

Fig. S1 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%.

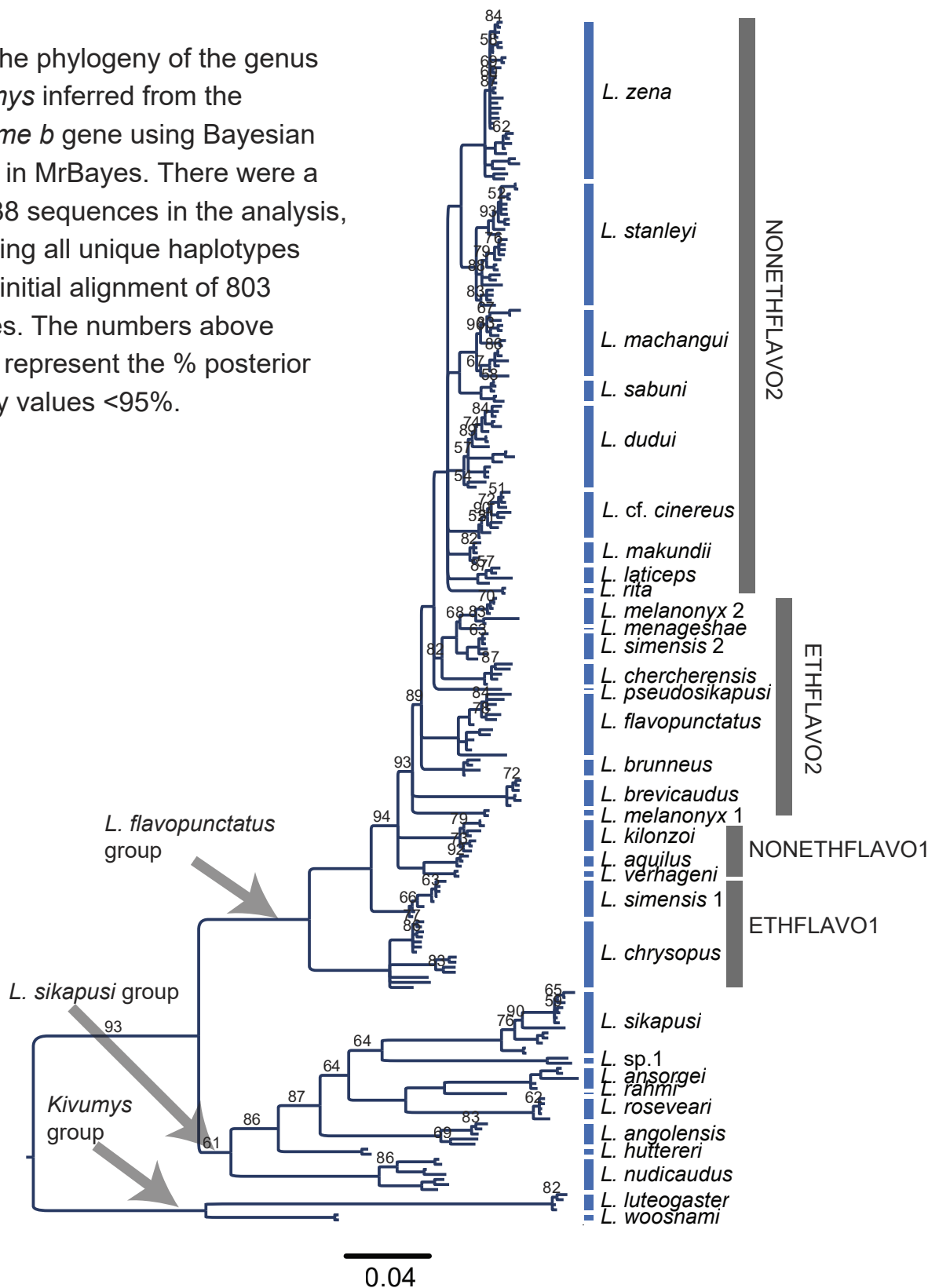
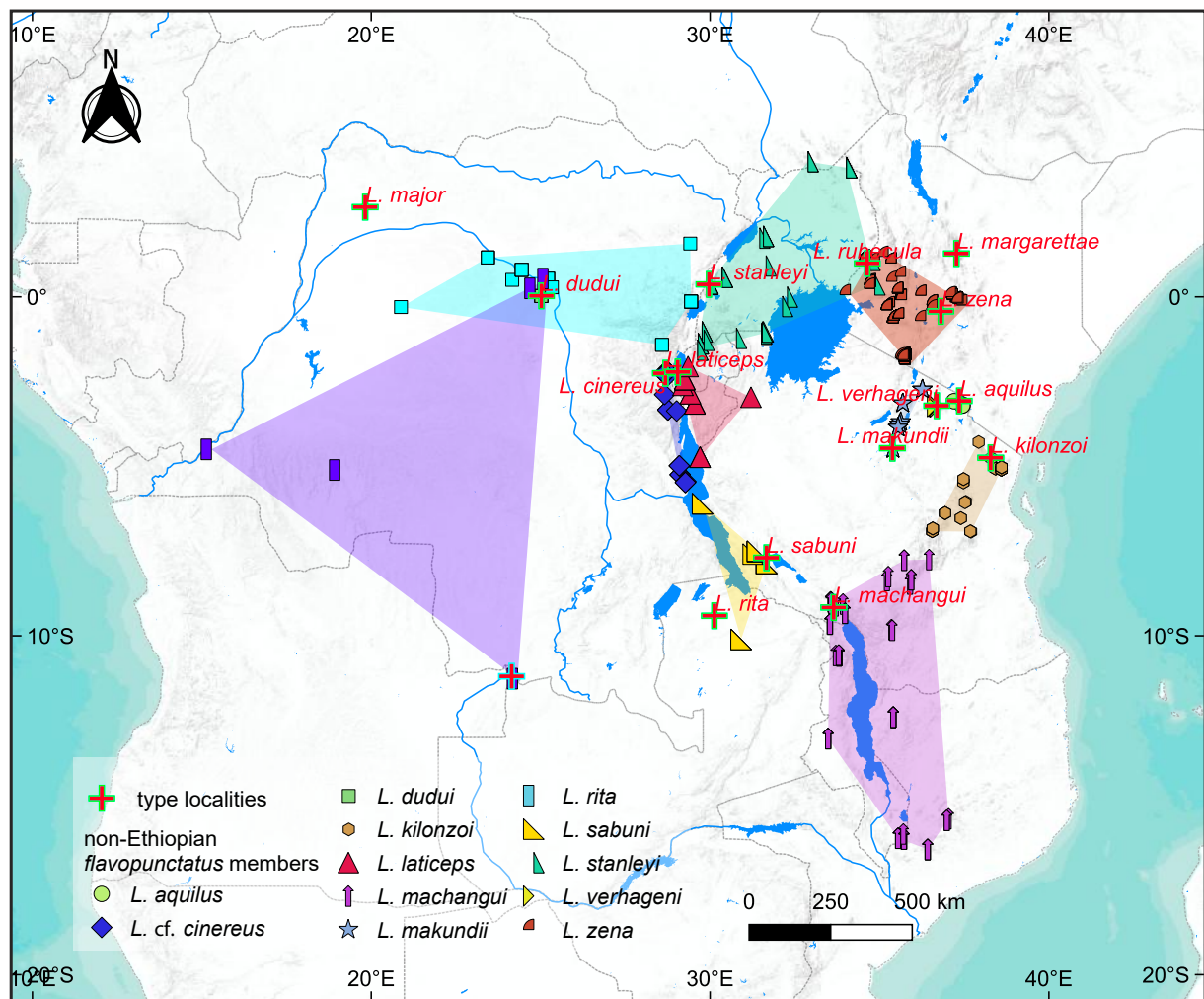
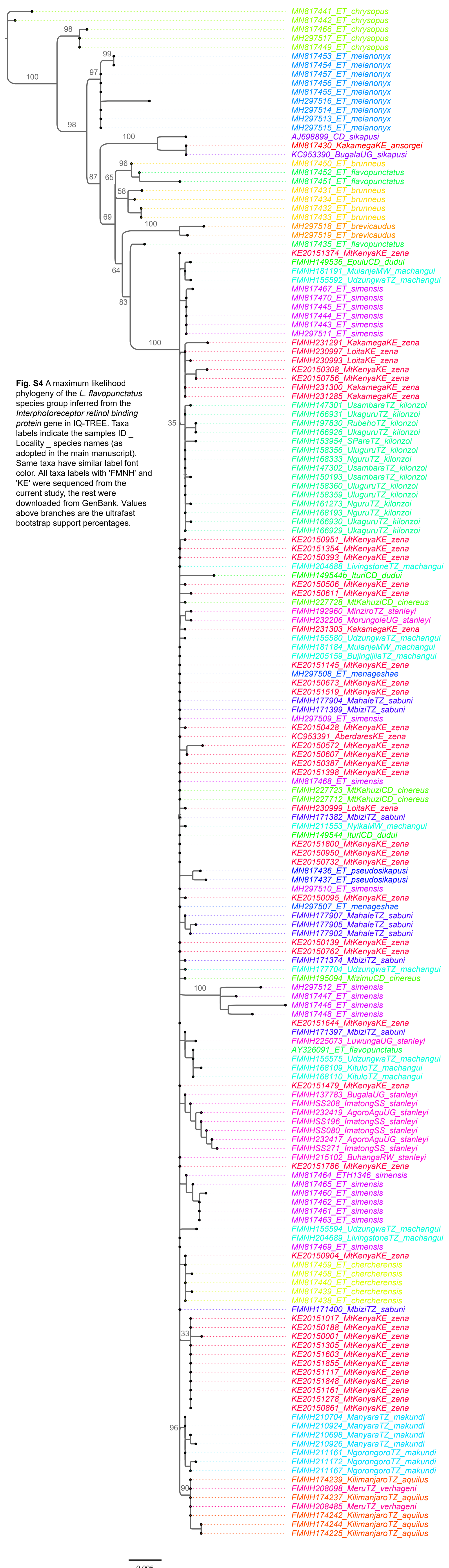


Fig. S2 Map showing the type localities (red, green outlined crosses '+') of species described under the non-Ethiopian *flavopunctatus* group, with the corresponding species names labeled in red fonts. The sampling points of samples used in the study are also shown, outlined to illustrate their distribution extents.





MN817441_ET_chrysopus
 MN817442_ET_chrysopus
 MN817466_ET_chrysopus
 MH297517_ET_chrysopus
 MN817449_ET_chrysopus
 MN817453_ET_melanonyx
 MN817454_ET_melanonyx
 MN817457_ET_melanonyx
 MN817456_ET_melanonyx
 MN817455_ET_melanonyx
 MH297516_ET_melanonyx
 MH297514_ET_melanonyx
 MH297513_ET_melanonyx
 MH297515_ET_melanonyx
 AJ698899_CD_sikapusi
 MN817430_KakamegaKE_ansorgei
 KC953390_BugalaUG_sikapusi
 MN817450_ET_brunneus
 MN817452_ET_flavopunctatus
 MN817451_ET_flavopunctatus
 MN817431_ET_brunneus
 MN817434_ET_brunneus
 MN817432_ET_brunneus
 MN817433_ET_brunneus
 MH297518_ET_brevicaudus
 MH297519_ET_brevicaudus
 MN817435_ET_flavopunctatus
 KE20151374_MtKenyaKE_zena
 FMNH149536_EpuluCD_dudui
 FMNH181191_MulanjeMW_machangui
 FMNH155592_UdzungwaTZ_machangui
 MN817467_ET_simensis
 MN817470_ET_simensis
