

Pearson correlation (Opt:0.40%) [0.0%-100.0%]

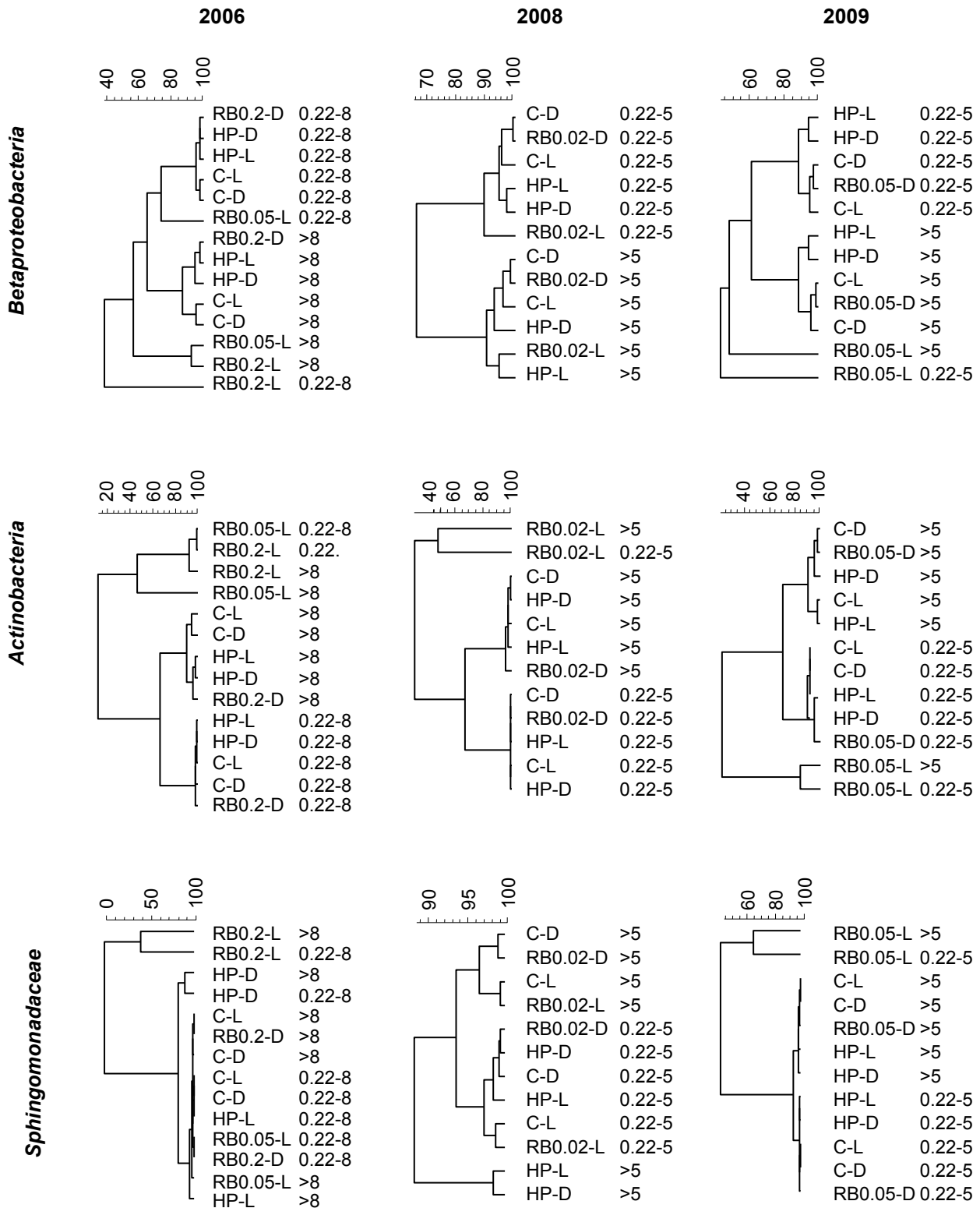


Figure S6

Cluster analysis of *Betaproteobacteria*, *Actinobacteria*, and *Sphingomonadaceae*-specific 16S rRNA gene based RT-PCR DGGE analysis. Free-living (0.22-8 μm in 2006 and 0.22-5 μm in 2008 and 2009) and particle-attached (>8 or >5 μm , respectively) bacteria of all treatments of the *in situ* experiments 2006, 2008, and 2009 were investigated. The UPGMA cluster analyses based on the Pearson correlation that considers the DNA band intensities. Abbreviations are given in Figure S2.