

Figure S1: Colonization experimental design. a) Picture of a geomicrobiology colonization system with its temperature sensor. b) Location of Eiffel Tower and Aisics vents (yellow triangles) and colonization systems LSTE1 and LSTE2 (orange star) on 2008 image mosaic of Eiffel Tower hydrothermal site.

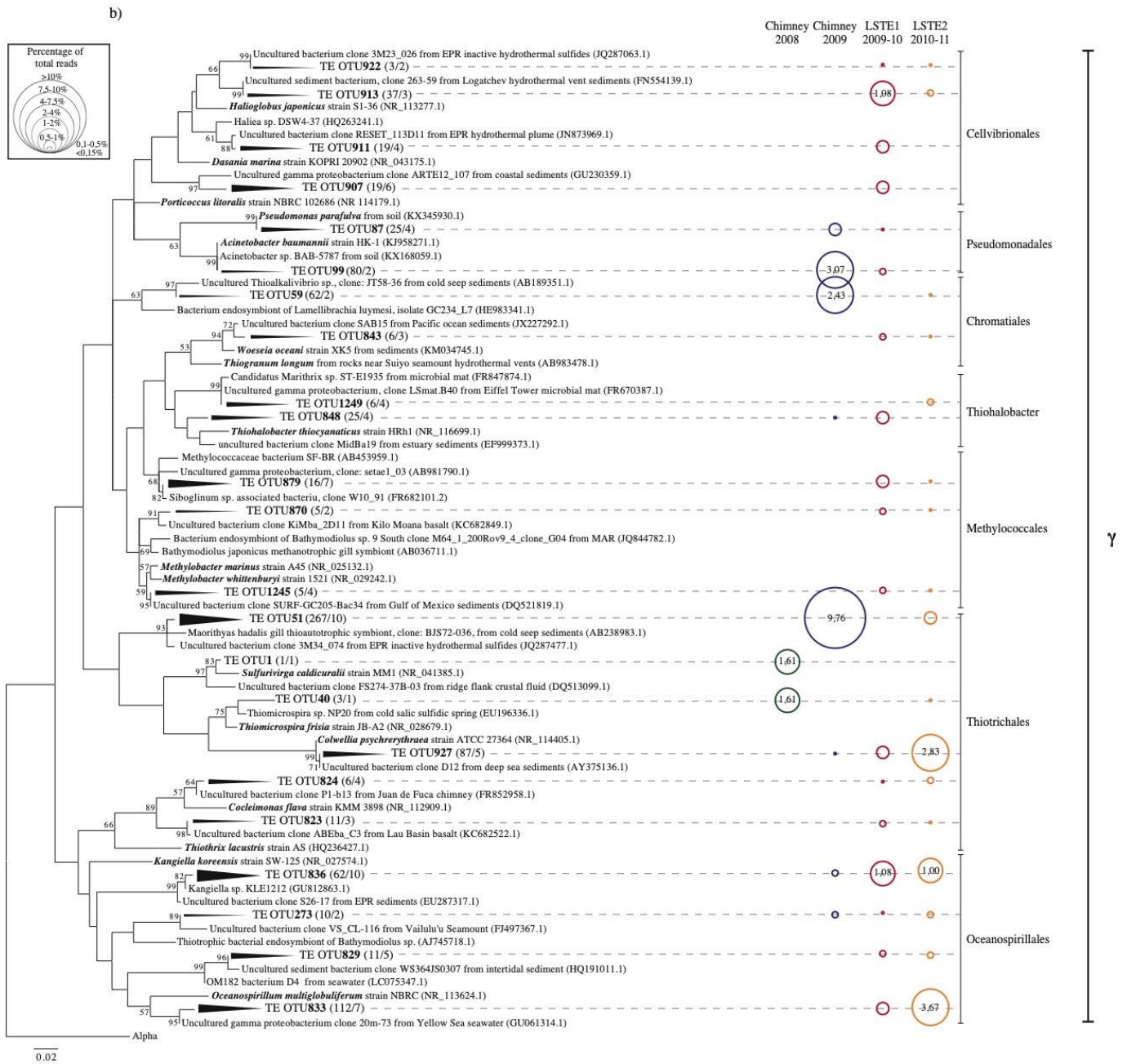


Figure S2: Phylogenetic relationships among the bacterial 16S rRNA gene sequences of representative OTUs of the four samples for Gammaproteobacteria. Sequences obtained in this study are designed by the prefix “TE”. The corresponding number of OTU/sequences obtained for each representative OTU is indicated in bracket. The size of the circle in the right part figures the percentage represented by each OTU with respect to the total number of sequences for each sample. The closest NCBI sequences are presented with their GenBank accession numbers. The tree was constructed by Maximum Likelihood method. Bootstrap values for nodes were obtained using 1,000 replicates. The scale bar represents 0.05 substitutions per nucleotide position

