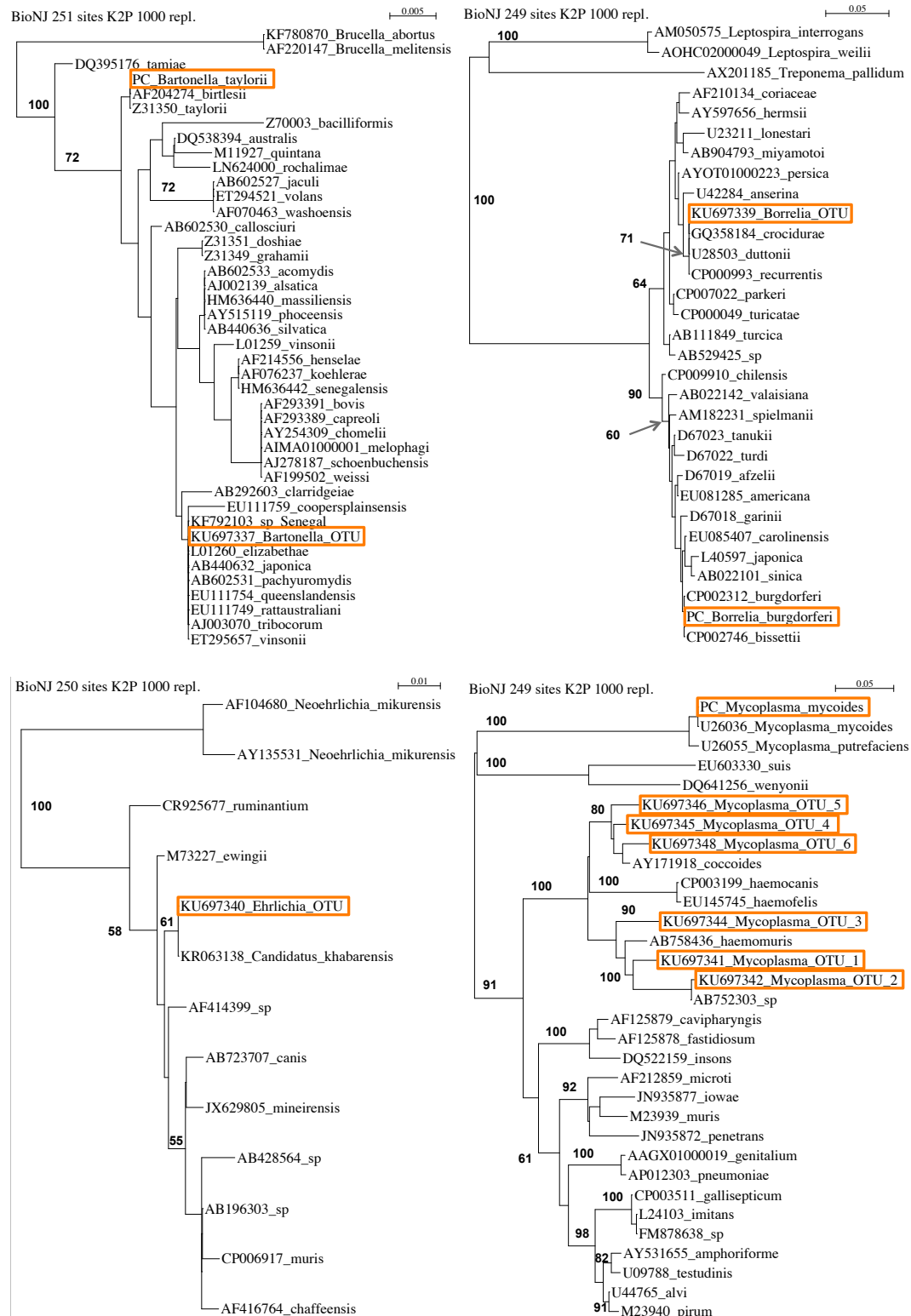
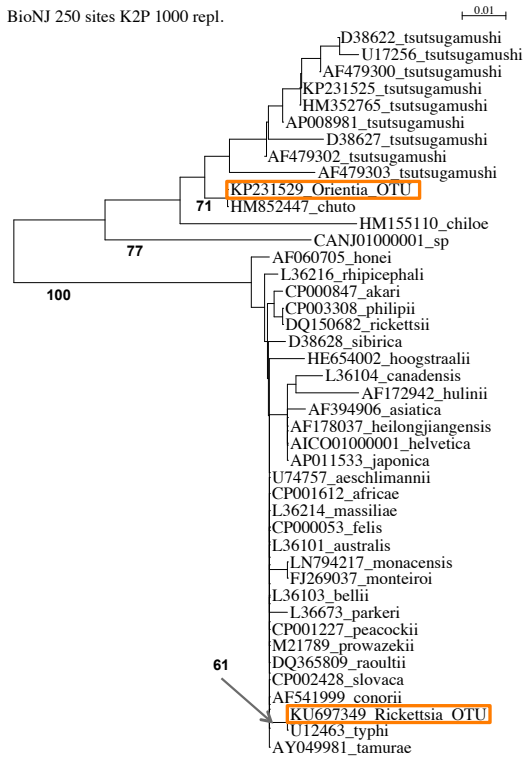


Figure S4. Phylogenetic trees of the 16S rRNA V4 sequences for 12 pathogenic bacterial OTUs detected in wild rodents from Senegal. Sequences boxed with an orange line were retrieved from African rodents and/or corresponds to positive controls (PC) for *Borellia burgdorferi*, *Mycoplasma mycoides* and *Bartonella taylorii*. The other sequences were extracted from the SILVA database and GenBank. Trees include all lineages collected for *Rickettsia*, *Bartonella*, *Ehrlichia* and *Orientia*, but only lineages of the Spotted Fever Group for *Borrelia*, and lineages of the pneumonia group for *Mycoplasma*. The numbers indicated are the bootstrap values >55%. Fasta files used have been deposited in the Dryad Digital Repository: <http://dx.doi.org/10.5061/dryad.m3p7d>.



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BioNJ 250 sites K2P 1000 repl.



BioNJ 251 sites K2P 1000 repl.

