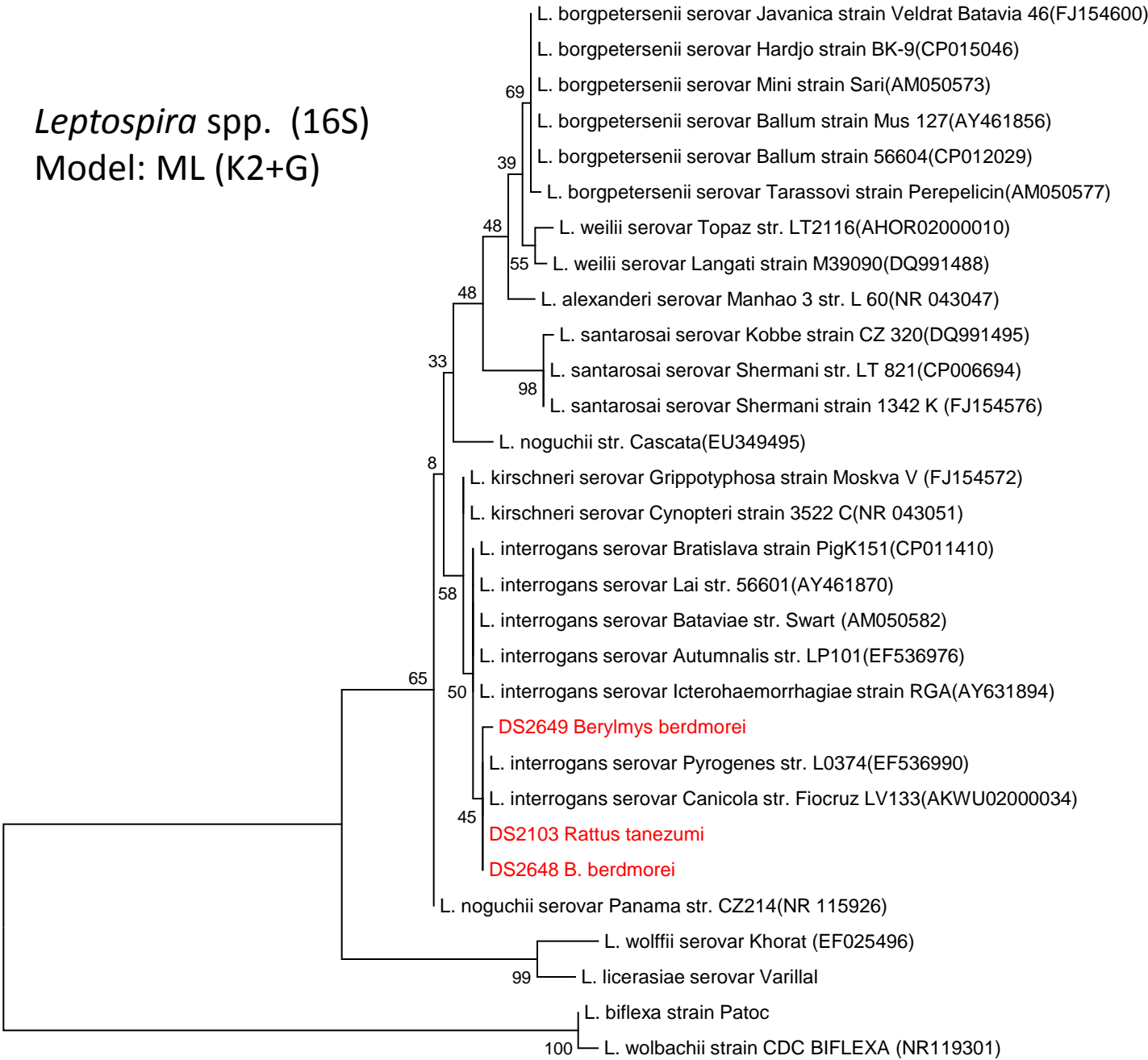


Phylogenetic analysis of pathogens detected from NGS results (red letters). All maximum likelihood trees were created using the best fit model of nucleotide substitution in the MEGA 6 program with bootstrapping (1000 replicates).

