

Figure S1. Screenshots of the 16S rDNA Alignment 1 (above) and 16S rDNA Alignment 3 (down).

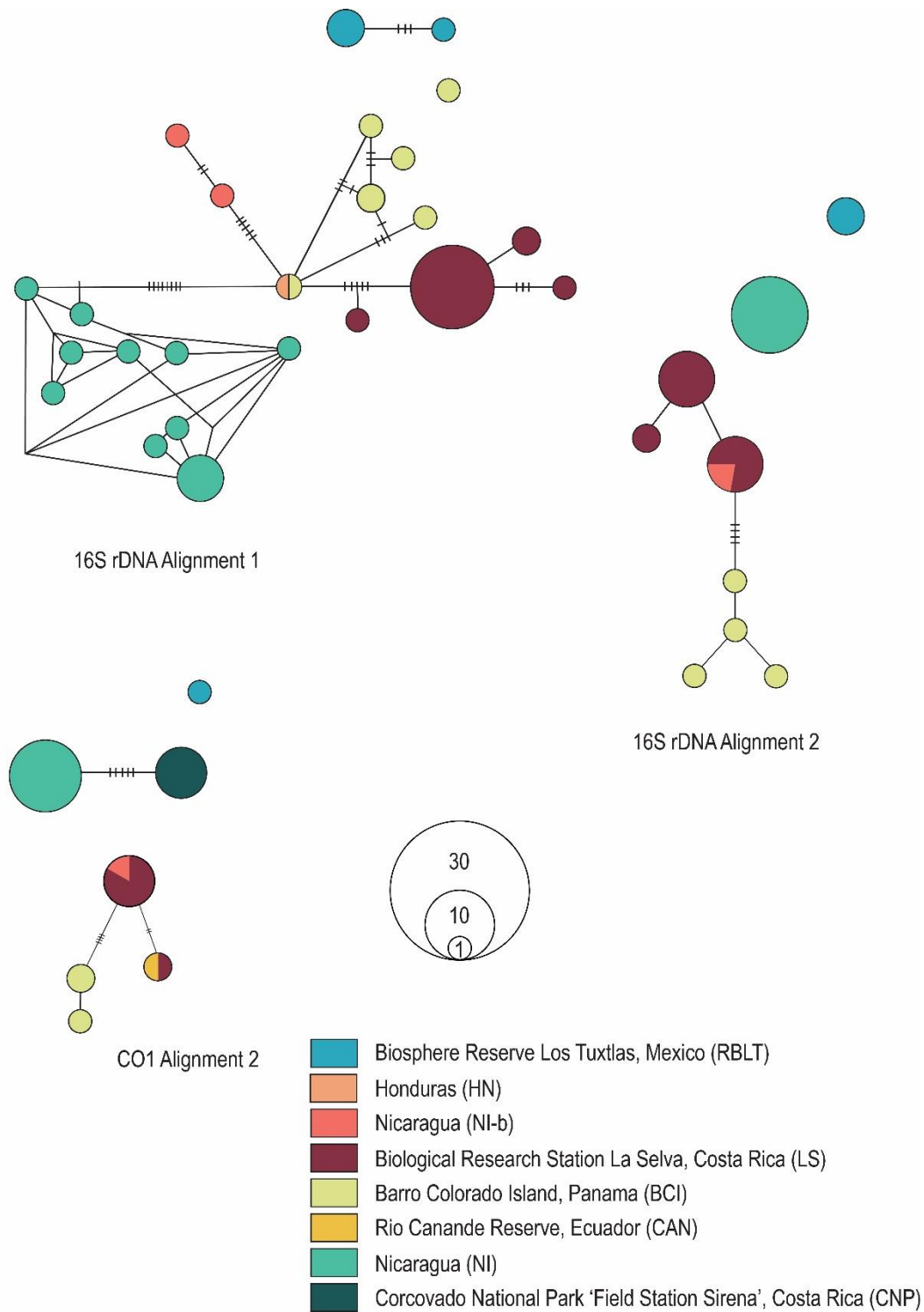


Figure S3. Genealogical relationships among *Megaloprepus* populations for the 16S rDNA Alignment 1 and 2, and the CO1 Alignment 2 based on statistical parsimony (95% connection limit) in TCS vers. 1.2.1. Populations are color coded according to their origin.

