Figure S1. Neighbor-joining phylogenetic tree based on 16S ribosomal DNA sequences of seven *Roseobacter* clade bacteria analyzed for this study. Sequences were aligned over >1300 positions using Clustal Omega (https://www.ebi.ac.uk/tools/msa/clustalo/) and assembled into a tree using the interactive Tree of Life ((Letunic and Bork, 2011; Letunic and Bork, 2007); http://itol.embl.de/). Sequence similarity is only an estimate of evolutionary relationships.