

Additional file.

Figure S1. Phylogenetic relationships were inferred from the partial sequence of *Anaplasma phagocytophilum* 16S rRNA gene by using the Maximum likelihood method (ML) and Kimura 2-parameter model with MEGA X software. Numbers at nodes correspond to bootstrap (1000 replicates) and values >40% are shown. Sequences of *Anaplasma* spp. retrieved from GenBank database were included. *A. phagocytophilum* sequence obtained in the present study is highlighted in bold. *Ehrlichia chaffeensis* NR074500 was used as outgroup.

