

Supplementary Information

Das, S., Greenbaum, E., Brecko, J., Pauwels, O. S. G., Ruane, S., Pirro, S. & Merilä, J.

Resolving the elapoid phylogeny: systematics of *Psammodynastes* and *Buhoma* (Elapoidea: Serpentes), with the description of a new Asian snake family

Reference genomes

The reference genomes listed here were used to harvest ultraconserved elements (UCE) loci and traditional nuclear markers *in silico*.

Bungarus multicinctus

Genome assembly: ASM2365372v1,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_023653725.1/

Publication: Xu *et al.* Genomic, transcriptomic, and epigenomic analysis of a medicinal snake, *Bungarus multicinctus*, to provides insights into the origin of Elapidae neurotoxins.

Acta Pharm. Sin. B, **13**, 2234–2249 (2023).

Daboia siamensis

Genome assembly: ASM2444931v1,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_024449315.1/

Publication: Saethang *et al.* Identification of *Daboia siamensis* venome using integrated multi-omics data. *Sci. Rep.*, **12**, 13140 (2022).

Remark: Only used for harvesting some traditional nuclear loci. UCEs for *D. palaestinae* were already available from [7].

Emydocephalus ijimae

Genome assembly: emylji_1.0,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_004319985.1/

Publication: Kishida *et al.* Loss of olfaction in sea snakes provides new perspectives on the aquatic adaptation of amniotes. *Proc. R. Soc. B*, **286**, 20191828 (2019).

Hydrophis cyanocinctus

Genome assembly: HCya_v2,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_019473425.1/

Publication: Li *et al.* Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. *Mol. Biol. Evol.*, **38**, 4867–4883 (2021).

Hydrophis curtus

Genome assembly: HCur_v2,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_019472885.1/

Publication: Li *et al.* Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. *Mol. Biol. Evol.*, **38**, 4867–4883 (2021).

Hydrophis melanocephalus

Genome assembly: hydMel_1.0,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_004320005.1/

Publication: Kishida *et al.* Loss of olfaction in sea snakes provides new perspectives on the aquatic adaptation of amniotes. *Proc. R. Soc. B*, **286**, 20191828 (2019).

Laticauda colubrina

Genome assembly: latCor_2.0,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_015471245.1/

Publication: Kishida *et al.* Loss of olfaction in sea snakes provides new perspectives on the aquatic adaptation of amniotes. *Proc. R. Soc. B*, **286**, 20191828 (2019).

Laticauda laticaudata

Genome assembly: latLat_1.0,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_004320025.1/

Publication: Kishida *et al.* Loss of olfaction in sea snakes provides new perspectives on the aquatic adaptation of amniotes. *Proc. R. Soc. B*, **286**, 20191828 (2019).

Myanophis thanlyinensis

Genome assembly: ASM1765603v1,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_017656035.1/

Publication: Köhler *et al.* A new genus and species of mud snake from Myanmar (Reptilia, Squamata, Homalopsidae). *Zootaxa*, **4915**, 301–325(2021).

Naja naja

Genome assembly: Nana_v5,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_009733165.1/

Publication: Suryamohan *et al.* The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. *Nat. Genetics*, **52**, pages 106–117 (2020).

Notechis scutatus

Genome assembly: TS10Xv2-PRI,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_900518725.1/

Publication: No specific publication (but the genome assembly has been used and cited by subsequent researches).

Ophiophagus hannah

Genome assembly: OphHan1.0,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000516915.1/

Publication: Vonk *et al.* The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. *Proc. Natl. Acad. Sci.*, **10**, 20651–20656 (2013).

Psammodynastes pulverulentus

Genome assembly: ASM2580229v1,

https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_025802295.1/

Publication: This paper.

Supplementary figures

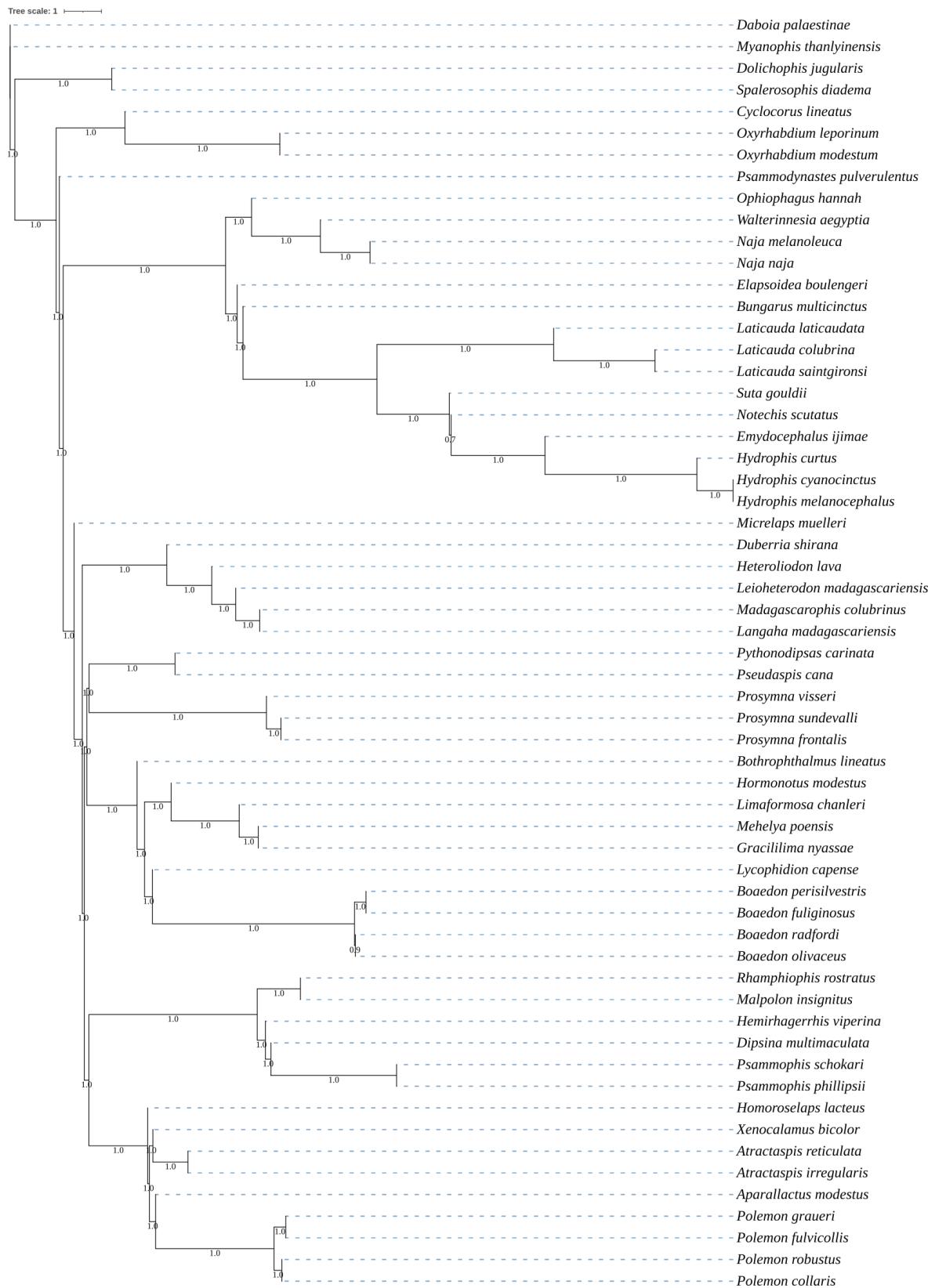


Fig. S1: 50 % complete UCE wASTRAL-h phylogeny. LocalPP on the branches.

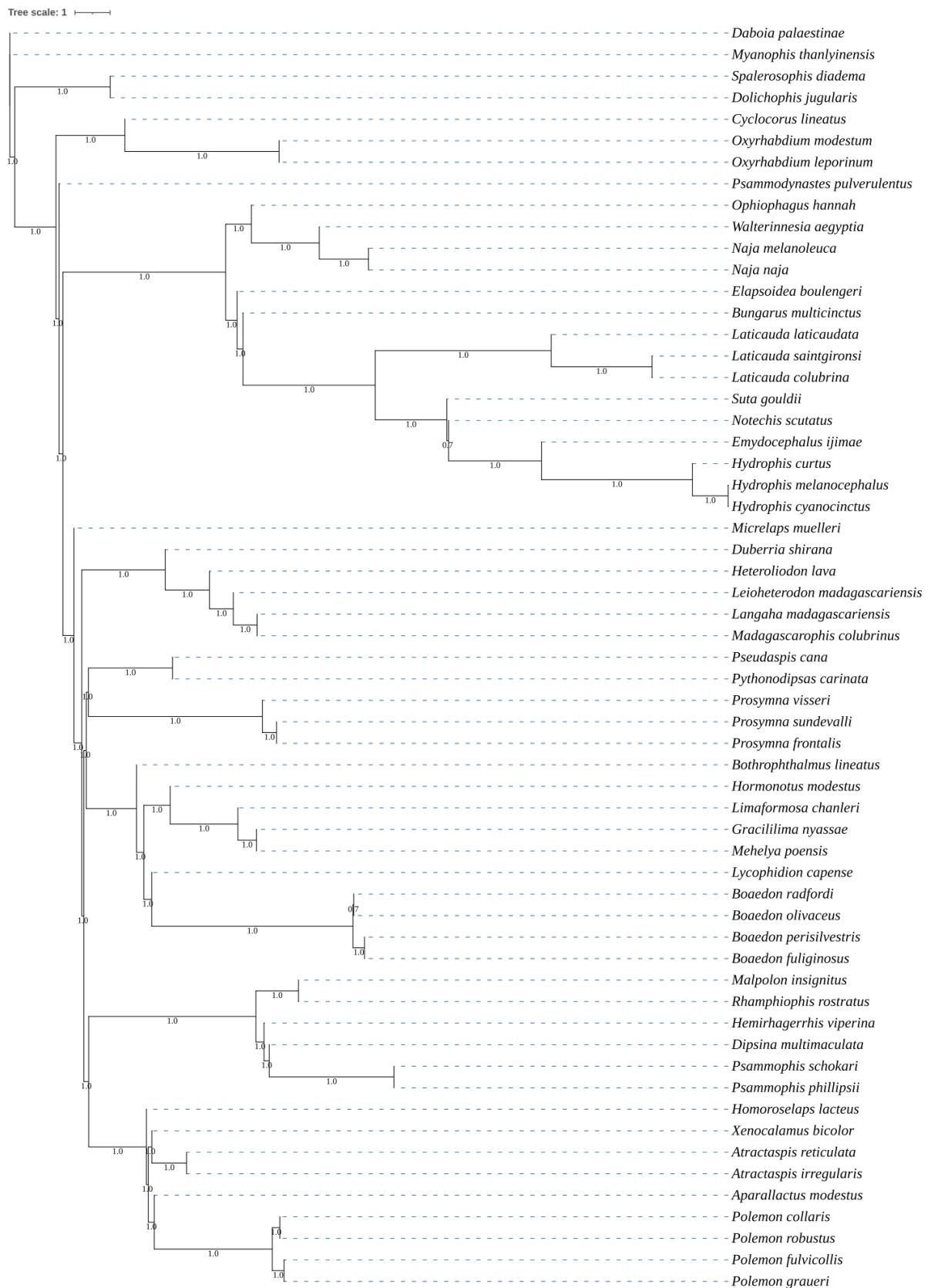


Fig. S2: 75 % complete UCE wASTRAL-h phylogeny. LocalPP on the branches.

