

Table S1. Sequencing results, including pre-target capture enrichment screening results and post-capture results. Endogenous content and enrichment factor estimated using mapping results from the whole mitochondrial genome reference sequence. Sequence data used in final analyses highlighted in green.

Species	Samples in final analysis	Pre-capture					Post-capture					Enrichment factor	% incr/ decr reads mapped
		Paired merged reads	Average coverage	Reads mapped	Reads mapped mtgenome	Estim. endogen. content	Paired merged reads	Average coverage	Reads mapped	Reads mapped mtgenome	Estim. endogen. content		
<i>G. thoracatus</i>	1	2,709,500	72.3 (mtgen) 0.17 (vwF) 0.34 (RAG1) 0.2 (RBP3) 0.39 (apoB) 0.38 (GHR)	16051 (mtgen) 5 (vwF) 7 (RAG1) 4 (RBP3) 9 (apoB) 8 (GHR)	12,927	0.477	5,405,344	63.14 (mtgen) 1.85 (vwF) 2.92 (RAG1) 1.31 (RBP3) 3.76 (apoB) 1.92 (GHR)	12927 (mtgen) 29 (vwF) 46 (RAG1) 23 (RBP3) 54 (apoB) 23 (GHR)	16,051	0.297	-61%	19%
<i>E. obliquus</i>	1	2,317,525	0.4 (mtgen) 0 (vwF) 0 (RAG1) 0 (RBP3) 0 (apoB) 0 (GHR)	6.18E-03 (mtgen) 0 (vwF) 0 (RAG1) 0 (RBP3) 0 (apoB) 0 (GHR)	6.18E-03	2.67E-07	4,426,535	0.45 (mtgen) 2.88 (vwF) 1.47 (RAG1) 2.9 (RBP3) 0.3 (apoB) 0.86 (GHR)	261 (mtgen) 146 (vwF) 71 (RAG1) 157 (RBP3) 16 (apoB) 31 (GHR)	261	0.006	100%	100%
		13,172,455	4.13 (mtgen) 2.07 (vwF) 1.41 (RAG1) 1.79 (RBP3) 0.59 (apoB) 1.07 (GHR)	3764 (mtgen) 132 (vwF) 845 (RAG1) 230 (RBP3) 378 (apoB) 490 (GHR)	3764	0.029	63,079,541	4.89 (mtgen) 20.71 (vwF) 14.15 (RAG1) 17.9 (RBP3) 5.91 (apoB) 10.72 (GHR)	4135 (mtgen) 1324 (vwF) 845 (RAG1) 1230 (RBP3) 378 (apoB) 490 (GHR)	4135	0.007	-336%	9%

Species	Samples in final analysis	Pre-capture					Post-capture					Enrichment factor	% incr/ decr reads mapped
		Paired merged reads	Average coverage	Reads mapped	Reads mapped mtgenome	Estim. endogen. content	Paired merged reads	Average coverage	Reads mapped	Reads mapped mtgenome	Estim. endogen. content		
<i>G. columbianus</i>	1	3,762,236	1.56 (mtgen) 6.67 (vwF) 3.27 (RAG1) 6.49 (RBP3) 0.86 (apoB) 0 (GHR)	1112 (mtgen) 447 (vwF) 186 (RAG1) 410 (RBP3) 57 (apoB) 0 (GHR)	1112	0.030	78,429,431	2.33 (mtgen) 6.95 (vwF) 5.03 (RAG1) 8.02 (RBP3) 0.82 (apoB) 3.87 (GHR)	3363 (mtgen) 396 (vwF) 281 (RAG1) 505 (RBP3) 51 (apoB) 160 (GHR)	3363	0.004	-589%	67%
		3,451,270	0.04 (mtgen) 0.69 (vwF) 0.10 (RAG1) 0.44 (RBP3) 0.16 (apoB) 0 (GHR)	23 (mtgen) 21 (vwF) 6 (RAG1) 26 (RBP3) 4 (apoB) 0 (GHR)	23	0.001	40,120,287	0.07 (mtgen) 0.37 (vwF) 0.11 (RAG1) 0.02 (RBP3) 0.39 (apoB) 0.08 (GHR)	109 (mtgen) 39 (vwF) 23 (RAG1) 2 (RBP3) 25 (apoB) 3 (GHR)	109	2.00E-04	-145%	79%
<i>I. portoricensis</i>	0	137,018	0.04 (mtgen) 0 (vwF) 0 (RAG1) 0 (RBP3) 0 (apoB) 0 (GHR)	14 (mtgen) 0 (vwF) 0 (RAG1) 0 (RBP3) 0 (apoB) 0 (GHR)	14	0.010	—	—	—	—	—	—	—

