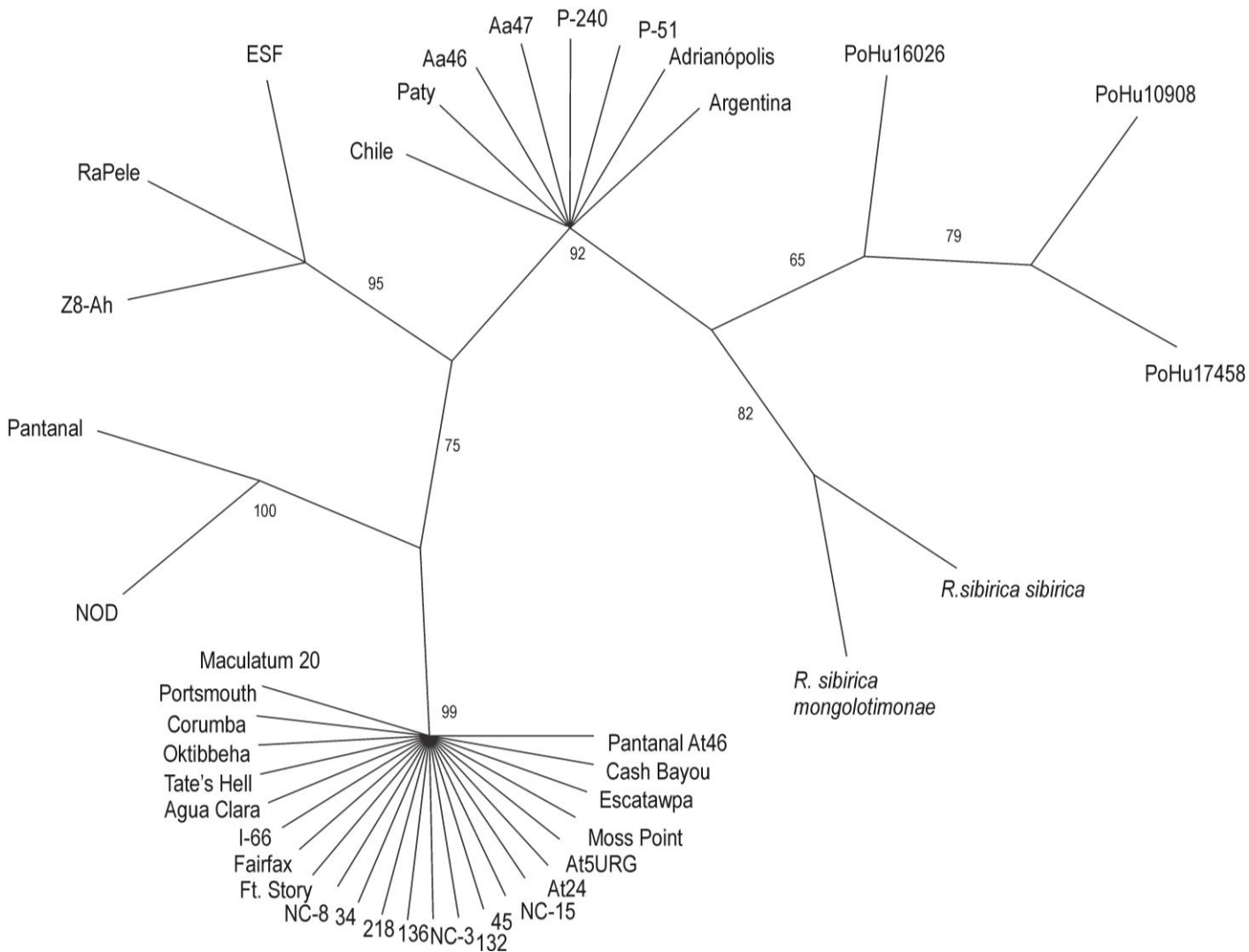
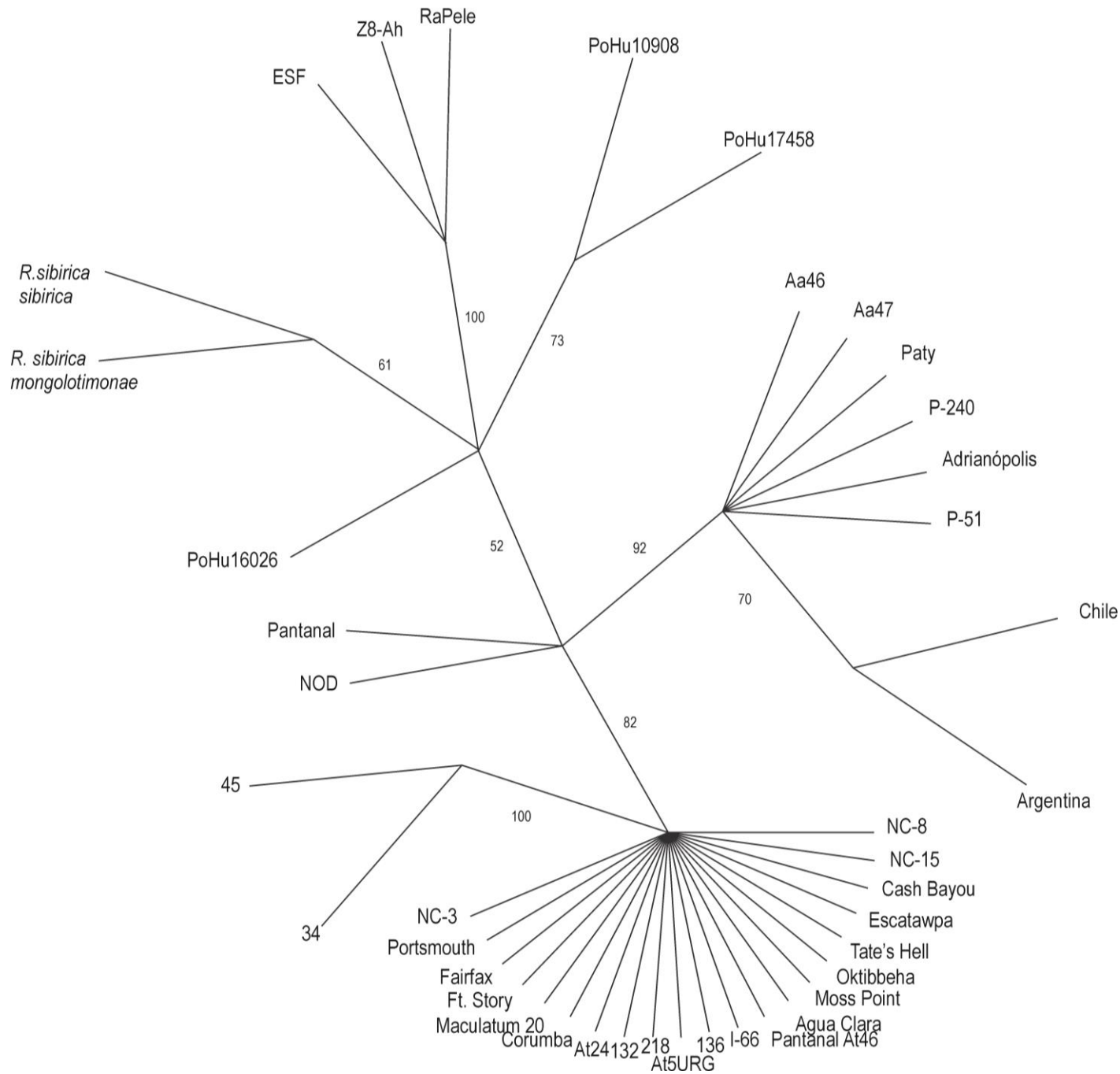


