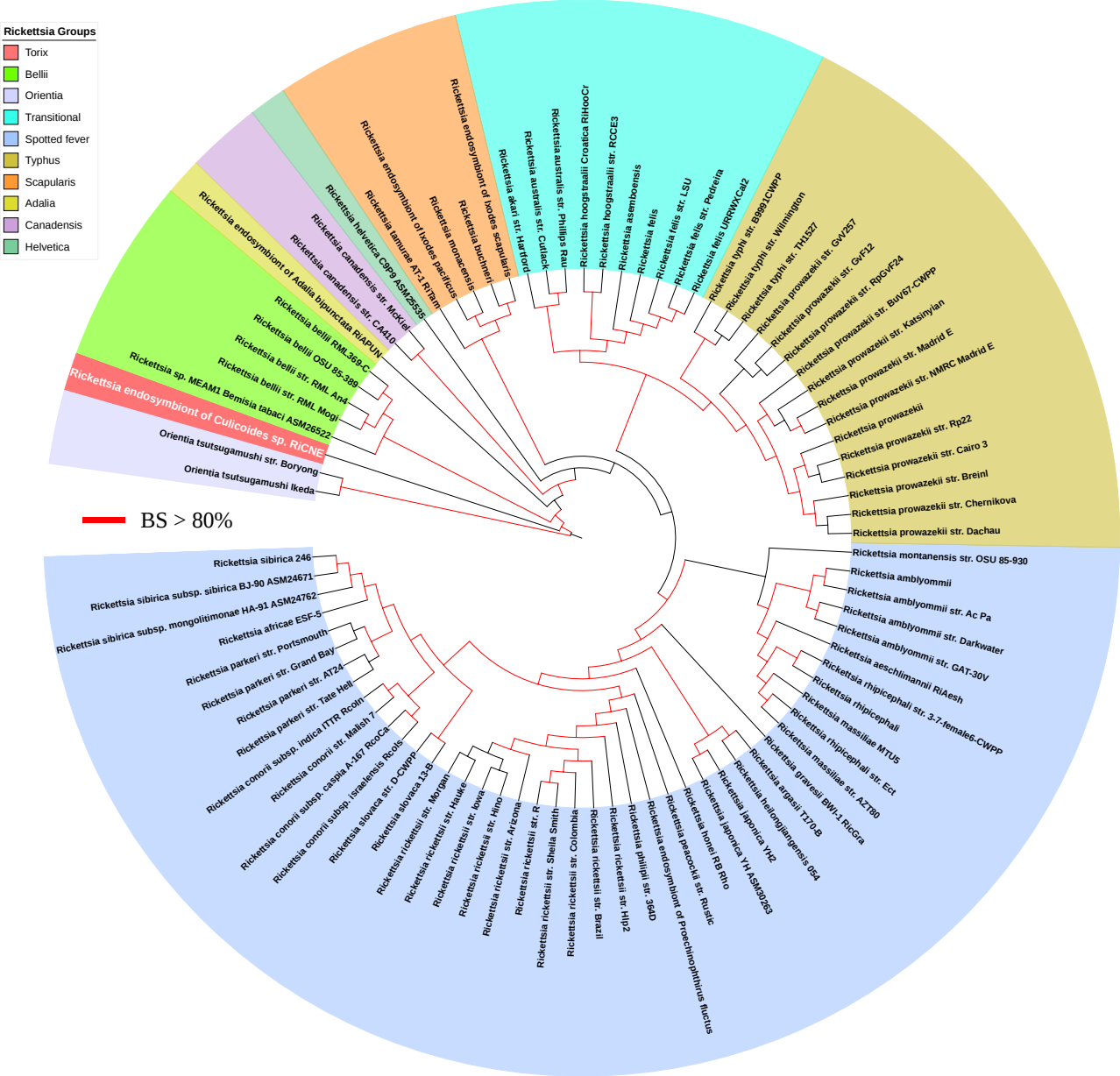


**Figure S4.** Cladogram of the complete core-genome phylogeny. Phylogenomic placement of the Rickettsia endosymbiont of C. newsteadii were inferred using maximum likelihood (RaxML, model: LG+G+I) from the concatenated protein allignments of 189 single copy ortholog genes. Support values are based on 100 rapid bootsrap replicates.