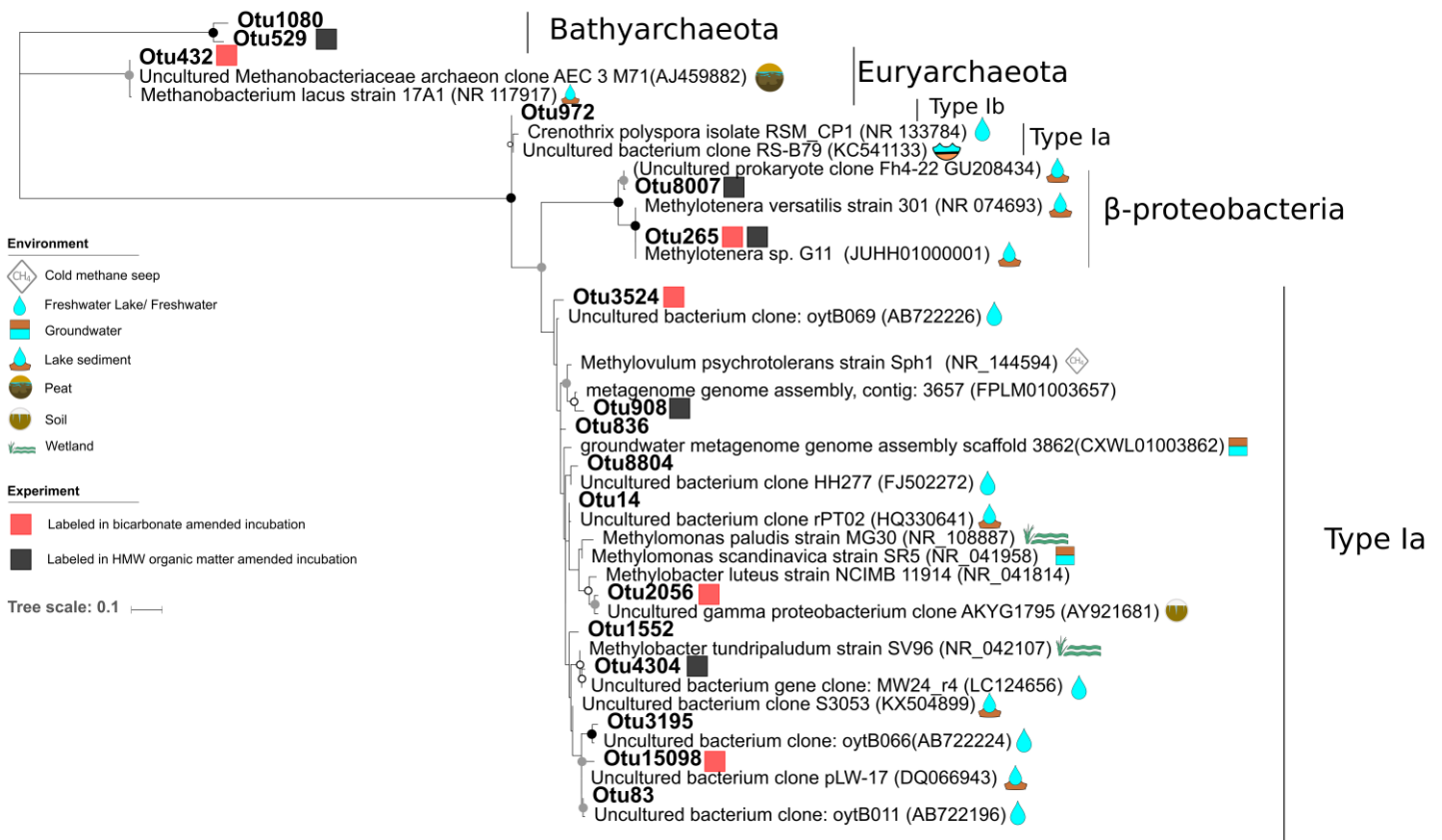
Supplementary Fig. 5 Mean \pm standard error ^{13}C EAF in the DNA of grouped taxa within class (Left top) order (Right top) and family (Bottom left) level after incubation with ^{13}C -labeled HMW organic matter (triangle) and ^{13}C -labeled (circle). Each taxonomic level was colored by phylum and the relative abundance of each taxonomic level is proportional to the size of symbols.



Supplementary Fig. 6. Maximum likelihood phylogenies (PhyML) of betaproteobacterial ammonia-oxidizers and nitrite-oxidizing *Nitrospira* and *Nitrospinae* 16S rRNA genes sharing 97% sequence identity with OTUs after a one-week incubation amended with ¹³C-labeled bicarbonate. OTUs which assimilated the labeled substrate represented as red stars next to each OTU. Black circles at nodes represent bootstrap support of 90%, gray circles represent bootstrap support from 70% to 90%, and white circles represent bootstrap support from 70% to 50%. Numbers represent NCBI GI accession IDs.



Supplementary Fig. 7. Maximum likelihood phylogenies (PhyML) of MDM 16S rRNA genes sharing 97% sequence identity with OTUs after a one-week incubation amended with ^{13}C -enriched organic matter. OTUs which assimilated the labeled organic matter and bicarbonate represented as red stars and black squares next to each OTU, respectively. Black circles at nodes represent bootstrap support of 90%, gray circles represent bootstrap support from 70% to 90%, and white circles represent bootstrap support from 70% to 50%. Numbers represent NCBI GI accession IDs.



Supplementary Fig. 8. Maximum likelihood phylogenies (PhyML) of methylotrophs and methanogens 16S rRNA genes sharing 97% sequence identity with OTUs after a one-week incubation amended with ¹³C-labeled HMW organic matter. OTUs which assimilated the labeled substrate represented as red stars next to each OTU. Black circles at nodes represent bootstrap support of 90%, gray circles represent bootstrap support from 70% to 90%, and white circles represent bootstrap support from 70% to 50%. Numbers represent NCBI GI accession IDs.