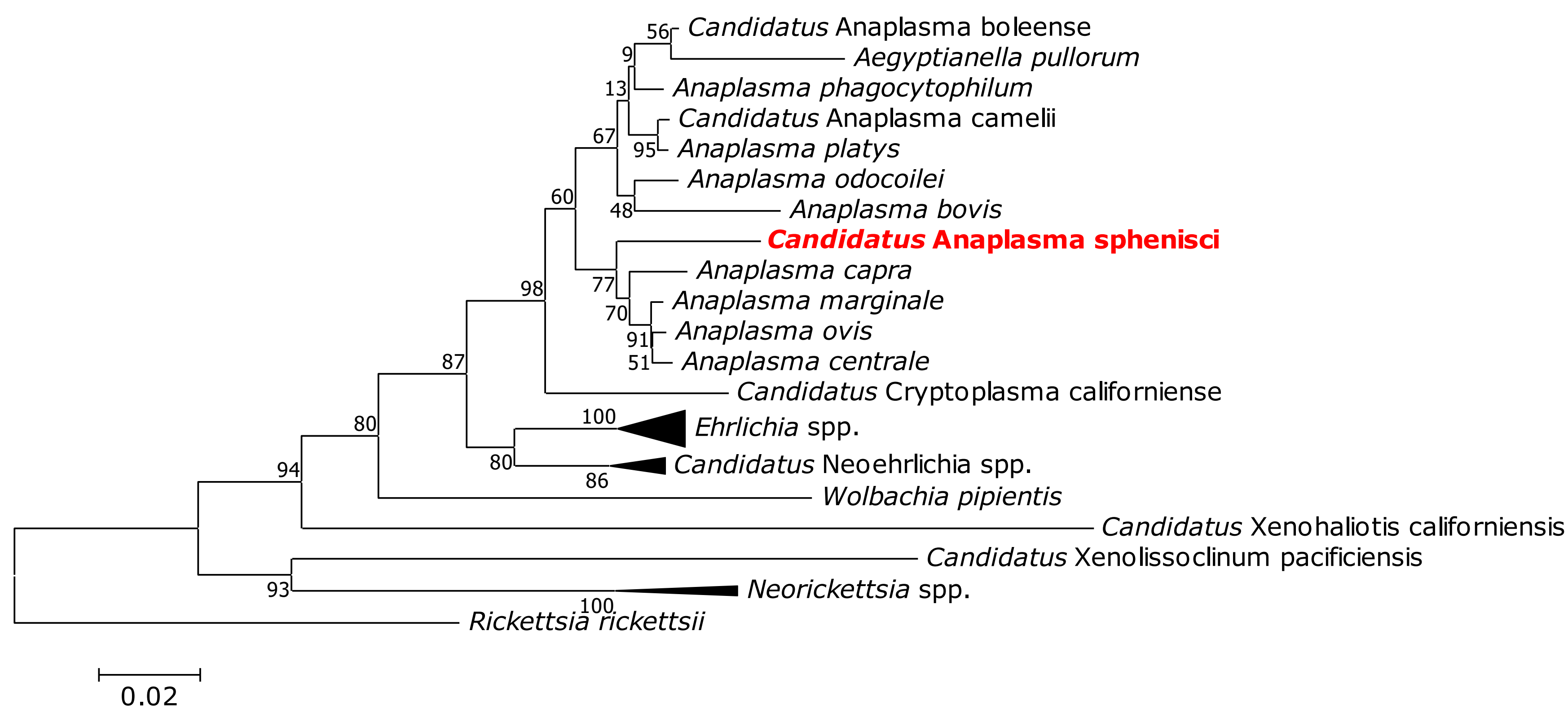
