The following supplement accompanies the article

Multilevel analysis of the bacterial diversity along the environmental gradient Río de la Plata–South Atlantic Ocean

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Aquatic Microbial Ecology 61: 57–72 (2010)

Supplement 1.

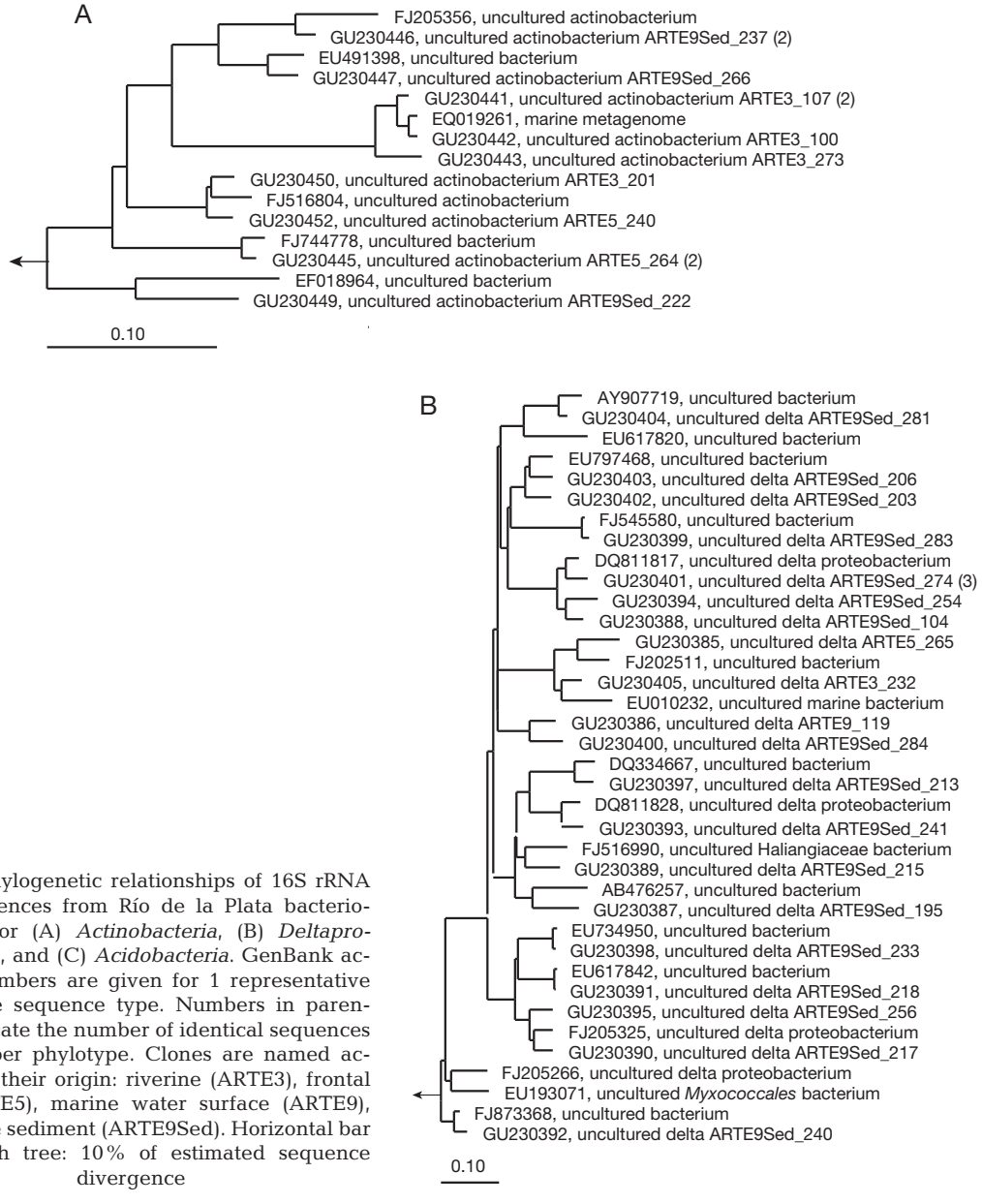
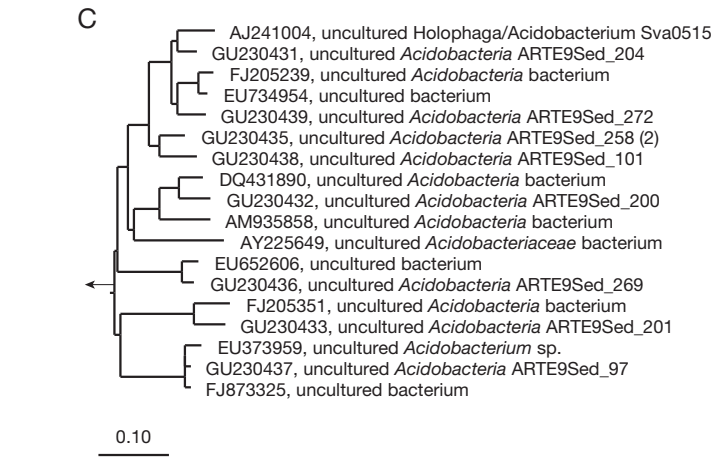


