

**Supplementary Fig. S1.** Phylogenetic analysis of the partial 16S rRNA gene in ticks of southern China.

The phylogenetic trees were constructed by the Neighbor-Joining method using the Kimura’s 2-parameter model. A total of 115 positions were included in the final analysis. Sequences are identified by their strain name and the origin, followed by the GenBank accession number. The detected 16S rRNA gene in ticks of the present study is marked in bold.