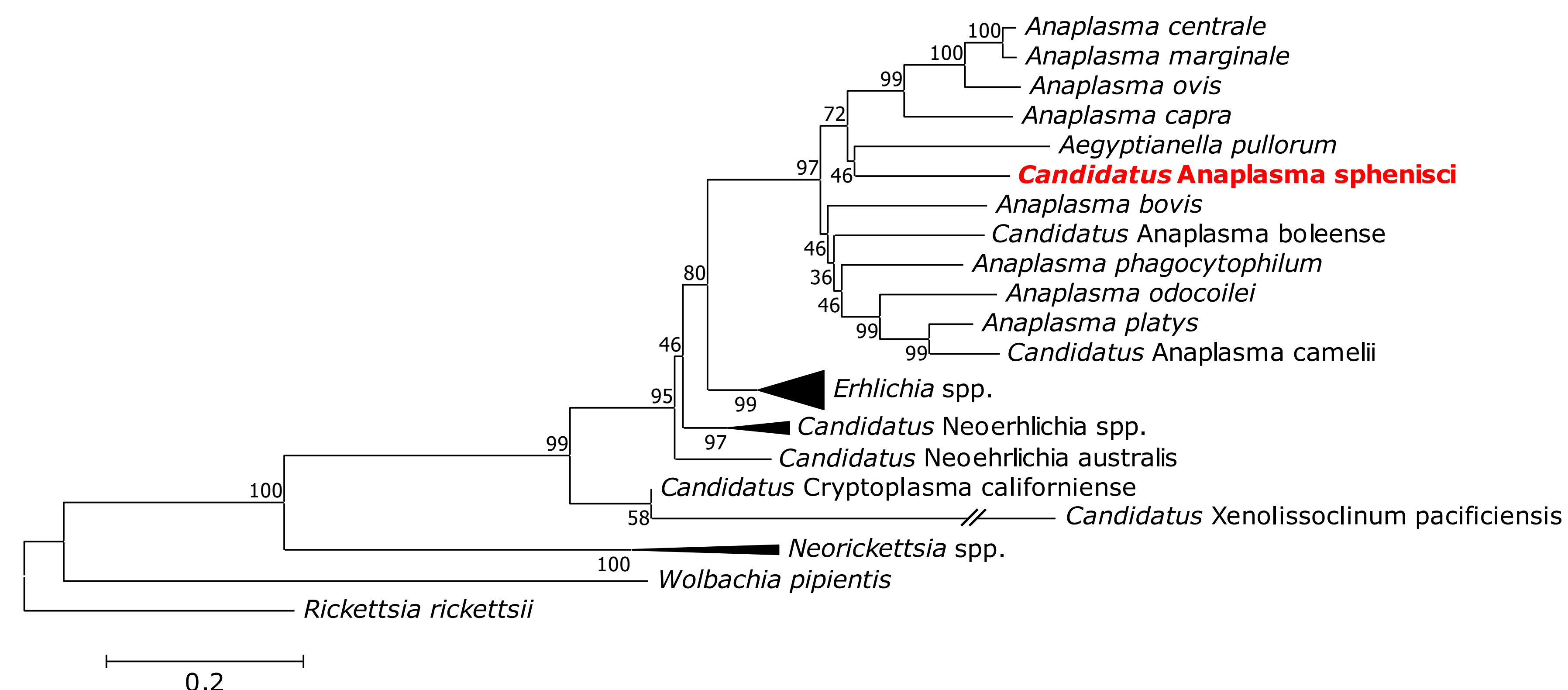