Table S2. Full details of final coverages of mitochondrial genomes and nuclear genes sequenced from extinct Caribbean caviomorphs.

Species	Gene	Missing data (bp)	Frequency (%)	GC content %	Sequence length (bp)
<i>B. offella</i>	mitochondrial genome	1,721	11.00	35.5	15,912
	vWF	241	37.60	61	809
<i>B. voratus</i>	mitochondrial genome	1,545	8.20	38.6	15,912
	vWF	8	1.40	61.1	809
	RAG1	32	3.00	53.2	1,073
	apoB	32	2.80	39.1	1,151
	GHR	19	2.20	49	842
<i>E. obliquus</i>	mitochondrial genome	1,666	8.40	38.9	15,912
	vWF	23	2.80	59.8	809
	RAG1	31	2.90	53.2	1,073
	RBP3	30	4.00	61.7	753
	apoB	45	3.90	39.4	1,151
	GHR	43	5.10	49.7	842
<i>G. columbianus</i>	mitochondrial genome	5,462	29.50	39.1	15,912
	vWF				
	RAG1	682	63.70	64.5	1,073
	RBP3	148	12.40	63.6	753
	GHR	293	36.10	50.9	842
<i>G. thoracatus</i>	mitochondrial genome	272	1.80	35.8	15,912
	RAG1	0	0.00	52.4	1,073
	RBP3	13	1.00	61.7	753
	apoB	3	0.30	39.3	1,151
	GHR	21	2.60	50.8	842

Table S3. Estimated divergence dates for numbered and lettered nodes in time-calibrated caviomorph phylogeny shown in Figure 3.

Node	Mean estimated divergence date (Mya)	95% HPD (Mya)	Node	Mean estimated divergence date (Mya)	95% HPD (Mya)
1	33.87	16.1, 42.1	27	3.52	2.0, 4.9
2	28.58	6.3, 37.7	28	14.55	11.7, 17.1
3	24.36	4.2, 35.2	29	10.28	7.0, 13.0
4	23.94	21, 27.5	30	8.61	5.5, 11.5
5	19.36	7.3, 23.0	31	7.46	4.7, 10.3
6	11.65	4.9, 16.1	32	15.63	6.9, 12.9
7	7.34	2.9, 11.4	33	10.36	7.0, 13.4
8	20.04	18.1, 22.4	34	2.70	1.3, 4.2
9	19.49	17.7, 21.7	35	15.43	9.2, 18.5
10	18.02	10, 21.2	36	14.47	8.1, 17.4
11	14.13	7.6, 17.4	37	10.21	5.5, 12.9
12	12.58	6.6, 15.8	38	7.39	3.9, 9.9
13	9.64	4.7, 13.1	39	5.24	2.6, 7.5
14	9.00	4.7, 13	40	13.21	7.4, 16.4
15	7.04	2.9, 9.7	41	18.08	9.9, 21.7
16	8.22	4.1, 11.9	42	12.05	7.1, 15.1
17	18.27	15.8, 20.3	43	11.20	7.1, 15.1
18	16.81	15.8 18.3	44	10.42	6.7, 14.1
19	15.57	14.1, 17.6	45	6.37	3.4, 8.8
20	13.47	11.5, 15.6	46	7.50	6.4, 13.3
21	9.79	6.5, 12.4	47	3.43	1.6, 4.6
22	11.00	8.8, 13.4	48	2.26	1.2, 3.2
23	9.98	7.5, 12.1	49	1.45	0.6, 2.2
24	6.46	4.4, 8.3	50	5.67	2.8, 7.6
25	5.61	3.7, 7.4	51	3.39	1.4, 4.9
26	4.90	3.1, 6.6			

Table S4. Genes used to generate baits for capture enrichment.