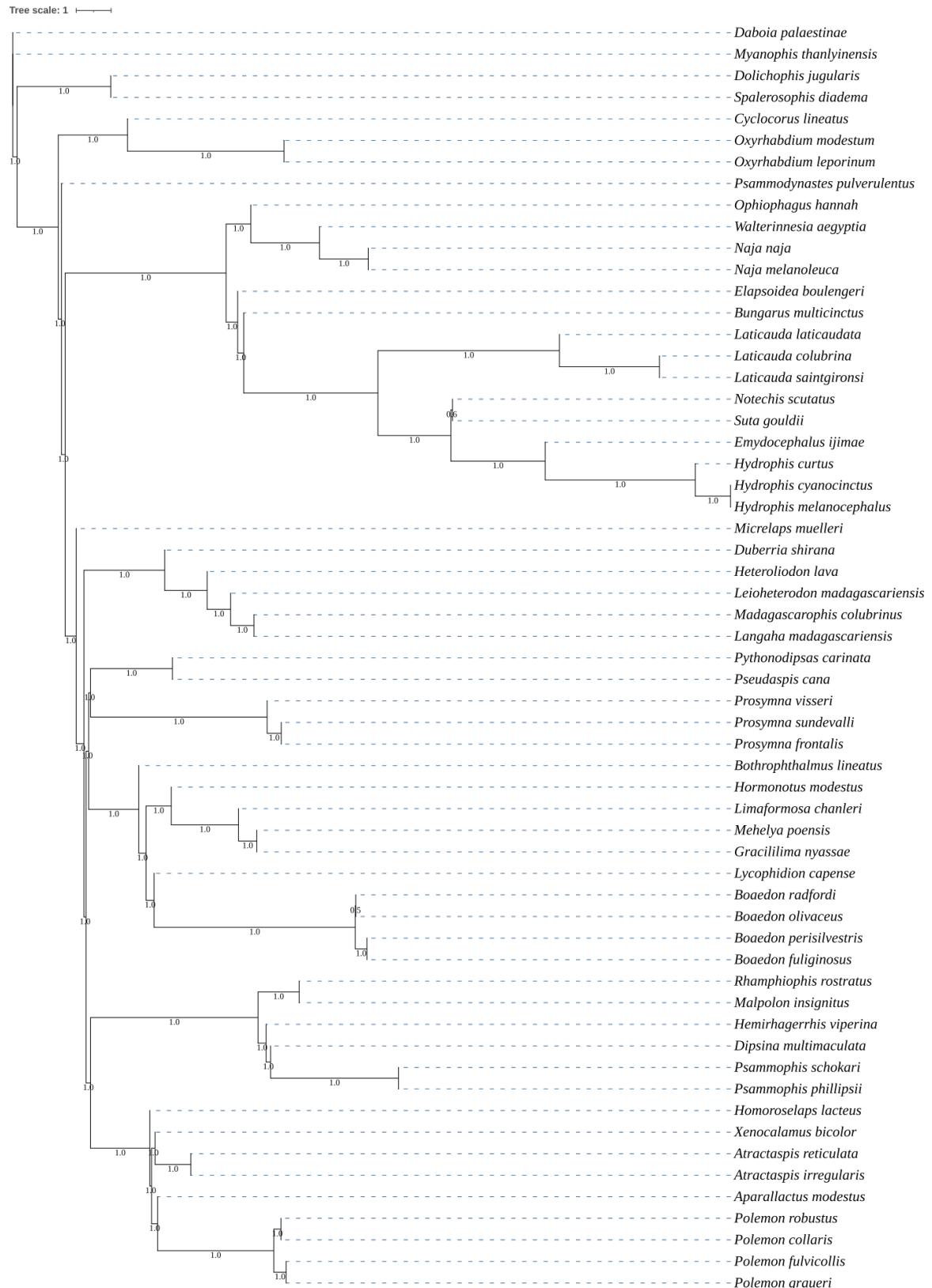


Fig. S3: 95 % complete UCE wASTRAL-h phylogeny. LocalPP on the branches.

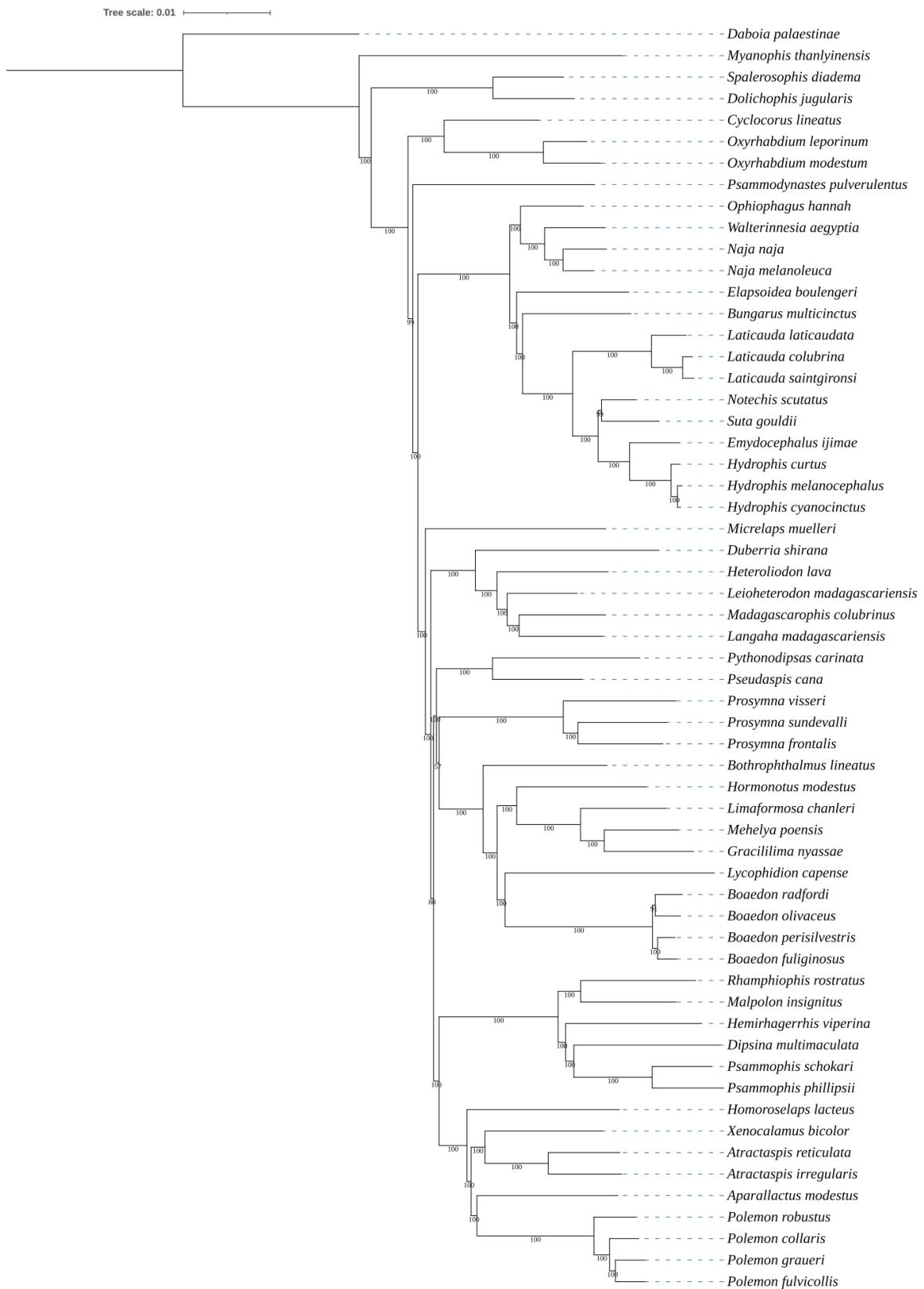


Fig. S4: 50 % complete UCE ML phylogeny. UFBoot on the branches.

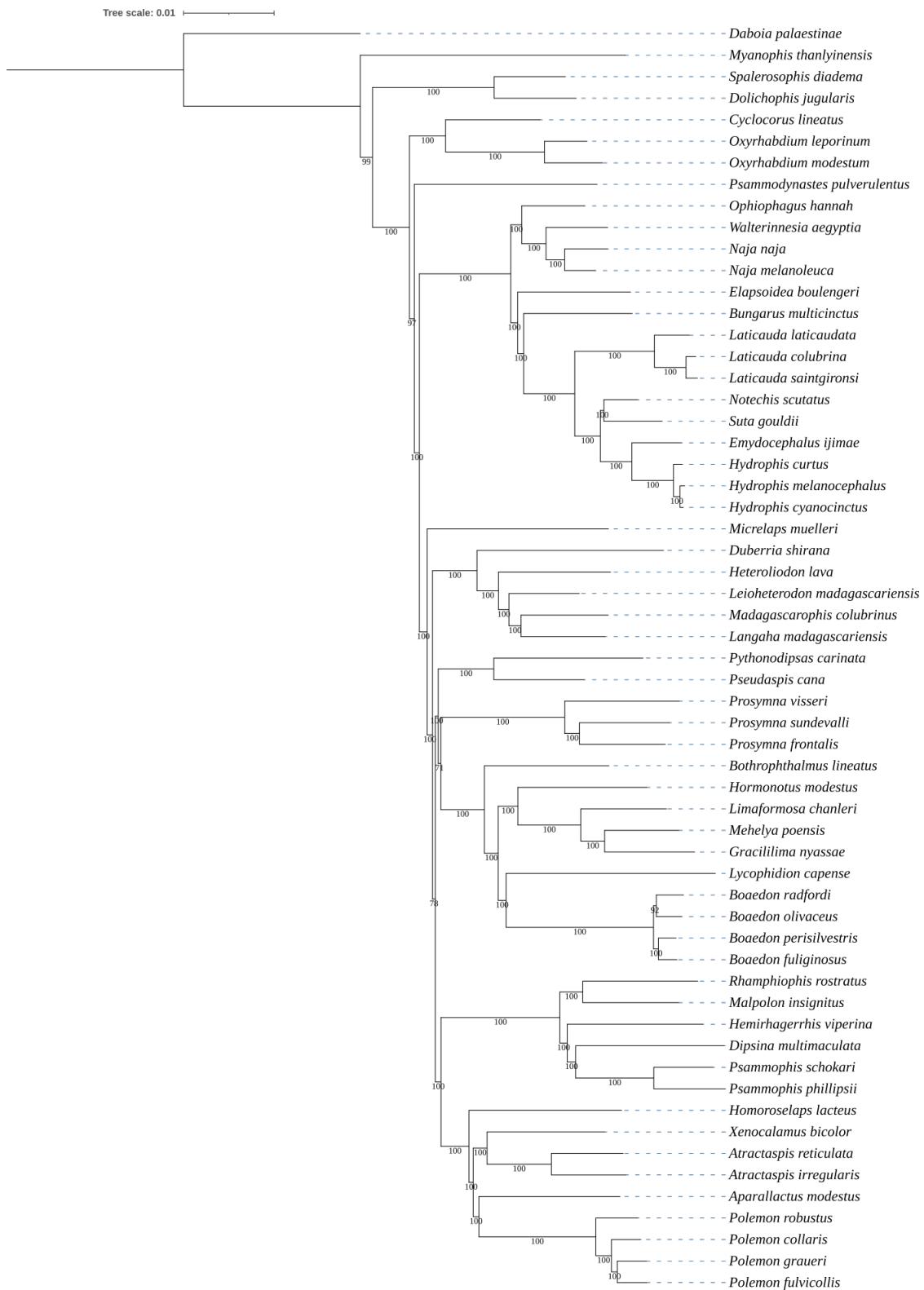


Fig. S5: 75 % complete UCE ML phylogeny. UFBoot on the branches.

