

SUPPORTING INFORMATION

Table S1. Quantitative and qualitative variables used for morphological comparisons

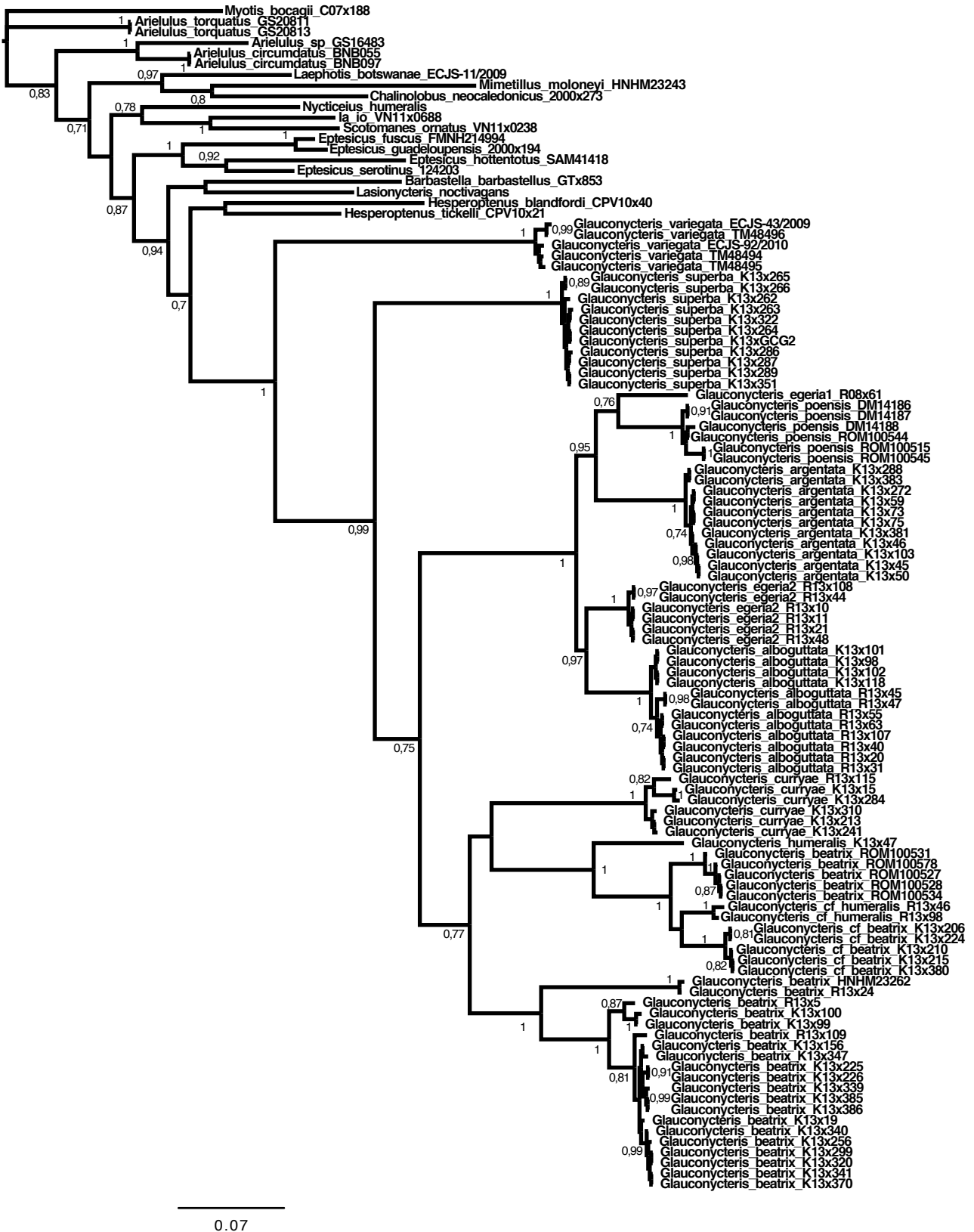
		M ₂ -M ₃ -C ₁ -C ₂			C-M ₃		C-M ₂	M ¹ -M ²	C ¹ -C ²																																
ID	sex	statut	species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	q1	q2	q3	q4	q5	q6	q7	q8	q9	q10	q11	
MNHN 2016-2772	M	Adult	<i>alboguttata</i>	4.46	2.67	4.557	4.19	6.47	4.83	8.96	7.64	12.87	9.67	7.73	4.53	8.62	7.58	2.53	38.1	18.7	41.6	46.5	4.5	36.7	38.7	15.2	25	36.3	33.9	q1-A	q2-A	q3-C	q4-A	q5-A	q6-A	q7-A	q8-A	q9-A	q10-A	q11-B	
MNHN 2016-2773	F	Lactating	<i>alboguttata</i>	4.57	2.78	4.509	4.42	6.7	4.79	8.94	7.62	12.2	9.11	7.66	4.4	8.5	7.53	2.82	40.8	18.8	41.5	51.3	5.2	37.2	39.1	14.55	25	37.4	35.4	q1-A	q2-A	q3-C	q4-A	q5-A	q6-A	q7-A	q8-A	q9-A	q10-A	q11-B	
MNHN 2016-2774	F	Lactating	<i>alboguttata</i>	4.5	2.86	4.642	4.44	6.61	5.01	9.24	7.87	13.3	9.8	8.04	4.84	8.78	7.47	2.78	39.2	18.7	42.5	49.2	5.9	38.2	39.4	14.9	25	37.8	35.1	q1-A	q2-A	q3-C	q4-A	q5-A	q6-A	q7-A	q8-A	q9-A	q10-A	q11-C	
MNHN 2016-2775	M	Adult	<i>alboguttata</i>	4.45	2.87	4.437	4.38	6.2	4.84	9.13	7.5	13.02	9.79	7.65	4.7	8.55	7.48	2.56	39.5	18.3	42.1	52.2	5.8	36.2	38.4	14.58	24	36.7	33.1	q1-A	q2-A	q3-C	q4-A	q5-A	q6-A	q7-A	q8-A	q9-A	q10-A	q11-B	
FMNH 151198	M	Adult	<i>argentata</i>	4.24	2.58	4.85	4.18	6.12	4.39	8.68	7.51	12.67	9.29	7.6	4.75	8.47	7.4	2.64	43	19.3	36.8	57	6.12	41.6	41.6	15.9	26	40.6	37.5	q1-A	q2-B	q3-C	q4-B	q5-B	q6-A	q7-B	q8-A	q9-B	q10-A	q11-C	
MNHN 2016-2776	M	Adult	<i>argentata</i>	3.99	2.58	4.091	4.06	5.86	4.19	8.1	7.06	12.13	8.96	7.75	4.77	8.07	7.21	2.52	39.4	18.3	40.7	46	4.9	40	41.2	13.8	25	37.5	35.5	q1-B	q2-B	q3-C	q4-B	q5-B	q6-A	q7-A	q8-A	q9-B	q10-A	q11-C	
MNHN 2016-2777	M	Adult	<i>argentata</i>	4.07	2.69	4.167	3.9	6.07	4.31	8.4	6.99	12.23	8.85	7.71	4.8	7.96	7.66	2.45	40.5	19.3	39.6	47.6	5.6	40	41.5	15.5	21.7	39.2	35.6	q1-B	q2-B	q3-C	q4-B	q5-B	q6-A	q7-A	q8-A	q9-B	q10-A	q11-C	
MNHN 2016-2778	M	Adult	<i>argentata</i>	4.42	2.49	4.306	4	6.13	4.18	7.89	6.89	11.76	9	7.51	4.69	7.84	7	2.59	39.6	18	40.2	48.5	4.5	38.6	39.4	14.3	26	37.3	33.5	q1-B	q2-B	q3-C	q4-B	q5-B	q6-A	q7-A	q8-A	q9-B	q10-A	q11-C	
MNHN 2016-2779	F	Lactating	<i>argentata</i>	3.88	2.54	4.151	4.09	6.02	4.56	8.43	6.3	12.24	9.3	8.03	4.75	8.22	7.46	2.41	41.6	18.8	45.1	51.5	5	39.9	41.2	14.7	27	39.1	36.1	q1-B	q2-B	q3-C	q4-B	q5-B	q6-A	q7-A	q8-A	q9-B	q10-A	q11-C	
MNHN 2016-2780	F	Nulliparous	<i>argentata</i>	3.82	2.57	4.045	3.97	6.23	4.13	8.37	6.61	12.07	8.86	7.46	4.61	7.86	7.14	2.43	40.7	18.5	41.5	48.8	4.6	39	41.4	14.6	27.1	38.1	35.2	q1-B	q2-B	q3-C	q4-B	q5-B	q6-A	q7-A	q8-A	q9-B	q10-A	q11-C	
MNHN 2016-2790	M	Adult	<i>atra sp. nov.</i>	4.06	2.49	4.276	4.21	5.86	4.7	8.44	7.33	12.11	9.1	7.19	4.45	7.92	7.3	2.43	36.8	17.4	40.8	50.7	4.1	36	37.2	13	20	35.2	32.5	q1-A	q2-A	q3-C	q4-A	q5-B	q6-C	q7-A	q8-A	q9-B	q10-A	q11-B	
MNHN 2016-2791	M	Adult	<i>atra sp. nov.</i>	4.04	2.46	4.09	4.15	5.72	4.16	8.12	7.09	12.22	9.2	7.5	4.67	7.97	7.5	2.32	34.5	16.3	39.43	45.6	4.3	33.8	35.2	12.6	21.6	30.4	31.1	q1-A	q2-A	q3-C	q4-A	q5-B	q6-C	q7-A	q8-C	q9-C	q10-A	q11-B	
MNHN 2016-2792	F	Lactating	<i>atra sp. nov.</i>	4.05	2.54	4.17	4.45	5.87	4.35	8.63	7.31	12.63	9.34	7.49	4.61	8.15	7.66	2.56	37.8	17.9	42.6	55.8	4.4	37.3	38.8	13.8	23	36.5	34.2	q1-A	q2-A	q3-C	q4-A	q5-B	q6-C	q7-A	q8-C	q9-C	q10-A	q11-B	
MNHN 2016-2793	F	Lactating	<i>atra sp. nov.</i>	4.05	2.49	4.407	4.17	5.78	4.32	8.49	7.44	12.16	9.13	7.49	4.64	8	7.51	2.29	36.1	17.8	41.9	50.9	3.9	35.4	36.2	13	22	34.9	32.8	q1-A	q2-A	q3-C	q4-A	q5-B	q6-C	q7-A	q8-C	q9-C	q10-A	q11-B	
MNHN 2016-2794	F	Lactating	<i>atra sp. nov.</i>	4.26	2.54	4.354	4.18	5.75	4.09	8.28	7.21	12.13	9.38	7.54	4.53	8.15	7.38	2.35	36.6	17.2	41.9	48	5	34.5	37.2	13	22.5	35	32.5	q1-A	q2-A	q3-C	q4-A	q5-B	q6-C	q7-A	q8-C	q9-C	q10-A	q11-B	