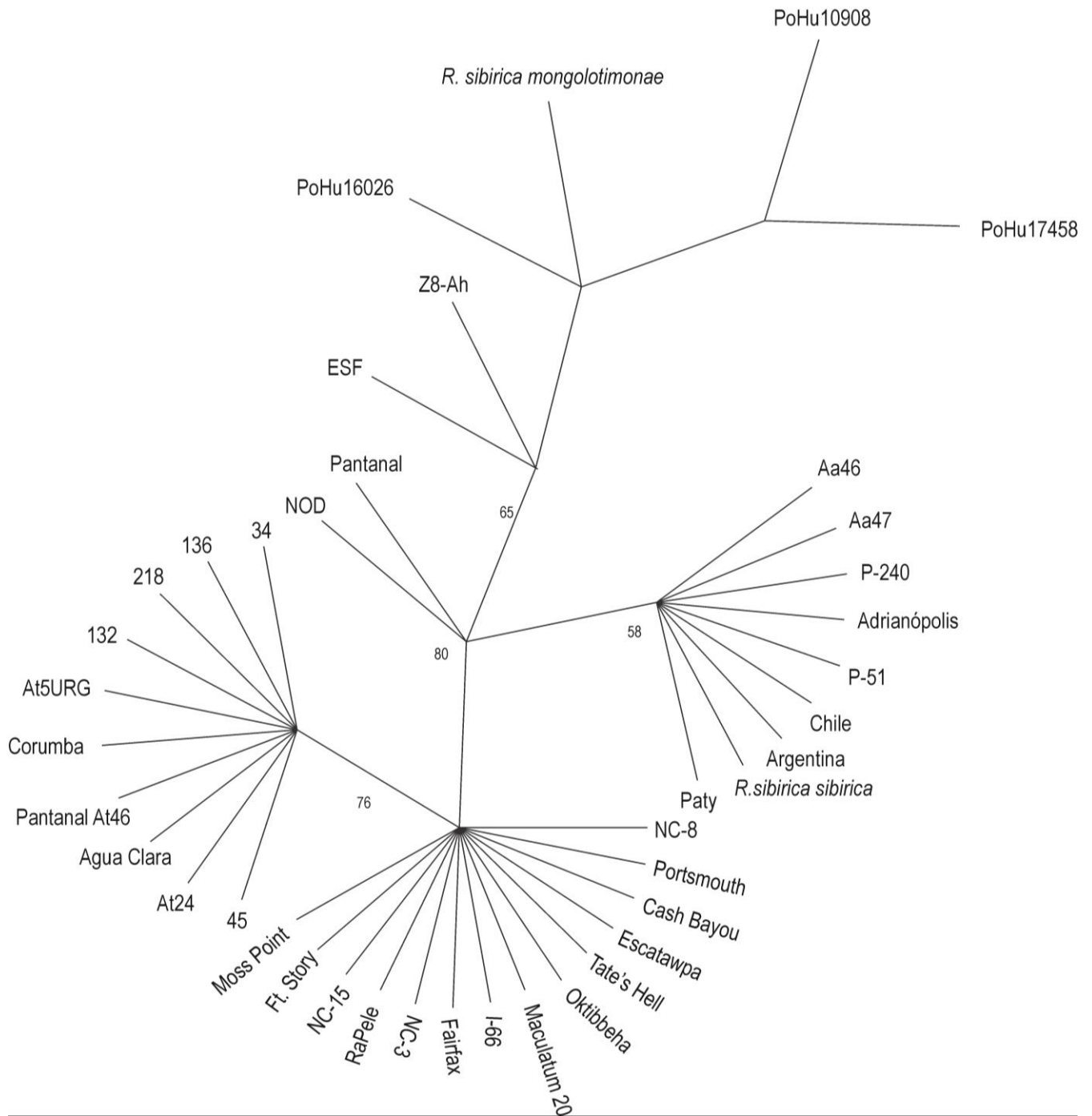
Supplemental Figure S1. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial *gltA* gene (257 nt). Please refer to Table 1 for data about the rickettsial isolates.