 MN817445_ET_simensis
 MN817444_ET_simensis
 MN817443_ET_simensis
 MH297511_ET_simensis
 FMNH231291_KakamegaKE_zena
 FMNH230997_LoitaKE_zena
 FMNH230993_LoitaKE_zena
 KE20150308_MtKenyaKE_zena
 KE20150756_MtKenyaKE_zena
 FMNH231300_KakamegaKE_zena
 FMNH231285_KakamegaKE_zena
 FMNH147301_UsambaraTZ_kilonzoi
 FMNH166931_UkaguruTZ_kilonzoi
 FMNH197830_RubehoTZ_kilonzoi
 FMNH166926_UkaguruTZ_kilonzoi
 FMNH153954_SPareTZ_kilonzoi
 FMNH158356_UluguruTZ_kilonzoi
 FMNH168333_NguruTZ_kilonzoi
 FMNH147302_UsambaraTZ_kilonzoi
 FMNH150193_UsambaraTZ_kilonzoi
 FMNH158360_UluguruTZ_kilonzoi
 FMNH158359_UluguruTZ_kilonzoi
 FMNH161273_NguruTZ_kilonzoi
 FMNH168193_NguruTZ_kilonzoi
 FMNH166930_UkaguruTZ_kilonzoi
 FMNH166929_UkaguruTZ_kilonzoi
 KE20150951_MtKenyaKE_zena
 KE20151354_MtKenyaKE_zena
 KE20150393_MtKenyaKE_zena
 FMNH204688_LivingstoneTZ_machangui
 FMNH149544b_IturiCD_dudui
 KE20150506_MtKenyaKE_zena
 KE20150611_MtKenyaKE_zena
 FMNH227728_MtKahuziCD_cinereus
 FMNH192960_MinziroTZ_stanleyi
 FMNH232206_MorungoleUG_stanleyi
 FMNH231303_KakamegaKE_zena
 FMNH155580_UdzungwaTZ_machangui
 FMNH181184_MulanjeMW_machangui
 FMNH205159_BujingijilaTZ_machangui
 KE20151145_MtKenyaKE_zena
 MH297508_ET_menageshae
 KE20150673_MtKenyaKE_zena
 KE20151519_MtKenyaKE_zena
 FMNH177904_MahaleTZ_sabuni
 FMNH171399_MbiziTZ_sabuni