Gene	Length (bp)	NCBI accession	Species
apolipoprotein B (apoB)	1155	JX515310.1	<i>Proechimys quadruplicatus</i>
recombination activating gene 1 (RAG1)	1072	EU313333.1	<i>Proechimys simonsi</i>
von Willebrand factor (vWF)	1150	AJ849311.1	<i>Echimys didelphoides</i>
interphotoreceptor retinoid binding (RBP3)	1245	JF297775.1	<i>Phyllomys</i> sp.
growth hormone receptor (GHR)	798	JX515330.1	<i>Trinomys setosus</i>
mitochondrial genome	16816	HM544128.1	<i>Proechimys longicaudatus</i>

Table S5. Sequence data used in post-sequencing data processing as reference sequences in read mappings.

Gene	Species	NCBI accession number
mitochondrial genome	<i>Plagiodontia aedium</i>	KU892771.1
	<i>Mysateles prehensilis</i>	KU892770.1
	<i>Chinchilla lanigera</i>	NC021386.1
	<i>Carterodon sulcidens</i>	KU892752.1
	<i>Capromys pilorides</i>	KU892766.1
	<i>Proechimys longicaudatus</i>	NC020657.1
	<i>Geocapromys brownii</i>	KU892767.1
	<i>Mesocapromys melanurus</i>	KU892769.1
GHR	<i>Trinomys paratus</i>	JX515330.1
	<i>Capromys pilorides</i>	AF433950.1
	<i>Geocapromys brownii</i>	KM013984.1
	<i>Geocapromys ingrahami</i>	KM013985.1
	<i>Mesocapromys auritus</i>	KJ742633.1
	<i>Mesocapromys angelcabrerai</i>	KJ742632.1
	<i>Mysateles prehensilis</i>	KJ742634.1
RAG1	<i>Proechimys simonsi</i>	EU313333.1
	<i>Capromys pilorides</i>	JN633628.1
	<i>Geocapromys ingrahami</i>	KM013990.1
	<i>Geocapromys brownii</i>	KM013989.1
	<i>Mesocapromys angelcabrerai</i>	KJ742694.1
	<i>Mesocapromys auritus</i>	KJ742693.1
	<i>Mesocapromys melanurus</i>	KJ742691.1
	<i>Mysateles prehensilis</i>	KJ742696.1
RBP3	<i>Phyllomys sp.</i>	JF297775.1
	<i>Capromys pilorides</i>	KM013993.1
	<i>Geocapromys ingrahami</i>	KM013995.1
apoB	<i>Proechimys quadruplicatus</i>	JX515310.1
vWF	<i>Echimys didelphoides</i>	AJ849311.1
	<i>Capromys pilorides</i>	AJ251142.1
	<i>Geocapromys ingrahami</i>	KM014000.1
	<i>Geocapromys brownii</i>	KM013999.1
	<i>Mesocapromys auritus</i>	KJ742623.1
	<i>Mesocapromys angelcabrerai</i>	KJ742622.1

Table S6. Results of reads-mapping analysis conducted in CLC Workbench v.8 for iterative consensus sequence generation.

