

Table S2. Uncorrected P-distances (number of base differences per site from averaging over all sequence pairs) are shown, obtained between (bottom left) and within (on diagonals in bold face; “n/c” indicates sample sizes too small for calculation) groups of pipistrelloid bats from Angola, Eswatini and South Africa in relation to Genbank sequences of comparable African species for the CO1 mitochondrial gene. See Table S1 for details of specimens used in the study. This analysis involved 118 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 478 positions in the final dataset. Analyses were conducted in MEGA X (Kumar et al. 2018). Abbreviations for groups are as follows: Anan = *Afronycteris nana*, Lang = *Laephotis angolensis*, Lbot = *L. botswanae*, Lcap(Ang) = *L. capensis* (Angola), Lcap(AngSA) = *L. capensis* (South Africa and Angola), Nanc = *Neoromicia anchietae*, Nsom = *N. somalica*, Nzul = *N. zuluensis*, Phesp = *Pipistrellus hesperidus*, Prust(Ang) = *P. rusticus* (Angola), Prust(SA) = *P. rusticus* (Southern Africa), Outgroup = outgroup (*Miniopterus* spp).

	Anan	Lang	Lbot	Lcap(Ang)	Lcap(AngSA)	Nanc	Nsom	Nzul(SA)	Phesp	Prust(Ang)	Prust(SA)	Outgroup
Anan	0.0135											
Lang	0.144	0.0028										
Lbot	0.138	0.014	n/c									
Lcap(Ang)	0.122	0.087	0.087	0.001								
Lcap(AngSA)	0.126	0.091	0.091	0.009	0.0068							
Nanc	0.130	0.161	0.155	0.142	0.143	0.0162						
Nsom	0.141	0.150	0.146	0.142	0.141	0.119	n/c					
Nzul(SA)	0.155	0.155	0.151	0.143	0.140	0.117	0.057	0.0042				
Phesp	0.153	0.167	0.161	0.156	0.156	0.157	0.170	0.166	0.0123			
Prust(Ang)	0.154	0.162	0.156	0.149	0.149	0.175	0.173	0.165	0.121	0.0056		
Prust(SA)	0.151	0.155	0.153	0.153	0.152	0.172	0.178	0.177	0.121	0.089	0.0032	
Outgroup	0.210	0.199	0.199	0.220	0.225	0.213	0.218	0.231	0.201	0.221	0.215	0.0211