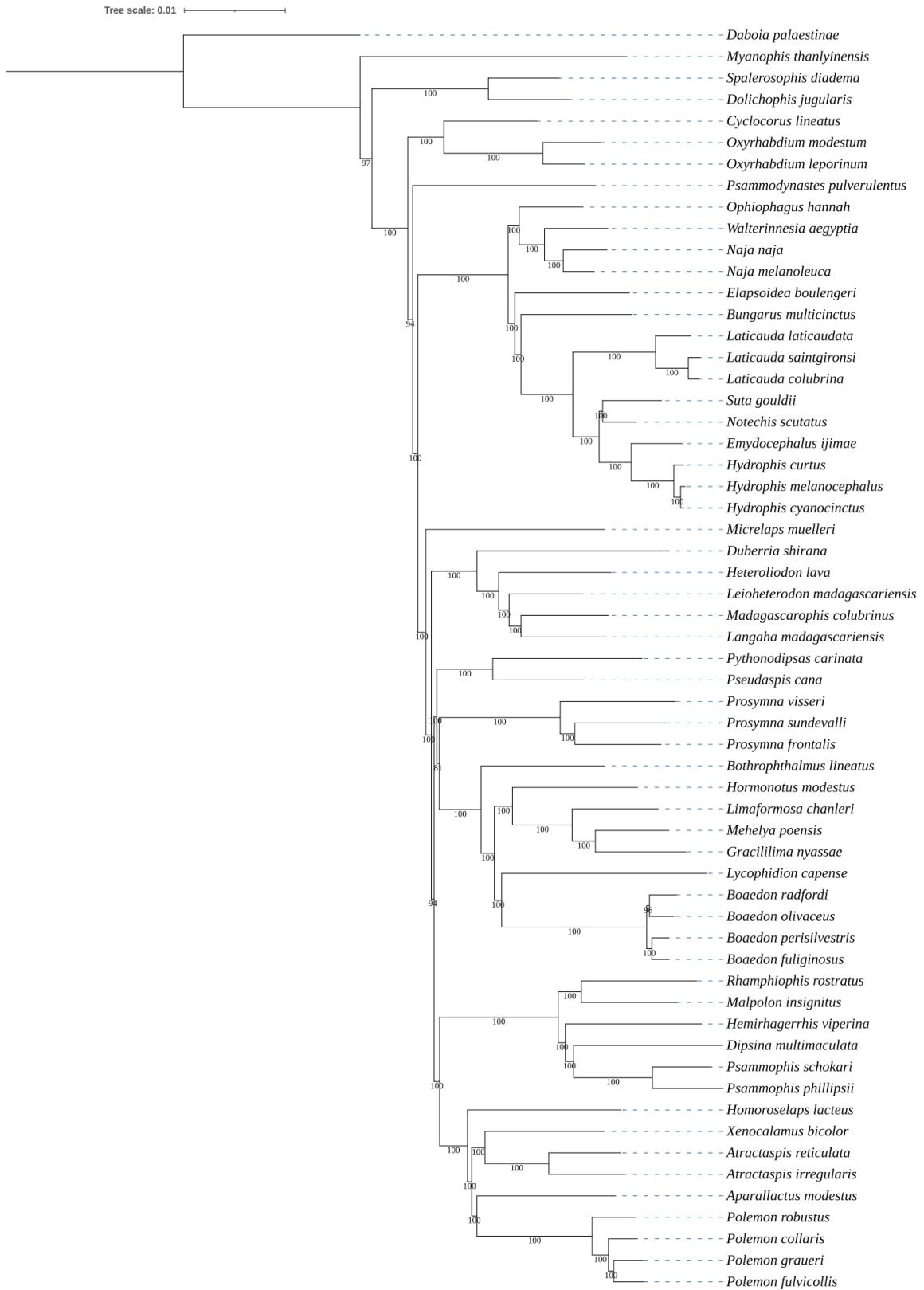


Fig. S6: 95 % complete UCE ML phylogeny. UFBoot on the branches.

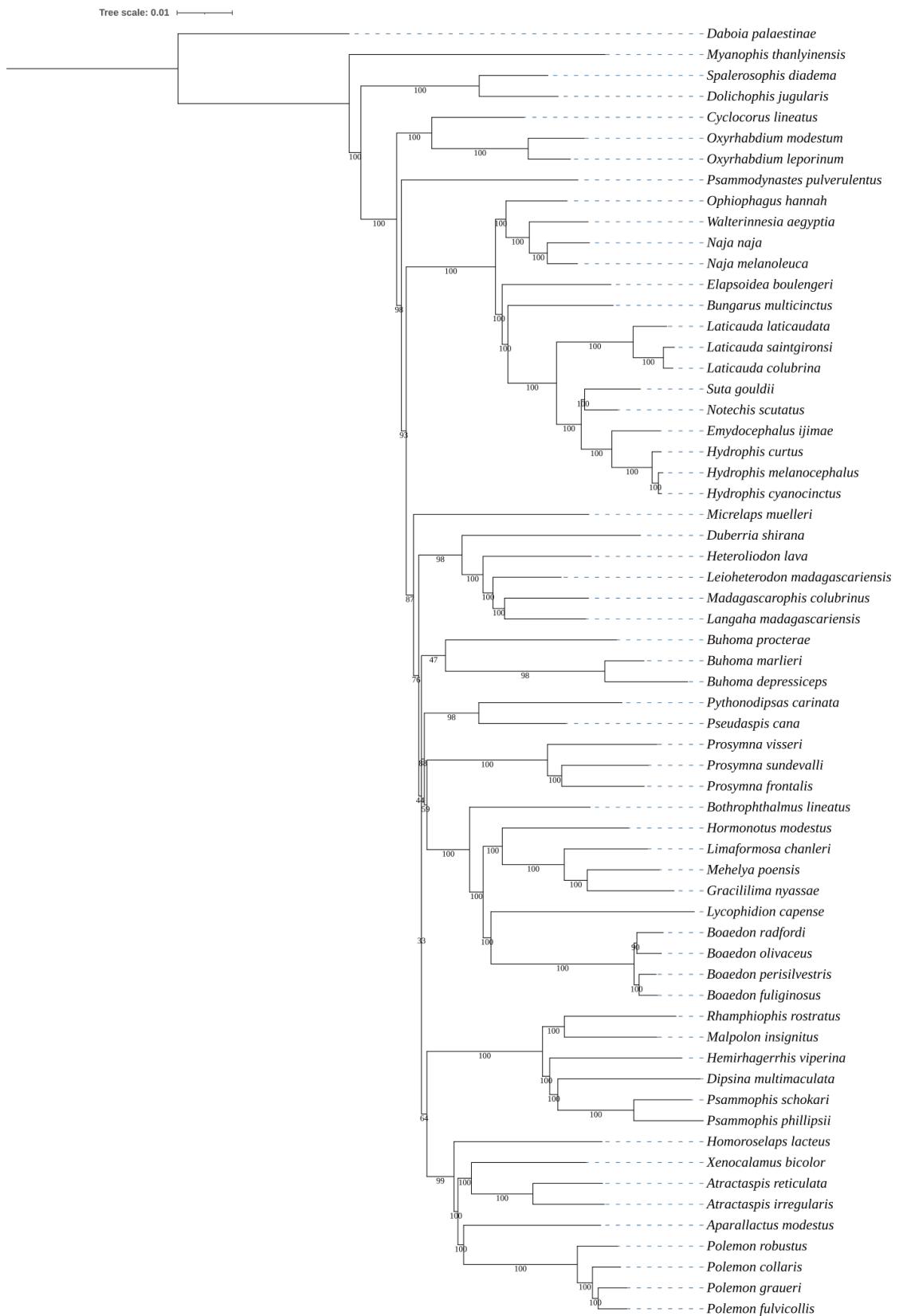


Fig. S7: 50 % UCE + tradition nuclear marker ML phylogeny. UFBoot on branches. For composite taxa (named here as in UCE datatset), see Figure 2 and Table S1.

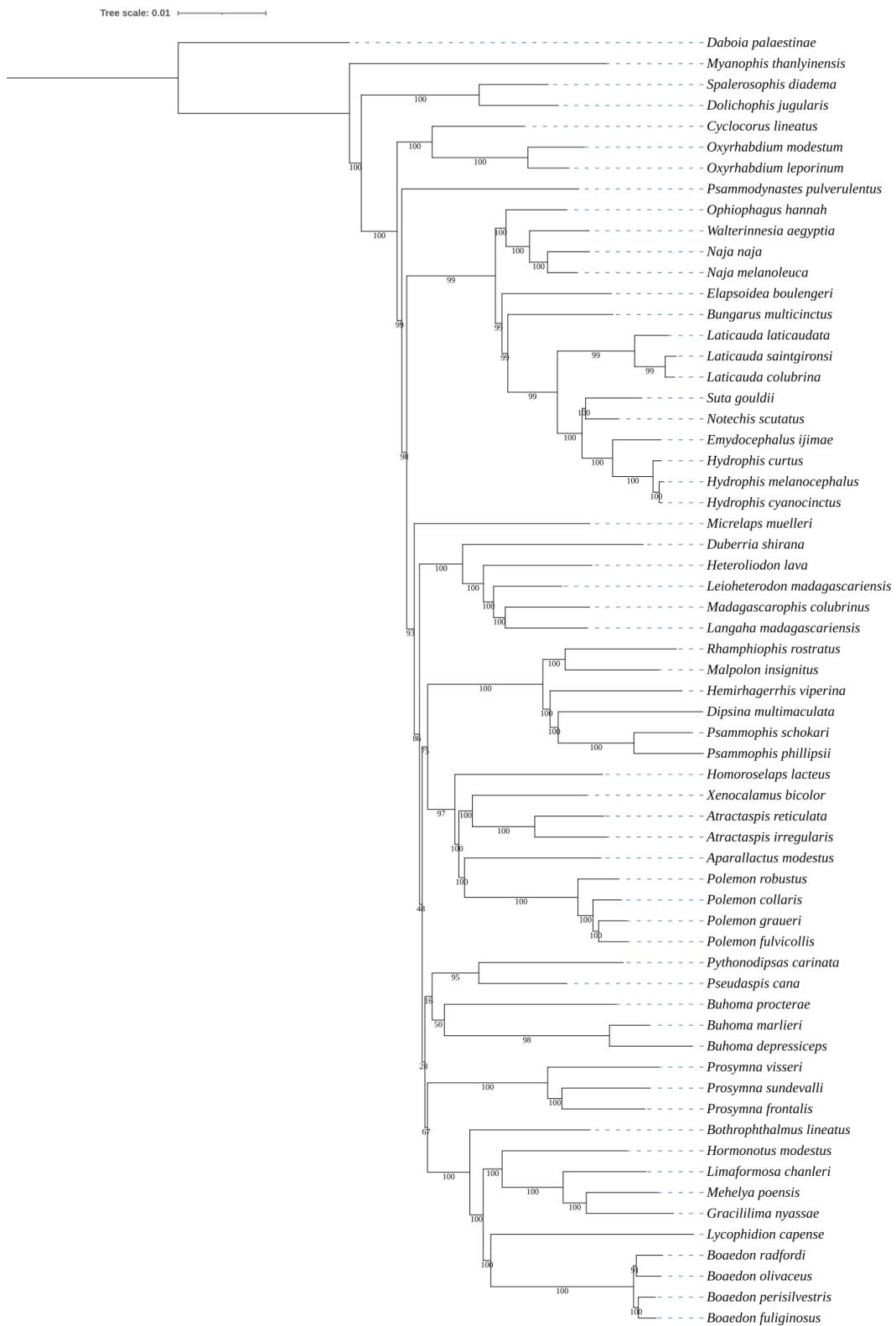


Fig. S8: 75 % UCE + tradition nuclear marker ML phylogeny. UFBoot on branches. For composite taxa (named here as in UCE datatset), see Figure 2 and Table S1.

