

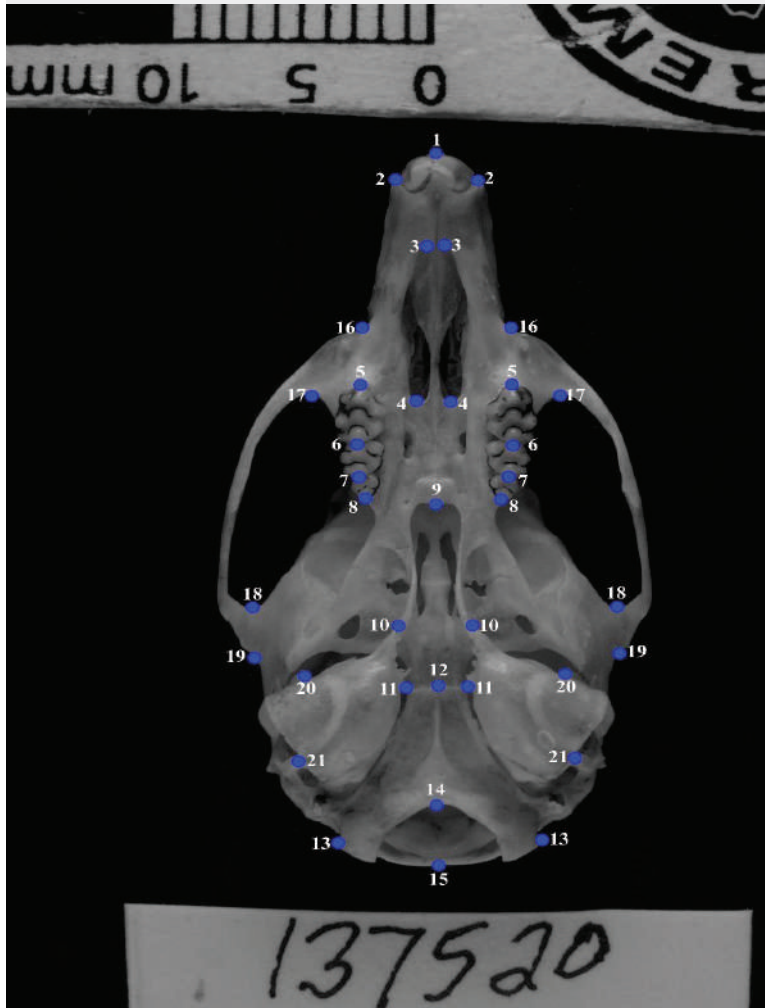


Fig. S2 Cranial landmarks used in geometric morphometric analyses of the non-Ethiopian *L. flavopunctatus* members. 1, Anteriormost point between upper incisors; 2, Superiormost point of upper incisive alveolus; 3, Anterior most margin of the incisive foramen; 4, Posteriormost margin of incisive foramen; ; 5, Anterior most margin of the first molar; 6, Between first molar and second molar; 7, Between the second molar and third molar; 8, Posteriormost margin of the third molar; 9, Posterior most point of the palate; 10, midpoint on the auditory bulla where it meets the piriform fenestra posteriorly; 11, Medial point of the junction between tympanic bullae and Eustachian tube; 12, Midpoint of suture between basisphenoid and basioccipital; 13, Posteriormost margin of occipital condyle; 14, Anterior most point of the Foramen magnum viewed ventrally; 15, Posteriormost point of superior margin of foramen magnum; 16, Anteriormost margin of zygomatic plate; 17, Posteriormost margin of the posterior zygomatic plate; 18, Posteriormost margin of the anterior zygomatic plate; 19, Posterior most point of suture between jugal and squamosal; 20, Tip of the eustachian tube; 21, caudal end of the external opening of the auditory channel.

Fig. S3 The phylogeny of the genus *Lophuromys* inferred from the *Cytochrome b* gene using Bayesian Inference in MrBayes. There were a total of 238 sequences in the analysis, representing all unique haplotypes from the initial alignment of 803 sequences. The numbers above branches represent the % posterior probability values <95%.

