Supplementary Material

Figure S1. Nitrate loss in cultures incubated with: unlabeled hexadecane, *d*$_{34}$-hexadecane, or unlabeled hexadecane with $NaH^{13}CO_3$. Arrows designate the time-point when cultures were extracted for metabolite analysis. Error bars are shown for the average of triplicate measurements. The average values of duplicate measurements are reported for the 7-month time-point for the $NaH^{13}CO_3$ cultures.

Figure S2. Neighbor-joining tree of consortium 16S rRNA gene OTUs and their closest GenBank matches. The (*) designate the number of clone sequences for each OTU. The tree was generated using MEGA3 and the Tajima Nei distance method. Five thousand bootstraps were performed, and values below 65 are not shown. Clone sequences that are $\geq$ 97% identical are grouped into OTUs.

Figure S3. Neighbor-joining tree of consortium 16S rRNA gene sequences obtained from DGGE analysis relative to other proteobacteria and representative OTUs from the 16S rRNA clone library. The tree was constructed in MEGA3 using the Tajima Nei distance method. Five thousand bootstraps were performed, and values below 65 are not shown.