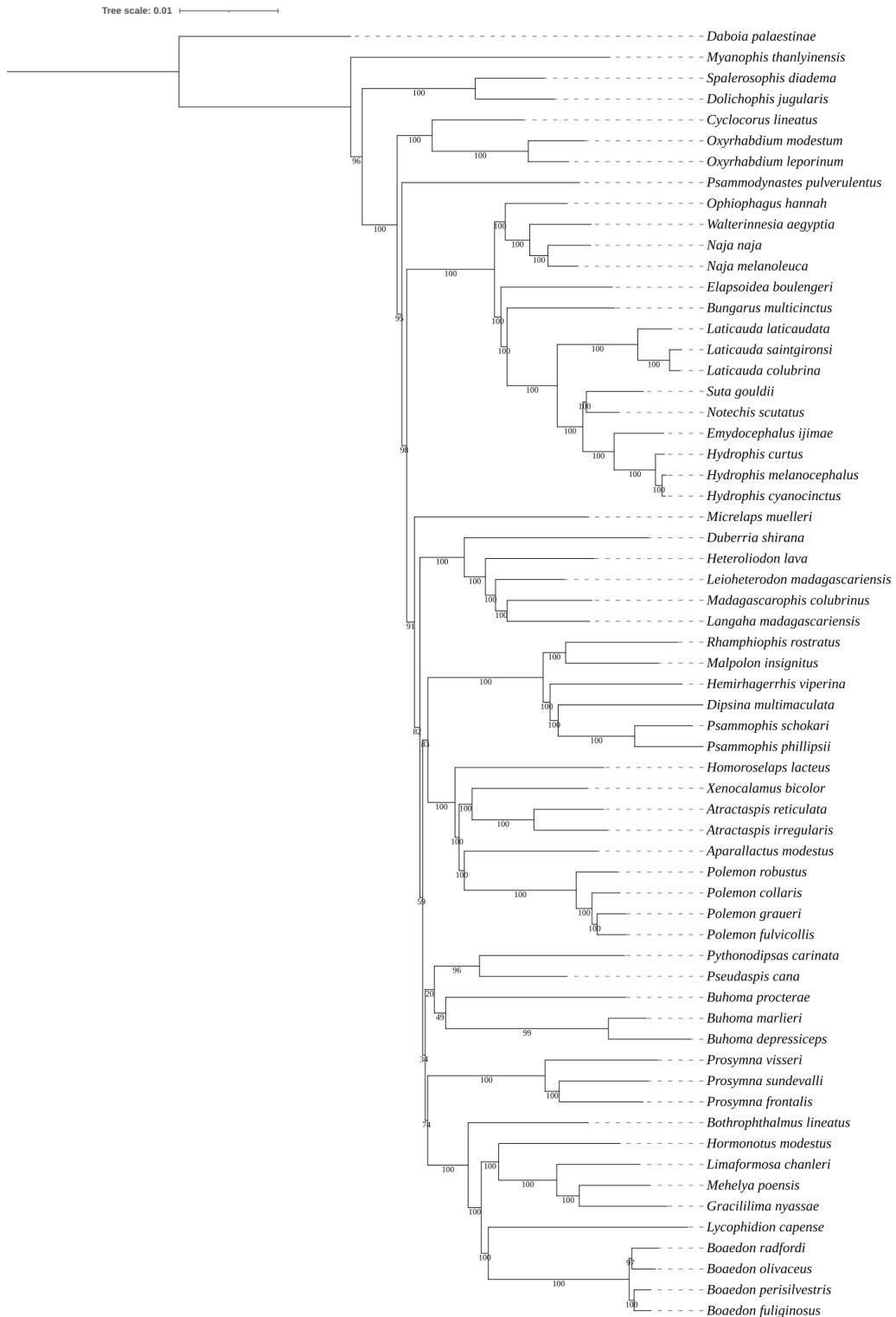


Fig. S9: 95 % UCE + tradition nuclear marker ML phylogeny. UFBoot on branches. For composite taxa (named here as in UCE datatset), see Figure 2 and Table S1.



Fig. S10: 50 % UCE + tradition mito-nuclear marker ML phylogeny. UFBoot on branches.

For composite taxa (named here as in UCE datatset), see Table S1.



Fig. S11: 75 % UCE + tradition mito-nuclear marker ML phylogeny. UFBoot on branches.

For composite taxa (named here as in UCE datatset), see Table S1.



Fig. S12: 95 % UCE + tradition mito-nuclear marker ML phylogeny. UFBoot on branches.

For composite taxa (named here as in UCE datatset), see Table S1.

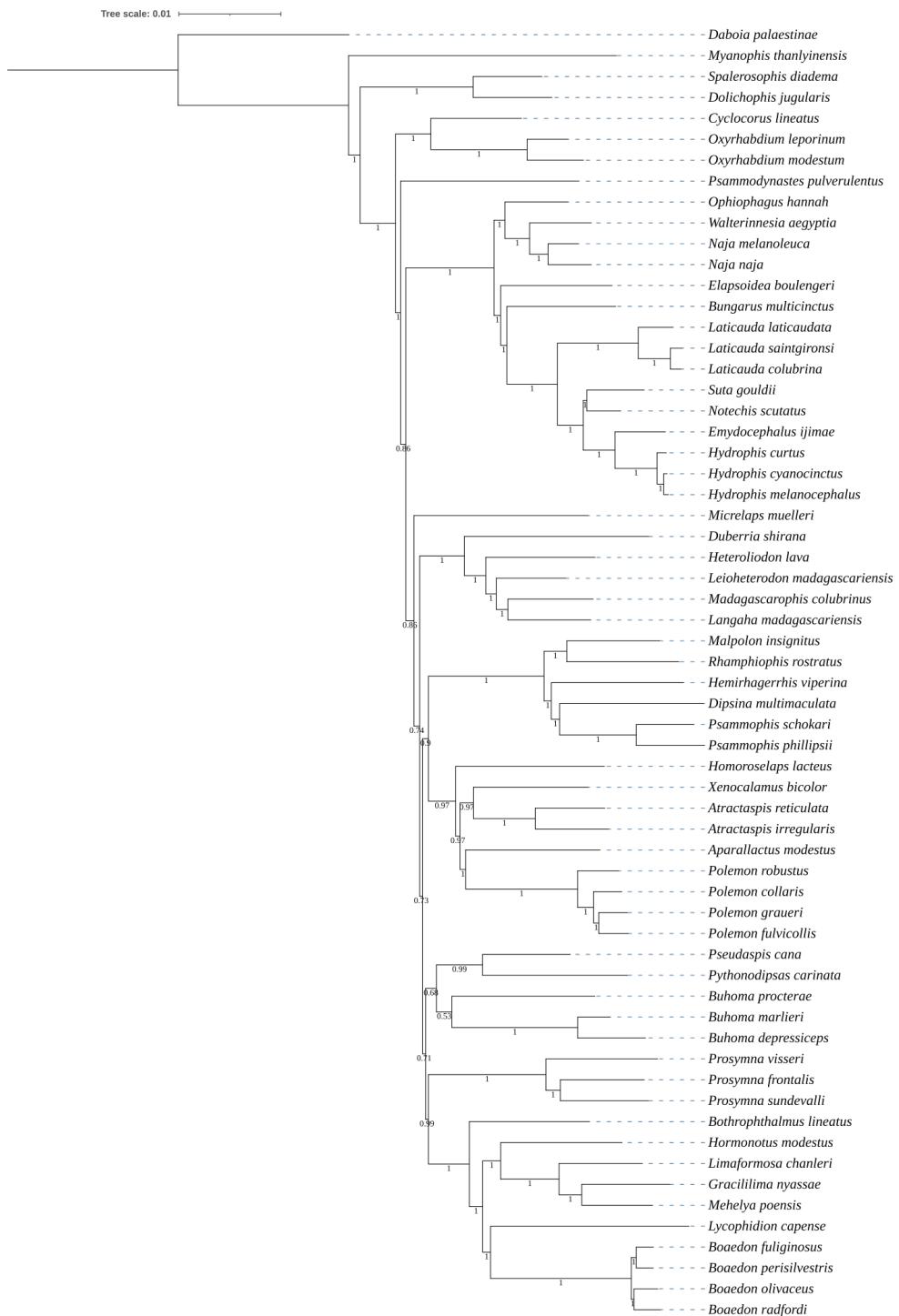


Fig. S13: 95 % UCE and traditional nuclear marker ExaBayes phylogeny. Posterior probability on the branches. For composite taxa (named here as in UCE dataset), see Figure 2 and Table S1.



Fig. S14: Traditional nuclear marker ML phylogeny. UFBoot on the branches. For composite taxa, see Table S1.