**Additional file 4: Figure S2.** Phylogenetic relationships of “*Candidatus Anaplasma sphenisci*” as determined by different phylogenetic methods based on partial sequences of the 16S *rRNA* and *groEL* genes. Branch lengths are drawn proportionally to evolutionary distance (scale-bars are shown). Numbers adjacent to nodes indicate bootstrap values (a, b, d, e) or posterior probabilities (c, g).

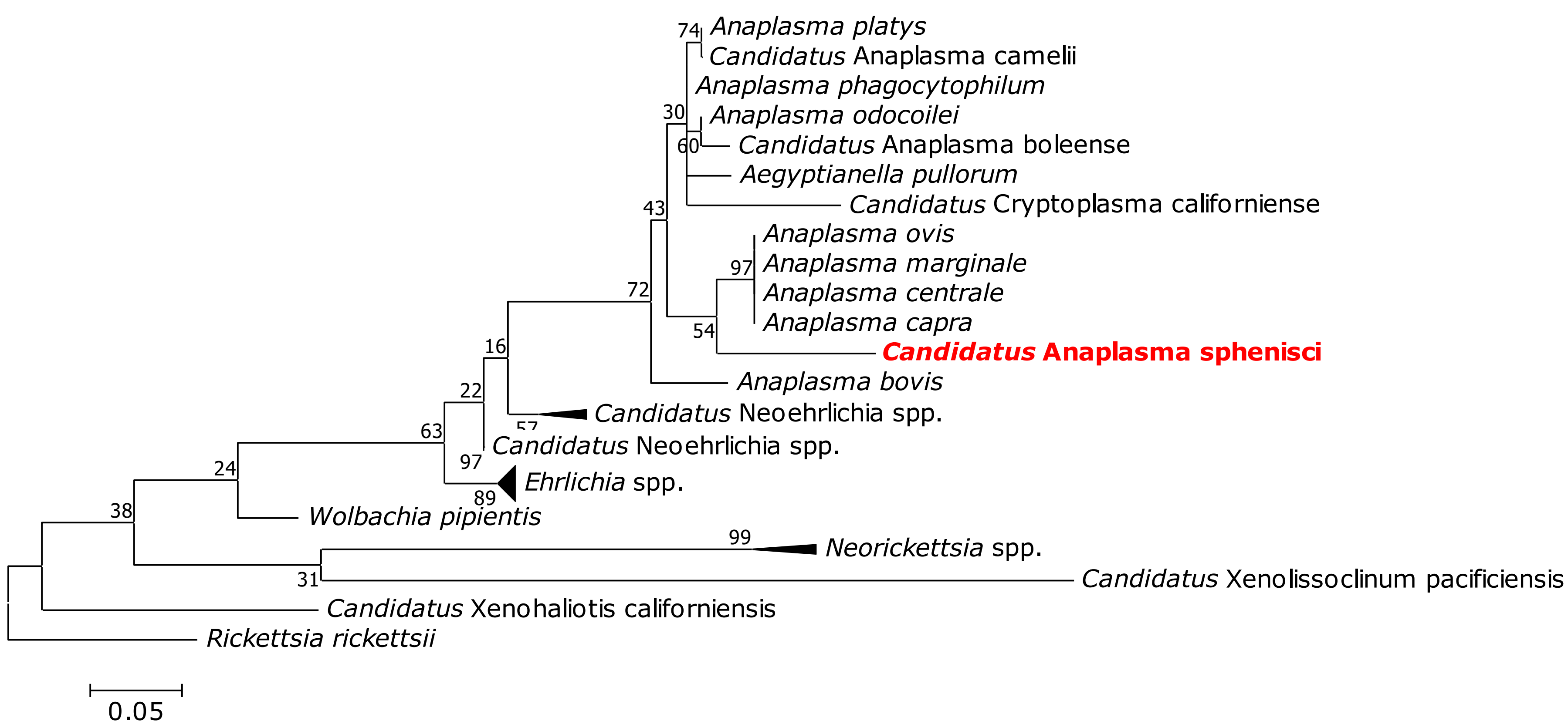
**(a)** 16S *rRNA*, Neighbor-Joining



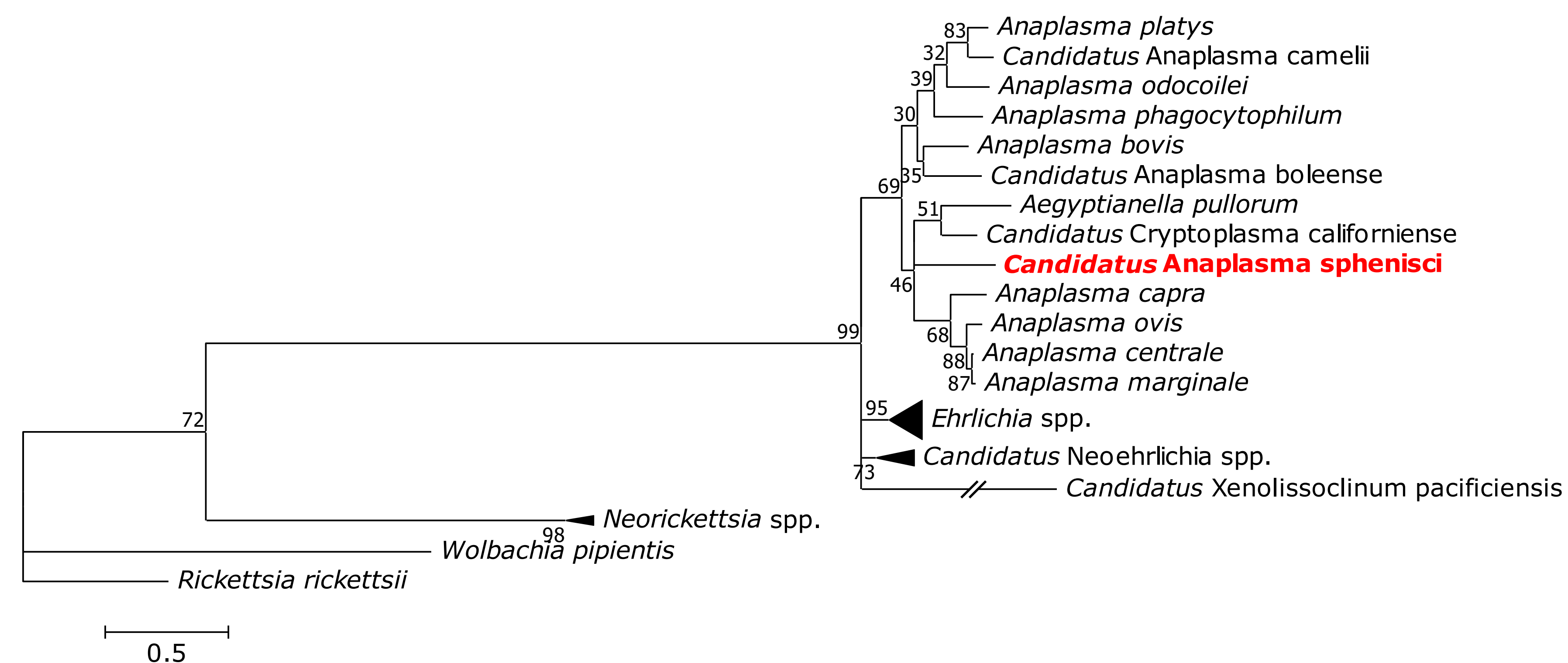
**(d)** *groEL*, Neighbor-Joining



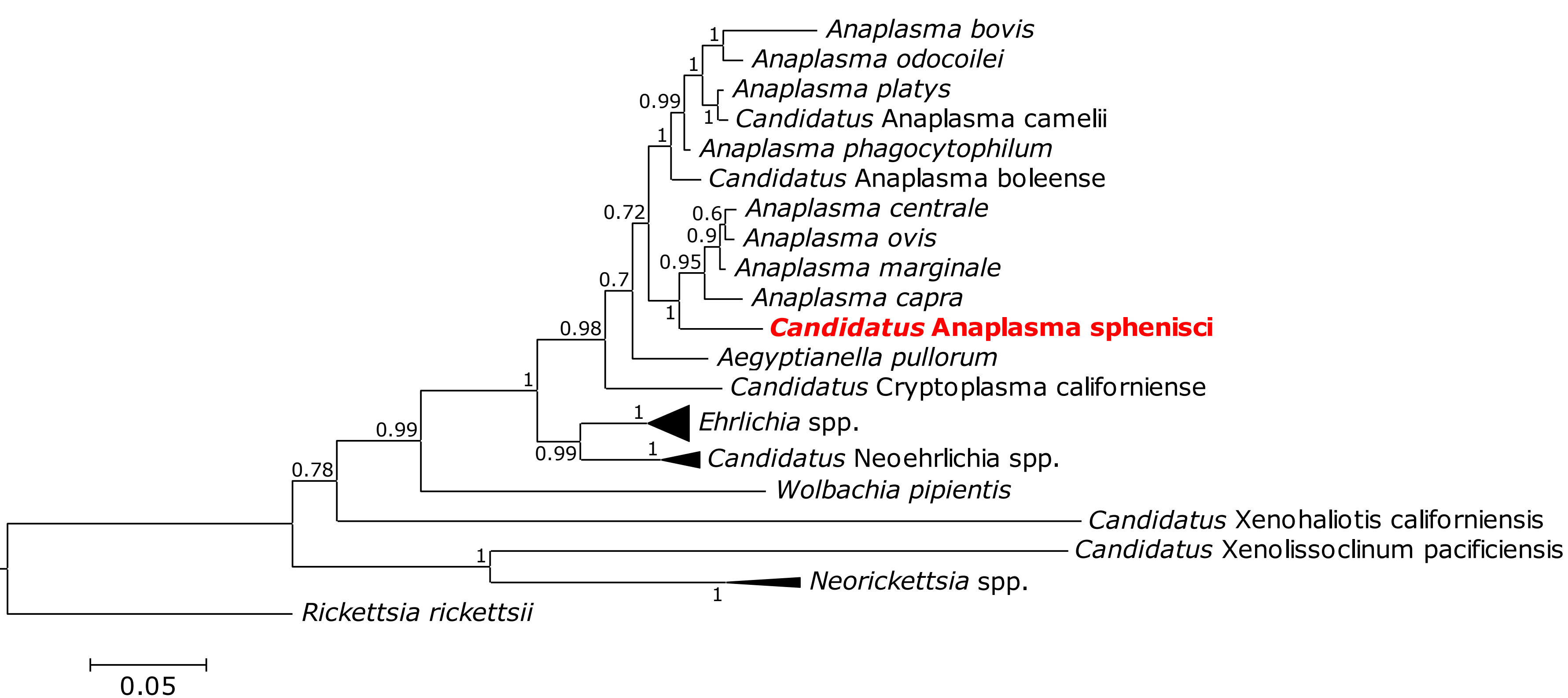
**(b)** 16S *rRNA*, Maximum Likelihood



**(e)** *groEL*, Maximum Likelihood



**(c)** 16S *rRNA*, Bayesian Inference



**(f)** *groEL*, Bayesian Inference