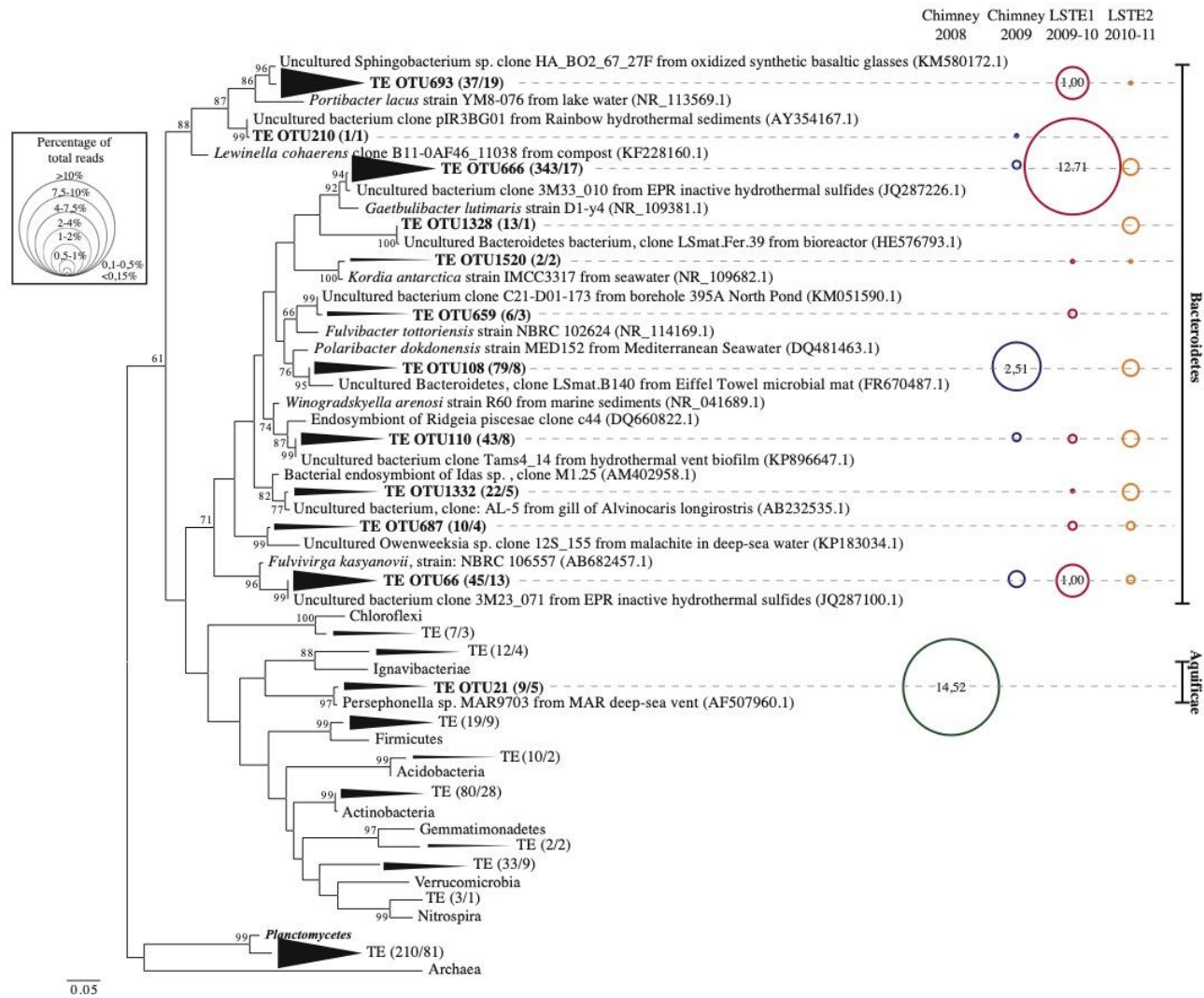


Figure S3: Phylogenetic relationships among the bacterial 16S rRNA gene sequences of representative OTUs of the four samples for Aquificae and Bacteroidetes. Sequences obtained in this study are designed by the prefix “TE”. The corresponding number of OTU/sequences obtained for each representative OTU is indicated in bracket. The size of the circle in the right part figures the percentage represented by each OTU with respect to the total number of sequences for each sample. The closest NCBI sequences are presented with their GenBank accession numbers. The tree was constructed by Maximum Likelihood method. Bootstrap values for nodes were obtained using 1,000 replicates. The scale bar represents 0.05 substitutions per nucleotide position

