



Suppl. Figure 3: Phylogenetic relationships between SSU rRNA gene clones from this study (in bold, with colony names provided), other members of the *Endozoicomonas* and representative sequences from the *Oceanospirillaceae* and *Gammaproteobacteria*. Numbers shown on branches are bootstrap values (1000 bootstraps) for neighbor joining and maximum parsimony, respectively. Bootstrap values less than 50% are not shown. The scale bar corresponds to 0.10 substitutions per nucleotide position.