Species	Mapping parameters	Reference sequence	Total reads mapped	Average coverage
<i>Geocapromys columbianus</i>	M1	<i>G. ingrahami</i>	124	0.21
		<i>M. prehensilis</i>	34	0.06
		<i>P. aedium</i>	25	0.05
		<i>P. longicaudatus</i>	43	0.04
	M	<i>G. ingrahami</i>	450	0.55
		<i>M. prehensilis</i>	337	0.75
		<i>P. aedium</i>	357	0.75
		<i>P. longicaudatus</i>	293	0.34
	L	<i>G. ingrahami</i>	679	1.78
		<i>M. prehensilis</i>	360	0.7
		<i>P. aedium</i>	560	1.03
		<i>P. longicaudatus</i>	618	1.17
<i>Geocapromys thoracatus</i>	XH	<i>G. ingrahami</i>	5987	16.89
		<i>M. prehensilis</i>	1387	3.42
		<i>P. aedium</i>	937	2.16
		<i>P. longicaudatus</i>	432	0.91
	H1	<i>G. ingrahami</i>	20573	82.3
		<i>M. prehensilis</i>	3592	10.73
		<i>P. aedium</i>	2260	6.23
		<i>P. longicaudatus</i>	1156	2.82
	H	<i>G. ingrahami</i>	30958	131.89
		<i>M. prehensilis</i>	5744	18.55
		<i>P. aedium</i>	3967	12.24
		<i>P. longicaudatus</i>	2559	7.47
	M1	<i>G. ingrahami</i>	33131	140.26
		<i>M. prehensilis</i>	6492	21.42
		<i>P. aedium</i>	5226	17.3
		<i>P. longicaudatus</i>	3914	12.67
M	<i>G. ingrahami</i>	34067	143.05	
	<i>M. prehensilis</i>	6847	22.43	
	<i>P. aedium</i>	5765	19.22	
	<i>P. longicaudatus</i>	4877	16.33	
L	<i>G. ingrahami</i>	37001	148.4	
	<i>M. prehensilis</i>	8653	25.06	
	<i>P. aedium</i>	7889	21.96	
	<i>P. longicaudatus</i>	7592	19.73	
<i>Elasmodontomys obliquus</i>	H	<i>G. ingrahami</i>	39	0.05
		<i>M. prehensilis</i>	25	0.04
		<i>P. aedium</i>	52	0.07
		<i>P. longicaudatus</i>	43	0.05

		<i>G. ingrahami</i>	149	0.18
	M1	<i>M. prehensilis</i>	123	0.15
		<i>P. aedium</i>	196	0.25
		<i>P. longicaudatus</i>	194	0.22
	M	<i>G. ingrahami</i>	345	0.42
		<i>M. prehensilis</i>	292	0.36
		<i>P. aedium</i>	450	0.56
		<i>P. longicaudatus</i>	471	0.53
	L	<i>G. ingrahami</i>	4429	4.87
		<i>M. prehensilis</i>	3657	3.99
		<i>P. aedium</i>	5374	6
		<i>P. longicaudatus</i>	5734	5.92
	H1	<i>G. ingrahami</i>	377	1
		<i>M. prehensilis</i>	383	1.1
		<i>P. aedium</i>	387	1.05
		<i>P. longicaudatus</i>	191	0.46
	H	<i>G. ingrahami</i>	1038	3.08
		<i>M. prehensilis</i>	990	2.91
		<i>P. aedium</i>	1310	3.9
		<i>P. longicaudatus</i>	551	1.51
<i>Brotomys voratus</i>	M1	<i>G. ingrahami</i>	1595	4.99
		<i>M. prehensilis</i>	1525	4.72
		<i>P. aedium</i>	2211	7.23
		<i>P. longicaudatus</i>	1056	3.16
	M	<i>G. ingrahami</i>	1961	6.12
		<i>M. prehensilis</i>	1869	5.62
		<i>P. aedium</i>	2747	8.89
		<i>P. longicaudatus</i>	1490	4.27
	L	<i>G. ingrahami</i>	6421	11.31
		<i>M. prehensilis</i>	6313	11.05
		<i>P. aedium</i>	9413	16.86
		<i>P. longicaudatus</i>	8761	12.23
	H1	<i>G. ingrahami</i>	325	0.75
		<i>M. prehensilis</i>	238	0.54
		<i>P. aedium</i>	453	1.06
		<i>P. longicaudatus</i>	224	0.48
<i>Boromys offella</i>	H	<i>G. ingrahami</i>	835	2
		<i>M. prehensilis</i>	599	1.46
		<i>P. aedium</i>	1236	3.07
		<i>P. longicaudatus</i>	626	1.42
	M1	<i>G. ingrahami</i>	1229	3
		<i>M. prehensilis</i>	878	2.16
		<i>P. aedium</i>	1815	4.63
		<i>P. longicaudatus</i>	1043	2.44
	M	<i>G. ingrahami</i>	1534	3.63

	<i>M. prehensilis</i>	1097	2.59
	<i>P. aedium</i>	2197	5.35
	<i>P. longicaudatus</i>	1432	3.19
	<i>G. ingrahami</i>	6025	8.53
L	<i>M. prehensilis</i>	5223	7.16
	<i>P. aedium</i>	8387	12.13
	<i>P. longicaudatus</i>	8587	10.56

Table S7. Mapping parameters used in CLC Workbench.