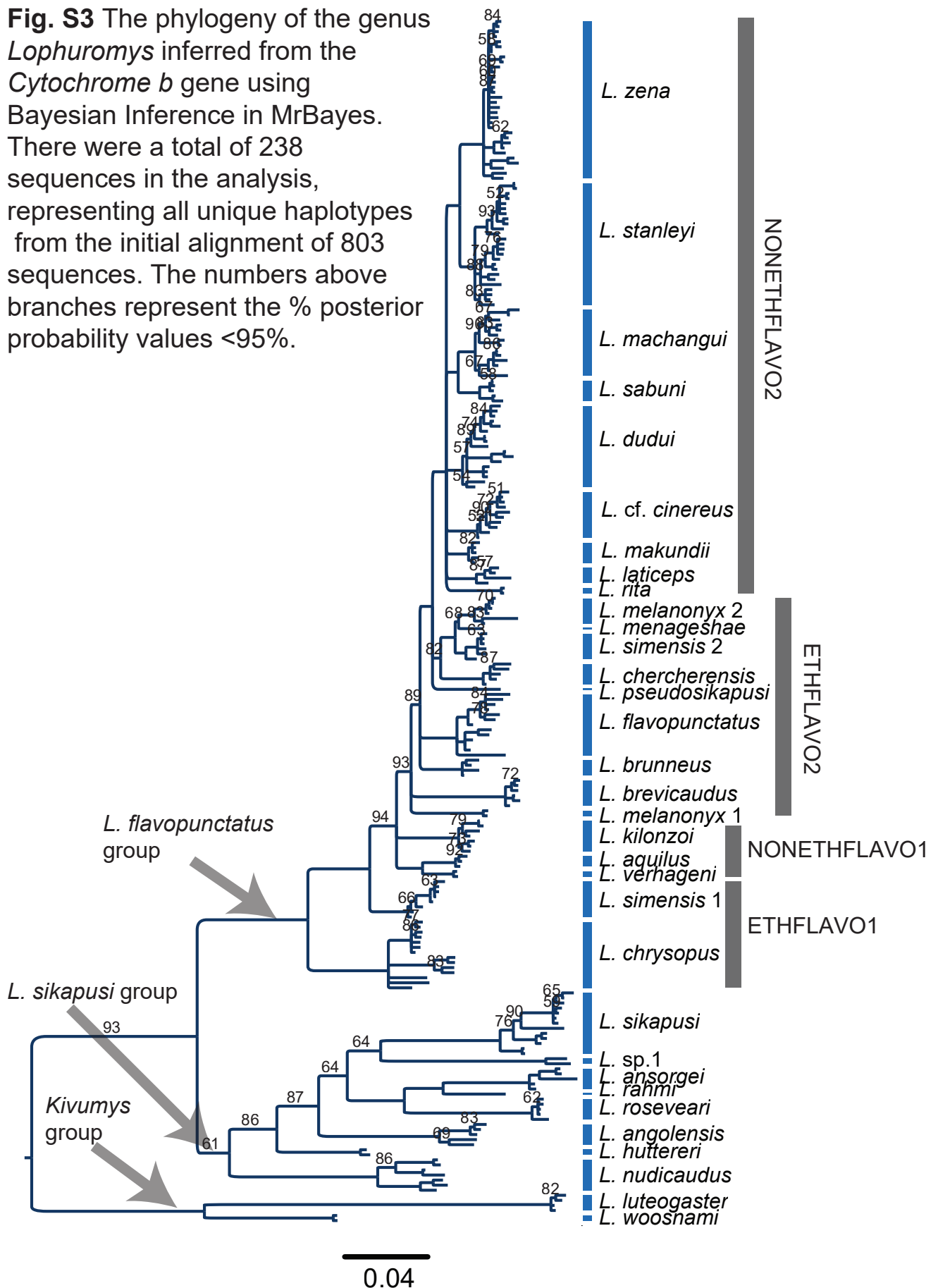
