

Supplementary Information

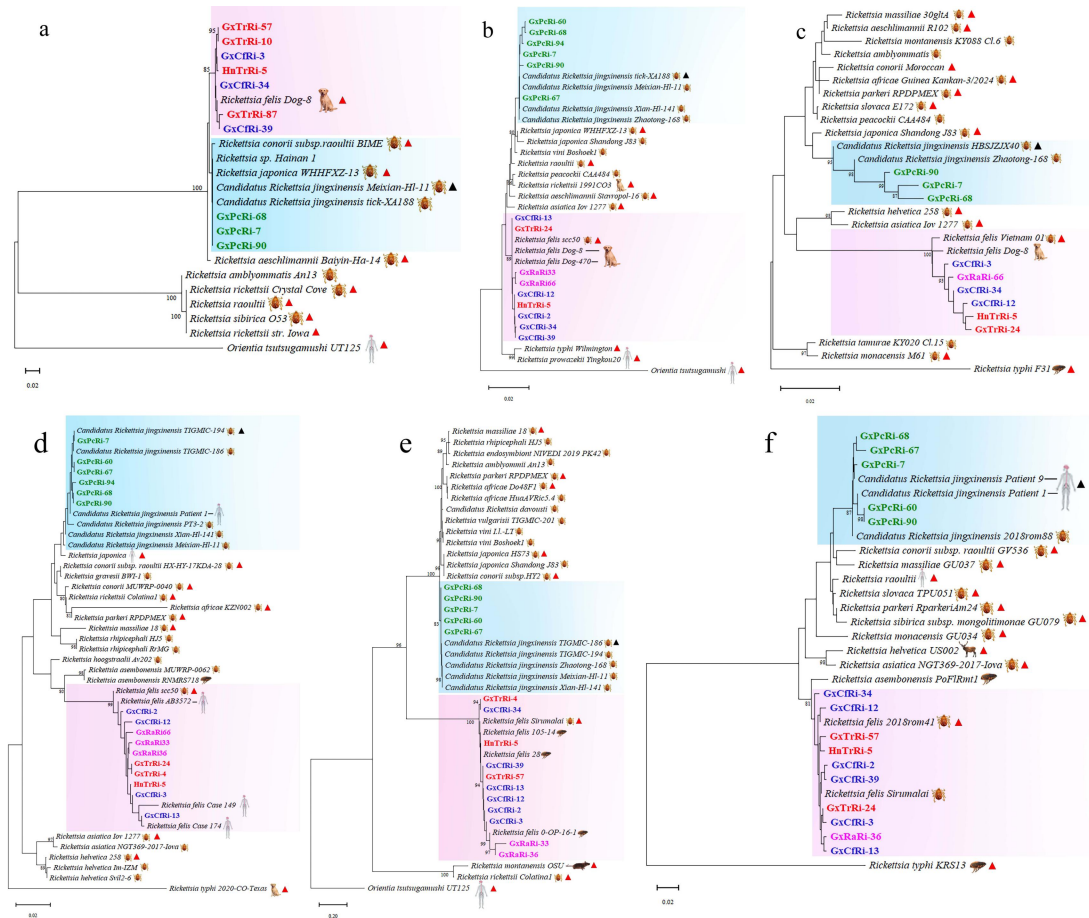


Fig. S1 Phylogenetic trees of *Rickettsia* spp. inferred from the *groEL* (a), *rrs* (b), *gltA* (c), 17-kDa (d), *ompA* (e), and *ompB* (f) gene sequences.

Sequences generated in this study from *Triatoma rubrofasciata*, *Ctenocephalides felis*, *Rattus norvegicus*, and *Rhipicephalus microplus* are highlighted in red, blue, purple, and green fonts, respectively; corresponding GenBank accession numbers are listed in Additional file 2: Table S2. Host species of reference sequences are denoted by pictograms. *Rickettsia* taxa documented as human pathogens are indicated by red triangles, whereas those detected in humans but of unresolved pathogenicity are marked with black triangles. Trees were constructed using the neighbor-joining algorithm in MEGA11 with 1,000 bootstrap replicates.