Mapping parameter	Length fraction	Similarity fraction
default	0.5	0.8
L	0.7	0.7
M	0.8	0.8
M1	0.85	0.85
H	0.9	0.9
H1	0.95	0.95
XH	1	1

Table S8. Echimyid outgroup taxa for whole mitochondrial genome and nuclear genes.

Species	GenBank accession number					
	mitogenome	apoB	RBP3	GHR	RAG1	vWF
<i>Callistomys pictus</i>	KU892754	KY303652.1	KY303656.1	KY303654.1	KY303658.1	KJ742614.1
<i>Capromys pilorides</i>	KU892766	KM013977	KM013993	KM013983	JX515322	KM013998
<i>Carterodon sulcidens</i>	KU892752	KY303653	KY303657	KY303655	KJ742678	—
<i>Cavia porcellus</i>	NC_000884.1	AJ399524	AJ427248	AF433930	JN414957	AJ224663
<i>Chinchilla lanigera</i>	NC_021386.1	—	AF297280	AF332036	KF590658.1	AJ238385.1
<i>Clyomys laticeps</i>	KU892753	JX515304	JX515316	JX515326	—	AJ849306
<i>Coendou</i> sp.	NC_021387.1	—	—	—	—	—
<i>Ctenomys</i> sp.	HM544130.1	JN414055.1	JN414816.1	FJ855214.1	JN414961.1	JN415078.1
<i>Dactylomys</i> sp.	KU762015	—	—	KF590681.1	EU313300.1	KF590667.1
<i>Echimyus chrysurus</i>	KU892781	JX515301	AJ427247	JX515533	EU313303	AJ251141
<i>Euryzgomatomys spinosus</i>	KU892755	—	JX515315	JX515327	KJ742680	AJ849319
<i>Geocapromys brownii</i>	KU892767	KM013978	—	KJ742644	KJ742692	KJ742621
<i>Geocapromys ingrahami</i>	KU892768	KM013979	KM013995	KM013985	KM013990	KM014000
<i>Hoplomys gymnurus</i>	KU892779	—	—	JN414758	JN633632	JN415080
<i>Isothrix sinnamariensis</i>	KU892785	JX515309	—	KF590685	EU313312	AJ849309
<i>Kannabateomys amblyonyx</i>	KU892775	—	—	—	—	AJ849310.1
<i>Lonchothrix emiliae</i>	KU892786	—	—	—	—	—
<i>Makalata didelphoides</i>	KU892782	JX515303	JF297756	JX515332	EU313314	AJ849311
<i>Mesocapromys melanurus</i>	KU892769	—	—	—	KJ742691	—
<i>Mesomys hispidus</i>	KU892787	JX515305	—	JX515335	EU313322	KF590671
<i>Mesomys stimulax</i>	KU892788	—	—	KJ742630.1	KJ742674.1	KJ742618.1
<i>Myocastor coypus</i>	KU892780	JX515307	JN414814	—	JN414955	AJ251140
<i>Mysateles prehensilis</i>	KU892770	KM013980	—	—	—	—
<i>Octodon lunatus/degus</i>	HM544134.1	—	AM050863	—	KJ742676	AJ238386
<i>Olallamys albicauda</i>	KU892774	—	—	KF590691.1	—	KF590673.1
<i>Pattonomys semivillosus</i>	KU892783	—	—	—	KJ742687.1	KJ742616.1
<i>Phyllomys blainvillii</i>	KU892756	JX515302	JF297781	JX515331	JX515323	AJ849314
<i>Phyllomys dasythrix</i>	KU892757	—	JF297757.1	KJ742641.1	KJ742689.1	JF297709.1
<i>Phyllomys lundii</i>	KU892758	—	JF297770.1	—	—	JF297721.1
<i>Phyllomys mantiqueirensis</i>	KU892759	—	JF297769.1	—	—	JF297720.1
<i>Phyllomys pattoni</i>	KU892760	—	JF297803	KJ742642	KJ742690	JF297754
<i>Plagiodontia aedium</i>	KU892771	KM013981	KM013996	KM013986	KM013991	KM014002
<i>Proechimys cuvieri</i>	KU892778	—	JX515318.1	KF590693.1	KF590665.1	KF590675.1
<i>Proechimys longicaudatus</i>	HM544128.1	—	—	FJ855217	KJ742681	KJ742619
<i>Proechimys roberti</i>	KU892772	—	—	—	—	—
<i>Santamartamys rufodorsalis</i>	KU892777	—	—	—	—	—
<i>Spalacopus cyanus</i>	HM544133.1	—	—	—	—	—
<i>Thrichomys apereoides</i>	KU892773	—	JX515319	JX515325	EU313334	KY303660
<i>Toromys grandis</i>	KU892784	—	—	KF590694.1	EU313336.1	KF590676.1
<i>Trinomys albispinus</i>	KU892761	KM013982	KM013997	KM013987	KM013992	KM014003
<i>Trinomys dimidiatus</i>	JX312694.1	—	—	—	KJ742682.1	KJ742620.1
<i>Trinomys iheringi</i>	KU892762	—	—	KF590695	EU313337	KF590677
<i>Trinomys paratus</i>	KU892763	JX515306	JX515320	JX515330	—	AJ849316
<i>Trinomys setosus</i>	KU892764	—	—	JX515329	—	AJ849317
<i>Trinomys yonenagae</i>	KU892765	KM013982	—	JX515328	—	AJ849318
<i>Tympanoctomys barrerae</i>	HM544132.1	—	—	KX646530.1	—	—