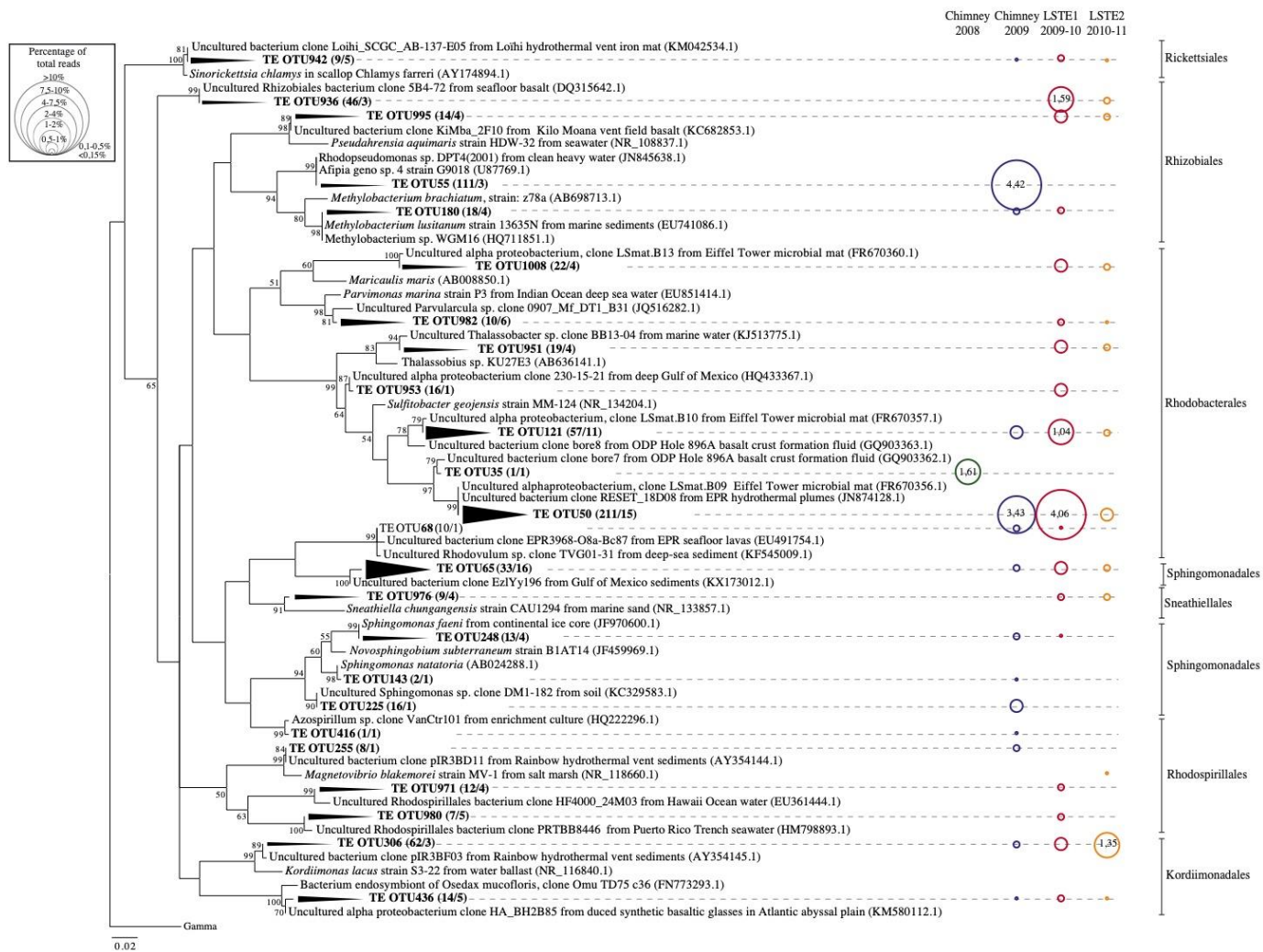


Figure S4. Phylogenetic relationships among the bacterial 16S rRNA gene sequences of representative OTUs of the four samples for Alphaproteobacteria. Sequences obtained in this study are designed by the prefix “TE”. The corresponding number of OTU/sequences obtained for each representative OTU is indicated in bracket. The size of the circle in the right part figures the percentage represented by each OTU with respect to the total number of sequences for each sample. The closest NCBI sequences are presented with their GenBank accession numbers. The tree was constructed by Maximum Likelihood method. Bootstrap values for nodes were obtained using 1,000 replicates. The scale bar represents 0.05 substitutions per nucleotide position.