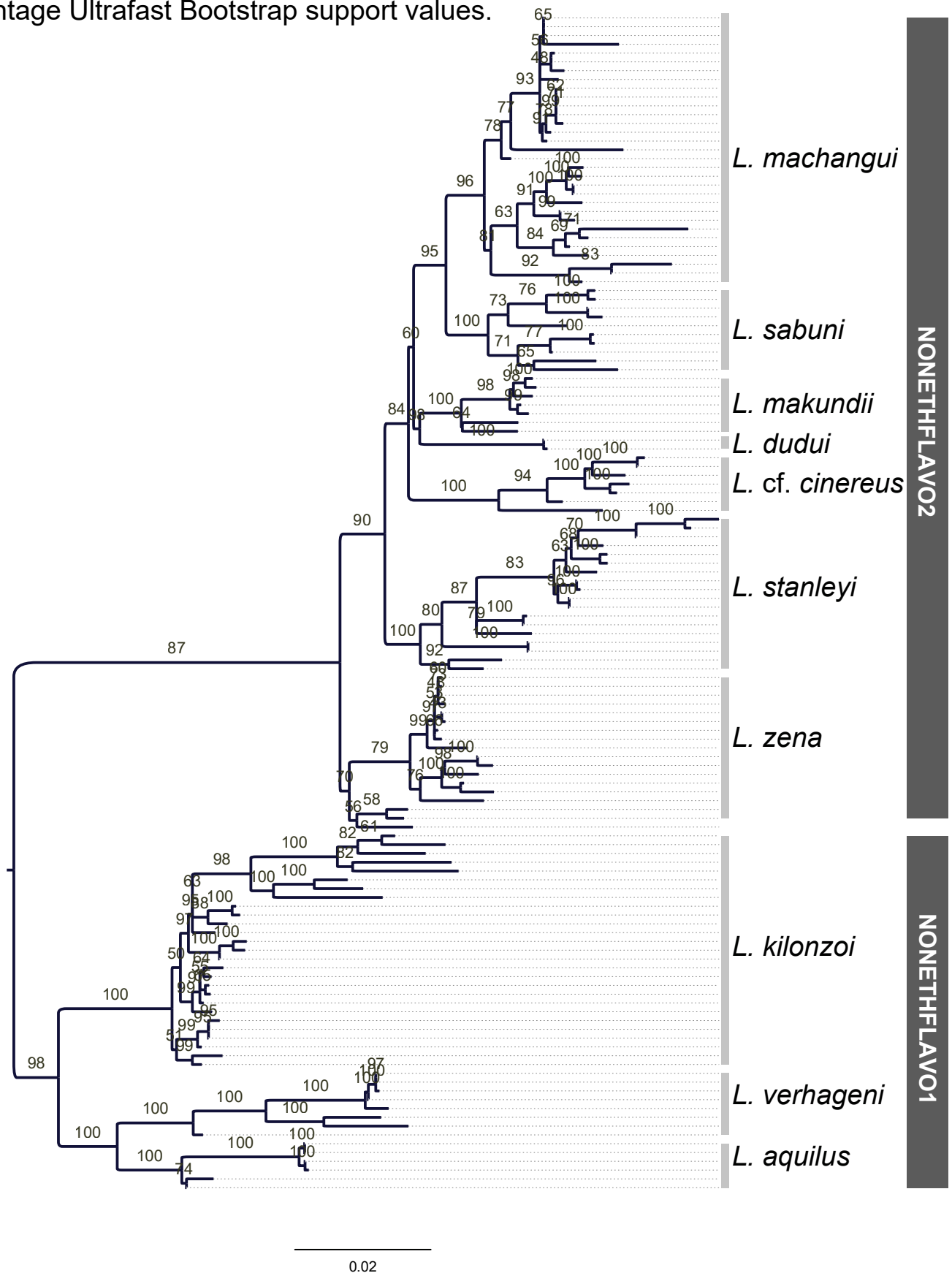