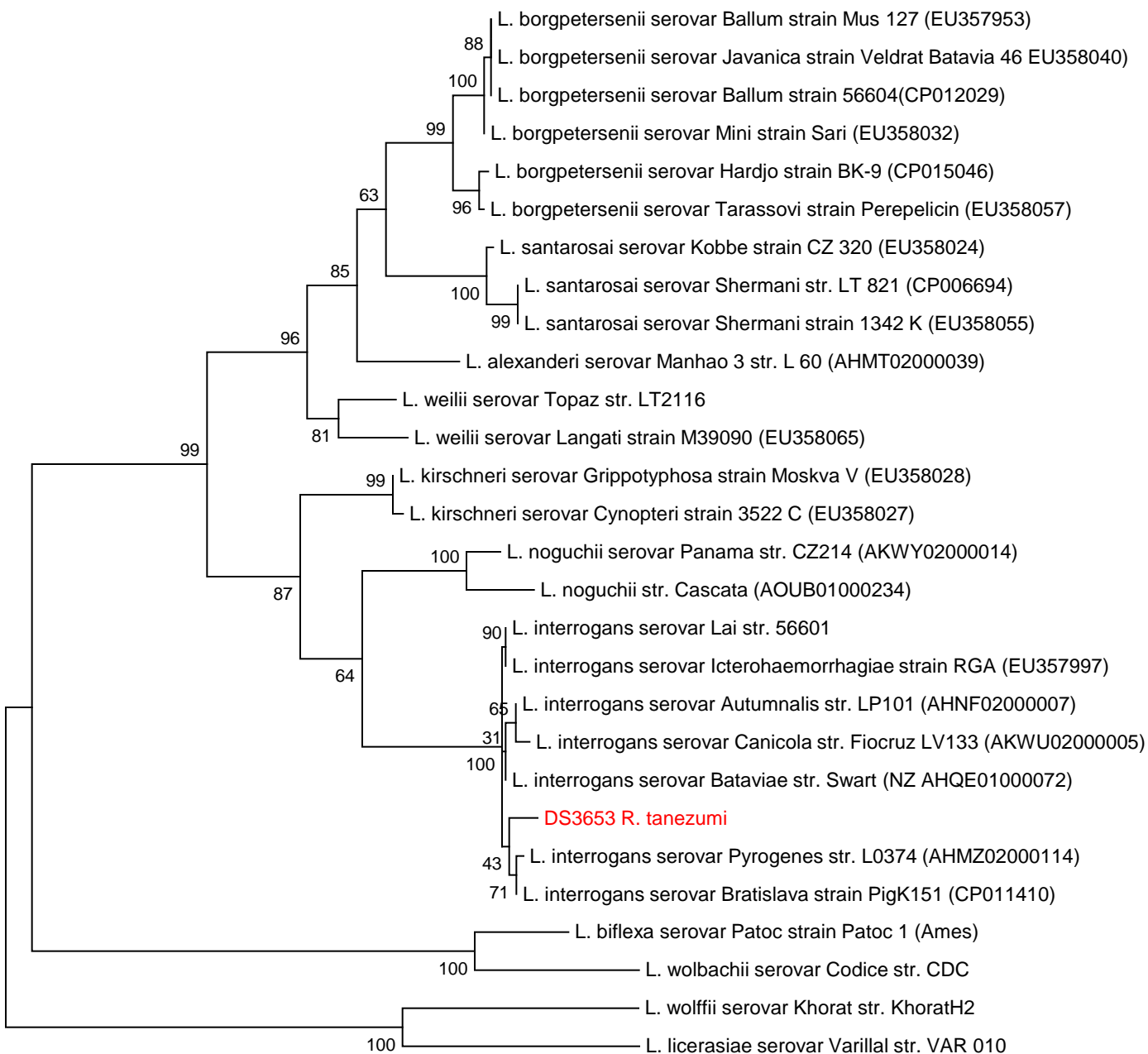
Leptospira spp. (16S)
Model: ML (K2+G)



0.02

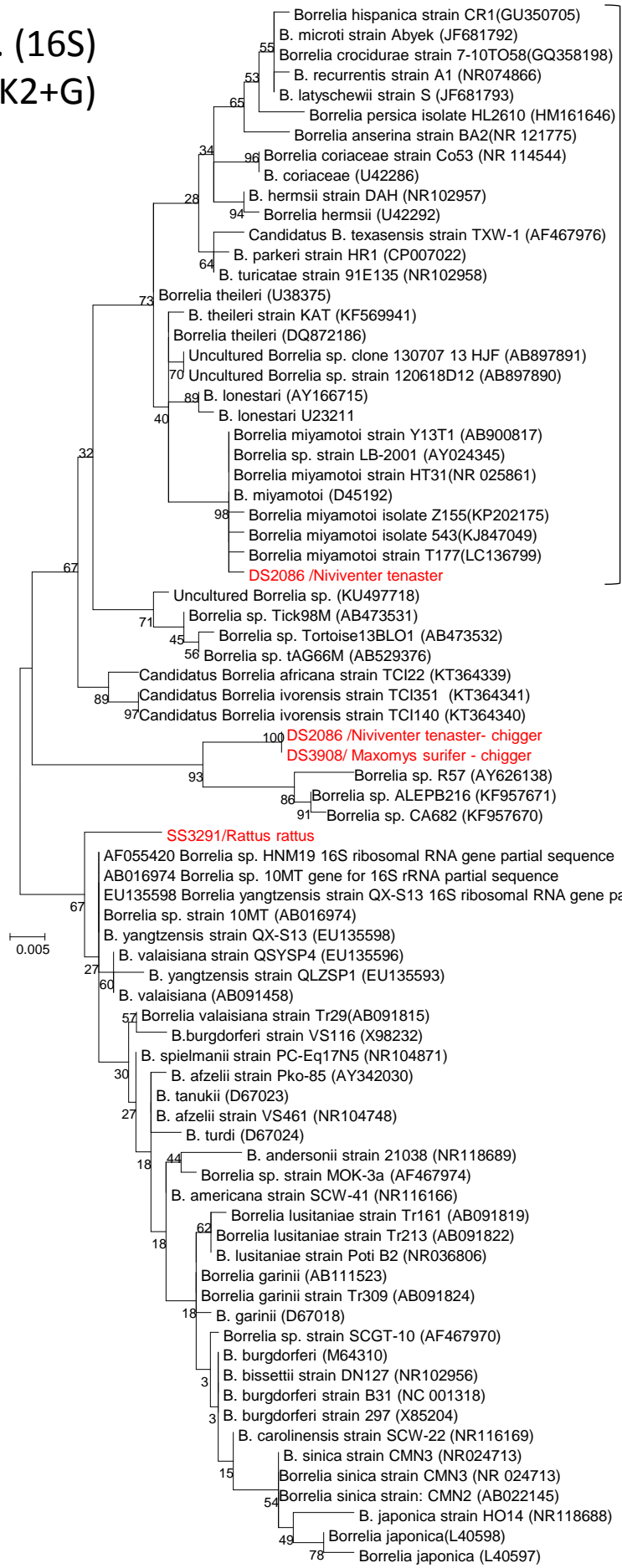
Leptospira spp. (*secY*)

