

Figure S1. Bayesian phylogeny of mitochondrial cytochrome oxidase one sequences (478 nucleotides) of Vespertilionidae genera *Afronycteris*, *Neoromicia*, *Laephotis*, *Pipistrellus* sampled from Angola, South Africa and Eswatini and the outgroup, *Miniopterus* spp. (Miniopteridae). Bayesian phylogenetic analysis was performed using the Hasegawa–Kishino–Yano model incorporating invariant sites and a gamma distribution (HKY+I+G). Posterior probabilities of > 0.7 are indicated at internal nodes. Samples obtained in this study are indicated in bold. Branch colours indicate posterior probabilities at each node.

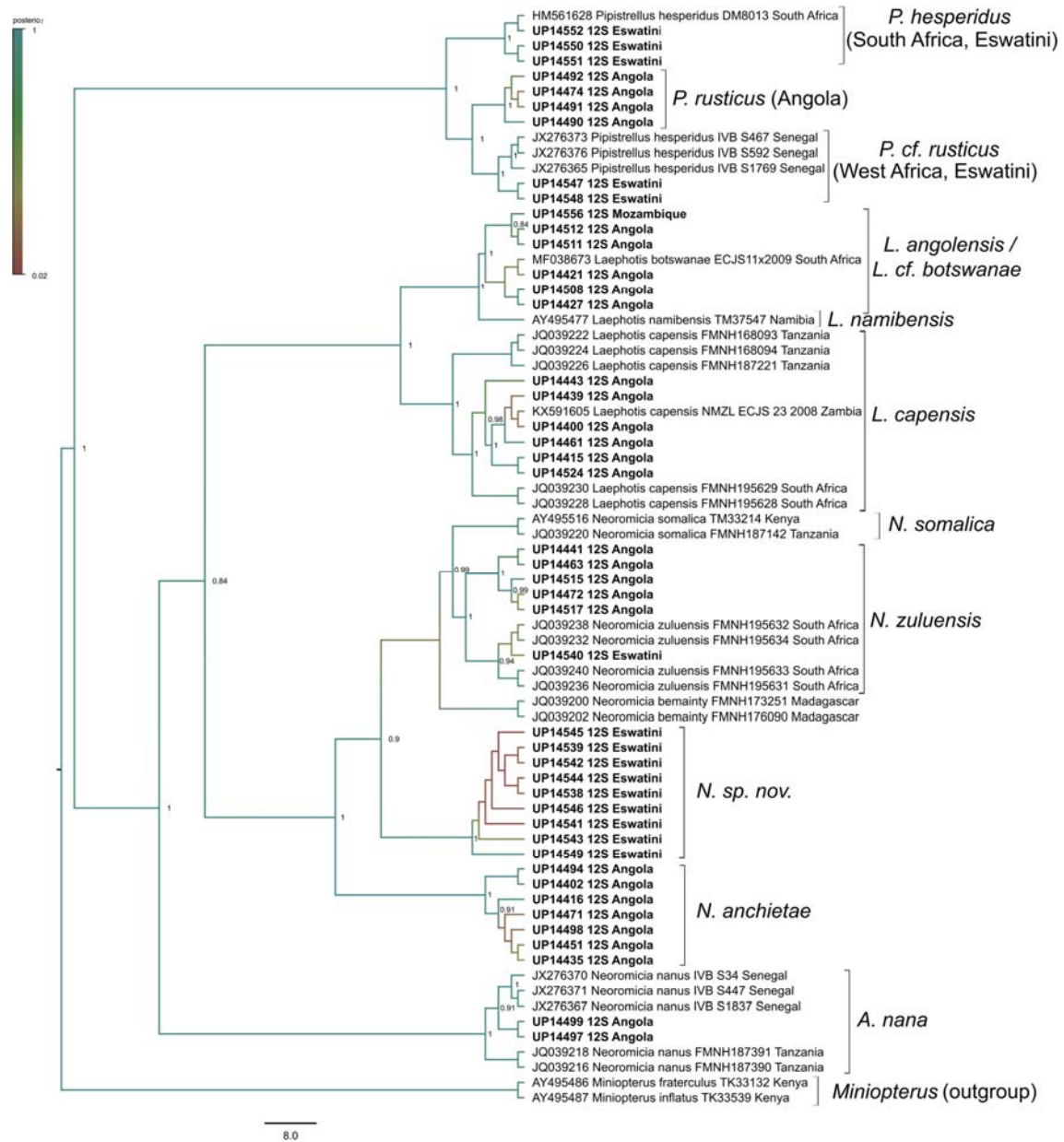


Figure S2. Bayesian phylogeny of mitochondrial 12S sequences (478 nucleotides) of pipistrelle-like Vespertilionidae genera *Afronycteris*, *Neoromicia*, *Laephotis* and *Pipistrellus* sampled from Angola, South Africa and Eswatini and outgroup *Miniopterus* spp. (Miniopteridae). Bayesian phylogenetic analysis was performed using the Hasegawa–Kishino–Yano model incorporating invariant sites and a gamma distribution (HKY+I+G). Posterior probabilities of > 0.7 are indicated at internal nodes. Samples obtained in this study are indicated in bold. Branch colours indicate posterior probabilities at each node.