

*The following supplement accompanies the article*

## **Bacterial community of oolitic carbonate sediments of the Bahamas Archipelago**

**Mara R. Diaz<sup>1,\*</sup>, Alan M. Piggot<sup>2</sup>, Gregor P. Eberli<sup>2</sup>, James S. Klaus<sup>2,3</sup>**

<sup>1</sup>Marine Biology and Fisheries, and <sup>2</sup>Marine Geology and Geophysics, Rosenstiel School of Marine and Atmospheric Science, University of Miami, Miami, Florida 33149, USA

<sup>3</sup>Department of Geological Sciences, University of Miami, Coral Gables, Florida 33146, USA

\*Email: mdiaz@rsmas.miami.edu

*Marine Ecology Progress Series 485: 9–24 (2013)*

---

**Supplement.** Phylogenetic distribution of environmental clones based on 16S rRNA gene sequence analysis. Phylogenetic trees were generated with PAUP\*4.0b10

Alphaproteobacteria

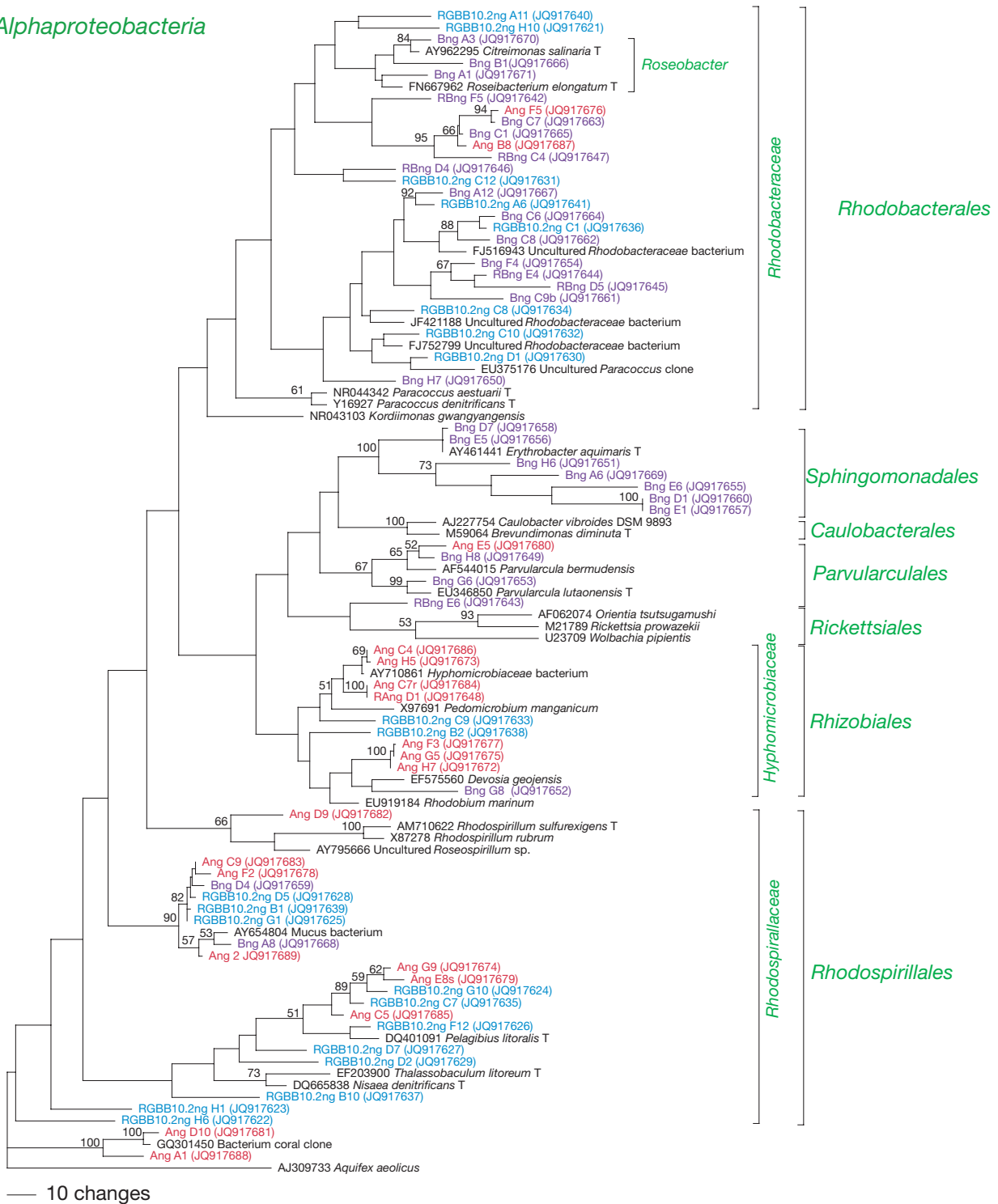


Fig. S1. 16S rRNA phylogenetic tree of *Alphaproteobacteria* clones based on parsimony analysis and heuristic search of 590 nucleotide positions. Numbers on tree represent bootstrap percentages obtained from 1000 replicates. *Aquifex aeolicus* was used as outgroup taxon. Red text denotes clones from the active environment, blue text clones from the non-active environment and purple text clones from the mat-stabilized environments.