 MH297509_ET_simensis
 KE20150428_MtKenyaKE_zena
 KC953391_AberdaresKE_zena
 KE20150572_MtKenyaKE_zena
 KE20150607_MtKenyaKE_zena
 KE20150387_MtKenyaKE_zena
 KE20151398_MtKenyaKE_zena
 MN817468_ET_simensis
 FMNH227723_MtKahuziCD_cinereus
 FMNH227712_MtKahuziCD_cinereus
 FMNH230999_LoitaKE_zena
 FMNH171382_MbiziTZ_sabuni
 FMNH211553_NyikaMW_machangui
 FMNH149544_IturiCD_dudui
 KE20151800_MtKenyaKE_zena
 KE20150950_MtKenyaKE_zena
 KE20150732_MtKenyaKE_zena
 MN817436_ET_pseudosikapusi
 MN817437_ET_pseudosikapusi
 MH297510_ET_simensis
 KE20150095_MtKenyaKE_zena
 MH297507_ET_menageshae
 FMNH177907_MahaleTZ_sabuni
 FMNH177905_MahaleTZ_sabuni
 FMNH177902_MahaleTZ_sabuni
 KE20150139_MtKenyaKE_zena
 KE20150762_MtKenyaKE_zena
 FMNH171374_MbiziTZ_sabuni
 FMNH177704_UdzungwaTZ_machangui
 FMNH195094_MizimuCD_cinereus
 MH297512_ET_simensis
 MN817447_ET_simensis
 MN817446_ET_simensis
 MN817448_ET_simensis
 KE20151644_MtKenyaKE_zena
 FMNH171397_MbiziTZ_sabuni
 FMNH225073_LuwungaUG_stanleyi
 AY326091_ET_flavopunctatus
 FMNH155575_UdzungwaTZ_machangui
 FMNH168109_KituloTZ_machangui
 FMNH168110_KituloTZ_machangui
 KE20151479_MtKenyaKE_zena
 FMNH137783_BugalaUG_stanleyi
 FMNHSS208_ImatongSS_stanleyi
 FMNH232419_AgoroAguUG_stanleyi
 FMNHSS196_ImatongSS_stanleyi
 FMNHSS080_ImatongSS_stanleyi
 FMNH232417_AgoroAguUG_stanleyi