HNHM 23262	F	Adult	<i>beatric</i>	3.78	2.25	3.958	3.91	5.18	3.99	8.02	6.57	11.18	8.36	7.47	4.27	7.56	6.37	2.27	39.02	20.1	45.76	39.45	4.8	35.95	36.98	14.45	24.94	33.67	33.5	q1-A	q2-E	q3-C	q4-B	q5-B	q6-C	q7-A	q8-B	q9-A	q10-A	q11-B	
MNHN 2016-2781	F	Lactating	<i>beatric</i>	3.63	2.31	4.08	3.95	5.41	3.69	8.01	6.18	11.19	8.24	7.34	4.6	7.66	6.59	2.39	39.5	20.1	51.3	44.7	3.7	38.7	40.4	13.6	23.2	39.6	37.4	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-B	
MNHN 2016-2782	M	Adult	<i>beatric</i>	3.51	2.21	4.039	3.97	5.31	3.73	7.82	6.21	11.22	8.18	6.67	4.47	7.33	6.43	2.2	36.4	17.9	43.3	39	4	34.4	37.1	12.8	23.8	34.3	33	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-C	
MNHN 2016-2783	M	Adult	<i>beatric</i>	3.68	2.37	3.922	3.84	5.33	3.37	7.85	6.04	11.17	8.08	6.93	4.25	7.37	6.52	2.28	33.6	17.4	40.8	40	3.6	32.7	34.7	12.14	23.5	32.8	31.2	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-B	
MNHN 2016-2784	M	Juvenile	<i>beatric</i>	3.3	2.28	3.965	3.82	5.11	3.56	7.72	6.09	11.02	8.13	7.25	4.52	7.57	6.78	2.31	36.2	18.1	40.5	39	3.3	36.8	37	12.5	21.7	35.3	33.6	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-B	
MNHN 2016-2785	M	Juvenile	<i>beatric</i>	3.4	2.02	3.929	3.72	5.23	3.24	7.69	6.05	11.15	8.01	7.23	4.49	7.36	6.25	2.39	36.3	18.8	44.8	39.9	4.8	35.5	37	12.9	21.7	34.6	33	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-C	
MNHN 2016-2786	F	Lactating	<i>beatric</i>	3.79	2.36	4.121	3.91	5.66	3.78	8	6.5	11.47	8.41	6.9	4.33	7.66	6.42	2.45	36.9	18.8	47.2	45	4.5	37.7	39.7	12.8	22.8	37.2	35.1	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-B	
MNHN 2016-2787	M	Adult	<i>beatric</i>	3.54	2.02	3.747	3.74	5.28	3.58	7.92	6.2	11.12	7.89	7.05	4.25	7.44	6.45	2.23	36.1	18.4	40.1	41.4	3.3	34.4	36.5	13.11	23.2	35.1	33.7	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-C	
MNHN 2016-2788	M	Adult	<i>beatric</i>	3.34	2.14	3.87	3.68	4.92	3.49	7.63	6.01	11.44	8.16	7.2	4.41	7.48	6.6	2.31	36.6	19.1	45.7	39.2	4	36.5	37.5	13.16	24	35.6	34.5	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-C	
MNHN 2016-2789	M	Adult	<i>beatric</i>	3.45	2.13	3.566	3.69	5.08	3.41	7.47	6.15	11.04	8	6.78	4.28	7.21	6.35	2.1	36.9	19.6	39.9	40.9	4.1	35.9	36.1	13.85	22	34.1	32.4	q1-A	q2-E	q3-C	q4-B	q5-C	q6-C	q7-A	q8-B	q9-A	q10-A	q11-B	
ROM 100531	M	Adult	<i>cf. beatric</i>	4.2	2.35	4.43	4.09	5.53	3.83	7.72	7.45	11.56	8.2	7.02	4.32	7.38	6.7	2.45	34	16.48	39.55	42.7	4.8	38.2	32.23	34.6	12.2	22.13	32.3	30.57	q1-A	q2-C	q3-C	q4-A	q5-C	q6-C	q7-A	q8-A	q9-A	q10-A	q11-A
ROM 100534	F	Adult	<i>cf. beatric</i>	3.79	2.3	4.42	4.01	5.42	4.03	7.93	6.8	11.77	8.26	6.73	4.27	7.25	6.31	2.15	35	17.54	40	44	4.8	34.07	34.05	12.06	21.5	32.95	30.8	q1-A	q2-A	q3-C	q4-A	q5-C	q6-C	q7-A	q8-A	q9-A	q10-A	q11-A	
ROM 100578	M	Adult	<i>cf. beatric</i>	4.11	2.42	4.47	4.18	5.43	4.05	7.94	7.2	11.79	8.3	6.86	4.3	7.46	6.85	2.4	35	16.57	39.8	43	4.92	34.12	34.69	12.3	21.4	32.11	30.4	q1-A	q2-C	q3-C	q4-A	q5-C	q6-C	q7-A	q8-A	q9-A	q10-A	q11-A	
MNHN 2016-2795	F	Lactating	<i>curryae</i>	4.2	2.39	4.299	4.15	5.69	3.9	8.24	6.7	12.41	9.03	7.04	4.19	7.77	6.56	2.53	36.5	16	44.3	42.1	5.6	38	39.9	14.3	23.4	38.9	35.1	q1-A	q2-D	q3-C	q4-A	q5-B	q6-C	q7-A	q8-D	q9-B	q10-A	q11-A	
MNHN 2016-2796	F	Lactating	<i>curryae</i>	3.8	2.31	4.096	4.06	5.56	3.71	8.4	6.83	12.18	9.02	6.87	3.98	7.73	6.39	2.51	36.8	17.4	37.3	42.4	4.1	36.5	38.9	15.2	21.3	36.2	34.3	q1-A	q2-D	q3-C	q4-A	q5-B	q6-C	q7-A	q8-D	q9-B	q10-A	q11-A	
MNHN 2016-2797	F	Lactating	<i>curryae</i>	3.82	2.41	4.119	3.96	5.47	3.66	8.04	6.65	11.85	8.77	7.2	3.85	7.79	6.13	2.56	35	16.1	39.5	39.6	5.3	34.6	36.2	13.5	22.8	34.3	33.2	q1-A	q2-D	q3-C	q4-A	q5-B	q6-C	q7-A	q8-D	q9-B	q10-A	q11-A	
MNHN 2016-2798	F	Lactating	<i>curryae</i>	3.67	2.18	4.563	4.16	5.67	3.68	8.09	6.5	11.8	8.87	6.87	4.19	7.73	6.22	2.2	36.1	16.8																					

