

Fig. S1: Ultrametric tree showing phylogenetic relationships among Cercopithecinae based on mitochondrial cytochrome b gene sequences. Given are Genbank accession number, species and geographic origin (countries as three-letter code). The newly described subspecies *Cercopithecus mitis manyarensis* is highlighted in green. Blue bars indicate 95% highest posterior densities. (AGO = Angola; BKF = Burkina Faso; CAF = Central African Republic; CIV = Ivory Coast; CMR = Cameroon; COD = Democratic Republic of Congo; ERI = Eritrea; ETH = Ethiopia; GAB = Gabon; GHA = Ghana; GNQ = Equatorial Guinea; KEN = Kenya; MOZ = Mozambique; MRT = Mauritania; MWI = Malawi; NGR = Nigeria; SDN = Sudan; SEN = Senegal; SLE = Sierra Leone; SOM = Somalia; SSD = South Sudan; TGO = Togo; TZA = Tanzania; UGA = Uganda; ZAF = South Africa; ZMB = Zambia)



Fig. S2: Maximum-likelihood phylogram showing phylogenetic relationships among Cercopithecinae based on mitochondrial cytochrome b gene sequences. Given are Genbank accession number and species. The newly described subspecies *Cercopithecus mitis manyarensis* is highlighted in green. Numbers at nodes refer to bootstrap values with those <90% indicated in red. The bar below indicates substitutions per site.

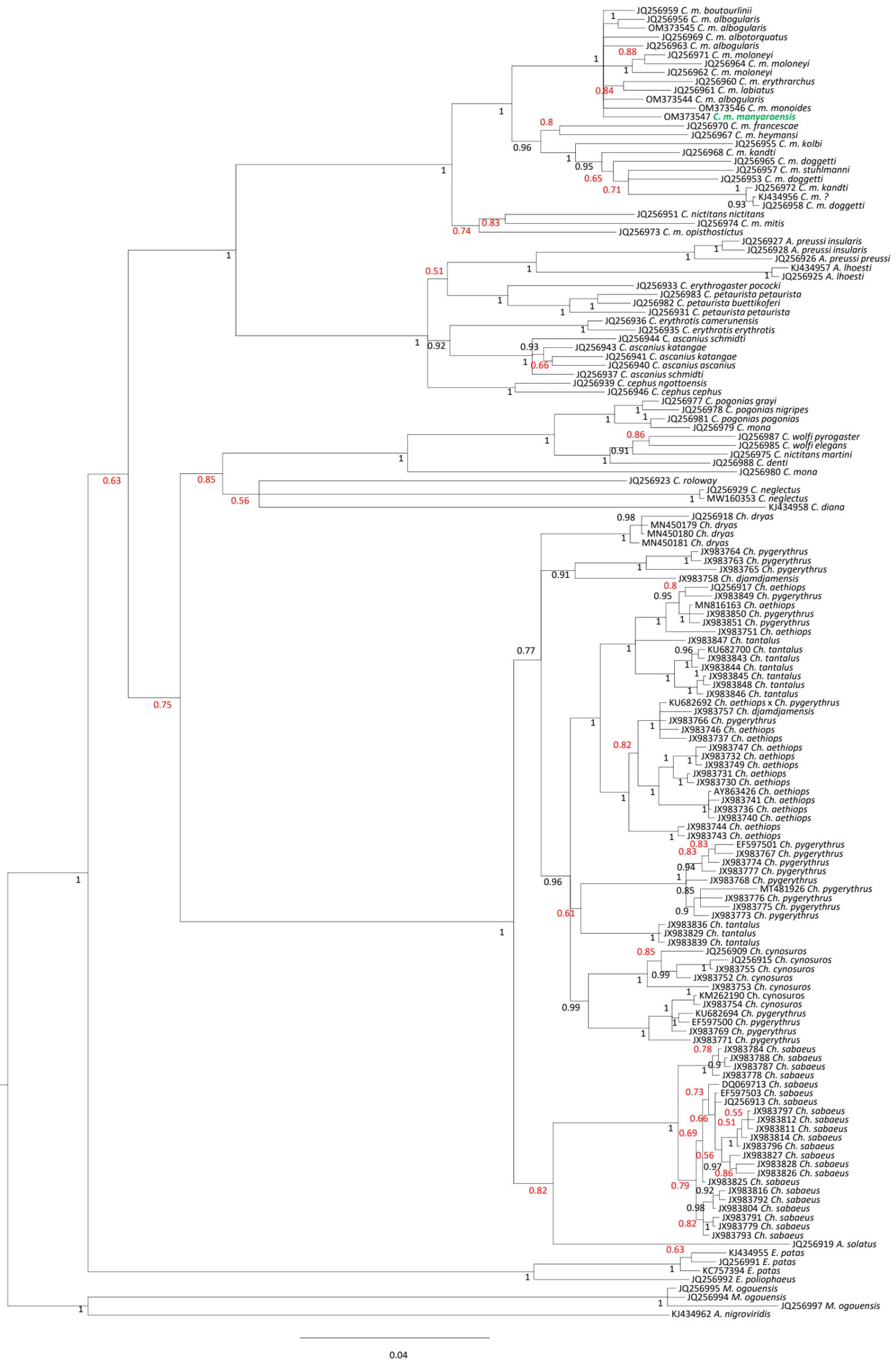


Fig. S3: Bayesian phylogram showing phylogenetic relationships among Cercopithecinae based on mitochondrial cytochrome b gene sequences. Given are Genbank accession number and species. The newly described subspecies *Cercopithecus mitis manyarensis* is highlighted in green. Numbers at nodes refer to posterior probabilities with those <0.90 indicated in red. The bar below indicates substitutions per site.