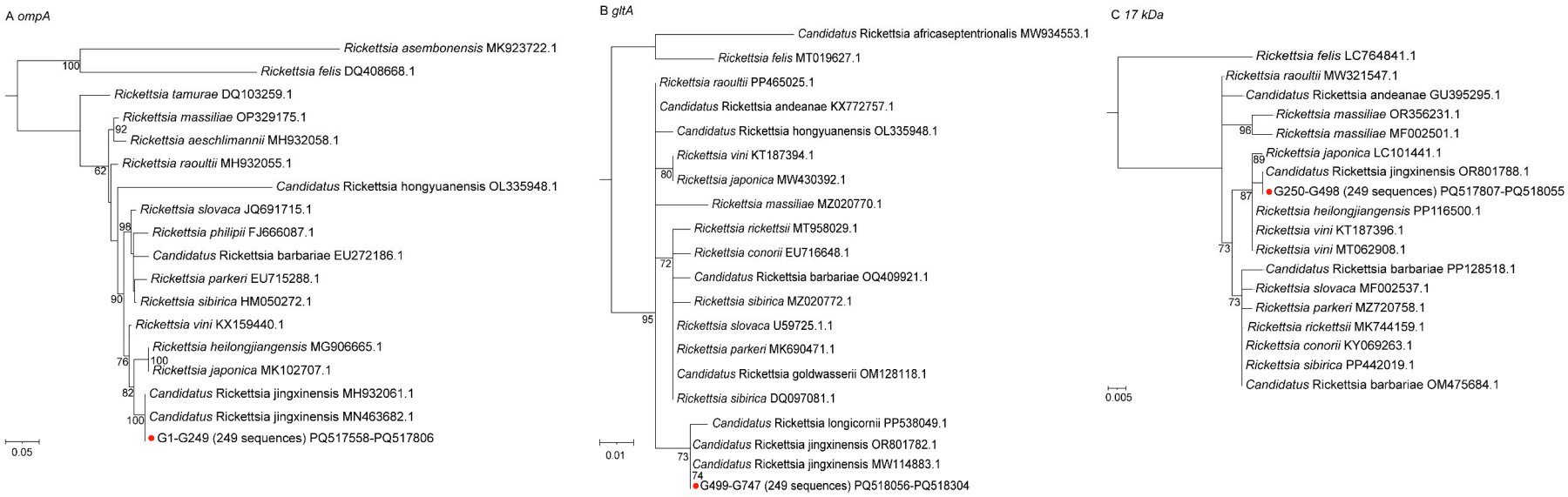

Figure S1. Phylogenetic trees of *Rickettsia* were constructed using the maximum likelihood (ML) method with 1000 bootstrap replicates. (A) *ompA* gene; (B) *gltA* gene; (C) *17 kDa* gene.