Model: ML(HKY+G)



0.05

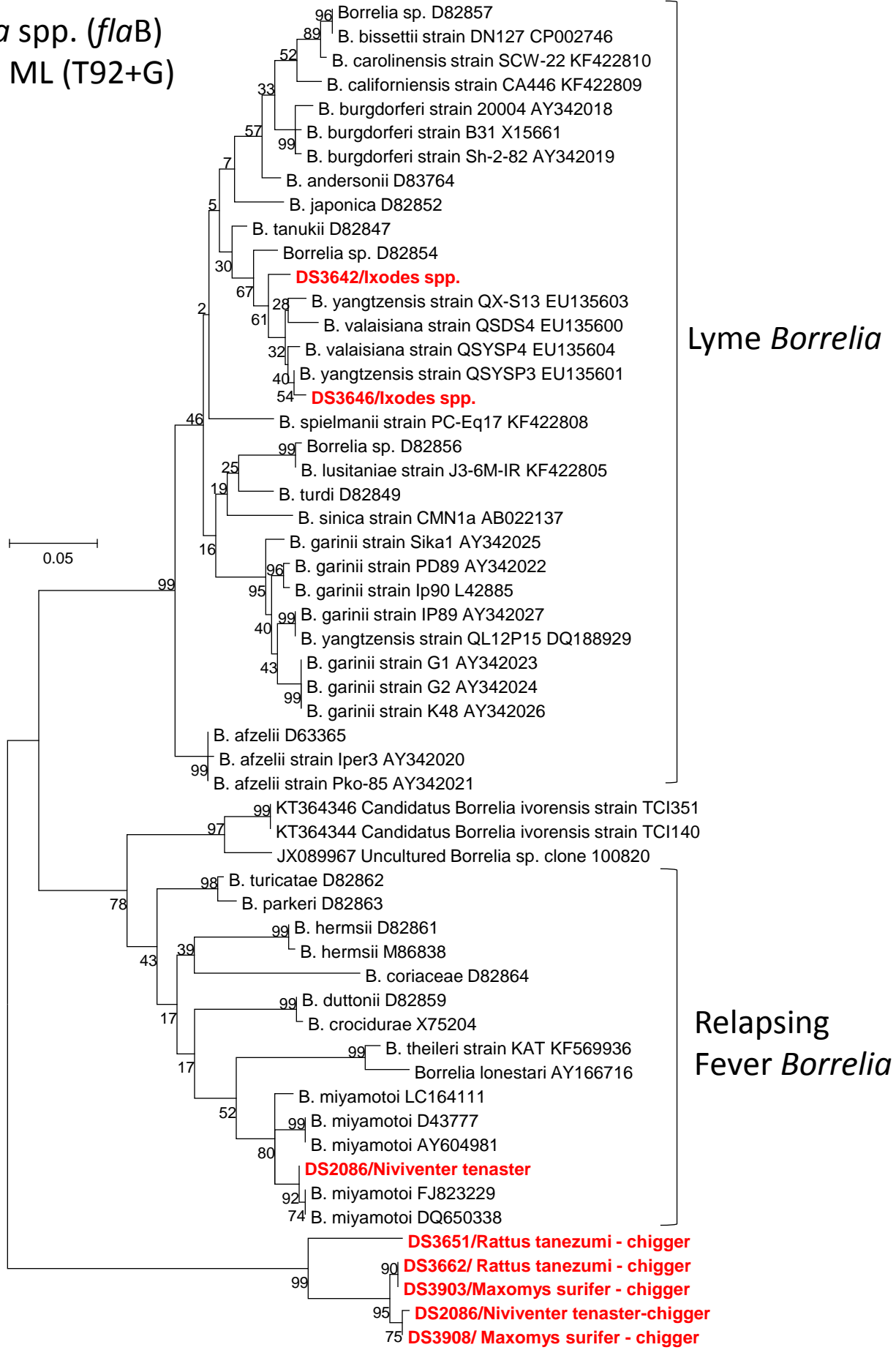
Borrelia spp. (16S)
Model: ML (K2+G)