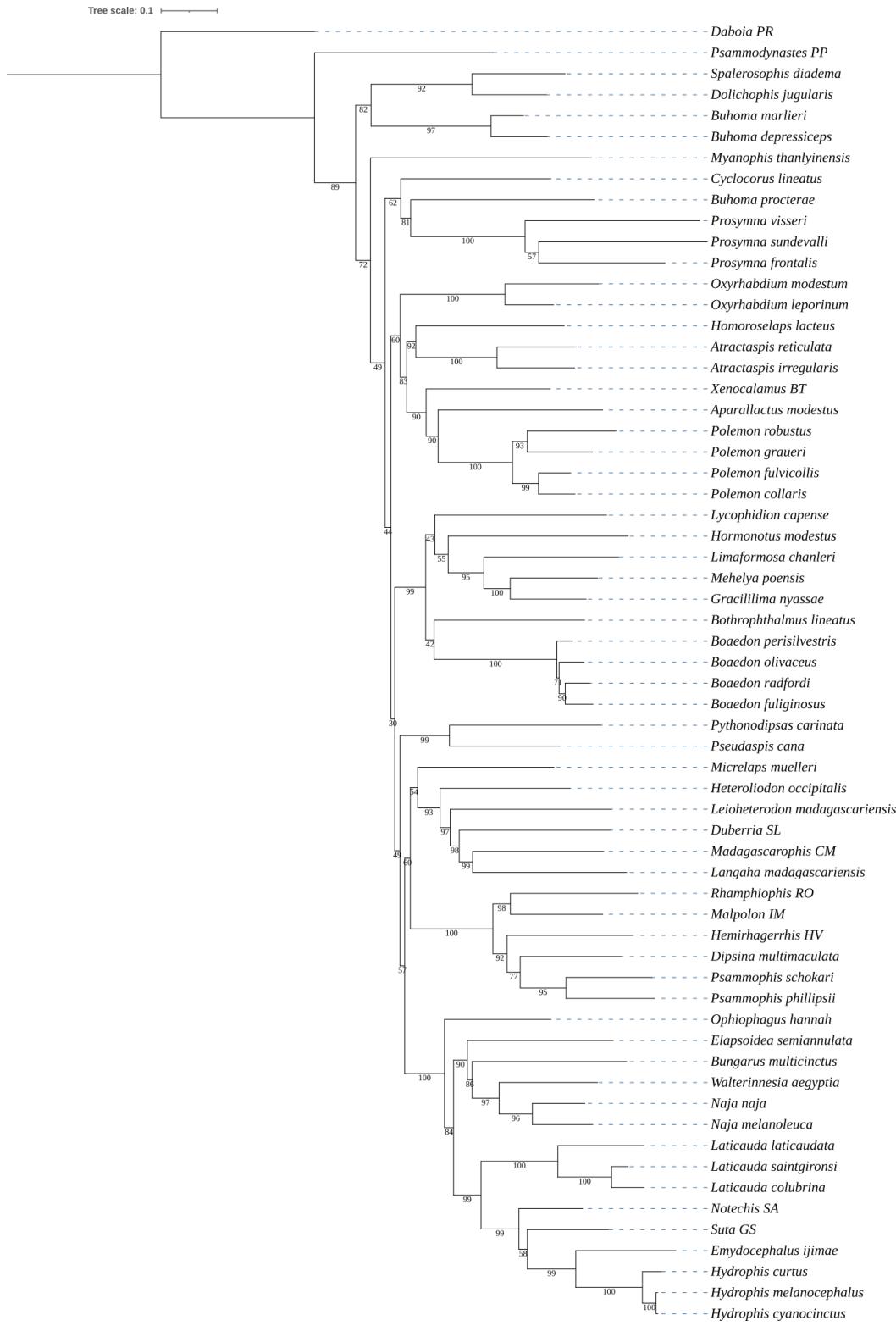


Fig. S15: Traditional mitochondrial marker ML phylogeny. UFBoot on the branches. For composite taxa (the ones with capital letters in the place of the specific epithet), see Table S1.

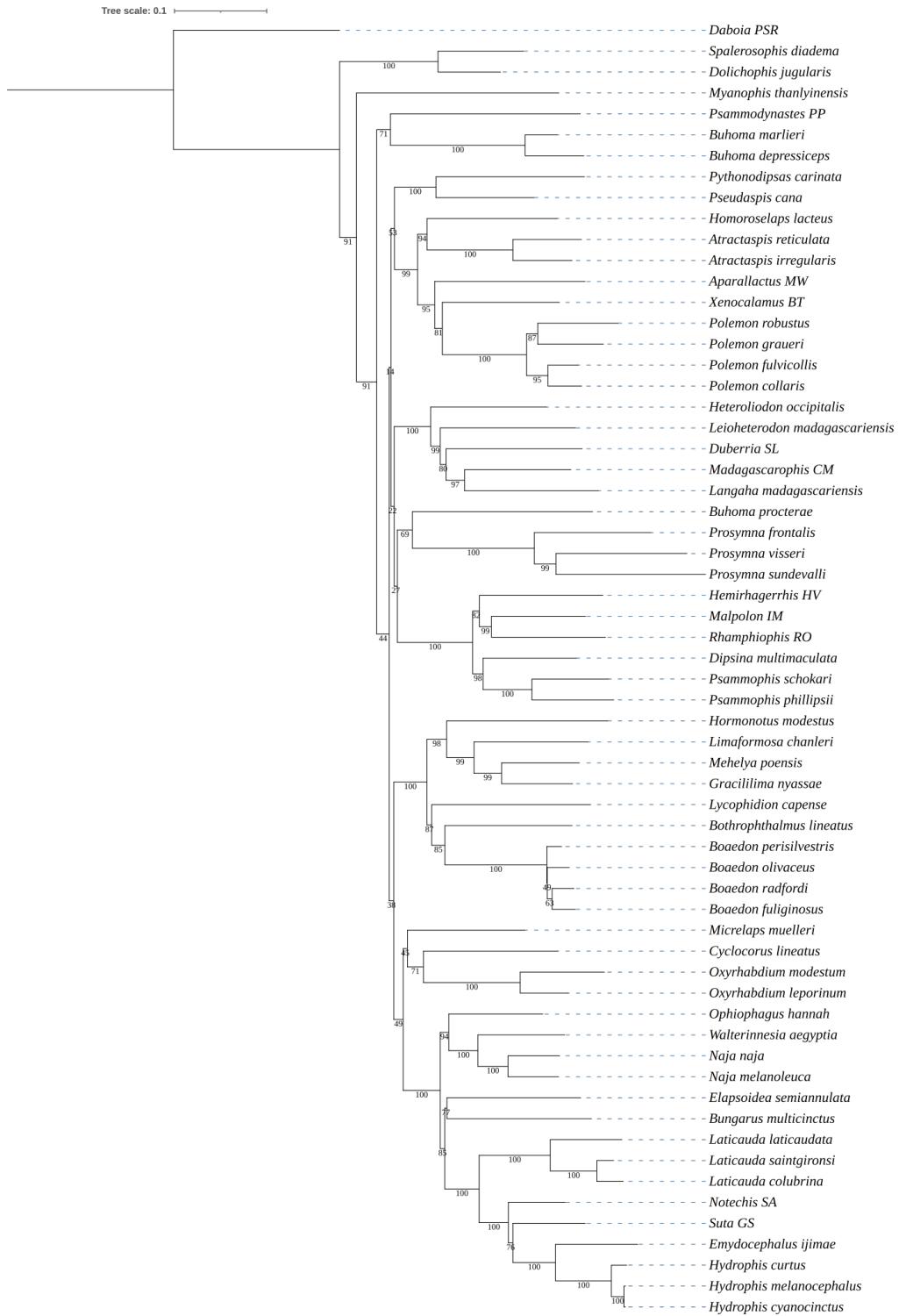


Fig. S16: Traditional mito-nuclear marker ML phylogeny. UFBoot on the branches. For composite taxa (the ones with capital letters in the place of the specific epithet), see Table S1.

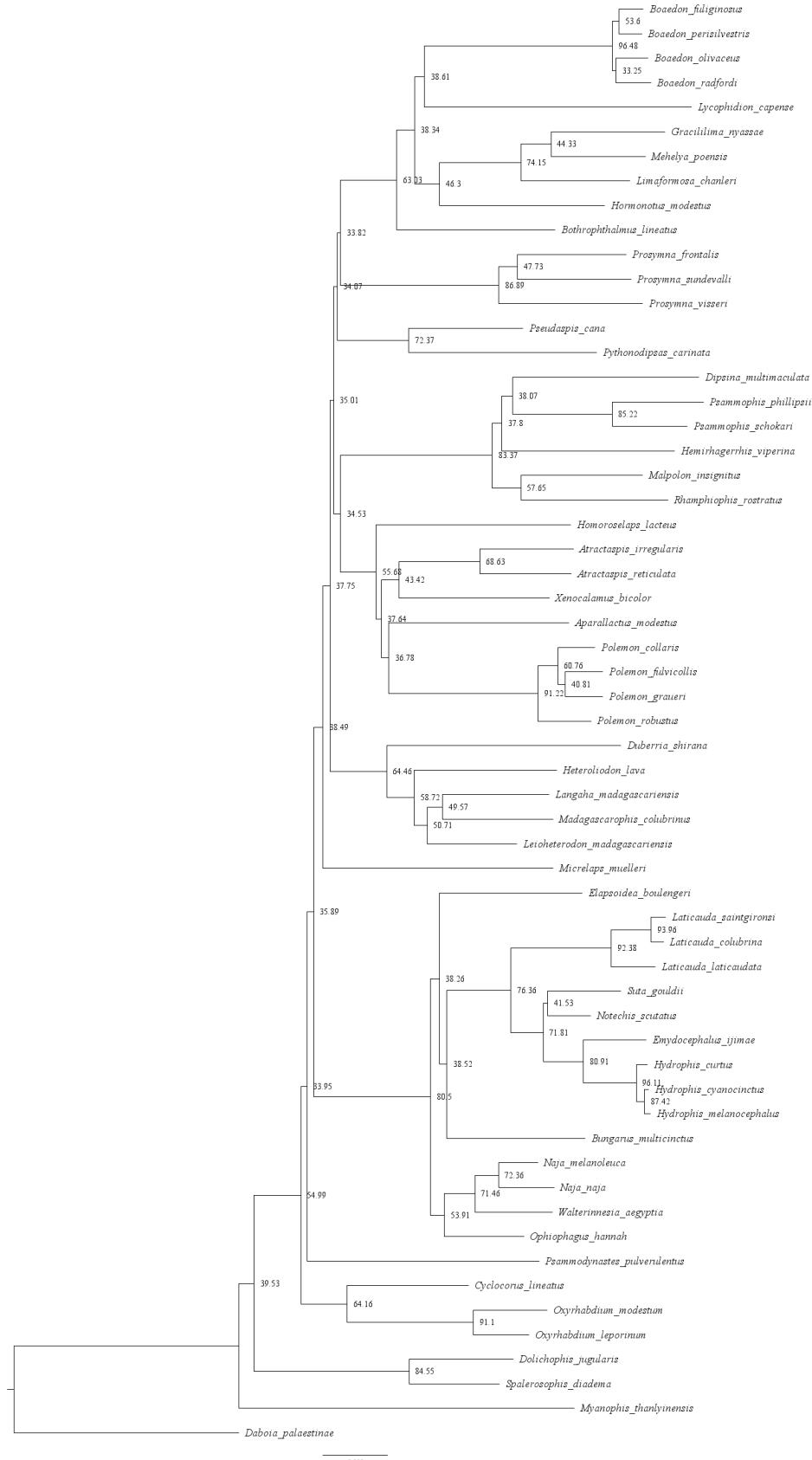


Fig. S17: Site concordance factors received by the branches in the 50 % complete UCE ML phylogeny.