Figure S1. Separate Bayesian analyses of the three mitochondrial genes

S1.1. Bayesian tree reconstructed with the alignment of 111 *COI* sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.

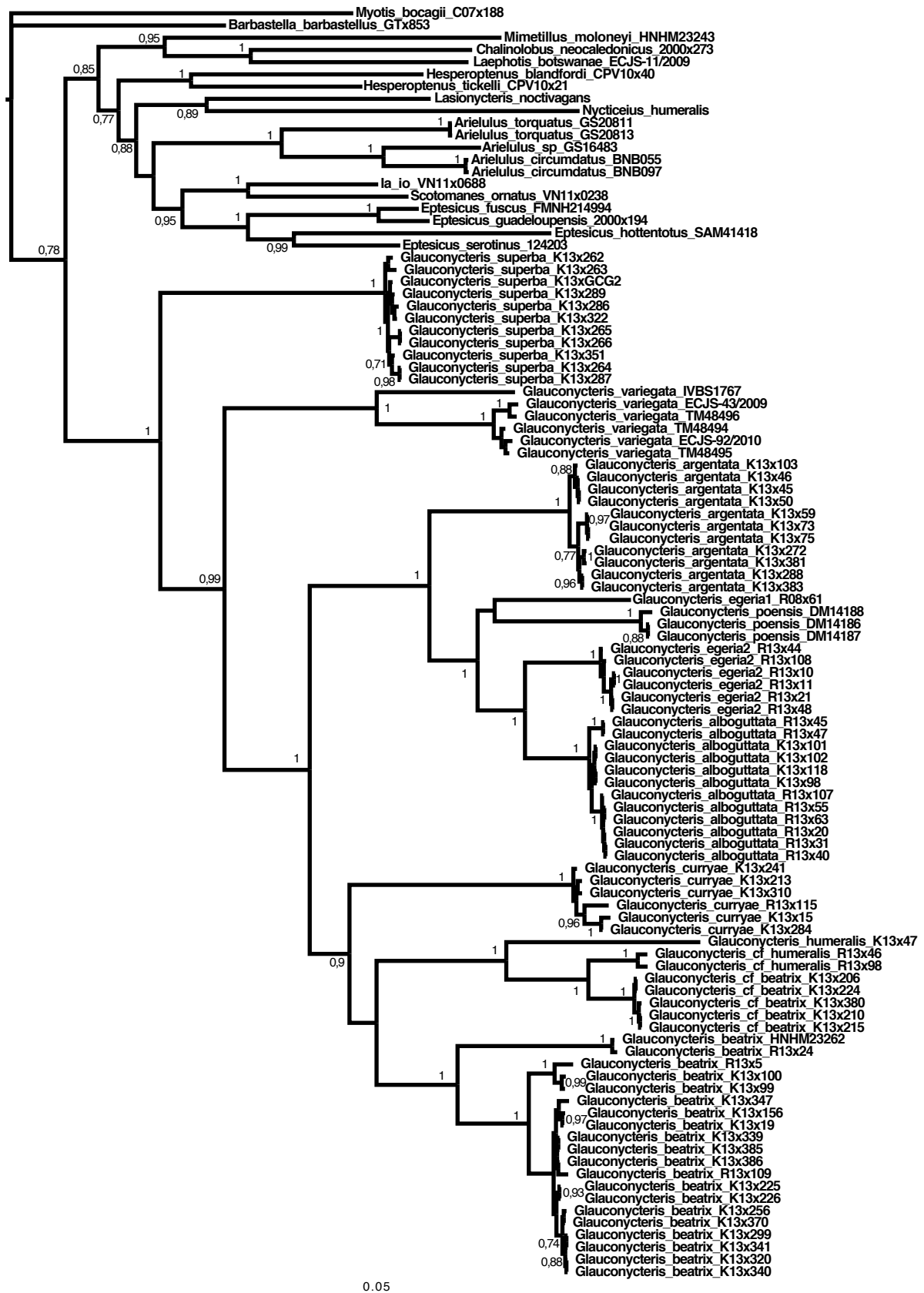
The length of all branches other than *Glaucocyteris* were divided by two.



S1.2. Bayesian tree reconstructed with the alignment of 104 Cytb sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.

The length of all branches other than *Glauconycteris* were divided by two.



S1.3. Bayesian tree reconstructed with the alignment of 103 *12S* sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.

The length of all branches other than *Glaucocycteris* were divided by two.

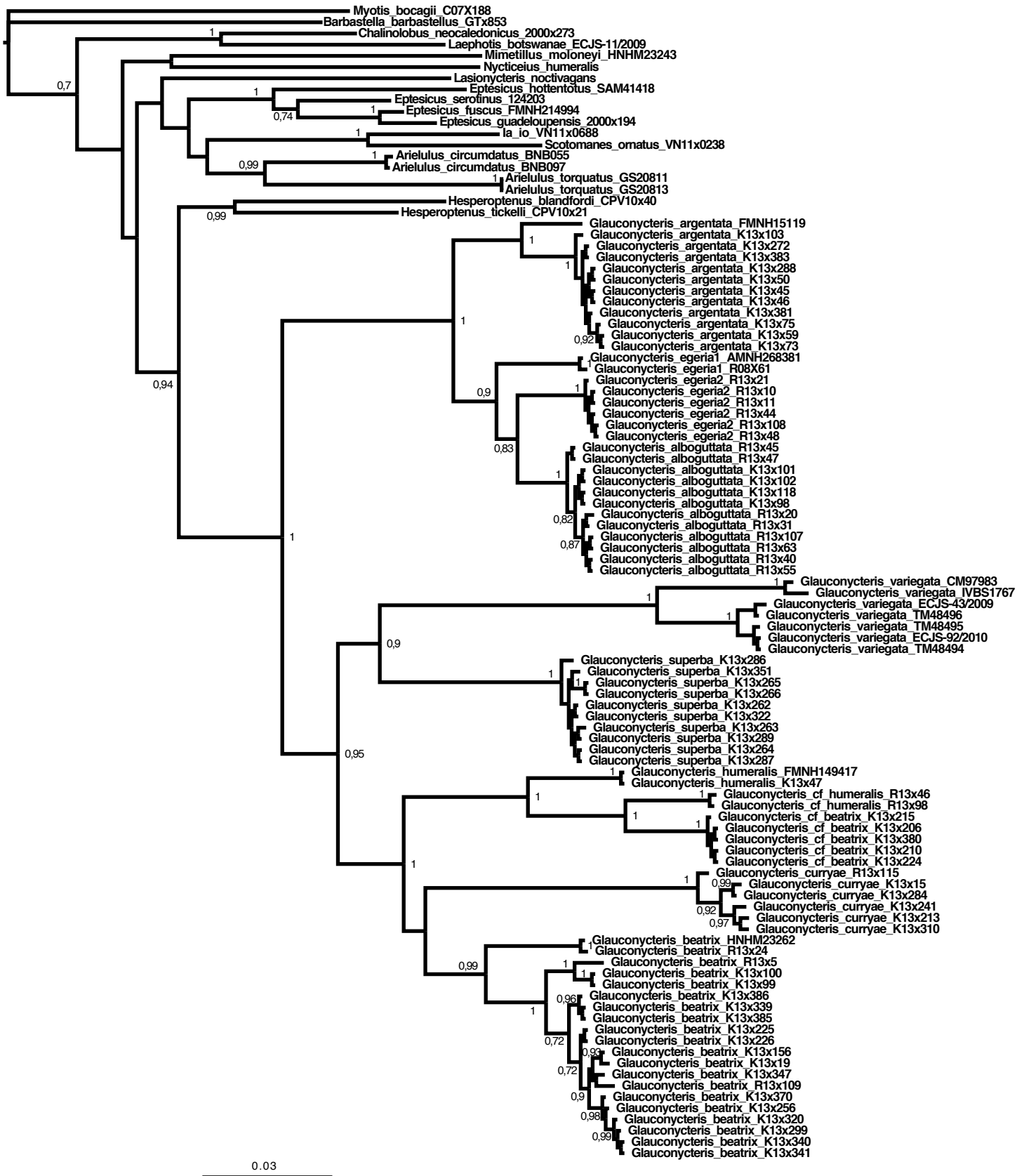
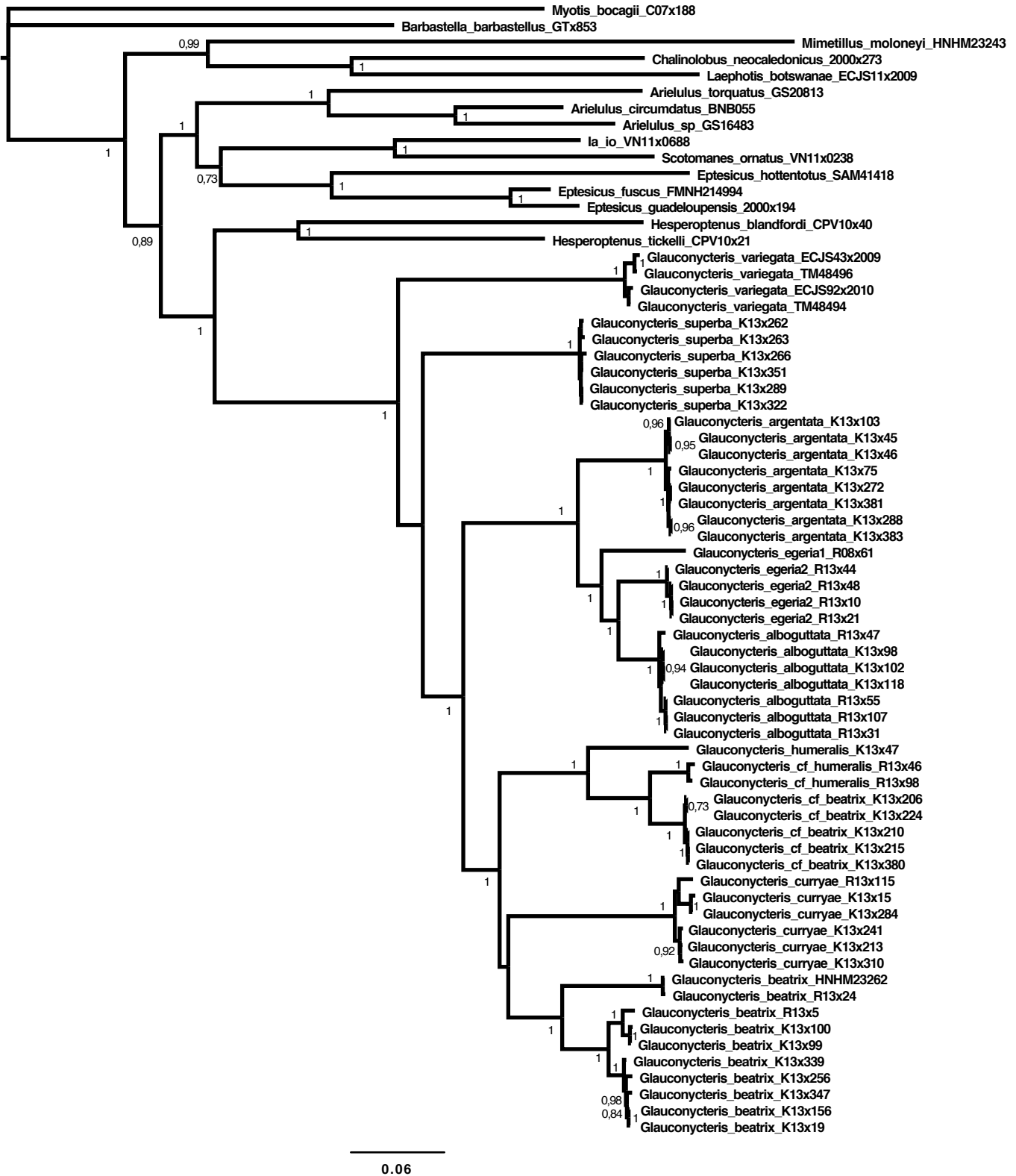


Figure S2. Separate Bayesian analyses of the five independent data sets based on 69 specimens.

