



Figure S1. Maximum-likelihood phylogenetic tree (1000 bootstraps) based on the 16S rRNA gene showing the phylogeny of the *Acidobacteria* cultures studied. *Acidobacterial* sequences from subdivision 8 were used as outgroup. Open and closed circles mark branchings with bootstrap values >60% and >90%, respectively. Subdivisions 1 and 3 are indicated. The bar indicates an evolutionary distance of 0.10 fixed point mutation per nucleotide position.