Table S9. Substitution models chosen for partitioned dataset.

Subset	Best model	Subset Partitions
Mitochondrial genome		
1	GTR+G	rrnL, rrnS, trnC, trnD, trnF, trnH, trnI, trnK, trnL1, trnL2, trnM, trnN, trnP, trnQ, trnR, trnS2, trnV, trnW, trnY
2	GTR+G	atp6, atp8, cob, cox3, nad1, nad2, nad3, nad4a, nad4l, nad5, nad6
3	GTR+G	cox1, cox2, trnA, trnE, trnG, trnS1, trnT
apoB (apolipoprotein B)		
1	HKY+G	Gene
RAG1 (recombination activating gene 1)		
1	K80+G	Gene
vWF (von Willebrand factor)		
1	K80+G	Gene
RBP3 (interphotoreceptor retinoid binding)		
1	HKY+G	Gene
GHR (growth hormone receptor)		
1	K80+G	Gene

Table S10. Fossil constraints and priors used in divergence dating analysis.

Node	Fossil and Deposit Locality	Age (Ma)	Prior distribution
Cavioidea–Erethizontoidea	Minimum: <i>Andemys termasi</i> (Tinguirirican) Maximum: <i>Canaanimys</i> and <i>Cachiyacuy</i> (Barrancan)	31.3–45.9	logNormalPrior mean="5.4" stdev="0.8" offset="31.3"
Octodontidae	Minimum: <i>Pseudoplateomys innominatus</i> (Huayquerian) Maximum: <i>Acarechimys</i> (Laventan)	6.8–11.8	logNormalPrior mean="1.846" stdev="0.8" offset="6.0"
<i>Trinomys</i> and <i>Clyomys</i> + <i>Euryzygomatomys</i>	<i>Theridomysops parvulus</i> (Huayquerian)	6.0–11.8	logNormalPrior mean="2.141" stdev="0.8" offset="6.0"
Echimyini	<i>Maruchito trilofodonte</i> (Colloncuran)	15.7–24.2	logNormalPrior mean="4.15" stdev="0.8" offset="15.7"
Myocastorini	<i>Pampamys emmonsae</i> (Huayquerian)	6.0–11.8	logNormalPrior mean="2.141" stdev="0.8" offset="6.0"