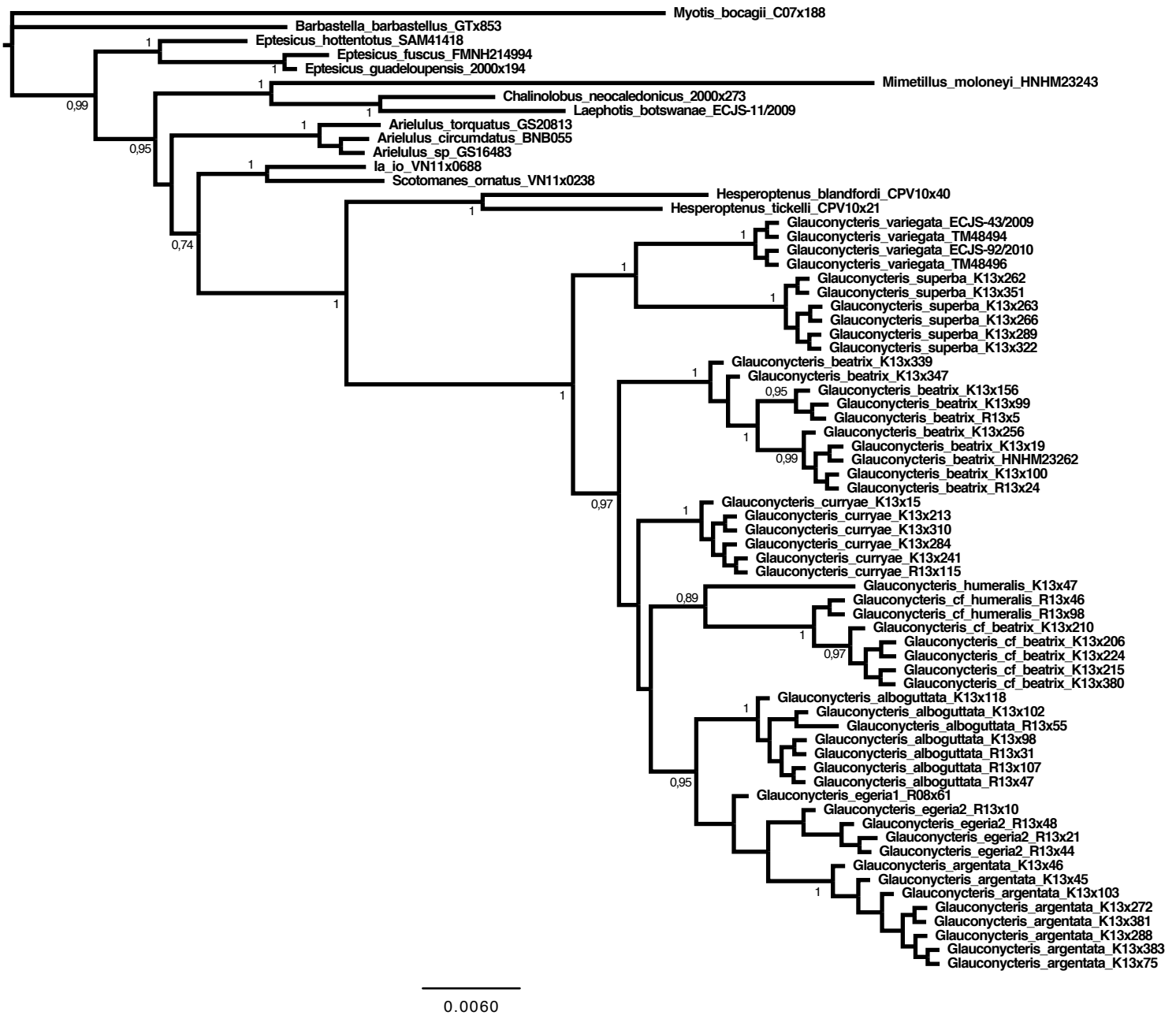
S2.1. Bayesian tree reconstructed with the concatenation of the three e mitochondrial genes

At the nodes, only posterior probabilities ≥ 0.7 were shown.



S2.2. Bayesian tree reconstructed with the alignment of *HDAC2* sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.



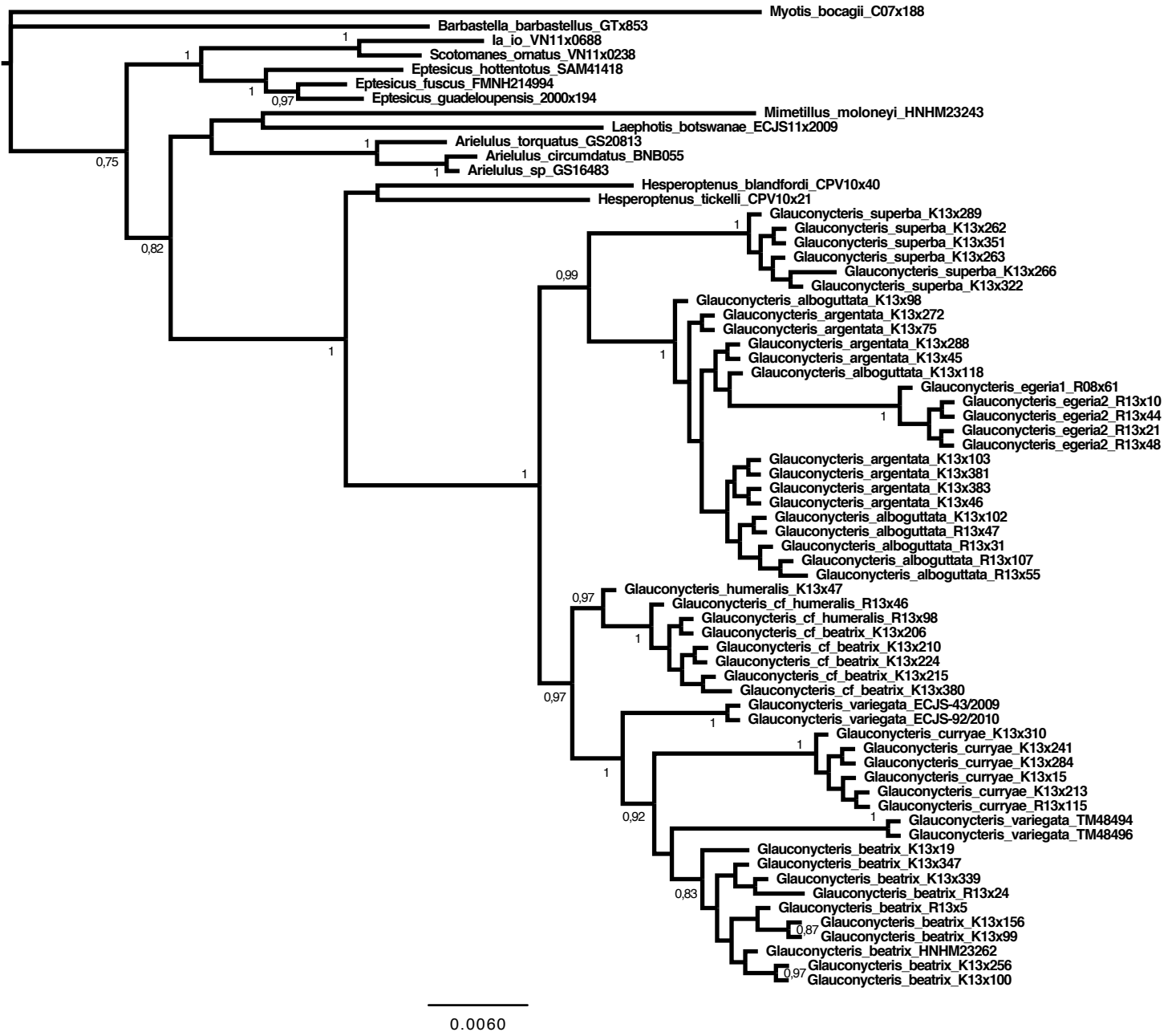
S2.3. Bayesian tree reconstructed with the alignment of RAG2 sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.



S2.4. Bayesian tree reconstructed with the alignment of *RIOK3* sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.



S2.5. Bayesian tree reconstructed with the alignment of *ZFYVE27* sequences

At the nodes, only posterior probabilities ≥ 0.7 were shown.