Relapsing
Fever *Borrelia*

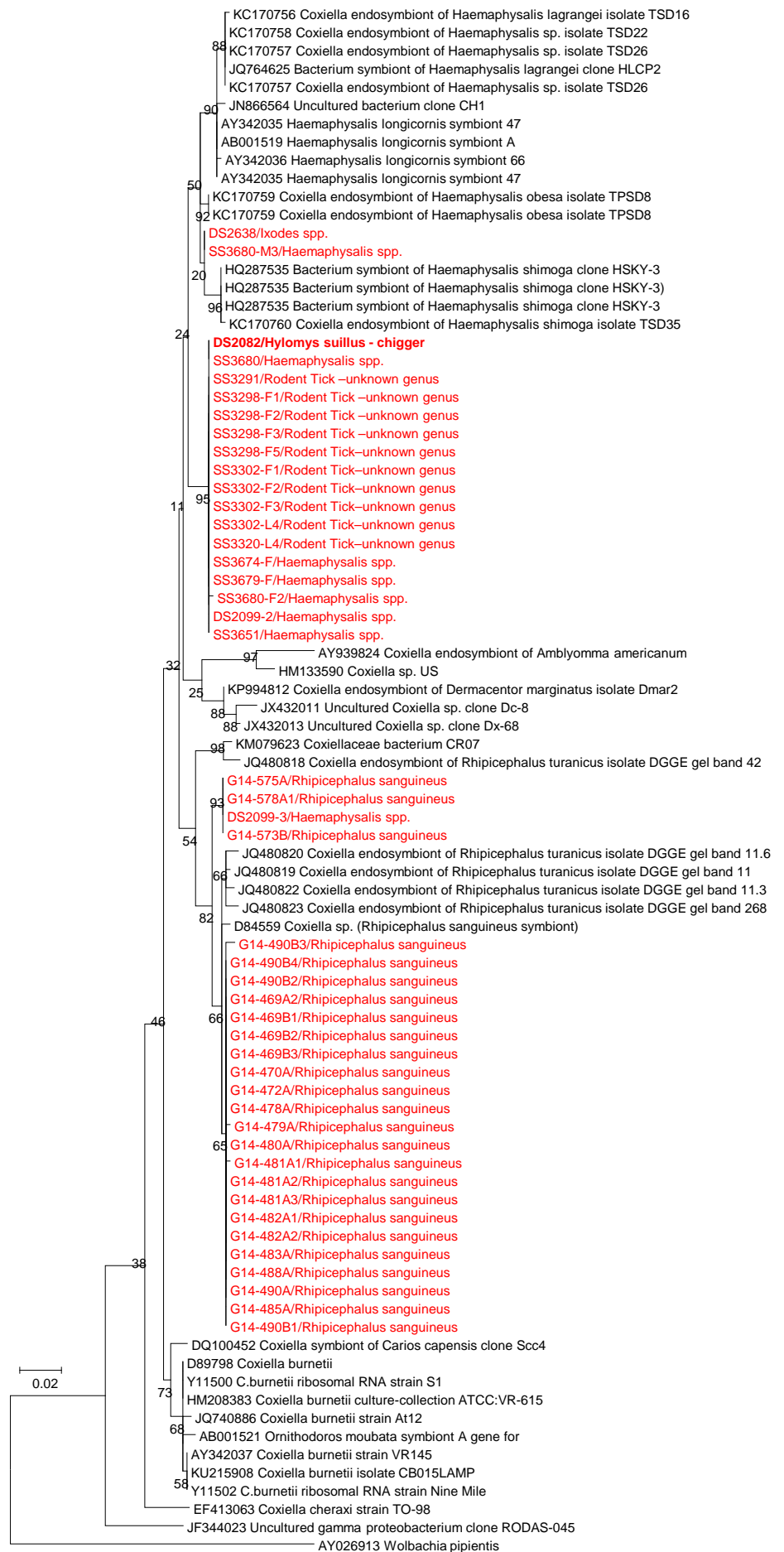
Lyme *Borrelia*

Borrelia spp. (*flaB*)
Model: ML (T92+G)



Coxiella spp. (16S)

Model: ML(K2+G)



Anaplasma spp.