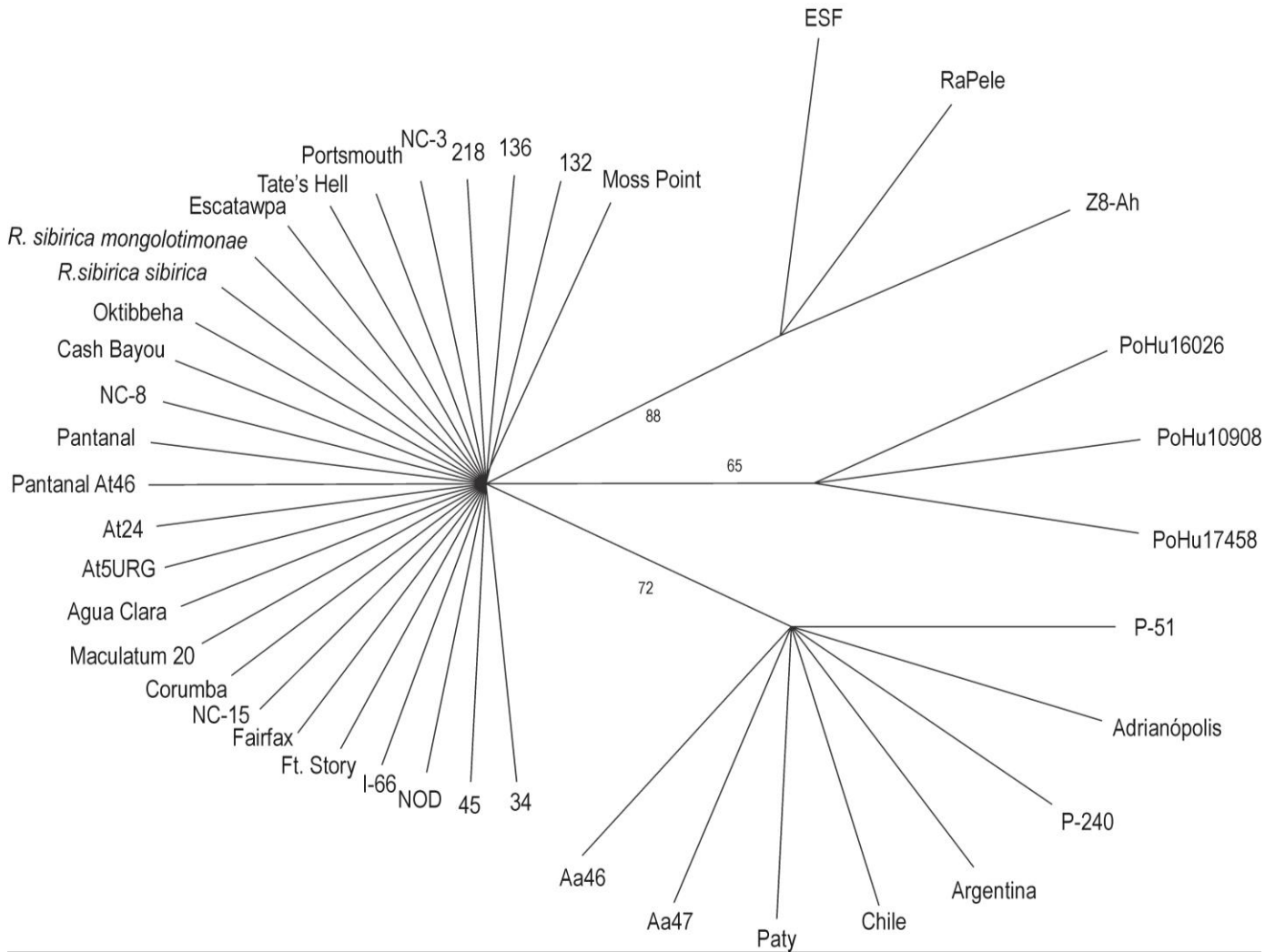
Supplemental Figure S2. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial *ompA* gene (490 nt). Please refer to Table 1 for data about the rickettsial isolates.