 FMNHSS271_ImatongSS_stanleyi
 FMNH215102_BuhangaRW_stanleyi
 KE20151786_MtKenyaKE_zena
 MN817464_ETH1346_simensis
 MN817465_ET_simensis
 MN817460_ET_simensis
 MN817462_ET_simensis
 MN817461_ET_simensis
 MN817463_ET_simensis
 FMNH155594_UdzungwaTZ_machangui
 FMNH204689_LivingstoneTZ_machangui
 MN817469_ET_simensis
 KE20150904_MtKenyaKE_zena
 MN817459_ET_chercherensis
 MN817458_ET_chercherensis
 MN817440_ET_chercherensis
 MN817439_ET_chercherensis
 MN817438_ET_chercherensis
 FMNH171400_MbiziTZ_sabuni
 KE20151017_MtKenyaKE_zena
 KE20150188_MtKenyaKE_zena
 KE20150001_MtKenyaKE_zena
 KE20151305_MtKenyaKE_zena
 KE20151603_MtKenyaKE_zena
 KE20151855_MtKenyaKE_zena
 KE20151117_MtKenyaKE_zena
 KE20151848_MtKenyaKE_zena
 KE20151161_MtKenyaKE_zena
 KE20151278_MtKenyaKE_zena
 KE20150861_MtKenyaKE_zena
 FMNH210704_ManyaraTZ_makundi
 FMNH210924_ManyaraTZ_makundi
 FMNH210698_ManyaraTZ_makundi
 FMNH210926_ManyaraTZ_makundi
 FMNH211161_NgorongoroTZ_makundi
 FMNH211172_NgorongoroTZ_makundi
 FMNH211169_NgorongoroTZ_makundi
 FMNH174239_KilimanjaroTZ_aquilus
 FMNH208098_MeruTZ_verhageni
 FMNH174237_KilimanjaroTZ_aquilus
 FMNH208485_MeruTZ_verhageni
 FMNH174242_KilimanjaroTZ_aquilus
 FMNH174244_KilimanjaroTZ_aquilus
 FMNH174225_KilimanjaroTZ_aquilus

Fig. S5 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.