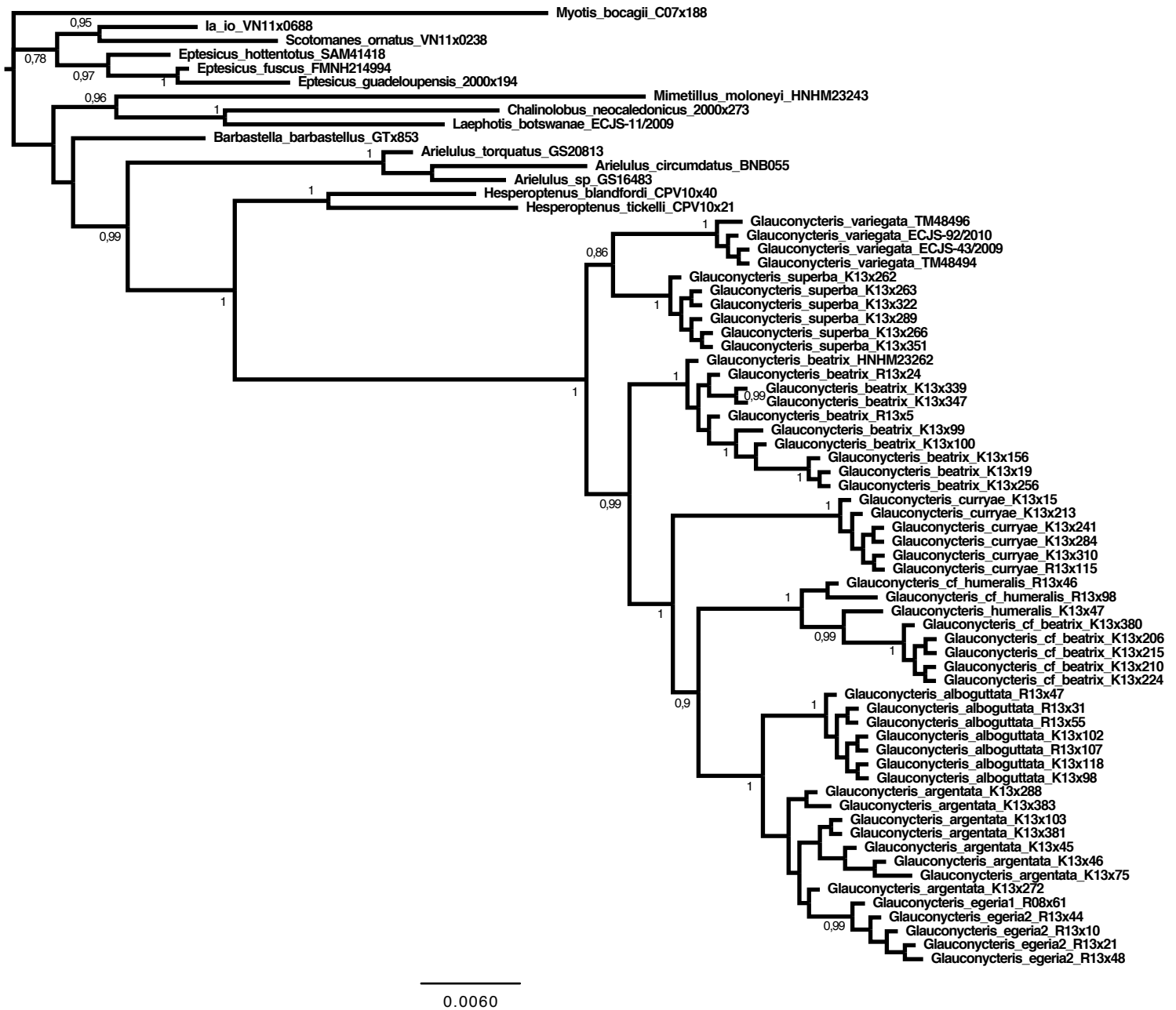


Figure S3. Sexual size dimorphism in species of *Glauconycteris*

The forearm lengths (FA in mm) were compared between females and males of all species of *Glauconycteris* caught in Central African Republic (CAR) and Democratic Republic of the Congo (DRC).

For each species and each sex, the number of individuals involved in the comparisons is indicated after the abbreviation used for females (F) and males (M).

The female of *G. humeralis* from Sukisa in DRC (MNHN 2016-2802) was compared to the females of the type series from Medje in DRC (Allen, 1917) and to the male FMNH 149417 from Epulu in DRC.

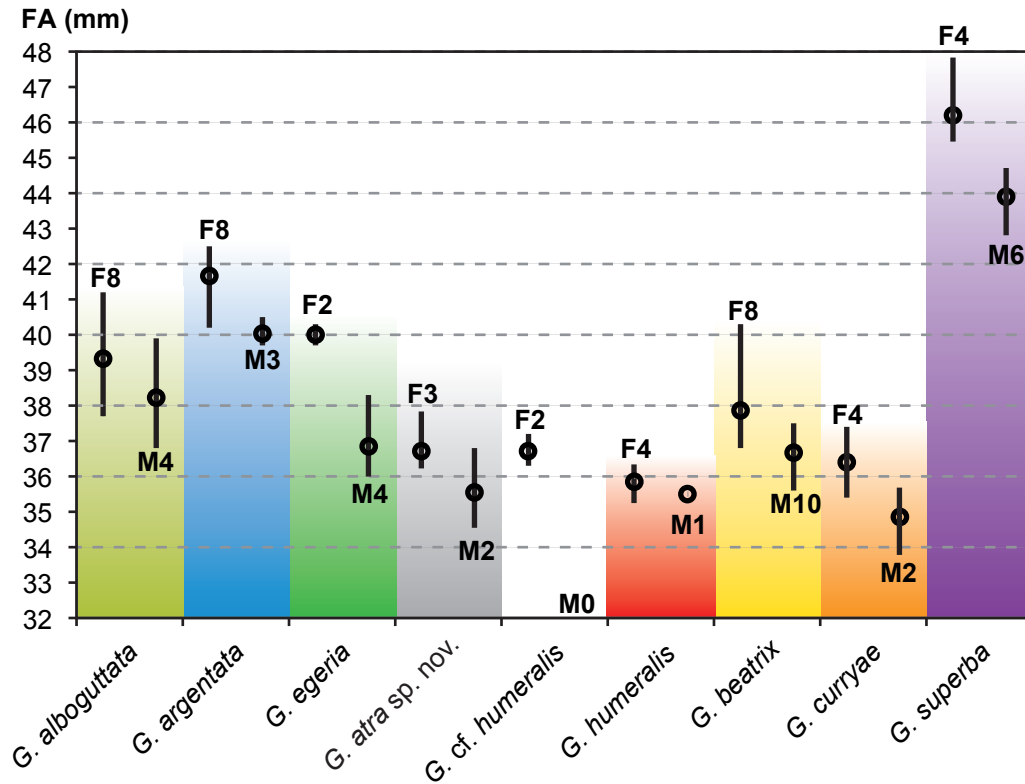


Figure S4. Bayesian tree reconstructed with the supermatrix combining all the seven genes (6,179 characters)
 At the nodes, only posterior probabilities ≥ 0.7 were shown.
 The length of all branches other than *Glauconycteris* were divided by two.

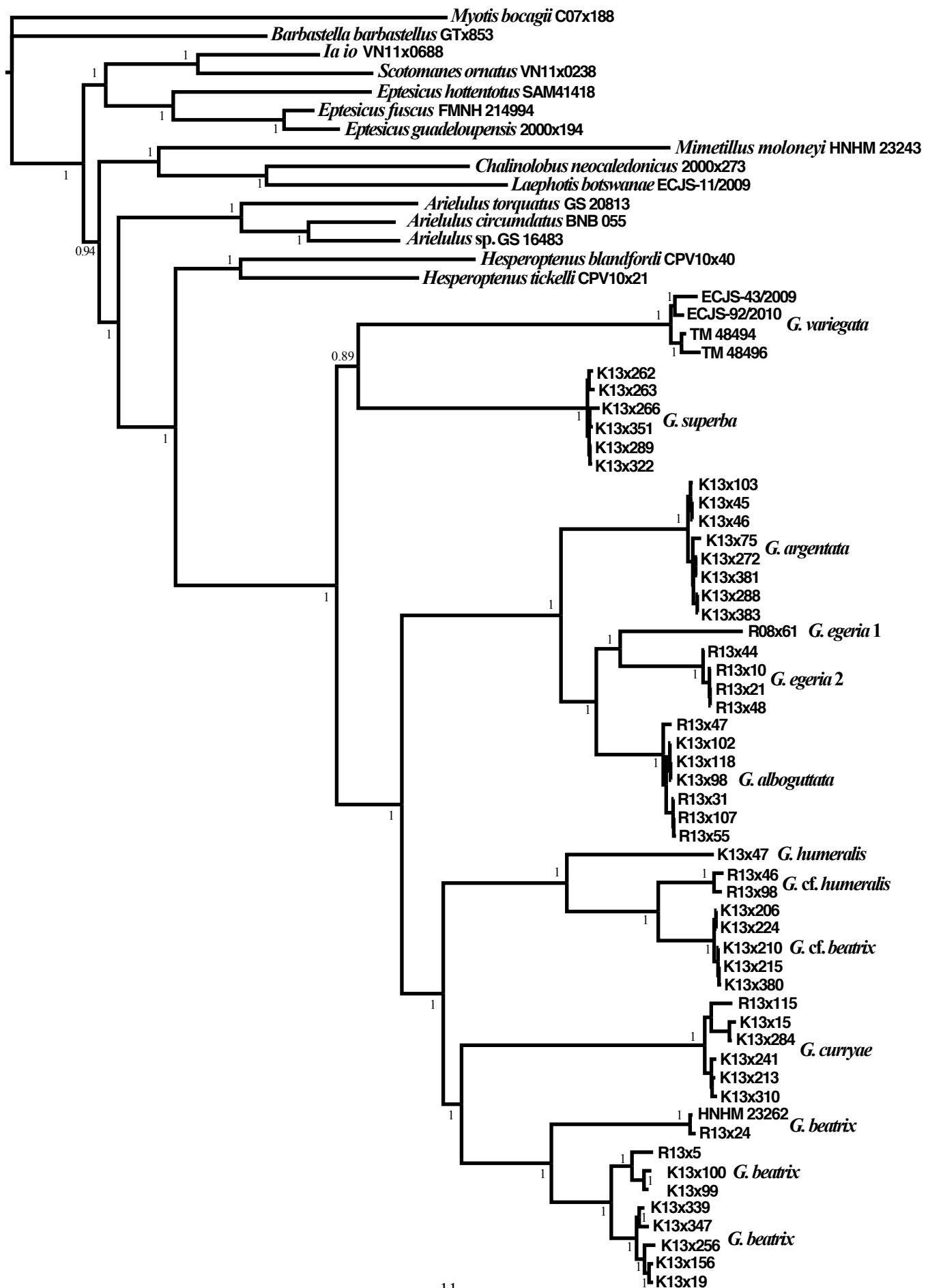


Figure S5.1. Chronogram estimated with the alignment of 126 RAG2 sequences (1017 characters)
 For better readability, the most deeper nodes are not shown.