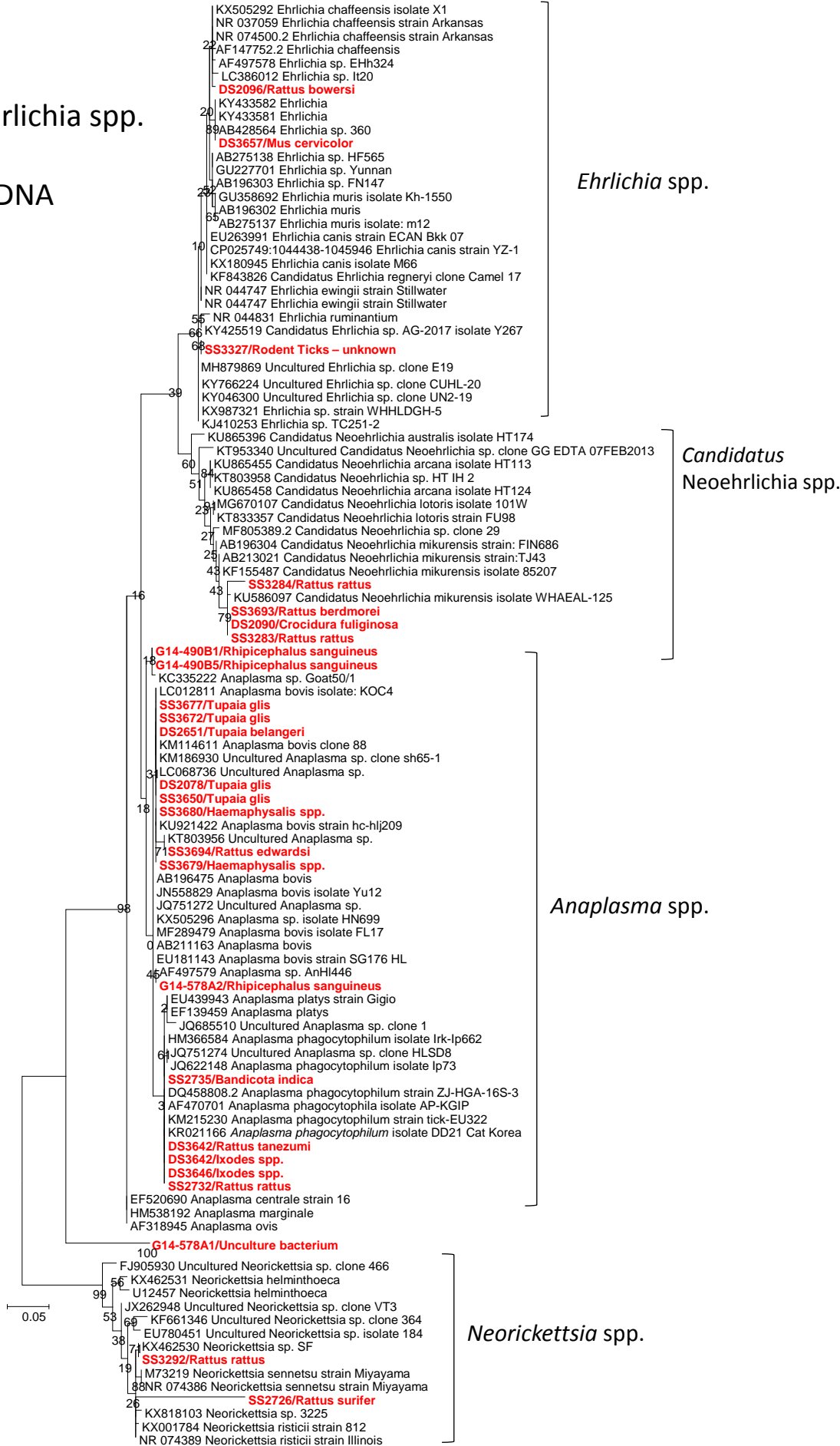
Ehrlichia spp

Candidatus Neoehrlichia spp.

Neorickettsia spp.

Target gene: 16S rDNA

Model: ML (K2+G)



Ehrlichia spp.