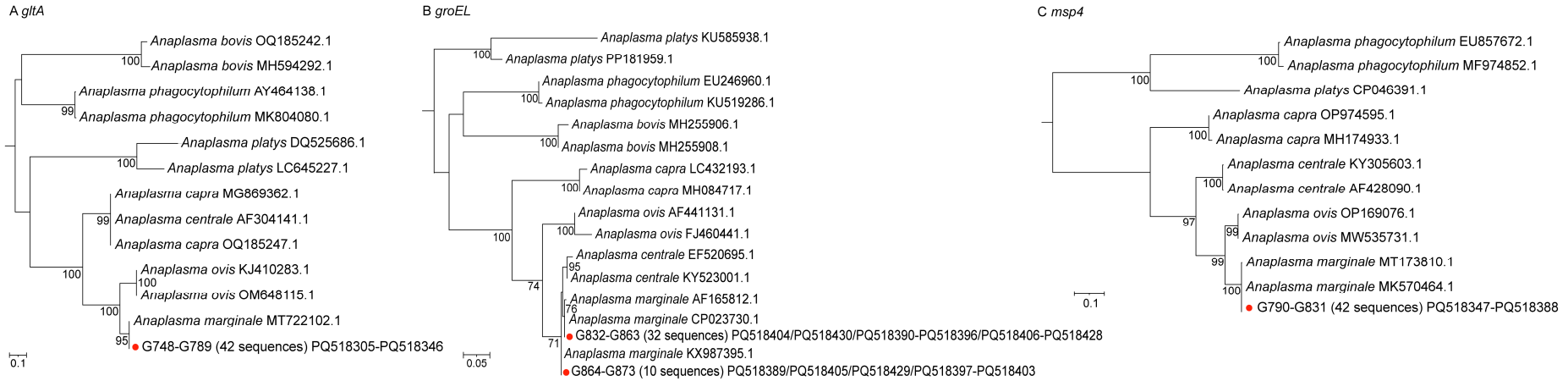

Figure S2. Phylogenetic trees of *Anaplasma* were constructed using the maximum likelihood (ML) method with 1000 bootstrap replicates. (A) *gltA* gene; (B) *groEL* gene; (C) *msp4* gene.

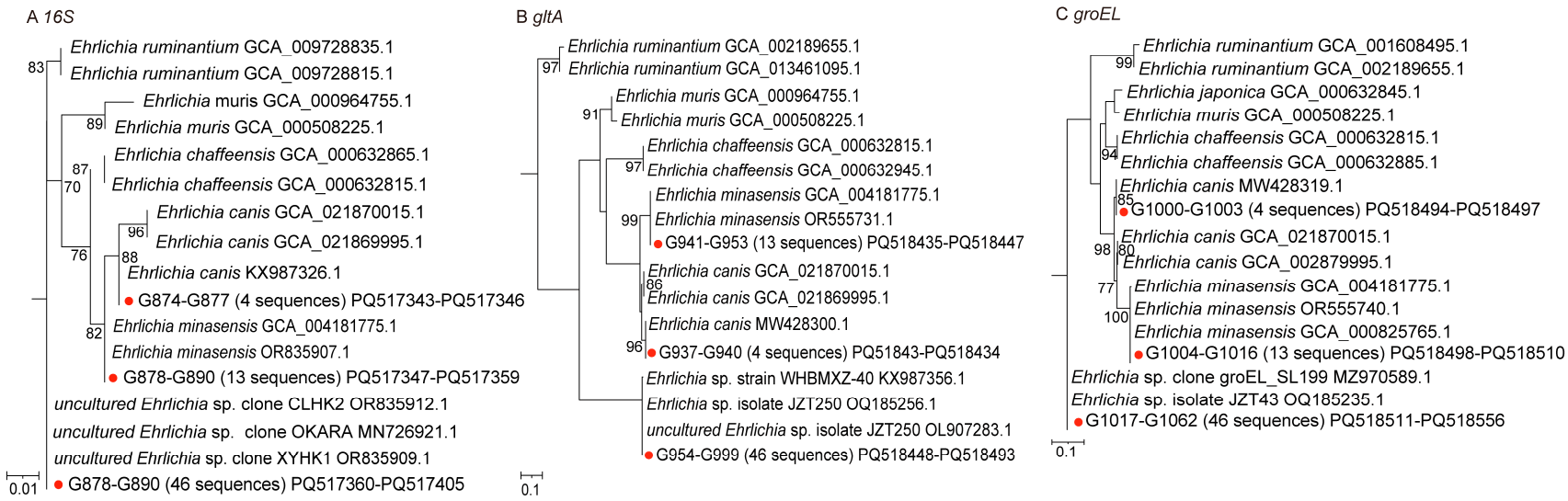

Figure S3. Phylogenetic trees of *Ehrlichia* were constructed using the maximum likelihood (ML) method with 1000 bootstrap replicates. (A) 16S rRNA gene; (B) *gltA* gene; (C) *groEL* gene.