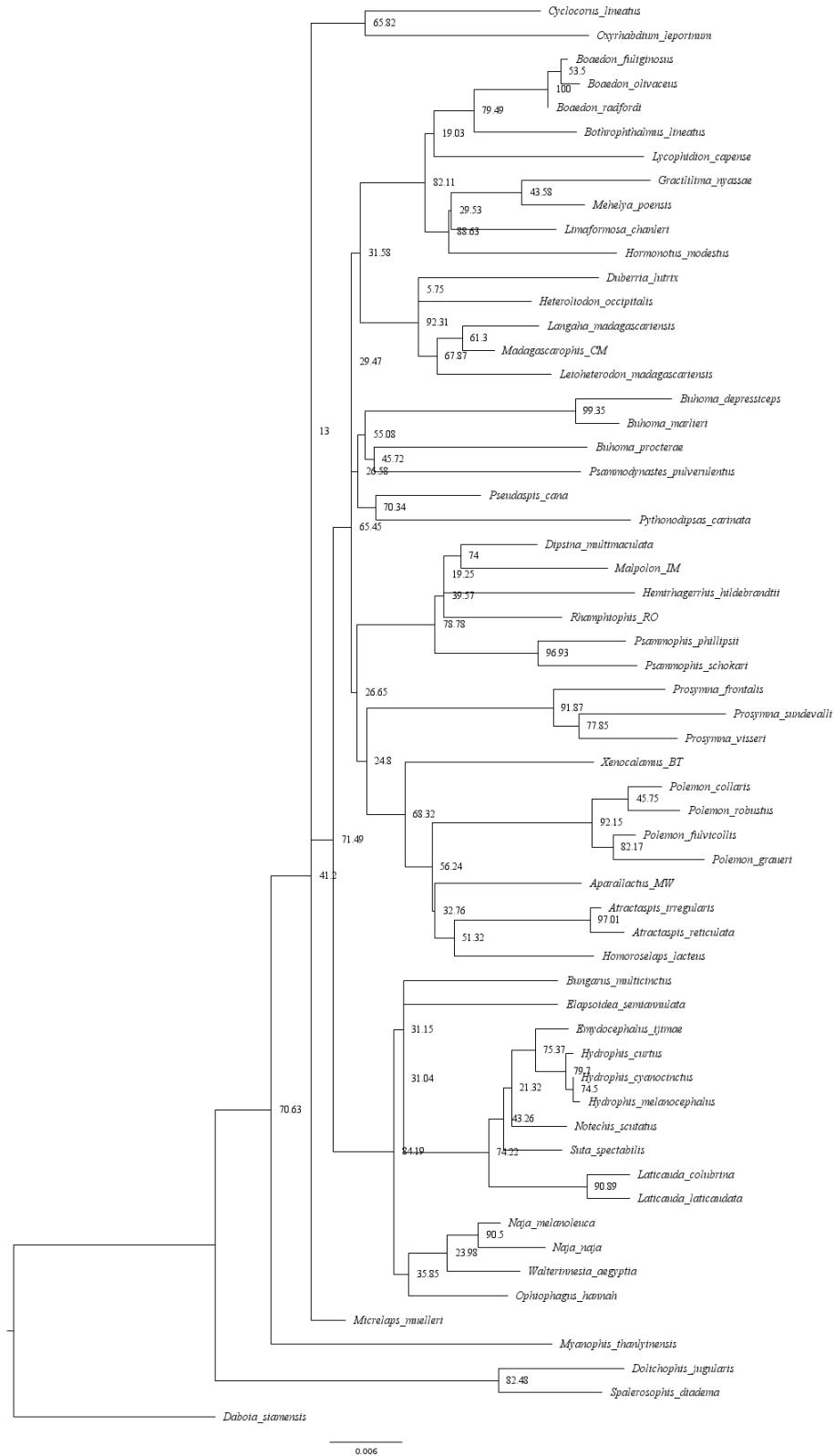


Fig. S18: Site concordance factors received by the branches in the traditional nuclear marker ML phylogeny.

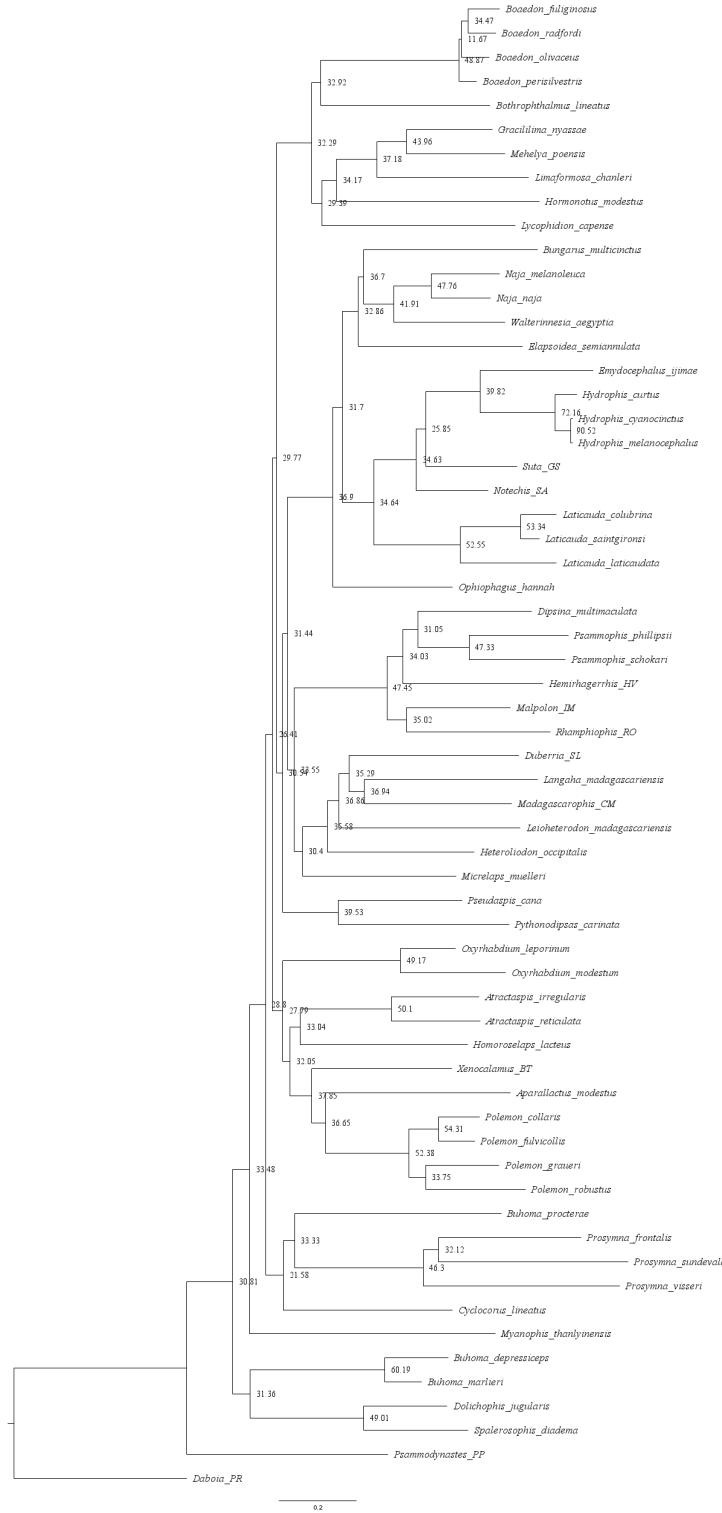


Fig. S19: Site concordance factors received by the branches in the traditional mitochondrial marker ML phylogeny.

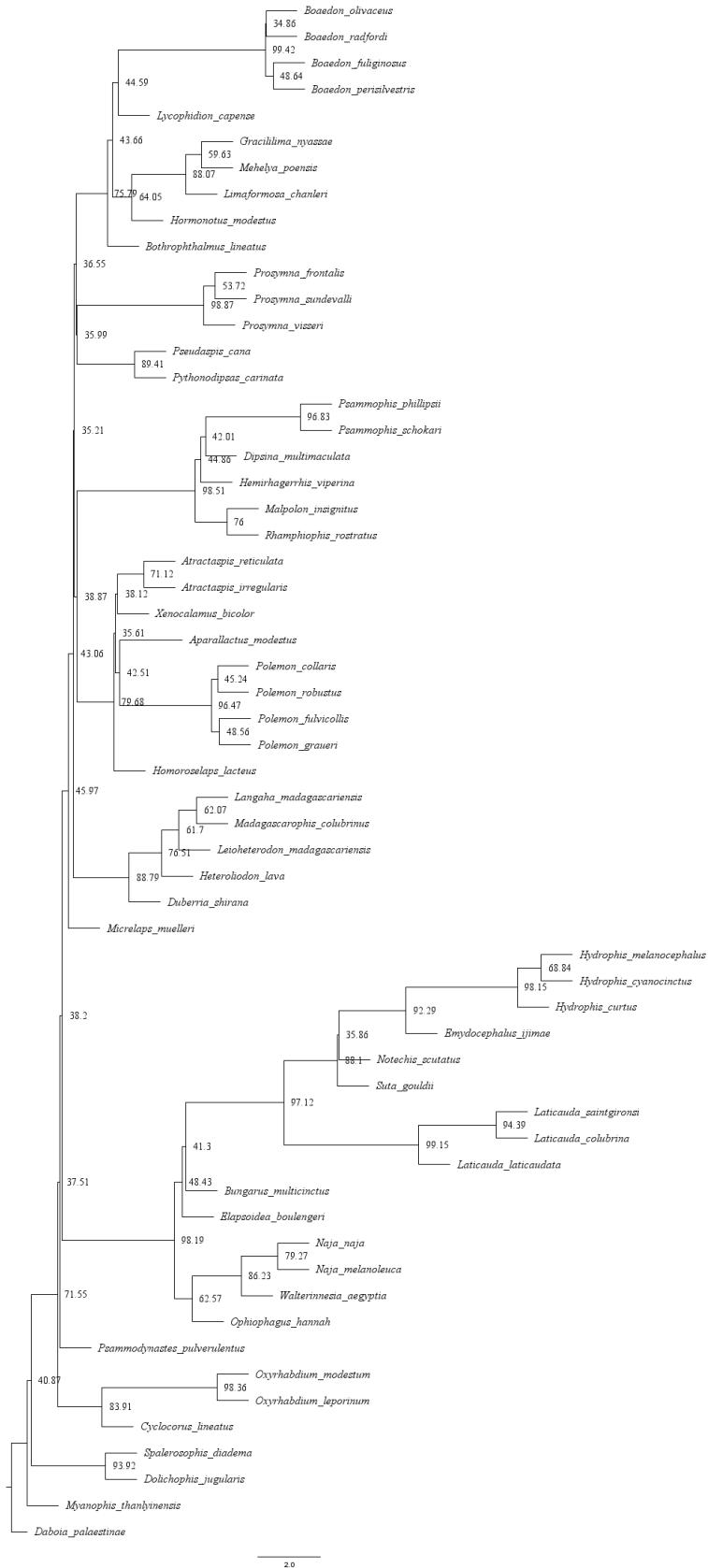


Fig. S20: Quartet support on the branches of the 50 % complete UCE wASTRAL-h phylogeny.