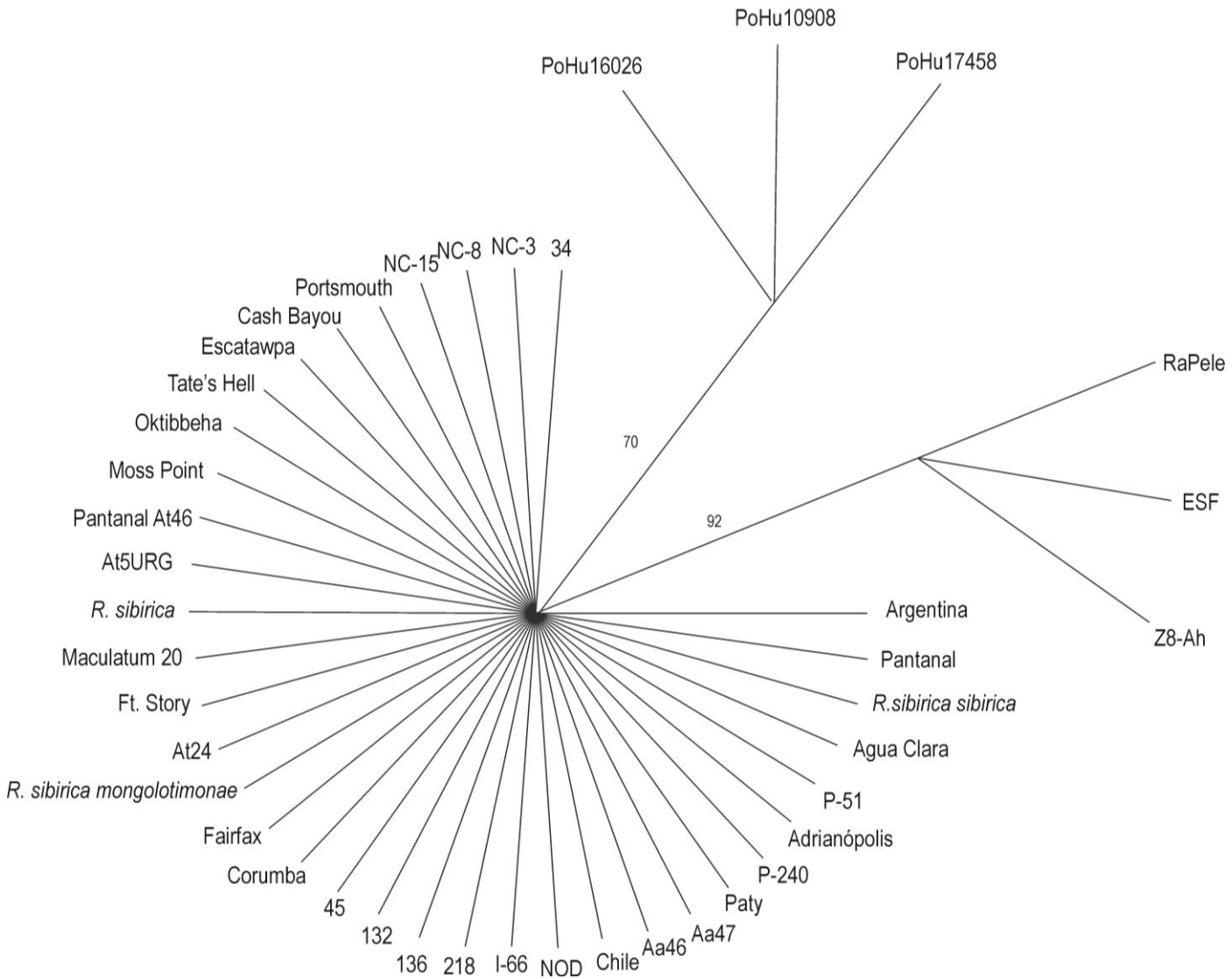
Supplemental Figure S3. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial *virB4* (684 nt). Please refer to Table 1 for data about the rickettsial isolates.