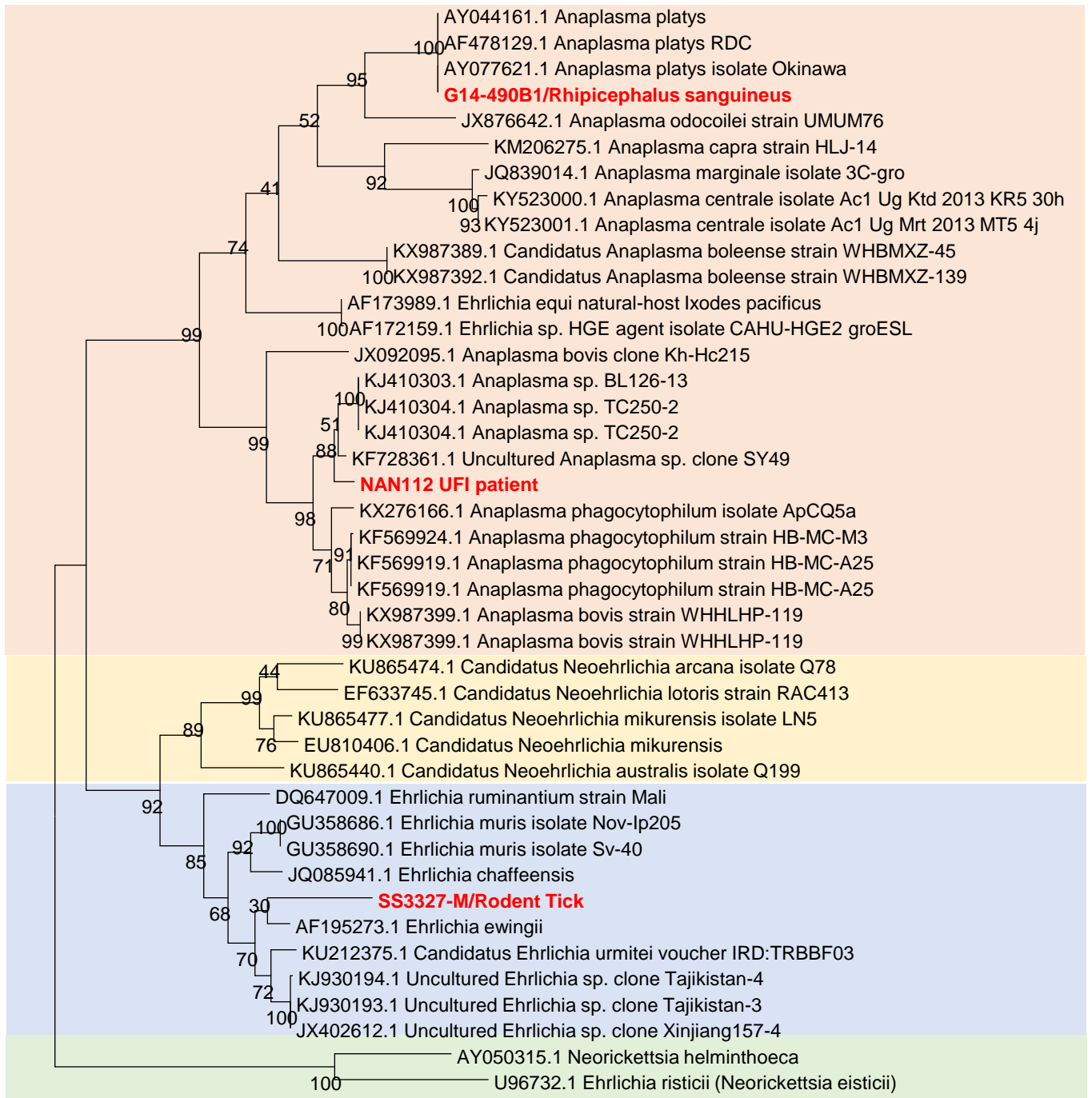
Candidatus Neoehrlichia spp.

Anaplasma spp.

Neorickettsia spp.

Anaplasma & *Ehrlichia* spp. (groEL)

