







**Figure S1.** Phylogenetic tree showing the relationship of the all cultured bacterial strains. The sequence alignment was performed using the SINA online tool (<http://www.arb-silva.de/aligner>) and trees were built in ARB starting from the SILVA SSU dataset Ref NR 99 (version 119) using MrBayes with 100,000 Markov Chain Monte Carlo (mcmc) cycles.