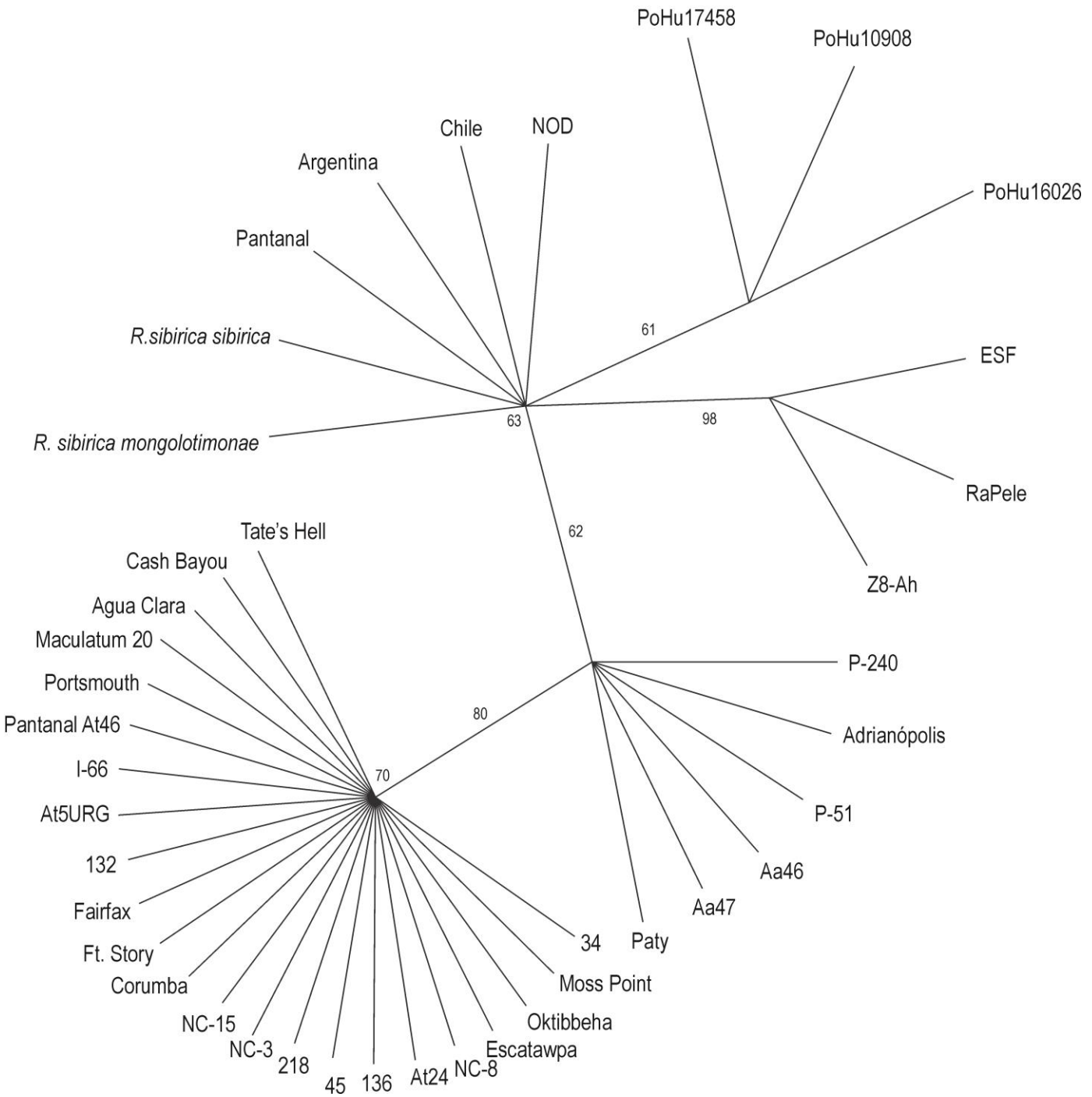
Supplemental Figure S4. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial *dnaA* gene (663 nt). Please refer to Table 1 for data about the rickettsial isolates.