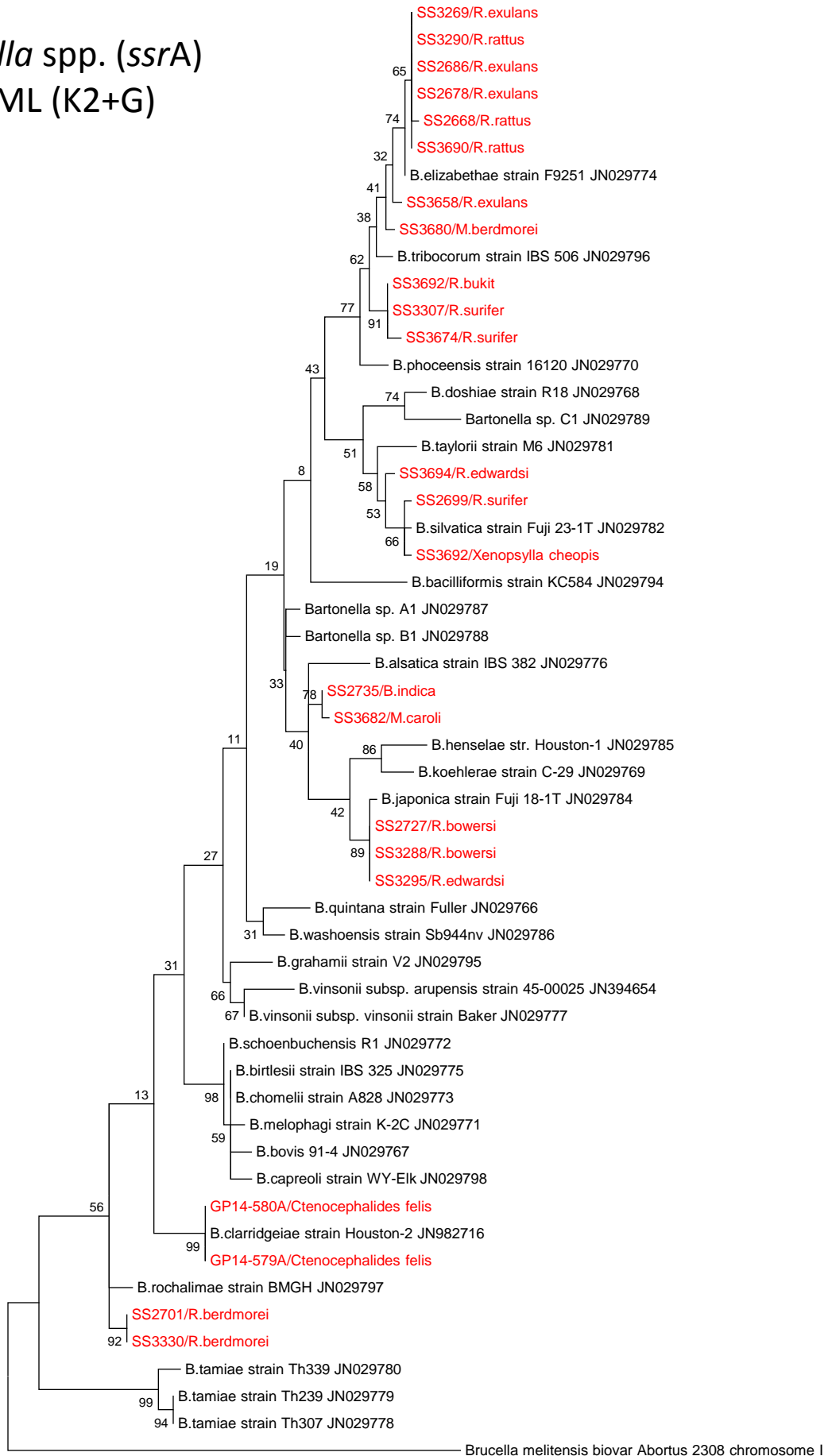
Model:T92+G



0.1

Bartonella spp. (*ssrA*)

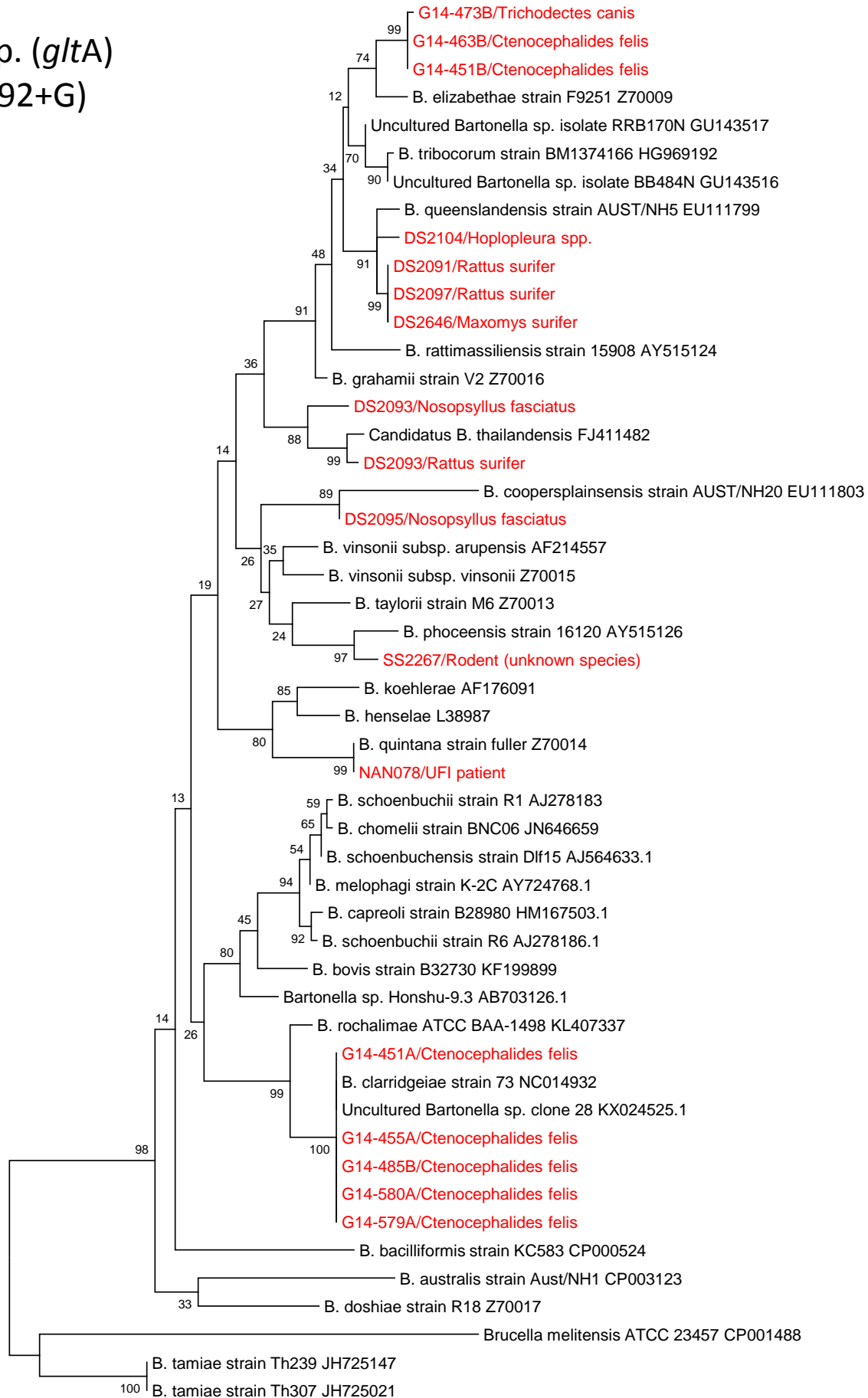
Model: ML (K2+G)