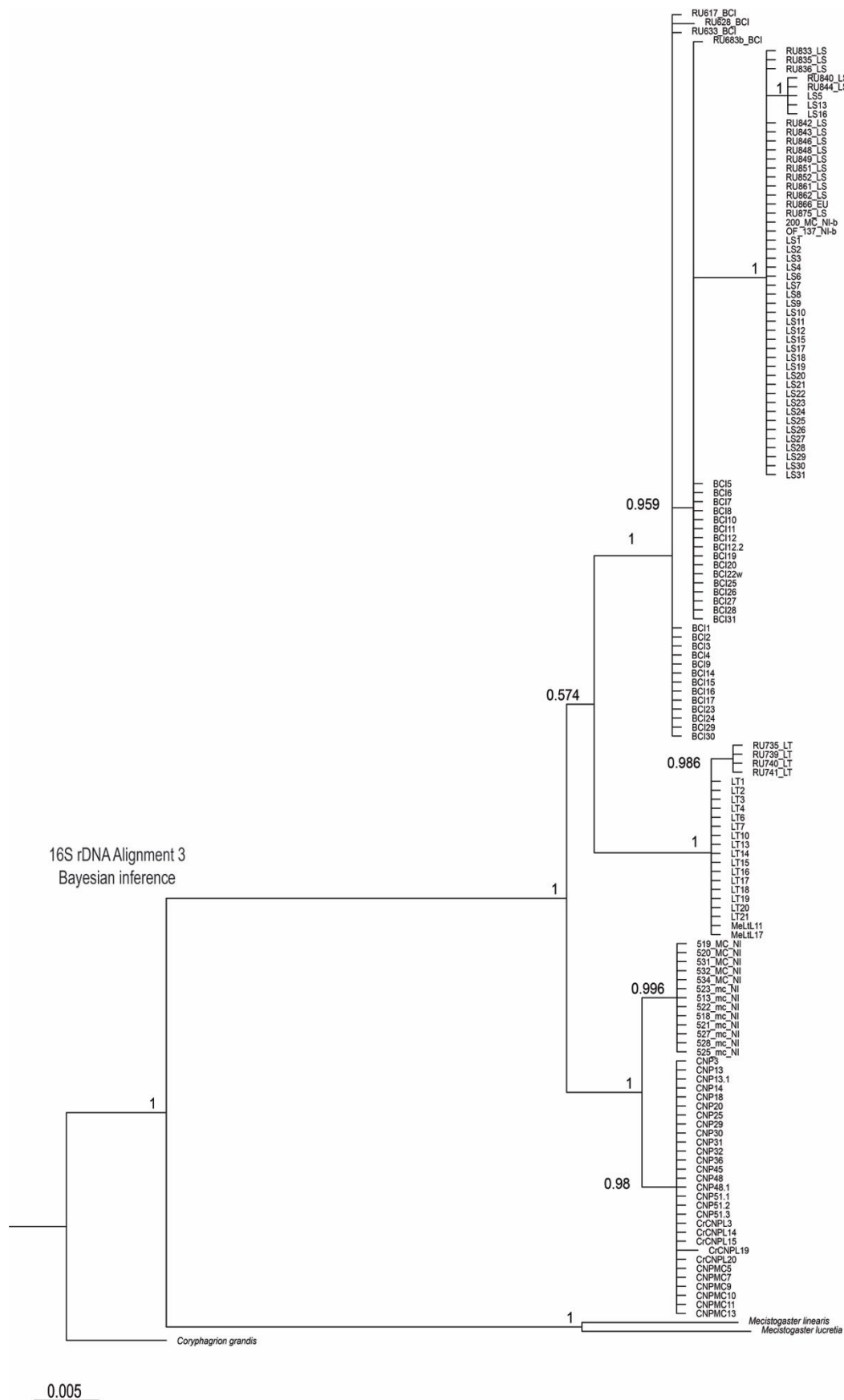


Figure S4. Phylogeny based on Bayesian inference using MrBayes vers. 3.7 for 16S rDNA Alignment3 the with posterior probabilities shown on the corresponding nodes. *Coryphagrion grandis*, *Mecistogaster linearis* and *Mecistogaster lucretia* are outgroups. For the species IDs please compare Table S1.