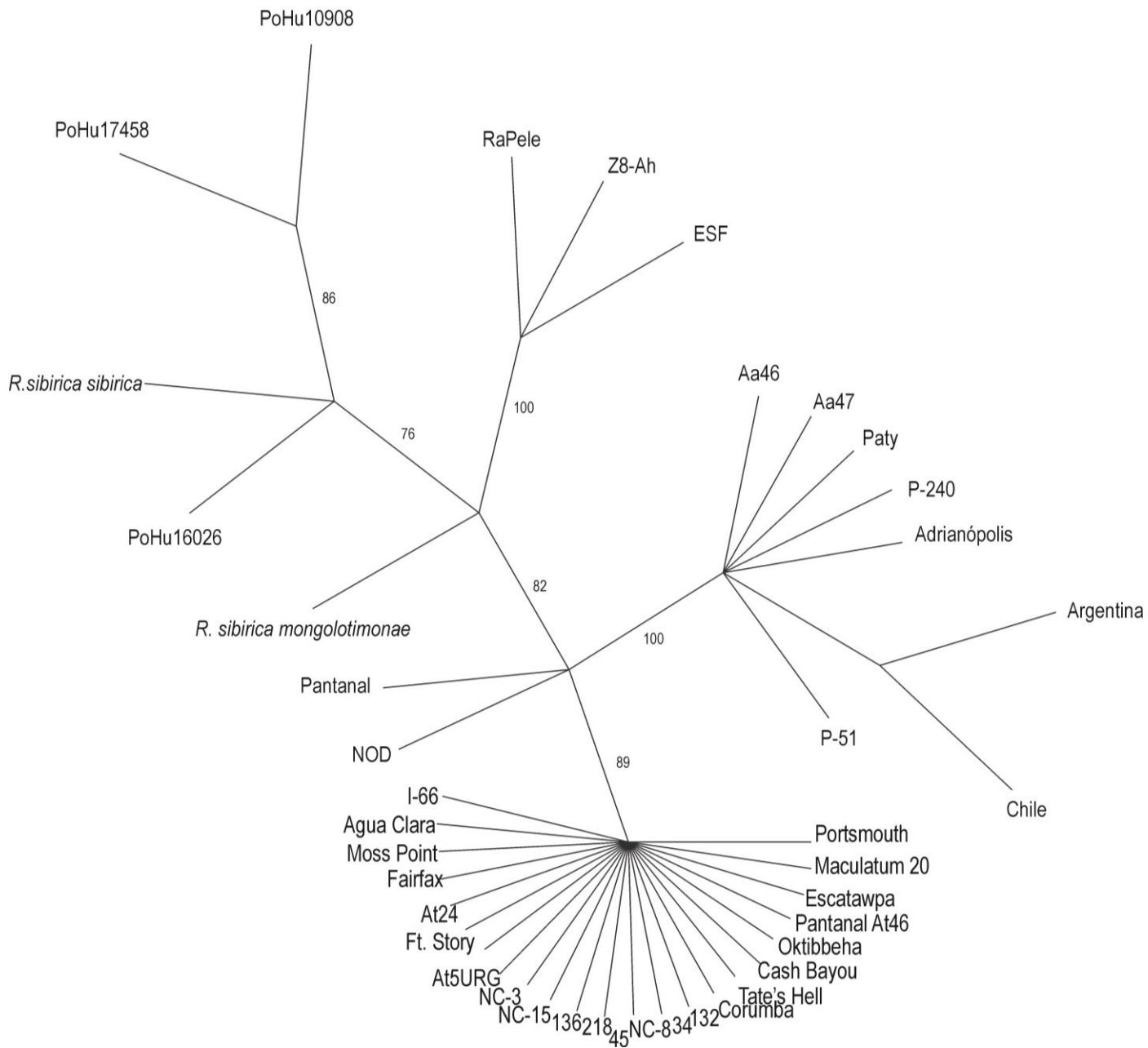
Supplemental Figure S5. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial *dnaK* gene (615 nt). Please refer to Table 1 for data about the rickettsial isolates.



Supplemental Figure S6. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial intergenic spacer *mppA-purC* (197 nt). Please refer to Table 1 for data about the rickettsial isolates.



Supplemental Figure S7. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial intergenic spacer *rrl-rrf*-ITS (330 nt). Please refer to Table 1 for data about the rickettsial isolates.



Supplemental Figure S8. Molecular phylogenetic analysis of New World isolates of *Rickettsia parkeri* sensu stricto, strains Atlantic rainforest, NOD, and Parvitarsum, in relation to Old World isolates of *Rickettsia africae*, *Rickettsia sibirica*, and *Rickettsia conorii*, inferred from a partial sequence of the rickettsial intergenic spacer *rpmE-tRNA^{fmet}* (343nt). Please refer to Table 1 for data about the rickettsial isolates.