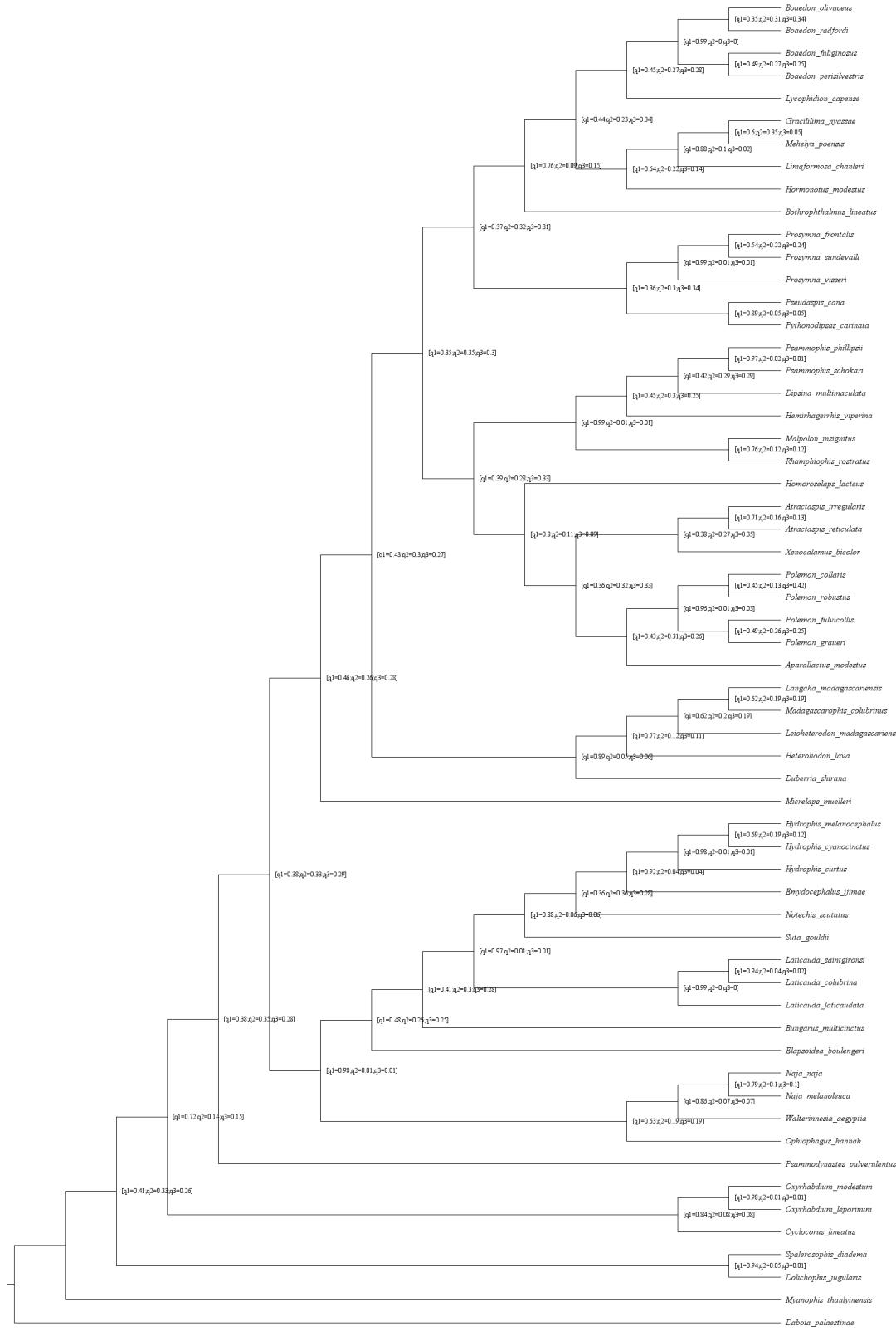


Fig. S21: Quartet support for the best and the alternative resolutions of the 50 % complete UCE wASTRAL-h phylogeny.

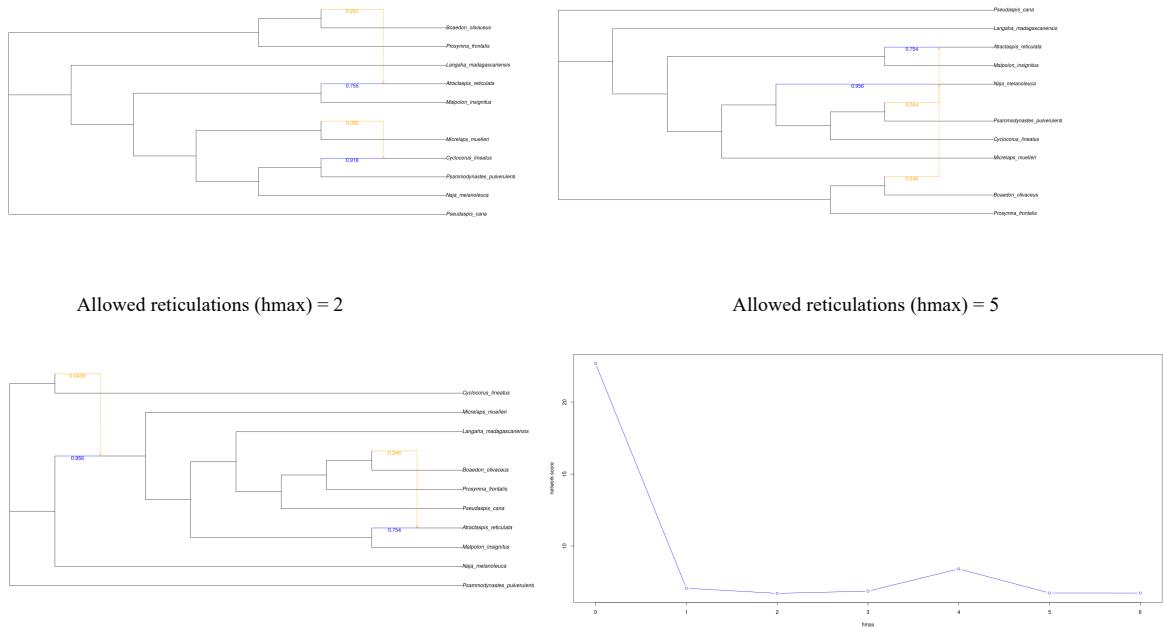
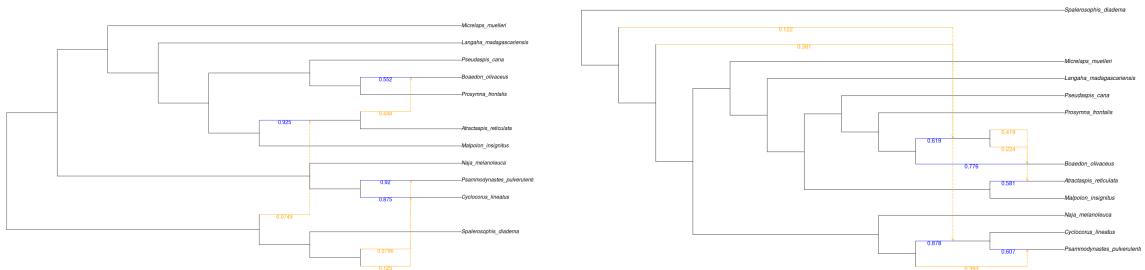


Fig. S22: Three top log-likelihood achieving MSCNs estimated by PhyloNetworks and plot of reticulations again the log-likelihoods in the visualisation format preferred by PhyloNetworks developers.



Allowed reticulations = 5

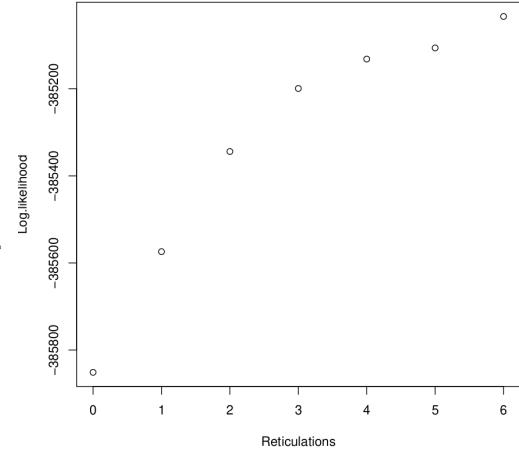
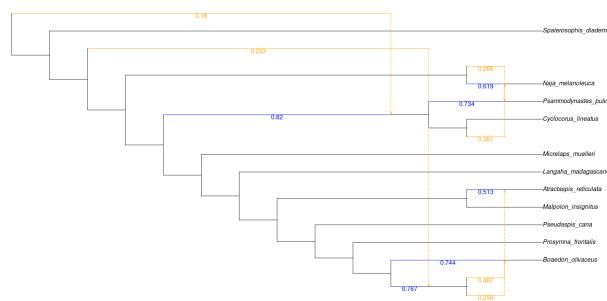


Fig. S23: Three top log-likelihood achieving MSCNs estimated by PhyloNet and plot of reticulations again the log-likelihoods (the plot basically conveys the same kind of information as in the previous figure).

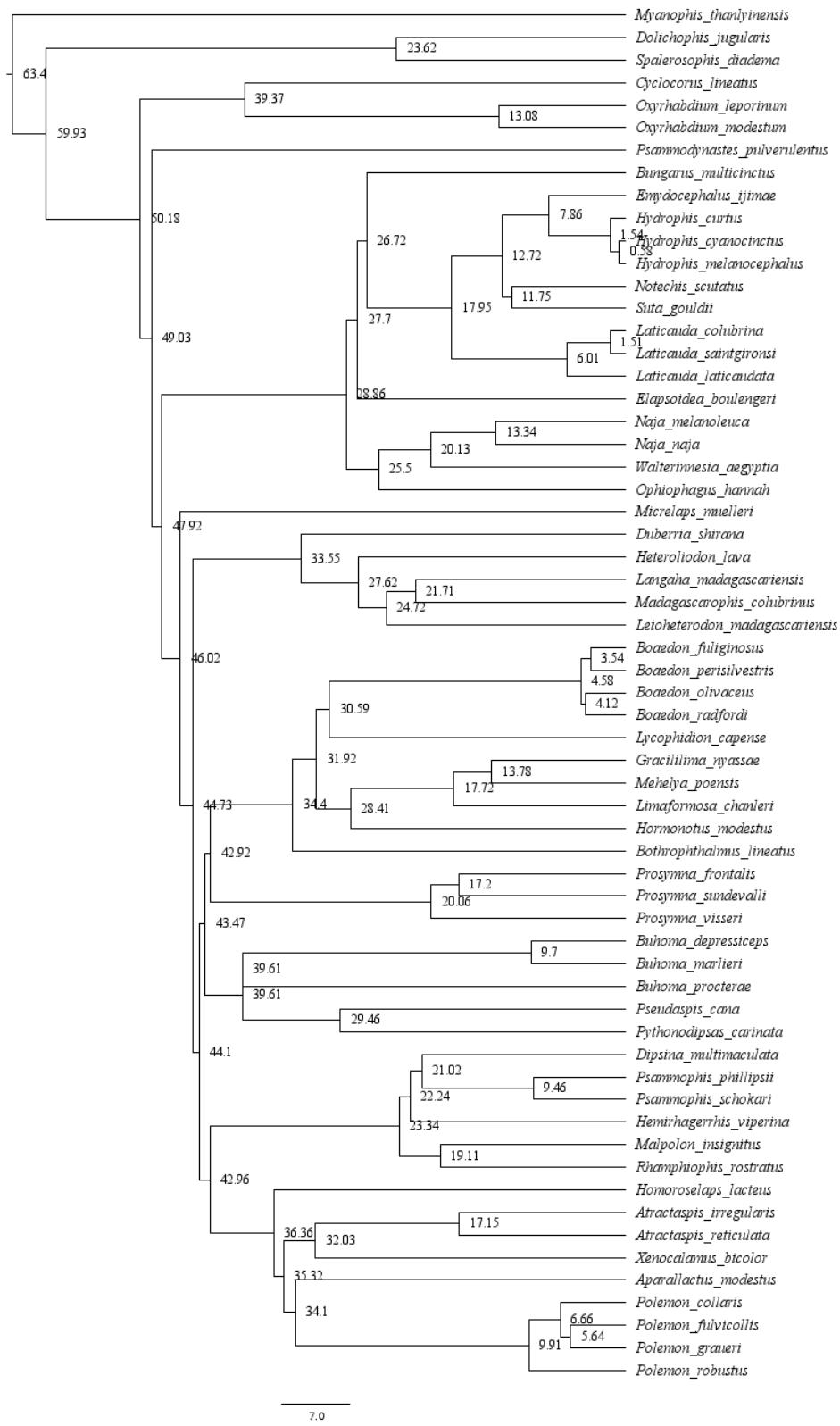


Fig. S24: Time-calibrated phylogeny of Elapoidea, from 95 % UCE and traditional nuclear loci dataset. Divergence times on the branches.

