



Fig. S2 Maximum-likelihood trees of the concatenated sequences of three pyruvate dehydrogenase components (PDH) and the peptide release factor (PRF) of *G. apicola* strains and *Frischella perrara*. The trees are based on nucleotide sequences and were rooted using homologs from *F. perrara*. Nodes with bootstrap values >50% are marked (1,000 replicates).