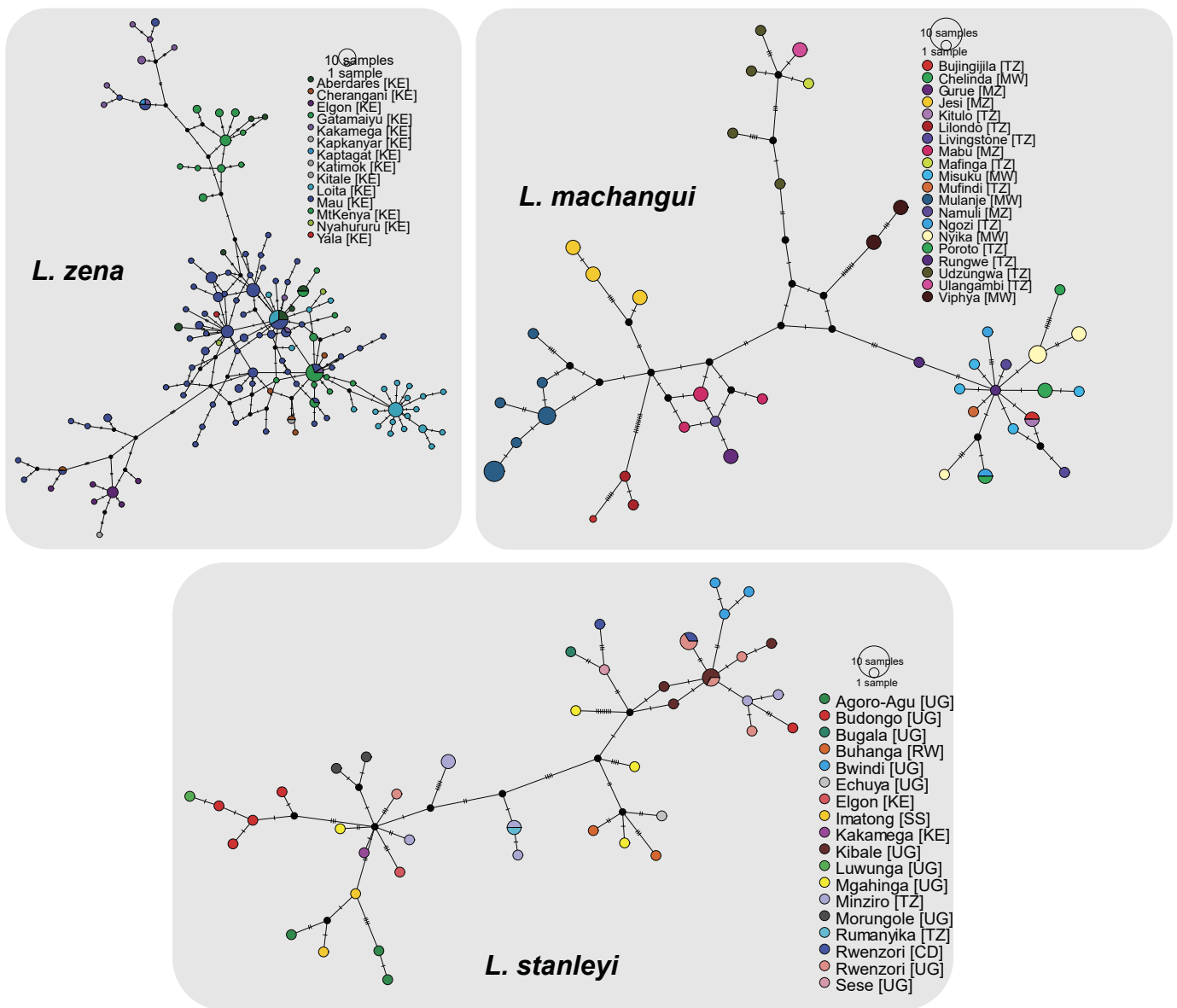


Fig. S6 Time calibrated maximum clade credibility tree of evolutionary relationships and divergence times of the non-Ethiopian *L. flavopunctatus* members reconstructed from concatenated alignments of *Cytochrome b* (*CYTB*), *cytochrome oxidase subunit 1*, and *Interphotoreceptor retinoid binding protein*, time-calibrated using most recent common ancestor ages. Branch labels show the posterior probability support values and node bars show the highest posterior density interval. The corresponding gene trees are also presented to illustrate the phylogenetic informativeness of the individual genes. Here it is apparent that only the *CYTB* topology offer a reliable outlook of the phylogenetic associations between the non-Ethiopian *L. flavopunctatus* members.

