



Supporting information 2. Maximum likelihood tree based on the Le_Gascuel_2008 model (Le and Gascuel, 1993) of the deduced peptide sequences of acetate kinase of available *Mollicutes* in HAMAP database, *Spiroplasma citri*, *Clostridium botulinum*, *Erysipelothrix rhusiopathiae*, *Bacillus subtilis* subsp. *subtilis*, *Lactobacillus plantarum*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, and *Lactococcus lactis* subsp. *lactis* employing *Escherichia coli* and *Salmonella typhimurium* as outgroup. The tree with the highest log likelihood (-14357.6146) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree for the heuristic search was obtained by applying the Neighbor-Joining method to a matrix of pairwise distances estimated using a JTT model. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4727)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 9.6080% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.