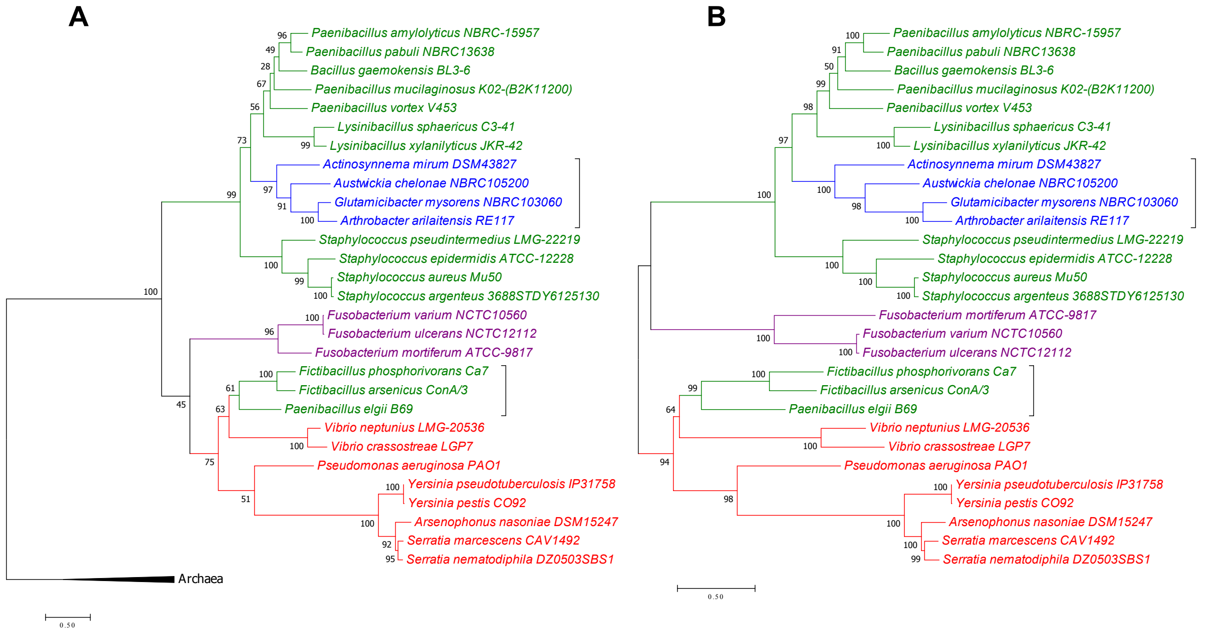
Electronic Supplementary Material (ESI) for Metallomics.

Supplementary Figures



Supplementary Figure 1: Molecular phylogenetic analyses of diverse CntL alone (A) and CntLM (B) amino acid sequences from bacteria. Theses evolutionary trees were constructed in MEGA 7.0.26 by using the Maximum Likelihood Method. They were based on a MUSCLE alignment and on best models chosen according to the Bayesian Information Criterion (BIC). The percentage of trees in which the associated taxa clustered together is shown next to the branches. The evolutionary history was inferred by using the LG (Le_Gascuel) model with a discrete Gamma distribution. The rate variation model allowed for some sites to be evolutionarily invariable. Number of bootstrap replications = 1000. Bacilli, Actinobacteria, Fusobacteria and γ-proteobacteria are depicted in green, blue, violet and red, respectively.