**S2 Text. Mitochondrial cytochrome b gene data base and analysis.**

We PCR-amplified and sequenced the cytochrome b gene of 65 tarsier individuals sampled in the framework of this study (Genebank accession numbers KR337026-KR337090) adopting PCR primers and conditions from Merker et al. (2009)[[1]](#footnote-1). Data sets of previous studies1[[2]](#footnote-2)[[3]](#footnote-3) comprising 86 individuals of Eastern tarsiers were also included in the tree reconstruction (Genbank accession numbers FJ214312-FJ214337, FJ614263-FJ614285, FJ614291-FJ614297, FJ614300-FJ614306, FJ614364-FJ614371, HM115970-HM115984). *Tarsius syrichta* served as outgroup (Genbank accession number AB371090).

We estimated a maximum likelihood phylogeny of 44 cytochrome b haplotypes (S1 Fig.) obtained from 151 individuals using PhyML-aBayes[[4]](#footnote-4)[[5]](#footnote-5) with the substitution model J3 and gamma distribution with five categories selected as described in the main text. Bootstrap support was assessed by 1000 replicates.

We preferred nuclear compared to matrilinear inherited DNA data for phylogenetic analyses to obtain reliable inferences about phylogenetic relationships and populations divergence times -mtDNA evolves more rapidly than nuclear DNA[[6]](#footnote-6)- and to minimize gender-biased admixture[[7]](#footnote-7), as we found strong indication for female philopatry and male dispersal (single-male multi-female groups at most study sites; nearly all cytochrome b haplotypes were unique to a single study locality).

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