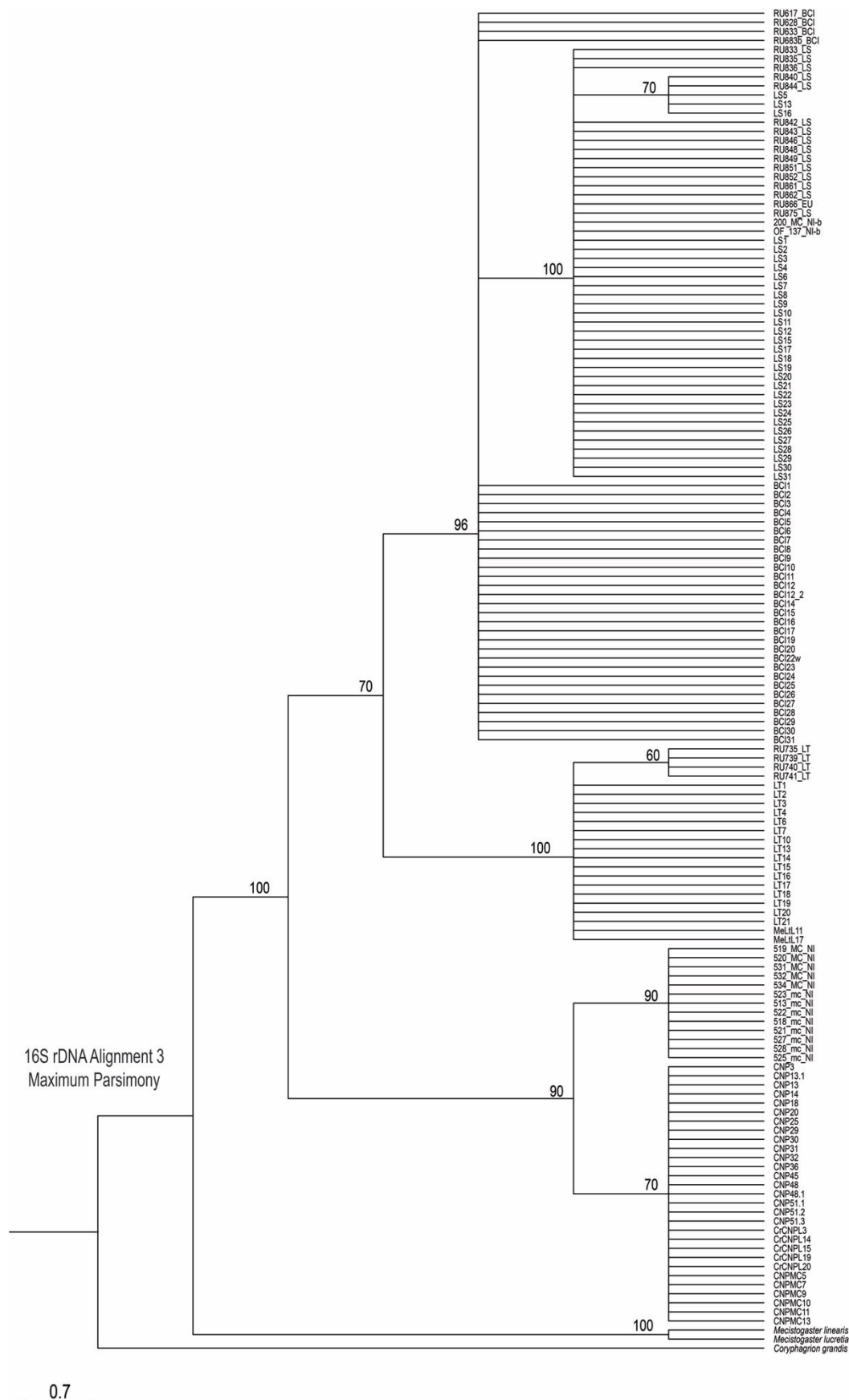


Figure S6. Maximum parsimony tree obtained with PAUP* vers. 4.0b8 for the 16S rDNA Alignment3 with 1000 bootstrap replicates. *Coryphagrion grandis*, *Mecistogaster linearis* and *Mecistogaster lucretia* are outgroups. For the species IDs please compare Table S1.