Fig. S4 A Maximum likelihood phylogeny of the non-Ethiopian *L. flavopunctatus* members inferred from the concatenated mitochondrial genes (Cytochrome b gene + cytochrome oxidase subunit 1) in IQ-TREE. The taxa labels represent the consensus species identities of main OTUs identified by species delimitation. Values above branches represent percentage Ultrafast Bootstrap support values.



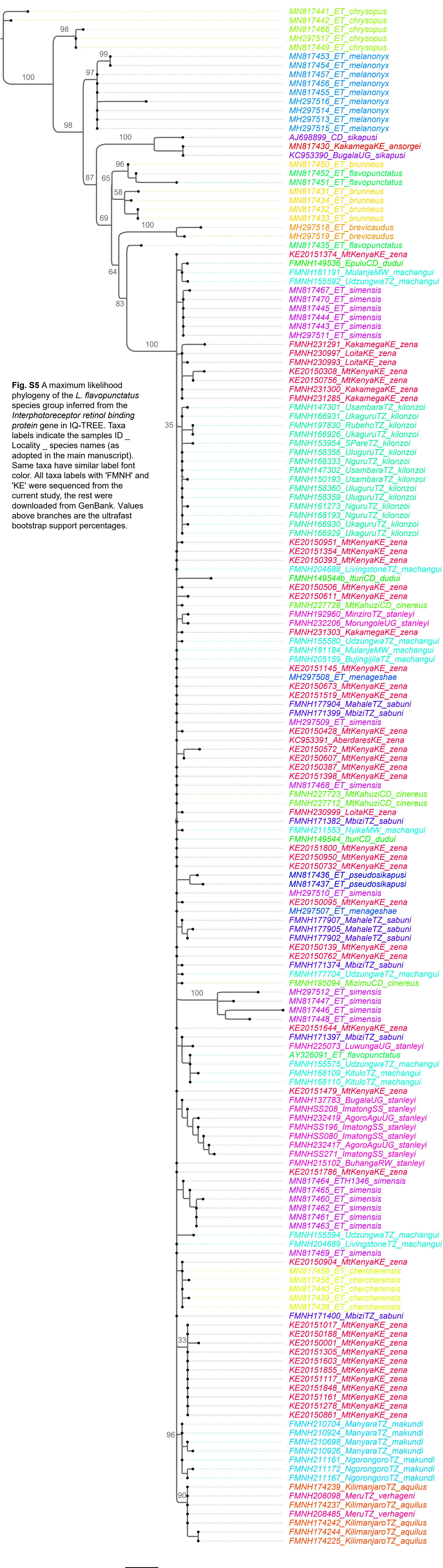


Fig. S6 Haplotype network structure in selected non-Ethiopian *L. flavopunctatus* members inferred from *Cytochrome b* using the Median Joining Network algorithm in PopART. The networks show genealogical relationships between sampling locality in the *L. zena*, *L. machangui*, and *L. stanleyi* clades which were selected for being sampled from more localities. The number of base substitutions between haplotypes are shown as hatchmarks on branches. The node sizes correspond to the haplotype frequency (number of samples per haplotypes) and branch lengths are relative to the number of mutations between haplotypes.

