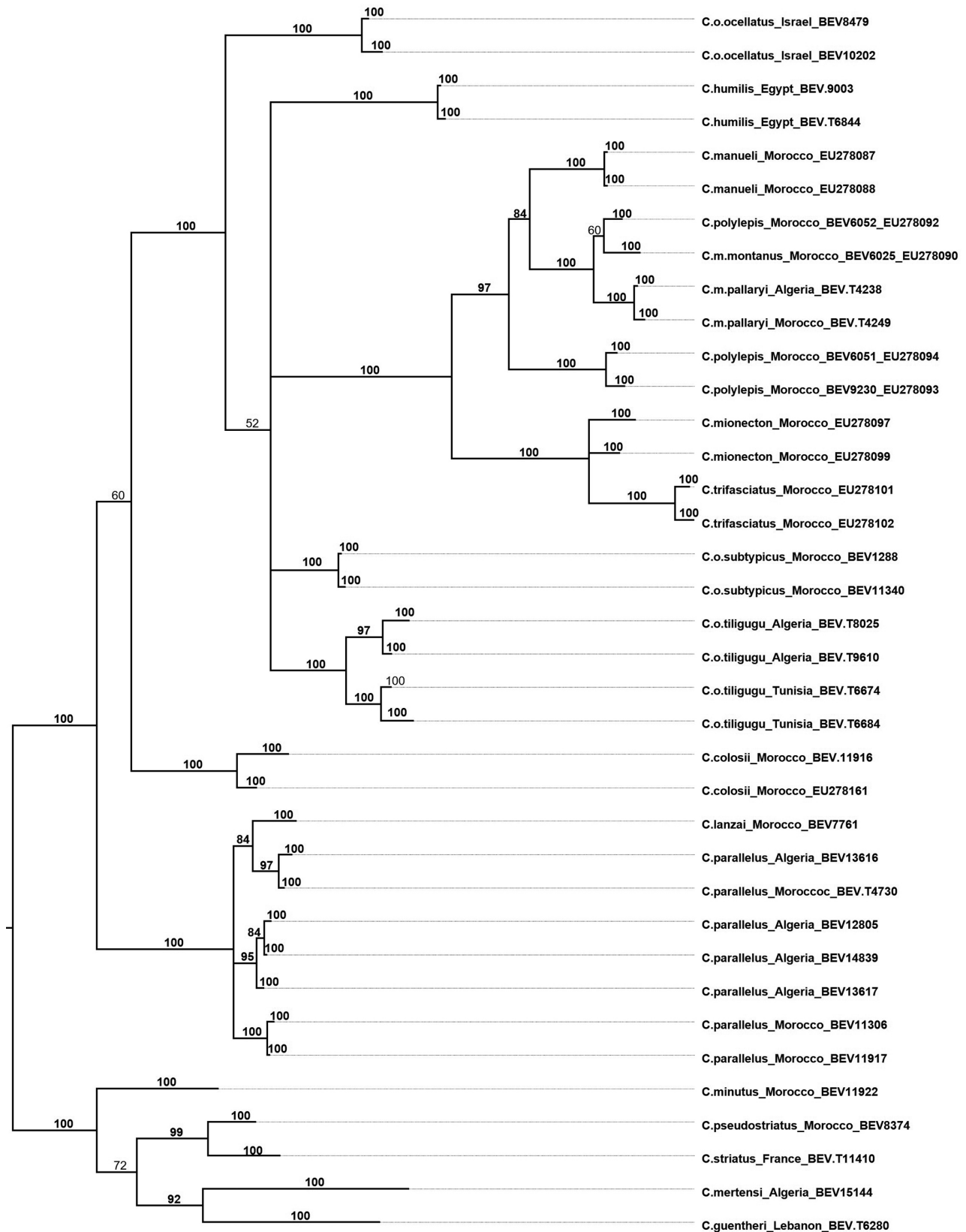


Supplementary Figure S1. Bayesian tree of the concatenated nuclear dataset. Bayesian posterior probabilities are expressed as percentages and shown on top of the branches. The scale bar denotes the number of substitutions per site.



Supplementary Figure S2. Bayesian tree of the mtDNA datasets. Bayesian posterior probabilities are expressed as percentages and shown on top of the branches. The scale bar denotes the number of substitutions per site.