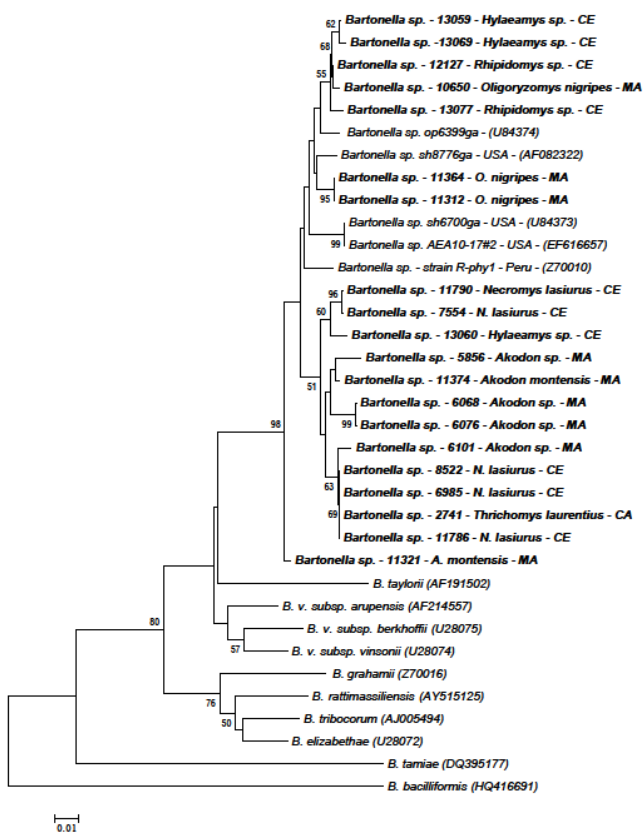
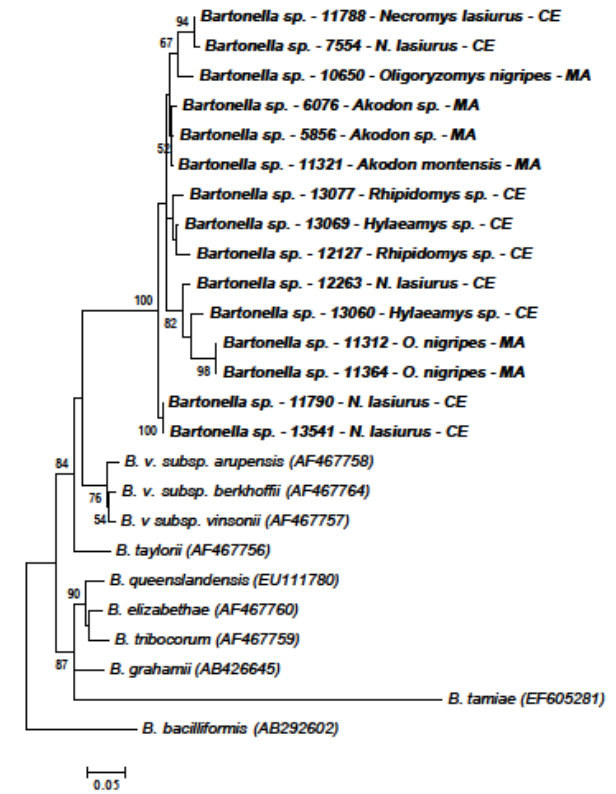


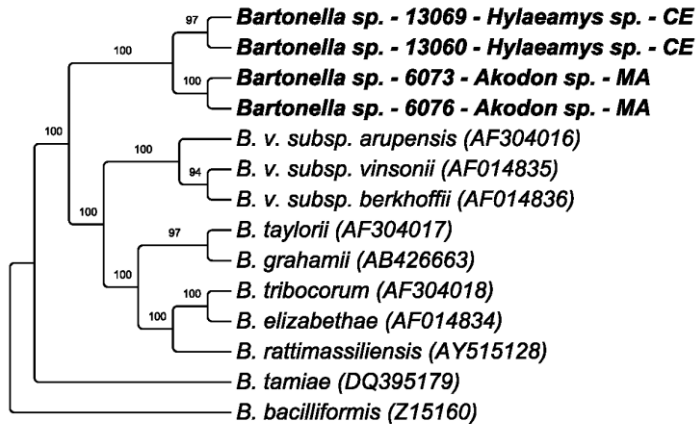
S 1



S 2



S 3



S 4

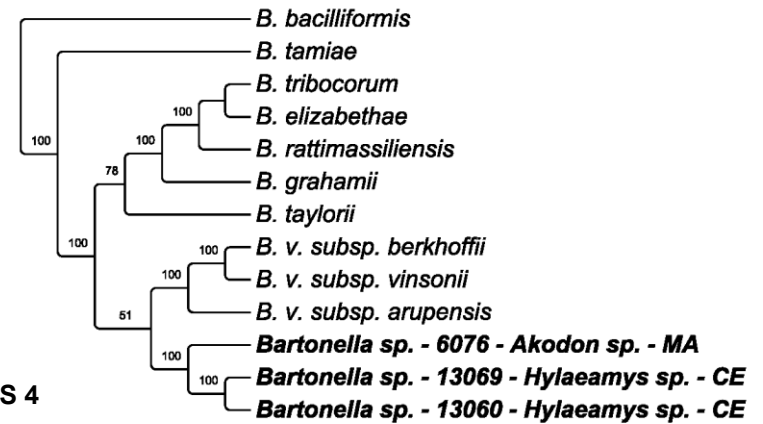


Figure supplementary 1-4. Phylogenetic relationships within the *Bartonella* genus based on the *gItA* (S 1 - BI), *ftsZ* (S 2 - ML), *groEL* (S 3 - BI) genes and concatenated (S 4 - BI). The tree was inferred by using the same beast model previously referred in the manuscript. The sequences detected in the present study are highlighted in bold. The numbers at the nodes correspond to bootstrap and/or posteriori probability values higher than 50% accessed with 1000 (ML) and/or 10^7 replicates. *Bartonella bacilliformis* was used as outgroup. MA: Mata Atlântica; CA: Caatinga; CE: Cerrado biomes.