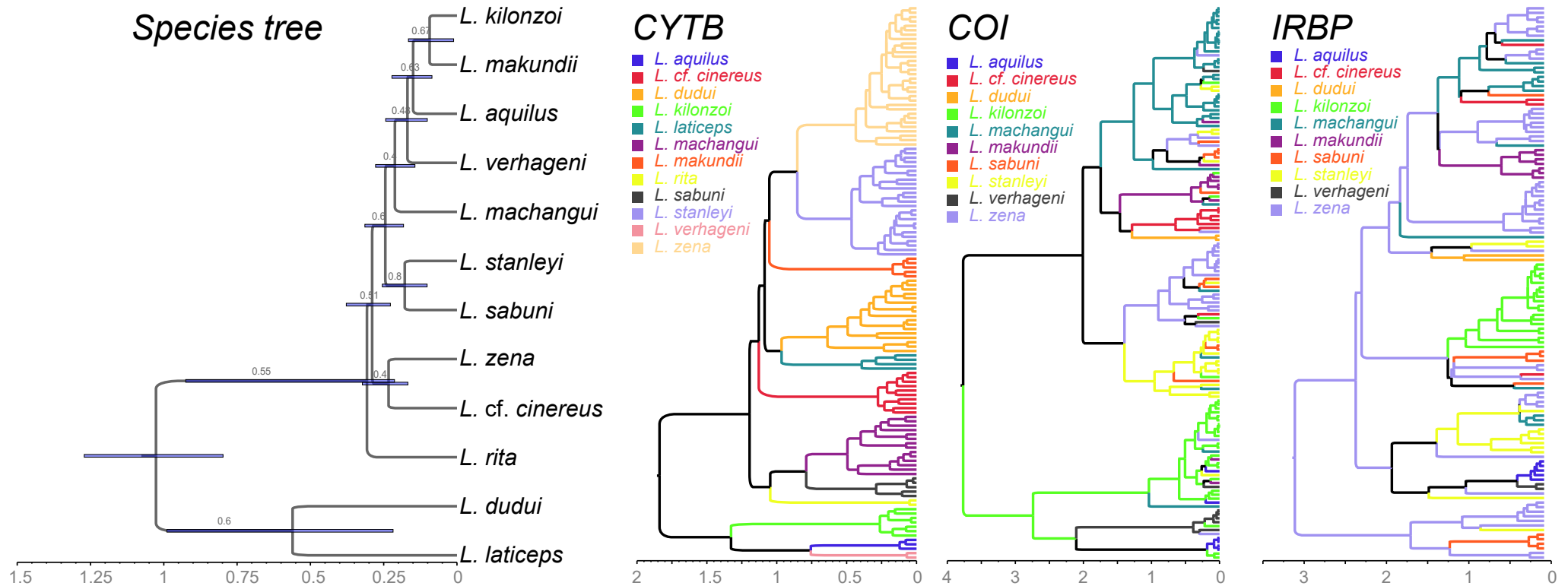
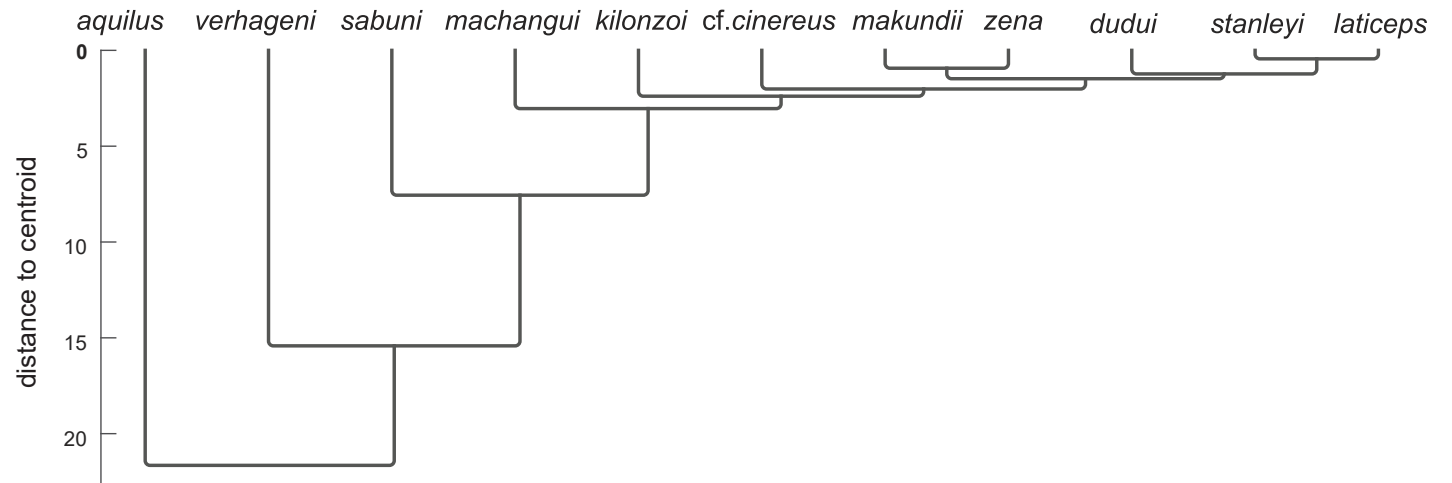


Fig. S7 Classification results following discriminant analysis in using linear and geometric craniodental datasets of the non-Ethiopian *L. flavopunctatus* members. Values indicate cross-validated (leave-one-out bootstrapping) percentage success by which samples were classified into a priori and predicted 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.

Dataset	Species	1	2	3	4	5	6	7	8	9	10	11	N
Linear	1 <i>L. aquilus</i>	92.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.7	0.0	13
	2 <i>L. cf. cinereus</i>	4.9	47.5	3.3	8.2	18.0	4.9	4.9	0.0	6.6	1.6	0.0	61
	3 <i>L. dudui</i>	0.0	13.8	55.2	3.4	17.2	0.0	0.0	0.0	6.9	0.0	3.4	29
	4 <i>L. kilonzoii</i>	1.4	12.2	2.7	35.1	14.9	12.2	4.1	0.0	9.5	2.7	5.4	74
	5 <i>L. laticeps</i>	0.0	23.1	3.8	11.5	38.5	3.8	0.0	3.8	15.4	0.0	0.0	26
	6 <i>L. machangui</i>	1.2	4.7	4.7	11.8	1.2	52.9	0.0	9.4	4.7	1.2	8.2	85
