



**Figure S3:** The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model (MEGA6). Initial tree(s) for the heuristic search were obtained by applying the BioNJ 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 = 0.7322)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 67 amino acid sequences. The coding data was translated assuming a Standard genetic code table. There were a total of 301 positions in the final dataset.