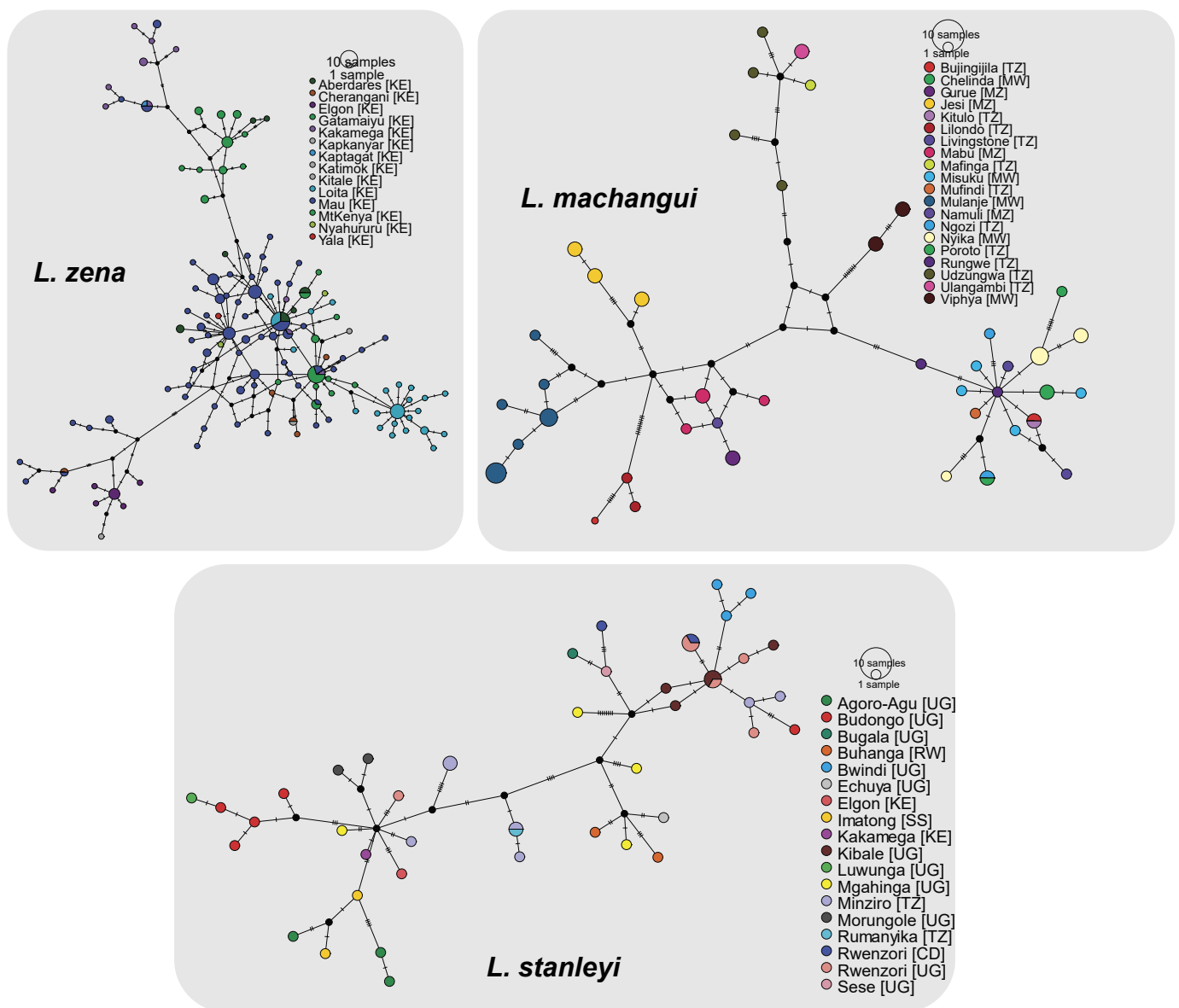


Fig. S7 Time calibrated maximum clade credibility tree of evolutionary relationships and divergence times of the non-Ethiopian *L. flavopunctatus* members reconstructed from a combination of *Cytochrome b*, *cytochrome oxidase subunit 1*, and *Interphotoreceptor retinoid binding protein*, time-calibrated using most recent common ancestor ages. Branch labels show the posterior probability support values, node labels illustrate the median divergence age, and node bars show the highest posterior density interval.