	7 <i>L. makundii</i>	0.0	3.3	0.0	0.0	0.0	0.0	83.3	0.0	6.7	0.0	6.7	30
	8 <i>L. sabuni</i>	0.0	0.0	0.0	9.1	0.0	9.1	0.0	77.3	0.0	0.0	4.5	22
	9 <i>L. stanleyi</i>	1.4	11.8	11.4	10.0	11.4	5.7	7.1	1.4	29.9	0.5	9.5	211
	10 <i>L. verhageni</i>	0.0	0.0	0.0	0.0	0.0	0.0	5.9	0.0	0.0	94.1	0.0	17
	11 <i>L. zena</i>	1.3	2.5	10.8	5.7	6.4	12.1	19.1	5.7	7.6	2.5	26.1	157
Geometric	1 <i>L. aquilus</i>	100	0	0	0	0	0	0	0	0	0	0	13
	2 <i>L. cf. cinereus</i>	0	52.6	8.8	1.8	7	5.3	5.3	0	17.5	0	1.8	57
	3 <i>L. dudui</i>	0	20.7	55.2	0	6.9	0	0	3.4	13.8	0	0	29
	4 <i>L. kilonzoii</i>	0	1.5	1.5	74.6	0	1.5	1.5	0	10.4	1.5	7.5	67
	5 <i>L. laticeps</i>	0	14.3	9.5	4.8	42.9	0	0	4.8	14.3	0	9.5	21
	6 <i>L. machangui</i>	2.5	0	2.5	5.1	0	75.9	1.3	6.3	2.5	1.3	2.5	79
	7 <i>L. makundii</i>	0	0	3.6	3.6	0	0	82.1	0	0	0	10.7	28
	8 <i>L. sabuni</i>	0	0	0	21.1	0	21.1	0	47.4	0	0	10.5	19
	9 <i>L. stanleyi</i>	0	12.1	5.5	8.5	8	3.5	3	0.5	48.7	0.5	9.5	199