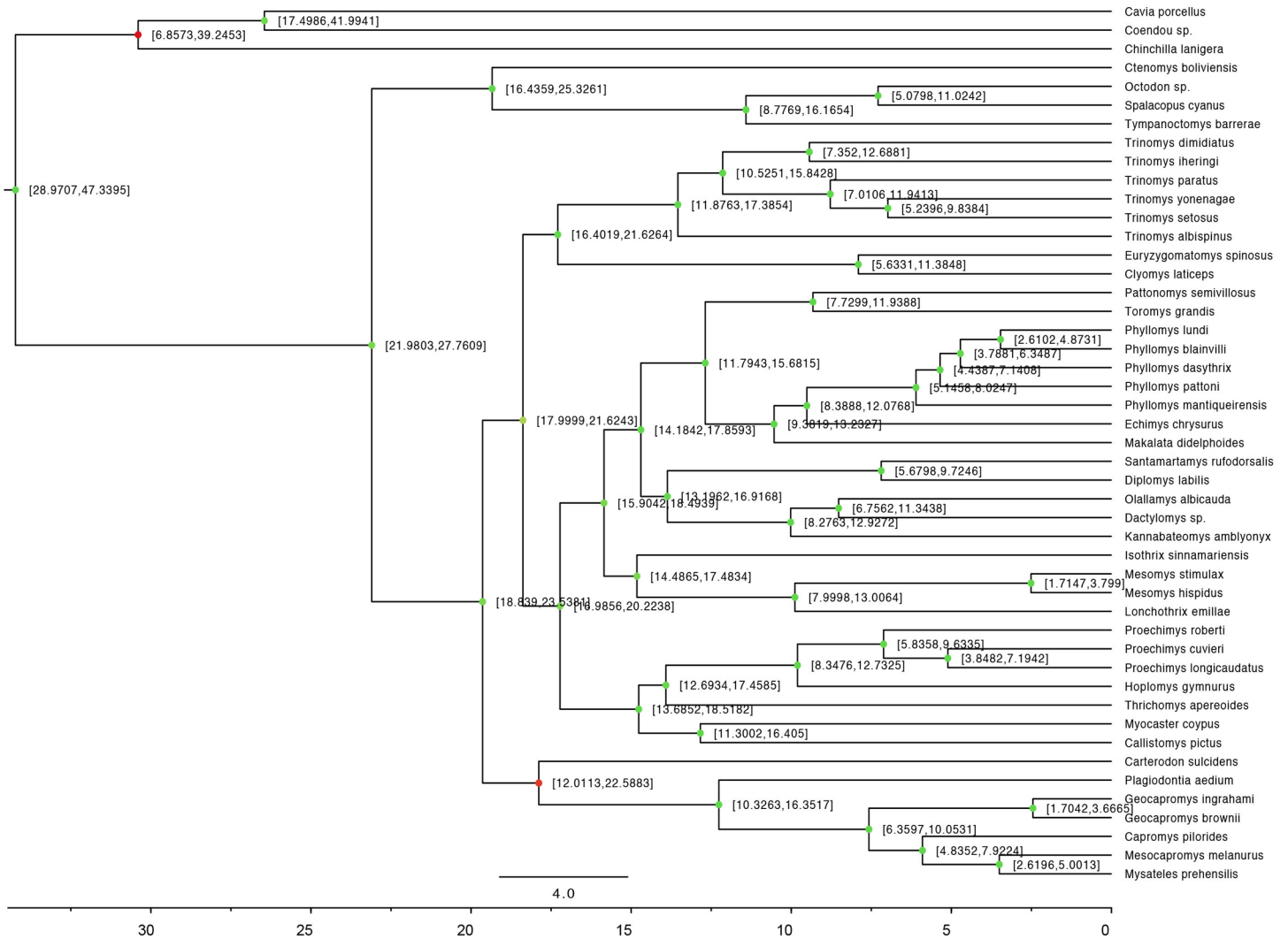


Figure S1. Time-calibrated phylogeny showing estimated divergence dates for Caribbean caviomorphs and mainland Neotropical caviomorphs, excluding extinct taxa. Node colours represent posterior probabilities (red <math>< 1</math>, green = 1). Numbered nodes include 95% error estimates for divergence dates in brackets.