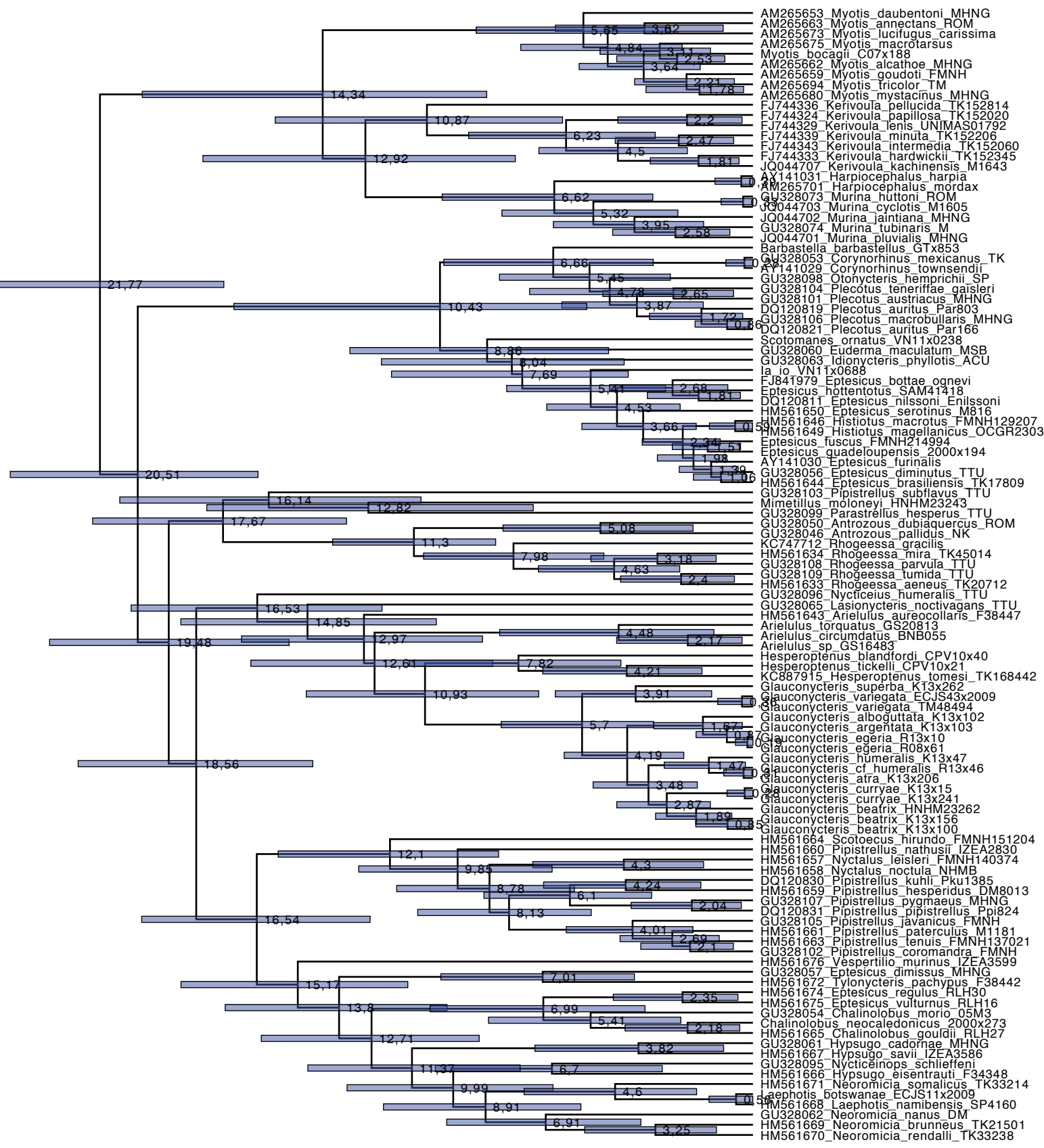


Figure S5.2. Chronogram estimated with the alignment of 77 cytochrome b sequences (1040 characters) and $R1 = 0.02 \pm 0.005$ per site per lineage per Myr.

For better readability, the most deeper nodes are not shown.

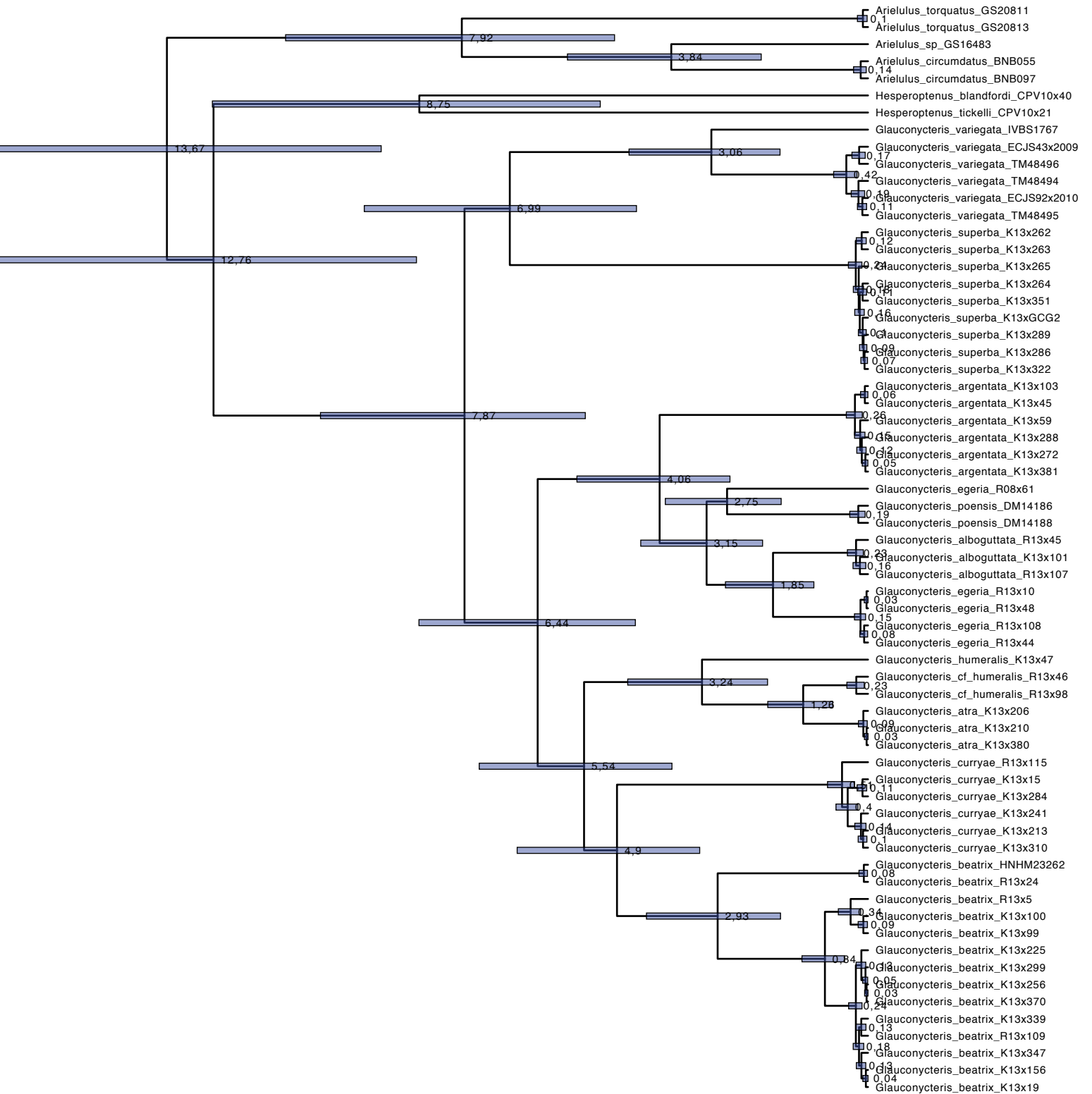


Figure S5.3. Chronogram estimated with the alignment of 77 cytochrome b sequences (1040 characters) and $R2 = 0.025 \pm 0.005$ per site per lineage per Myr.

For better readability, the most deeper nodes are not shown.

