**Supporting Information**

Limited clone libraries were generated for the 16S rRNA, *amoA*, and *nifH* genes to identify representative sequences to be used for the calibration curves. Two time points were selected for this analysis, the TC material at t0 and a consolidated sample from the three BG mesocosms at t3. Amplicons were produced from DNA extracts using a modified protocol from Colores *et al*. (2000) for all three primer sets. Each 25 μL reaction contained 3 μL DNA extract, 2.5 μL of 10× HotStar buffer with 15 mM MgCl2 (Qiagen Sciences), 200 μM dNTP, 0.4 μM of each primer, 5% dimethyl sulfoxide (Sigma, St. Louis, MO), 0.4 g/L unacetylated bovine serum albumin (Sigma), and 0.5 U HotStar Taq DNA polymerase (Qiagen Sciences). Thermocycler conditions were 95°C for 15 min followed by 30 cycles (16S rRNA) or 37 cycles (*nifH* and *amoA*) of 94°C for 45 s, 55°C (16S rRNA) or 59°C (*nifH*) or 56°C (*amoA*) for 45 s, and 72°C for 30 s (16S rRNA) or 45 s (*nifH* and *amoA*), followed by a 72°C extension for 7 min. PCR products were confirmed by gel electrophoresis using an Alpha Imager (Alpha Innotech).

The amplicons were purified using QIAquick PCR Purification kit (Qiagen Sciences) and cloned into the pCR 2.1 TOPO vector using standard protocols (Invitrogen, Carlsbad, CA). Twenty five clones were randomly selected to represent each gene at each time point (TC-t0 and BG-t3). The clone-amplicon inserts were confirmed and the plasmids extracted from *E. coli* cells using the QIAprep Spin Miniprep kit (Qiagen Sciences) following the manufacturer’s protocol. The clones were sequenced by The University of Arizona Genetics Core (UAGC, Tucson, AZ) using primers M13F/M13R and the sequences were analyzed using CodonCode Aligner v 3.7.1 (CodonCode Corporation, Dedham, MA). Sequences > 400 bp were checked for chimeras using Bellerophon (Huber *et al.* 2004).

From the twenty-five clones processed for each target gene (16S rRNA, *nifH*, and *amoA*) at each of the two time points, 14 to 24 usable sequences were recovered after quality filtering (Table S1). Phylogenetic classifications were determined for the 16S rRNA genes using the Ribosomal Database Project (RDP) v.10 classifier (Wang *et al.* 2007) and the closest taxonomic identifications were determined using the NCBI GenBank Nucleotide BLAST (Table S2). *nifH* clones clustered in four OTU groups, three of which were most similar (93-98% identity) to a rice paddy clone (GU097349) and one (OTU 4) that had 97% identity to a clone previously identified from copper mine tailings (HM565863). The majority of *amoA* clones had 99-100% identity with clones isolated from cattle (AB465017) or swine (AB688086) manure compost.

**References**

Colores, G.M., Macur, R.E., Ward, D.M., Inskeep, W.P., 2000. Molecular analysis of surfactant-driven microbial population shifts in hydrocarbon-contaminated soil. Applied and Environmental Microbiology 66, 2959-2964.

Huber, T., Faulkner, G., Hugenholtz, P., 2004. Bellerophon: a program to detect chimeric sequences in multiple alignments. Bioinformatics 20, 2317-2319.

Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R, 2007. Naïve Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. Applied and Environmental Microbiology 73, 5261-5267.