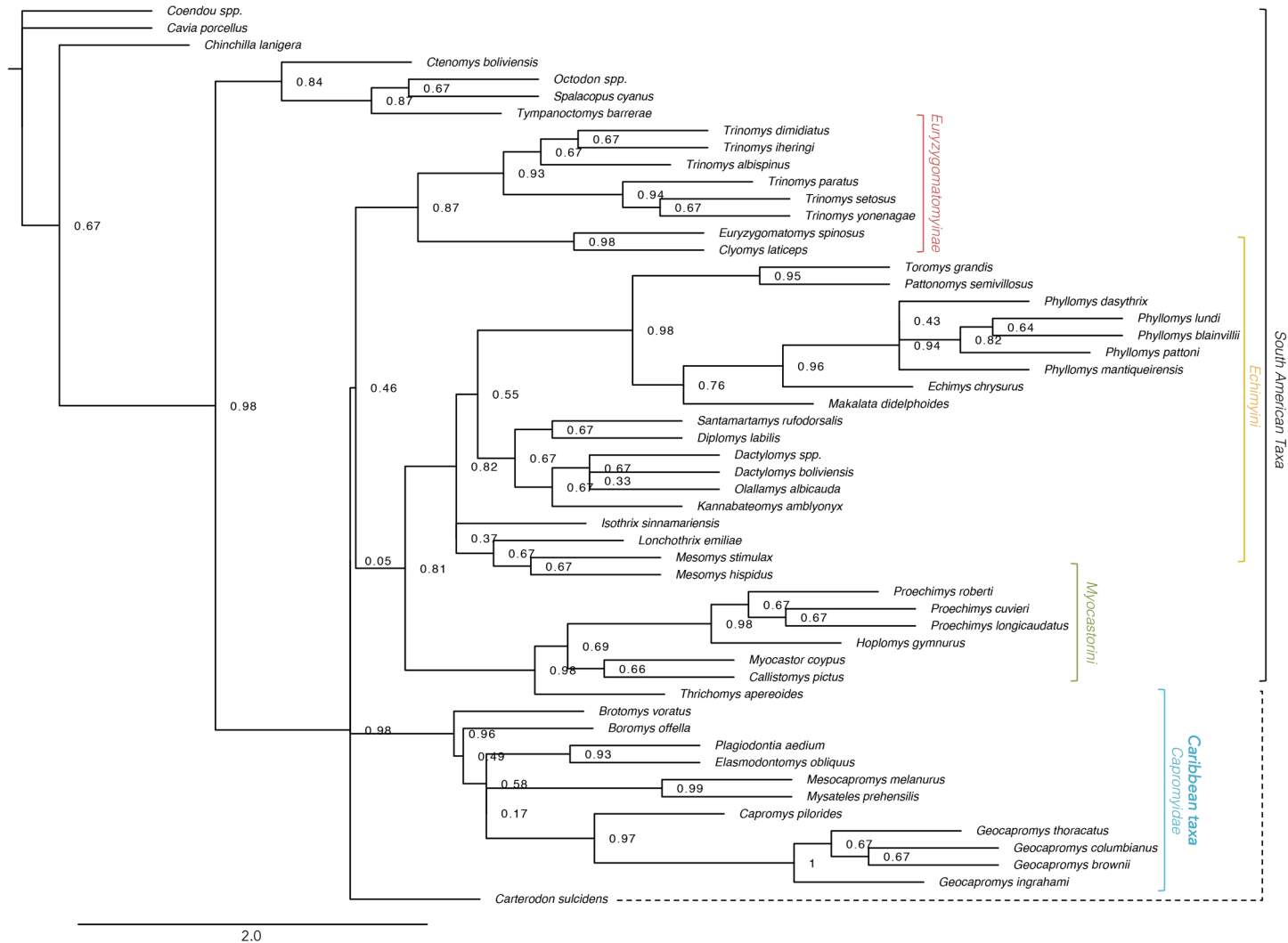


Figure S2. Coalescent species tree inferred using six gene trees. Node values represent the local posterior probability. Normalised quartet score = 0.8. Main clades are colour-coded and named.