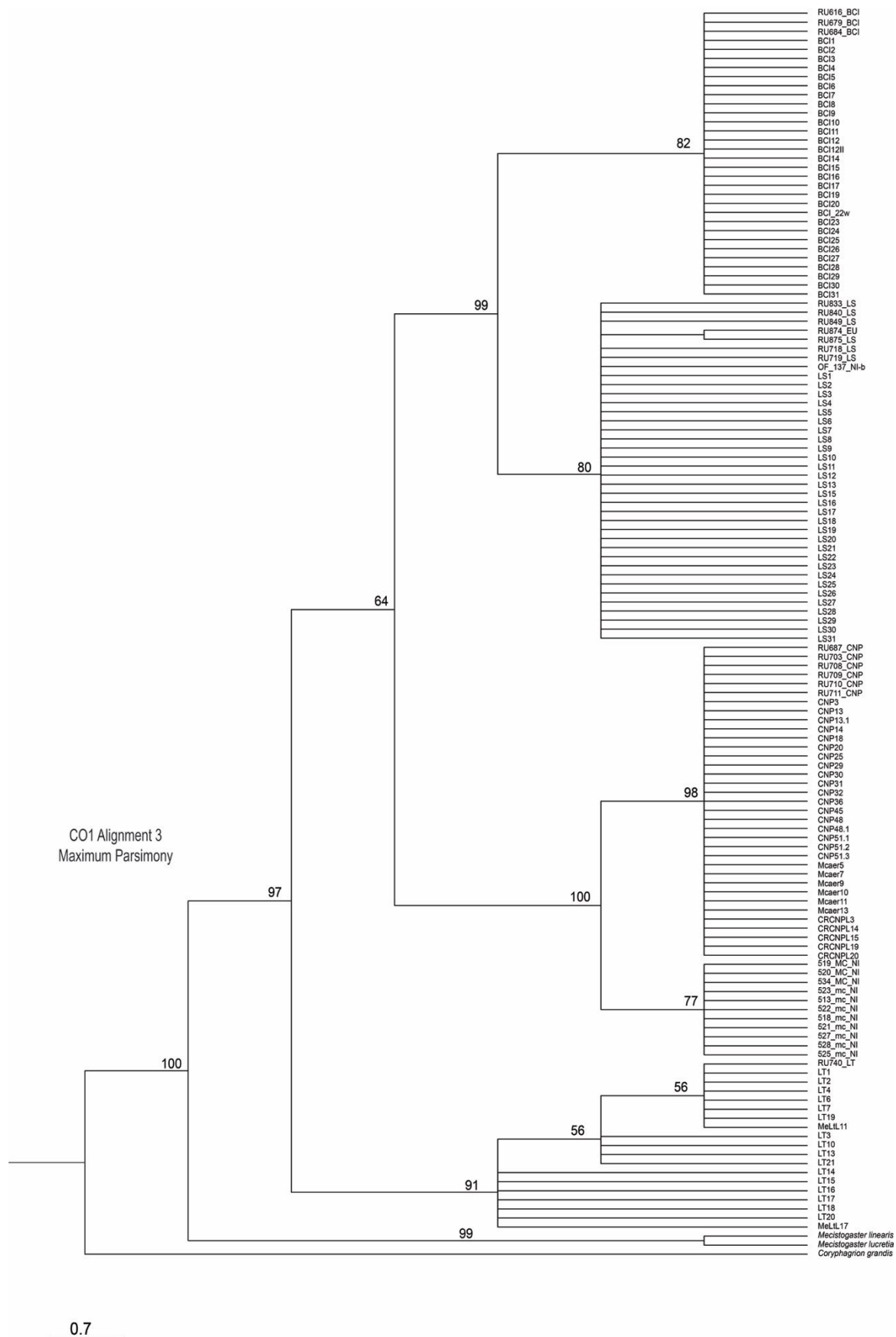


Figure S7. Maximum parsimony tree obtained with PAUP* vers. 4.0b8 for the CO1 Alignment3 with 1000 bootstrap replicates. *Coryphagrion grandis*, *Mecistogaster linearis* and *Mecistogaster lucretia* are outgroups. For the species IDs please compare Table S1.