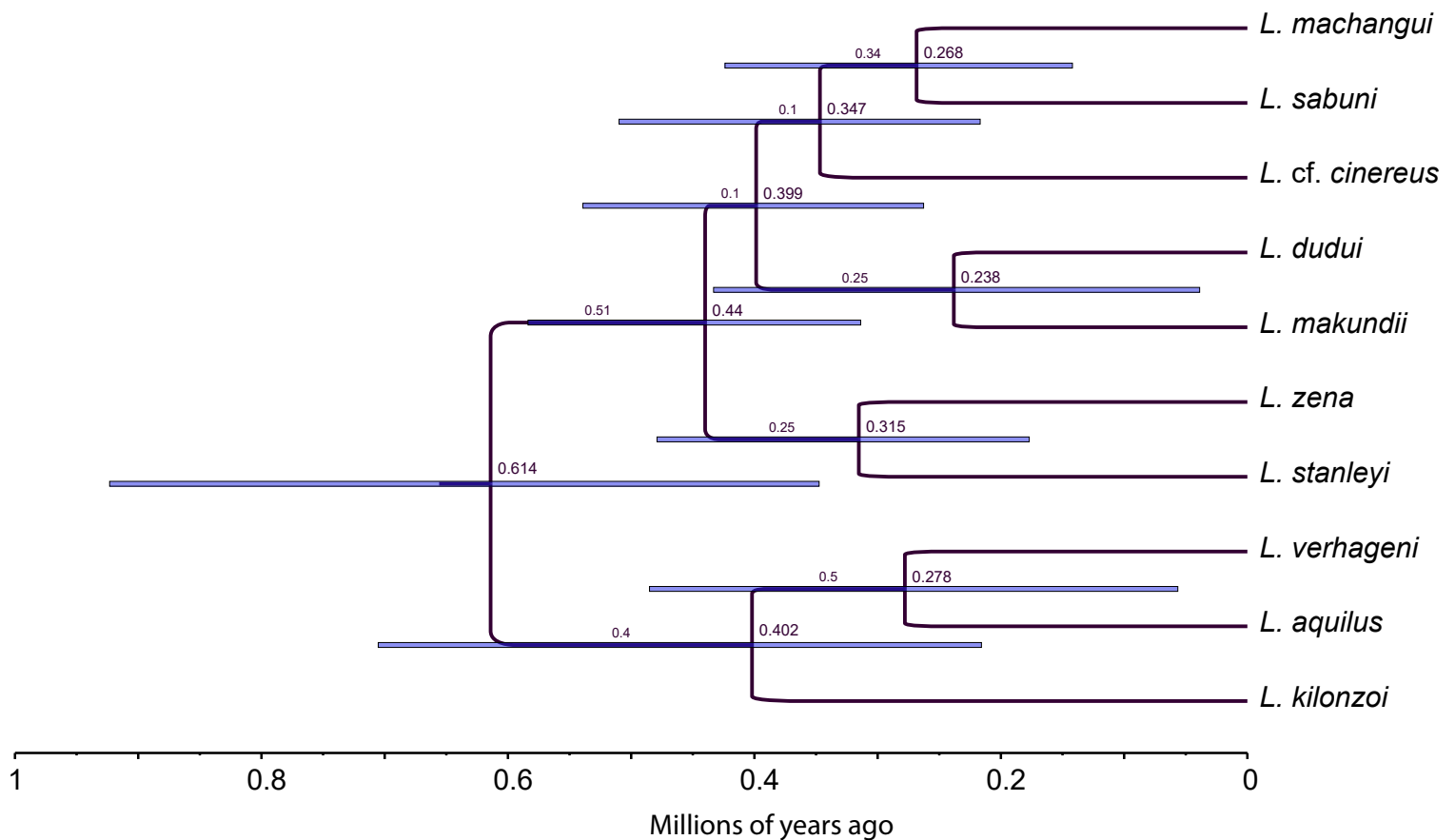


Fig. S8 Classification results following discriminant analysis in using linear and gometric craniodental datasets of the non-Ethiopian *L. flavopunctatus* members. Values indicate cross-validated (leave-one-our bootstrapping) % success by which samples were classified into a priori and predicted species groups. The shaded diagonal values indicate the success by which samples were predicted into their own groups which correspond to distinct *Cytochrome b* clades. N = number of samples. See Fig. 6 in main manuscript for stratified species classification results.