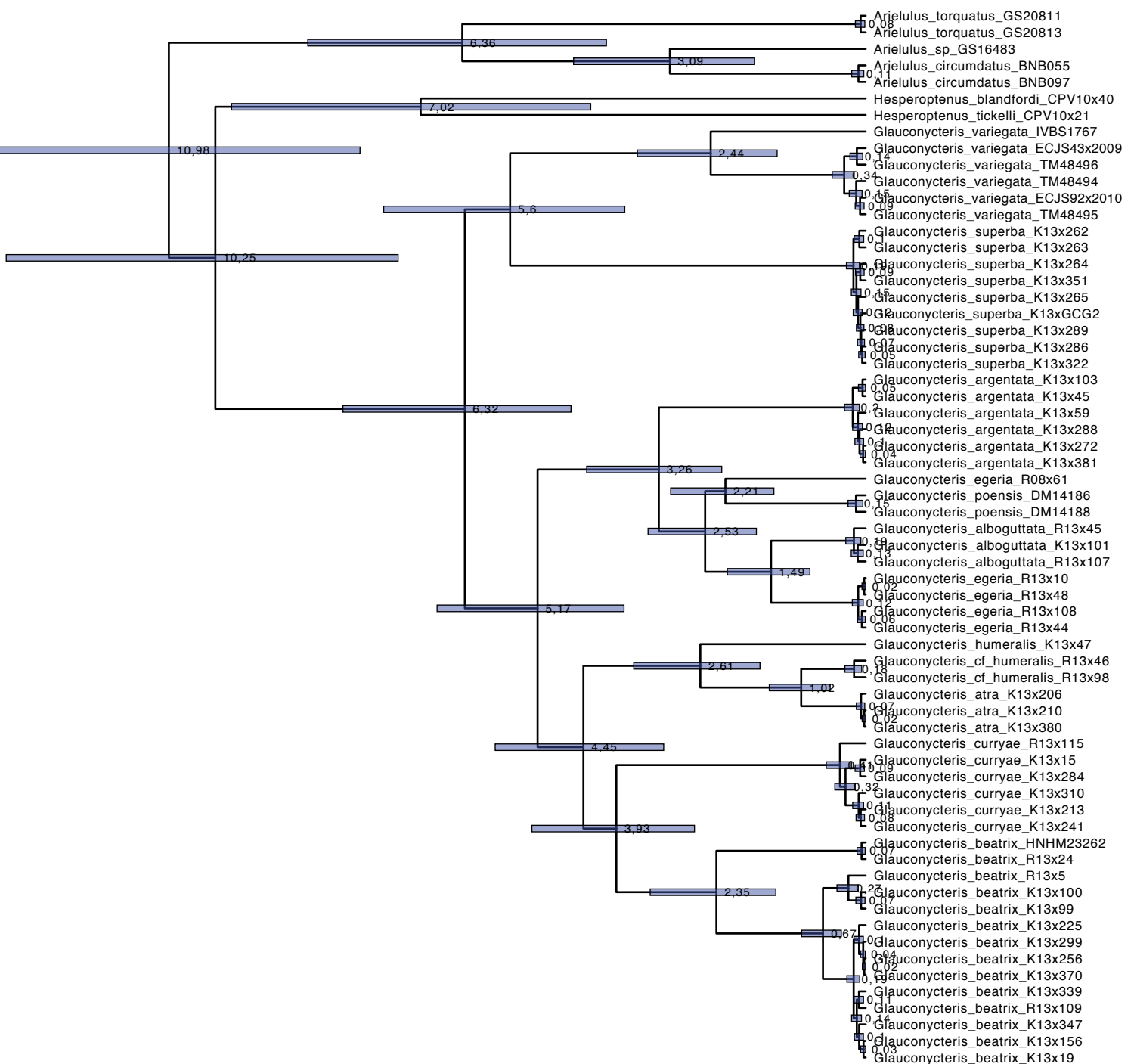
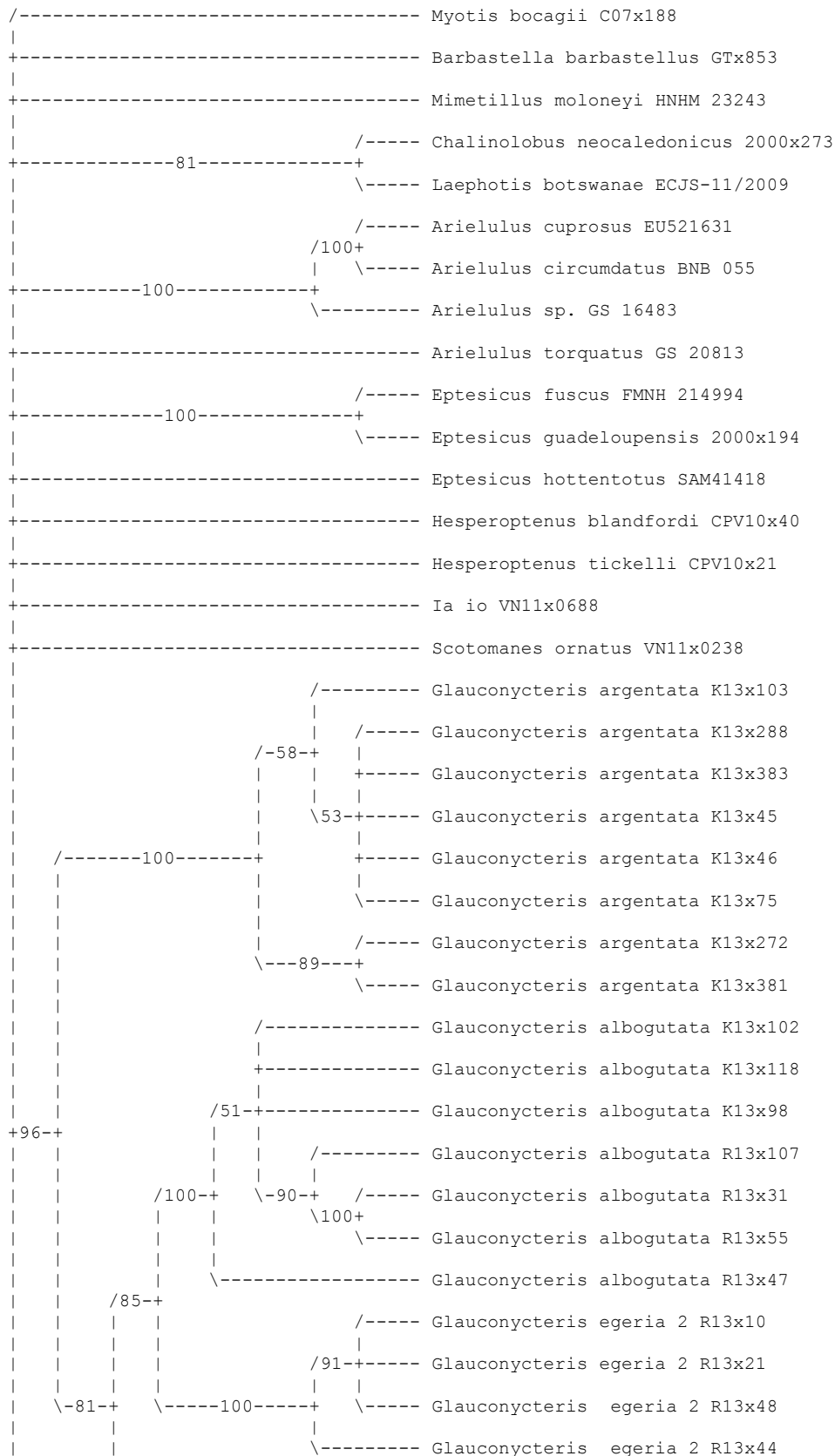


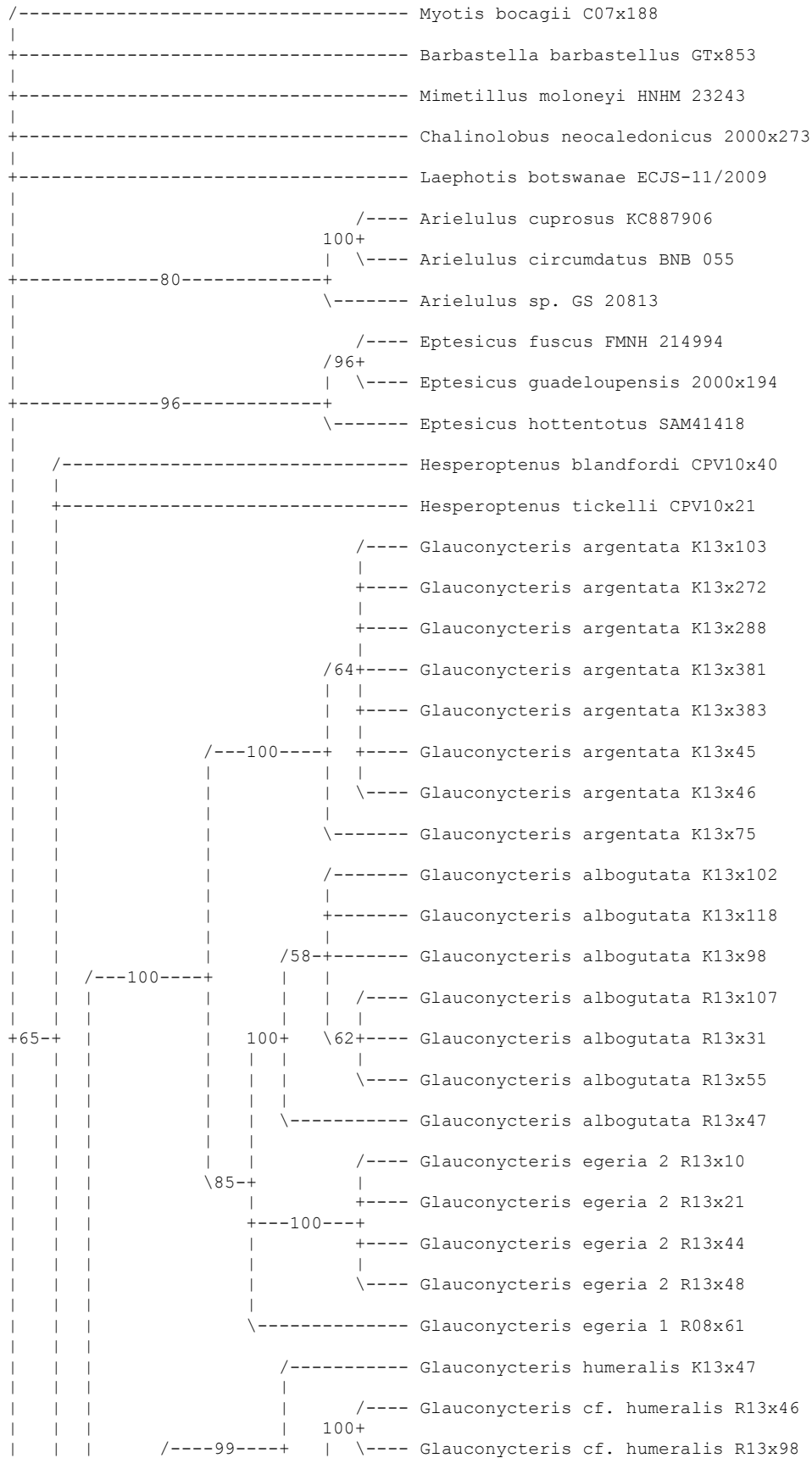
Figure S6. Phylogenetic position of *Arielulus cuprosus* based on *Cytb*, 12S and RAG2 alignments