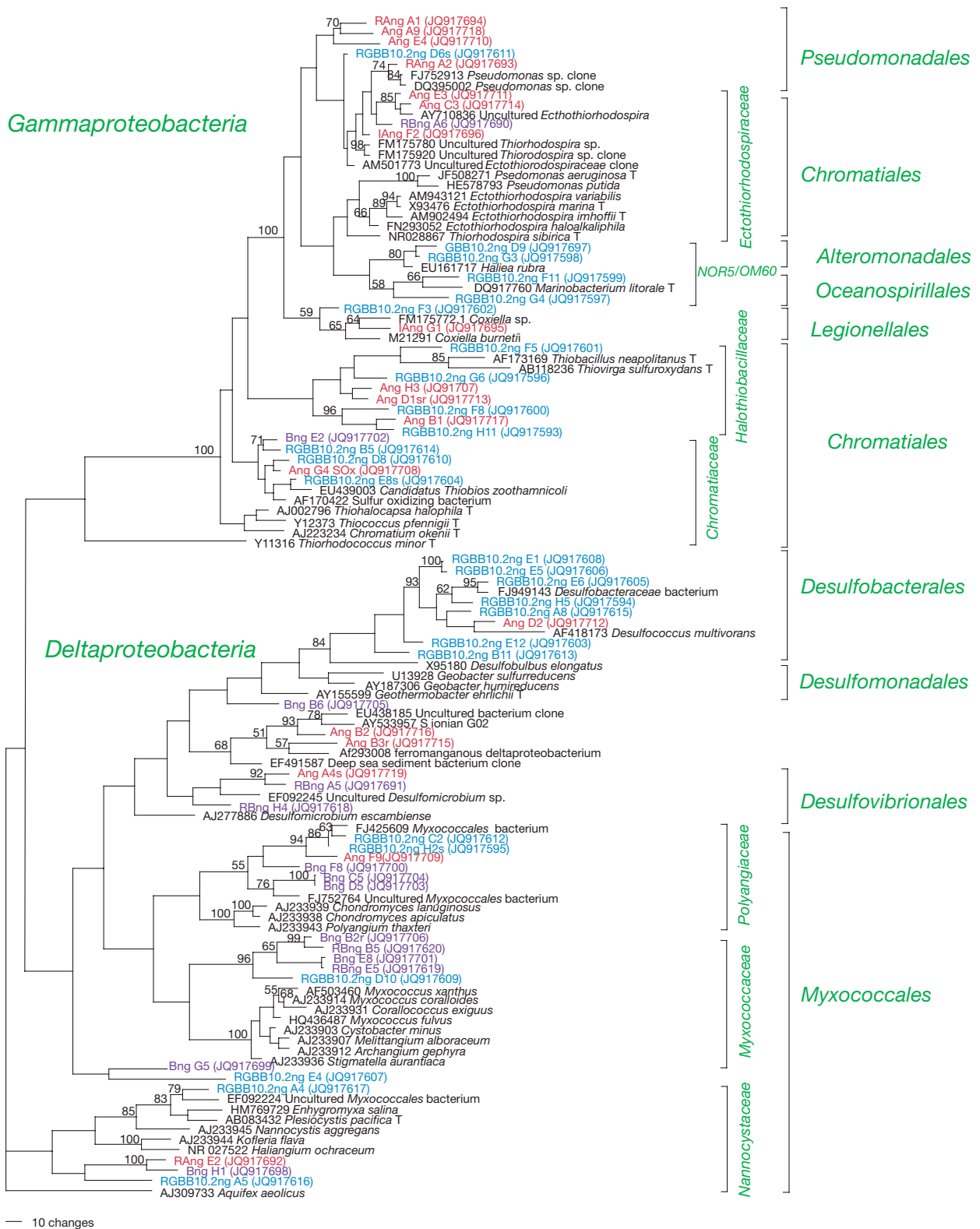
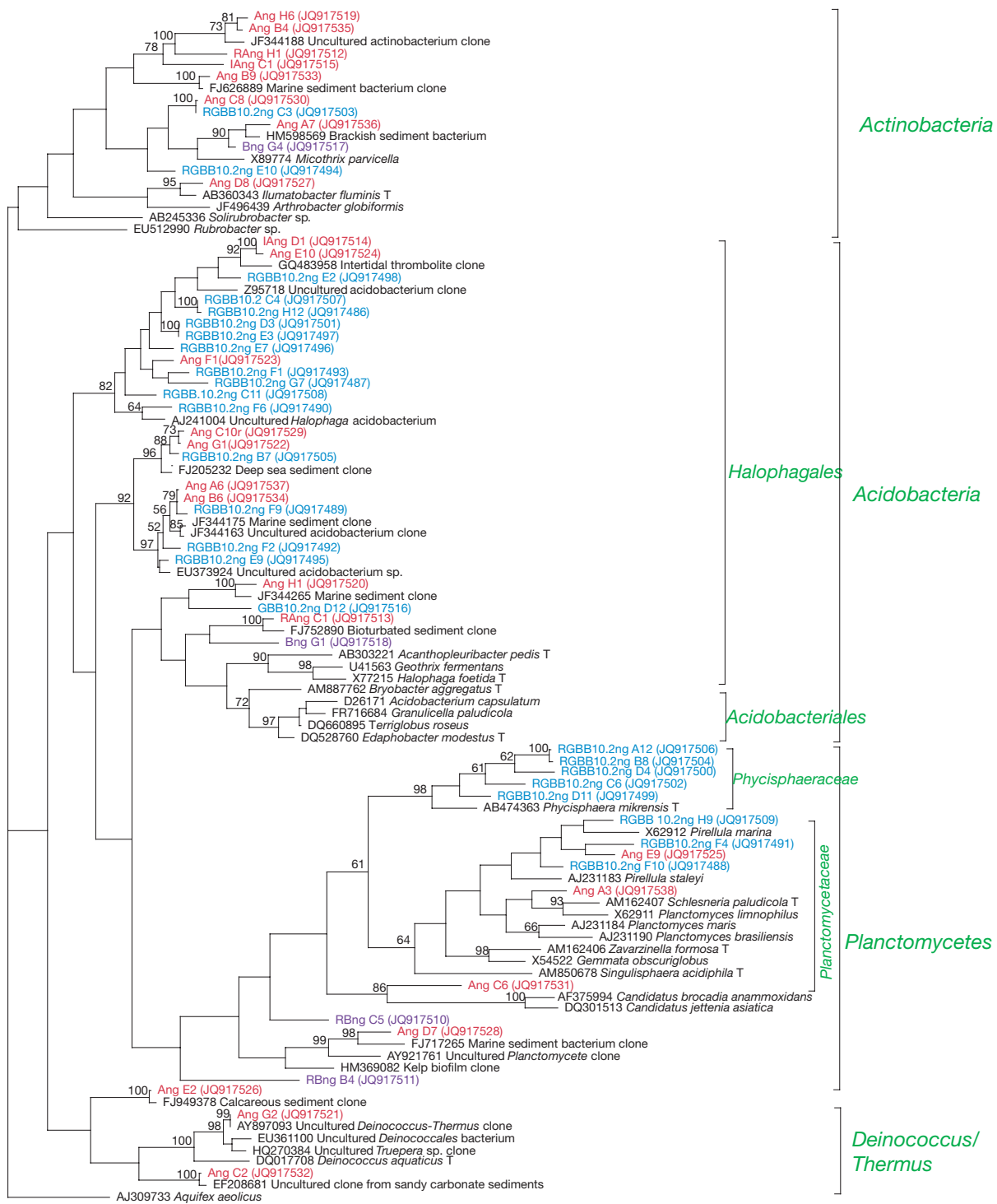


Fig. S2. 16S rRNA phylogenetic tree of *Gammaproteobacteria* and *Deltaproteobacteria* clones based on parsimony analysis and heuristic search of 540 nucleotide positions. Numbers on tree represent bootstrap percentages obtained from 1000 replicates. *Aquifex aeolicus* was used as outgroup taxon. Red text denotes clones from the active environment, blue text clones from the non-active environment and purple text clones from the mat-stabilized environments.