	10 <i>L. verhageni</i>	0	6.7	0	0	0	0	0	6.7	0	80	6.7	15
	11 <i>L. zena</i>	2.8	1.9	1.9	6.5	5.6	5.6	7.5	3.7	6.5	4.7	53.3	107



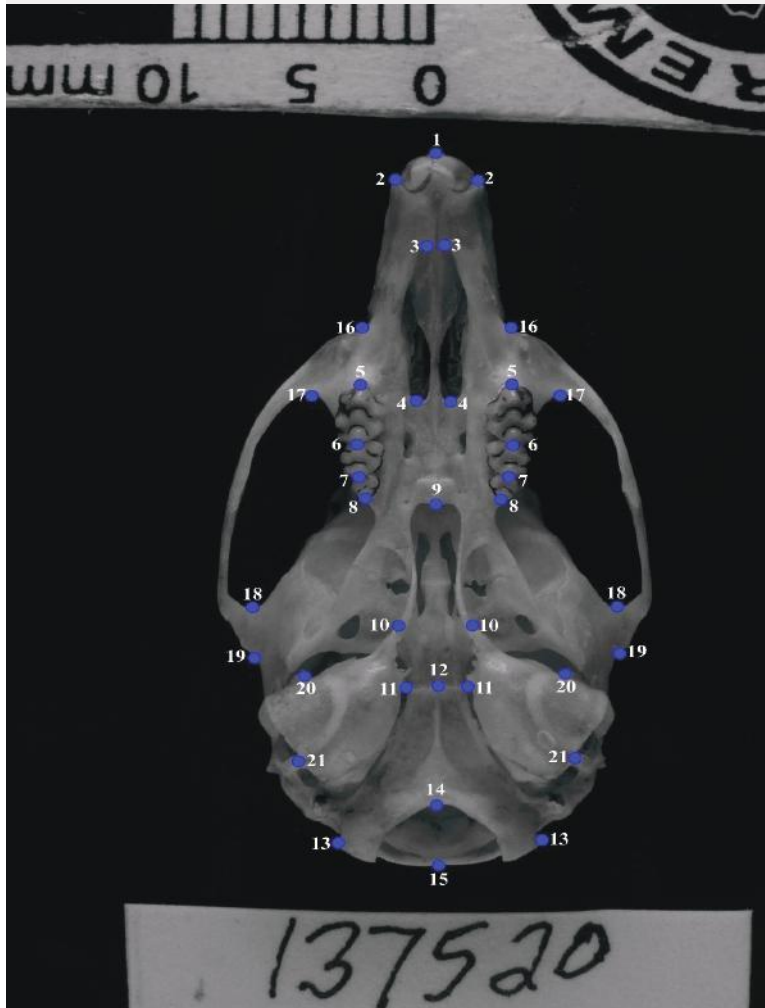


Fig. S8 Cranial landmarks used in geometric morphometric analyses of the non-Ethiopian *L. flavopunctatus* members. 1, Anteriormost point between upper incisors; 2, Superiormost point of upper incisive alveolus; 3, Anterior most margin of the incisive foramen; 4, Posteriormost margin of incisive foramen; ; 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. S9 Principal component analysis (PCA) of linear measurements used in the study. The plots show how samples cluster based on the first and second component scores. The top left scatter plot shows samples do not cluster in a distinct pattern consistent with the taxonomic units currently acknowledged in literature (top right). The bottom left plot shows the variances accounted for by all the component loadings.