Brucella melitensis biovar Abortus 2308 chromosome I

0.05

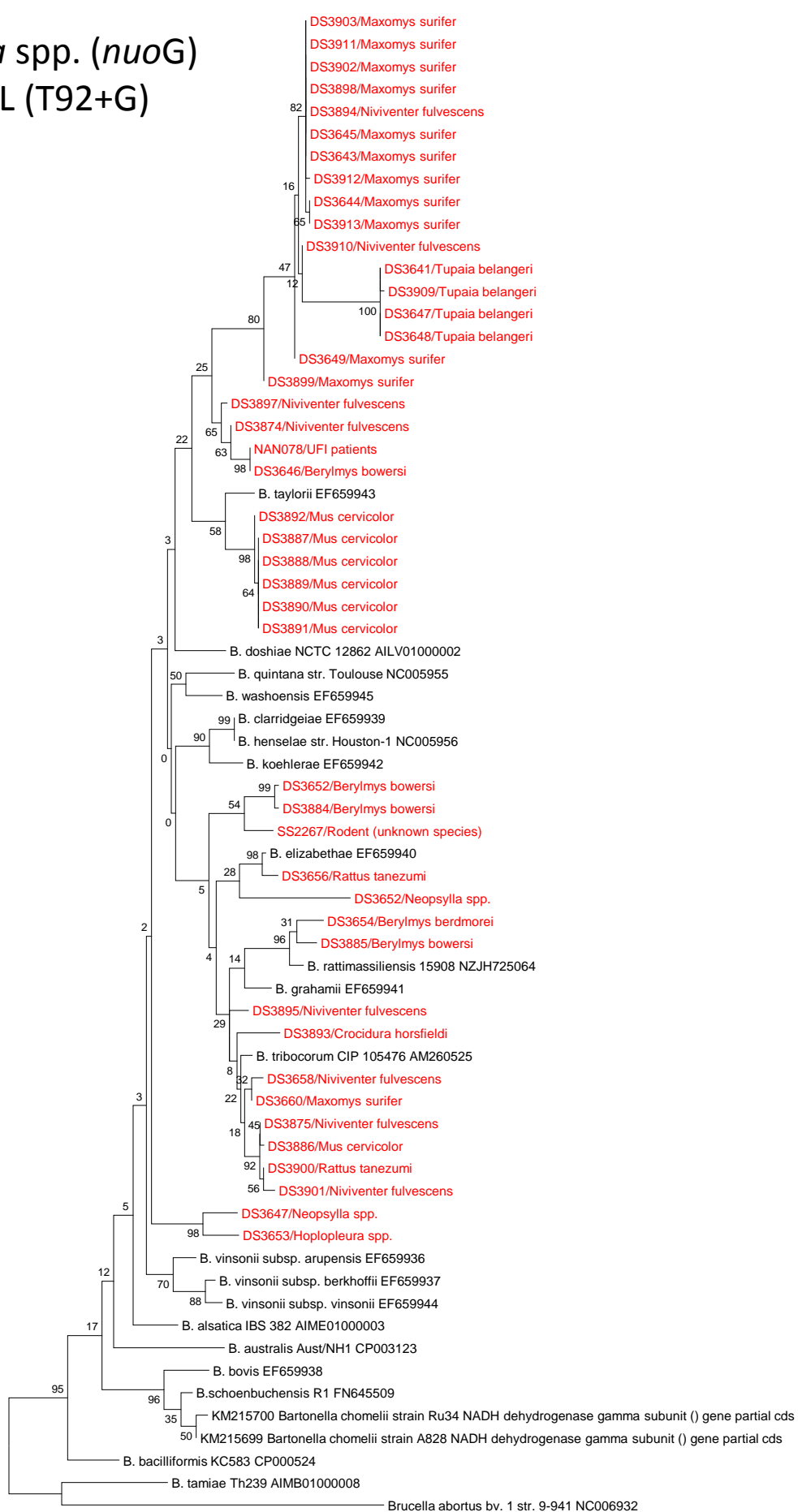
Bartonella spp. (*gltA*)
 Model: ML (T92+G)



0.05

Bartonella spp. (*nuoG*)

Model: ML (T92+G)



0.05

Rickettsia spp. (*gltA*)

Model: ML(T92+G)