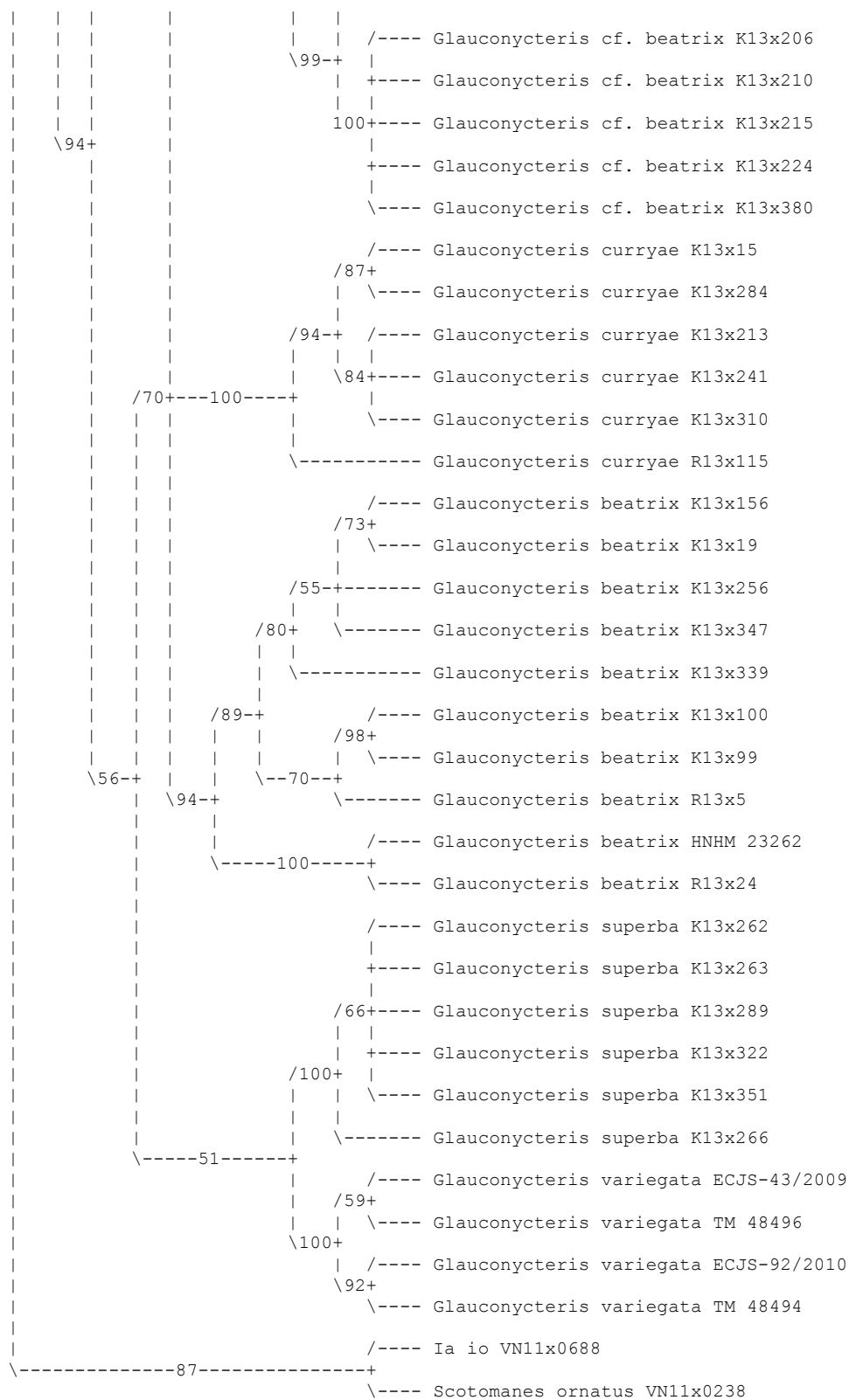
S6.1. Bootstrap 50% majority-rule consensus tree obtained from the Neighbour-Joining analysis of *Cytb* sequences





S6.2. Bootstrap 50% majority-rule consensus tree obtained from the Neighbour-Joining analysis of 12S sequences





S6.3. Bootstrap 50% majority-rule consensus tree obtained from the Neighbour-Joining analysis of RAG2 sequences

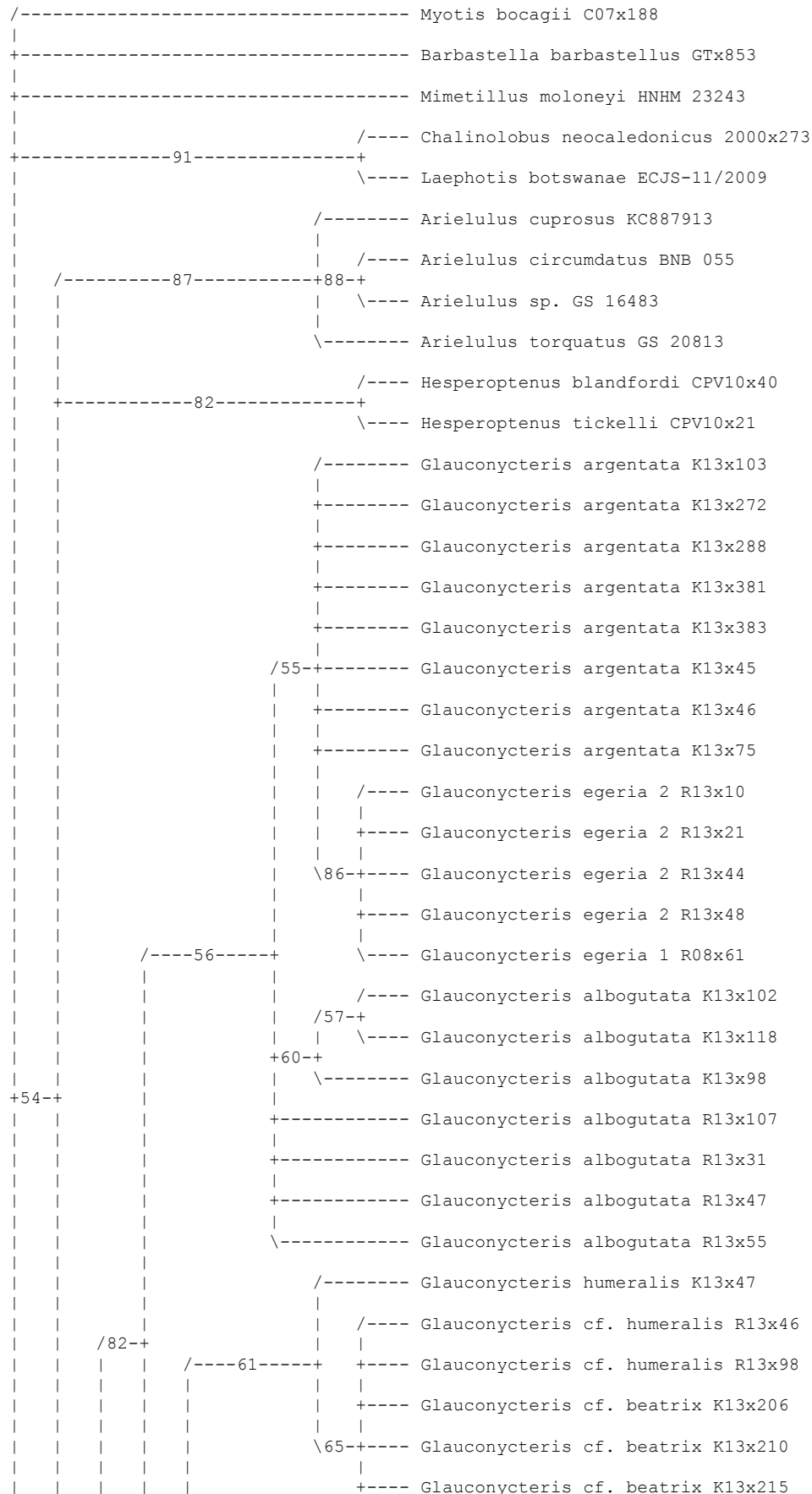


Figure S7. Map showing the geographic localities of *Glauconycteris* analysed in this study.

- 1: Niokolo-Koba NP (Senegal); 2: Mt Nimba (Liberia); 3: Mont Peko NP (Republic of Côte d'Ivoire);
4: Ifon (Nigeria); 5: Nki NP (Cameroon); 6: Dzanga-Sangha (CAR); 7: Mbaéré-Bodingué (CAR)
8: Melume (DRC); 9: Bongandjola (DRC); 10: Sukisa (DRC); 11: Yaengo-Yatolema (DRC); 12: Yoko (DRC);
13: Mbiye (DRC); 14: Epulu (DRC); 15: Western Province (Kenya); 16: Gonja FR (Tanzania);
17: Kafue NP (Zambia); 18: Chitabe (Botswana); 19: Kruger NP (South Africa).