Fig. S1. Phylogenetic relationships of 16S rRNA gene sequences from Río de la Plata bacterioplankton for (A) *Actinobacteria*, (B) *Deltaproteobacteria*, and (C) *Acidobacteria*. GenBank accession numbers are given for 1 representative per unique sequence type. Numbers in parenthesis indicate the number of identical sequences retrieved per phylotype. Clones are named according to their origin: riverine (ARTE3), frontal zone (ARTE5), marine water surface (ARTE9), and marine sediment (ARTE9Sed). Horizontal bar below each tree: 10% of estimated sequence divergence



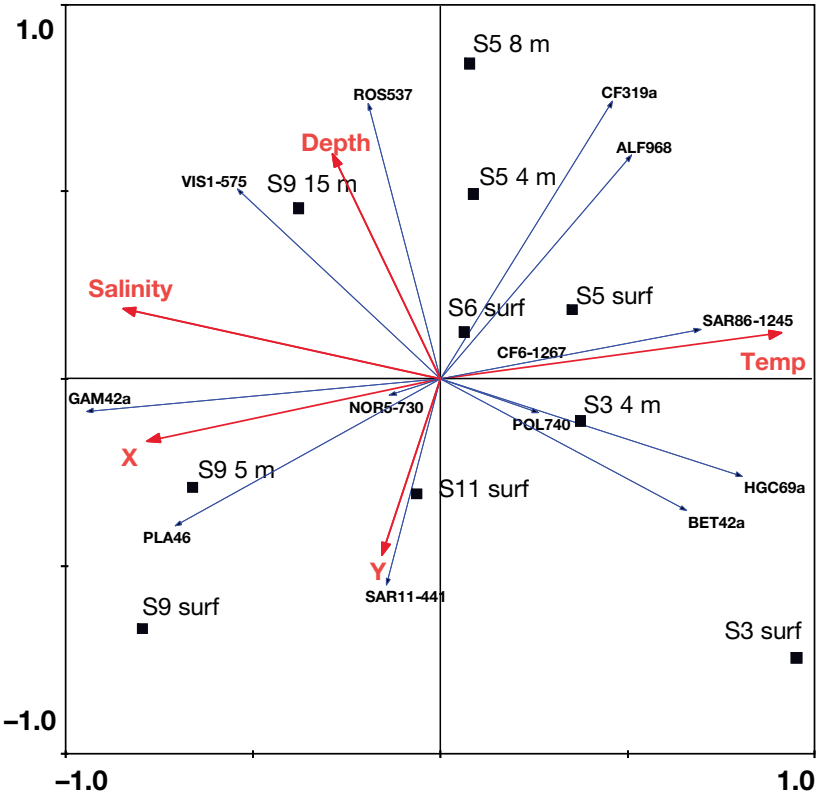


Fig. S2. Redundancy analysis triplot representing the variation in catalyzed reporter deposition-fluorescence *in situ* hybridization (CARD-FISH) abundance data as a function of environmental and spatial parameters. Longitude and latitude coordinates were converted into Euclidean distances in km, where the largest dimension becomes *x* and the second, perpendicular dimension becomes *y*. Ordination plot represents 62% of the biological variation and 82% of the taxa-environment relationships. Constrained ordination was overall significant (trace = 0.753, *F*-ratio = 2.44, p = 0.020) as determined by 1000 permutations of the data. S3 = Stn 3, S5 = Stn 5, etc.; sed = sediment; surf = surface; 4 m = 4 m depth, 5 m = 5 m depth, etc.; ROS537, CF319a, etc. were the probes used in CARD-FISH