— 10 changes

Fig. S3. Phylogenetic tree of *Actinobacteria*, *Acidobacteria*, *Planctomycetes* and *Deinococcus-Thermus* clones based on parsimony analysis and heuristic search of 525 nucleotide positions. Numbers on tree represent bootstrap percentages obtained from 1000 replicates. *Aquifex aeolicus* was used as outgroup taxon. Red text denotes clones from the active environment, blue text clones from the non-active environment and purple text clones from the mat-stabilized environments.

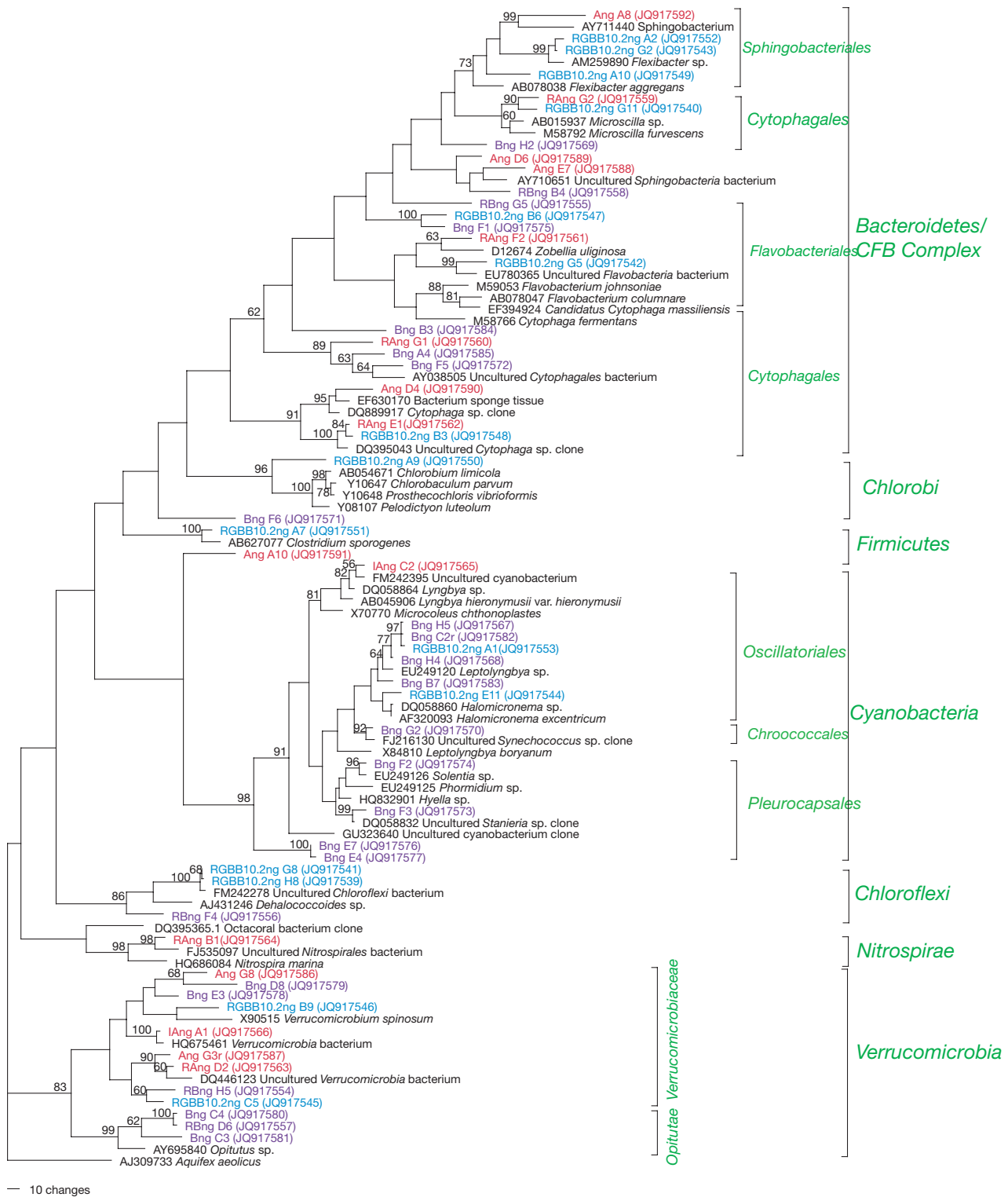


Fig. S4. 16S rRNA phylogenetic analysis of bacterial clones based on parsimony analysis and heuristic search of 550 nucleotide positions. Numbers on tree represent bootstrap percentages obtained from 1000 replicates. *Aquifex aeolicus* was used as the outgroup. Red text denotes clones from the active environment, blue text clones from the non-active environment and purple text clones from the mat-stabilized environments.