

**Additional file 4.** Maximum likelihood phylogeny of 350 mitochondrial cytochrome-*b* sequences of *Rhinolophus*. The phylogeny was inferred in IQ-TREE and its topology was very similar to the Bayesian phylogeny calculated in MRBAYES. Filled black circles on nodes denote bootstrap values (BS)  $\geq 70\%$  and Bayesian posterior probabilities (PP)  $\geq 0.95$ , left-half-filled circles indicate BS  $\geq 70\%$  and PP  $< 0.95$ , right-half-filled circles indicate BS  $< 70\%$  and PP  $\geq 0.95$ , and unmarked nodes indicate BS  $< 70\%$  and PP  $< 0.95$ . Branch colors indicate individual clade membership. Species groups are from Csorba et al. (2003). Specimen localities include counties for Kenya. Museum acronyms are defined in Additional file 1.