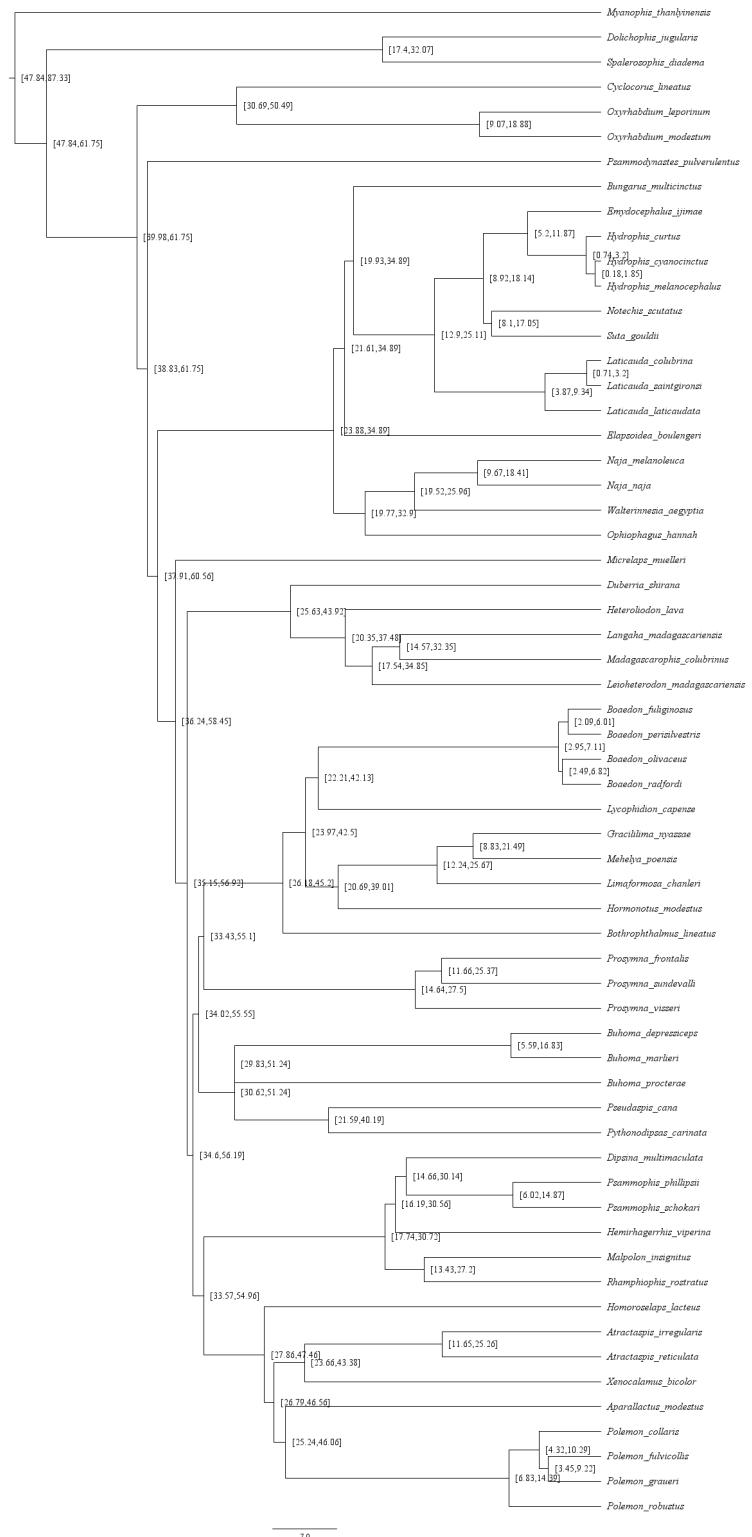


Fig. S25: Time-calibrated phylogeny of Elapoidea, from 95 % UCE and traditional nuclear loci dataset. 95 % confidence interval around the divergence times on the branches.

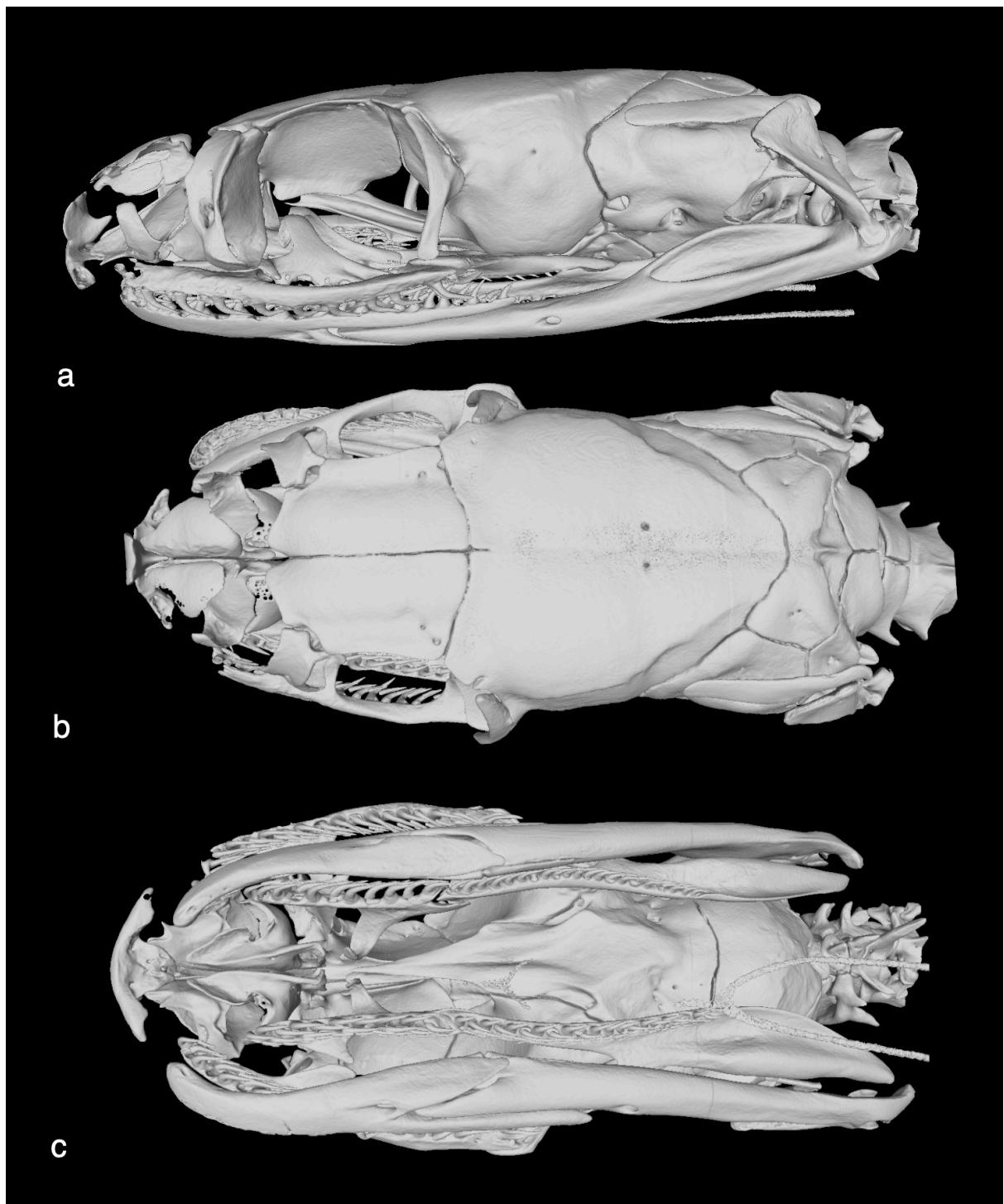


Fig. S26: Lateral (a), dorsal (b) and ventral (c) views of the cranium of *Buhoma marlieri* (BE-RBINS-VER-REP-8620)

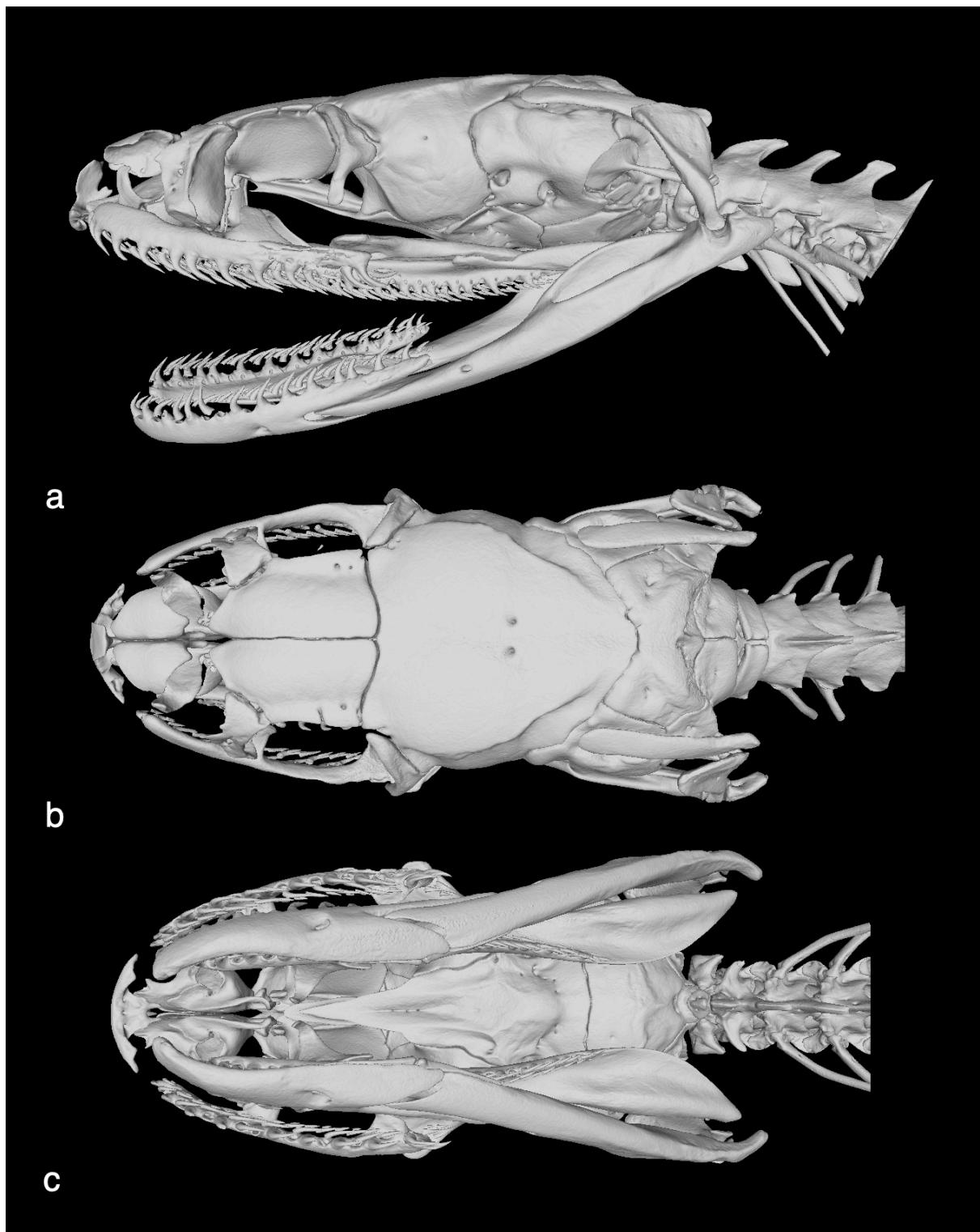


Fig. S27: Lateral (a), dorsal (b) and ventral (c) views of the cranium of the holotype of *Buhoma marlieri* (BE-RMCA-VER-REP 18091).

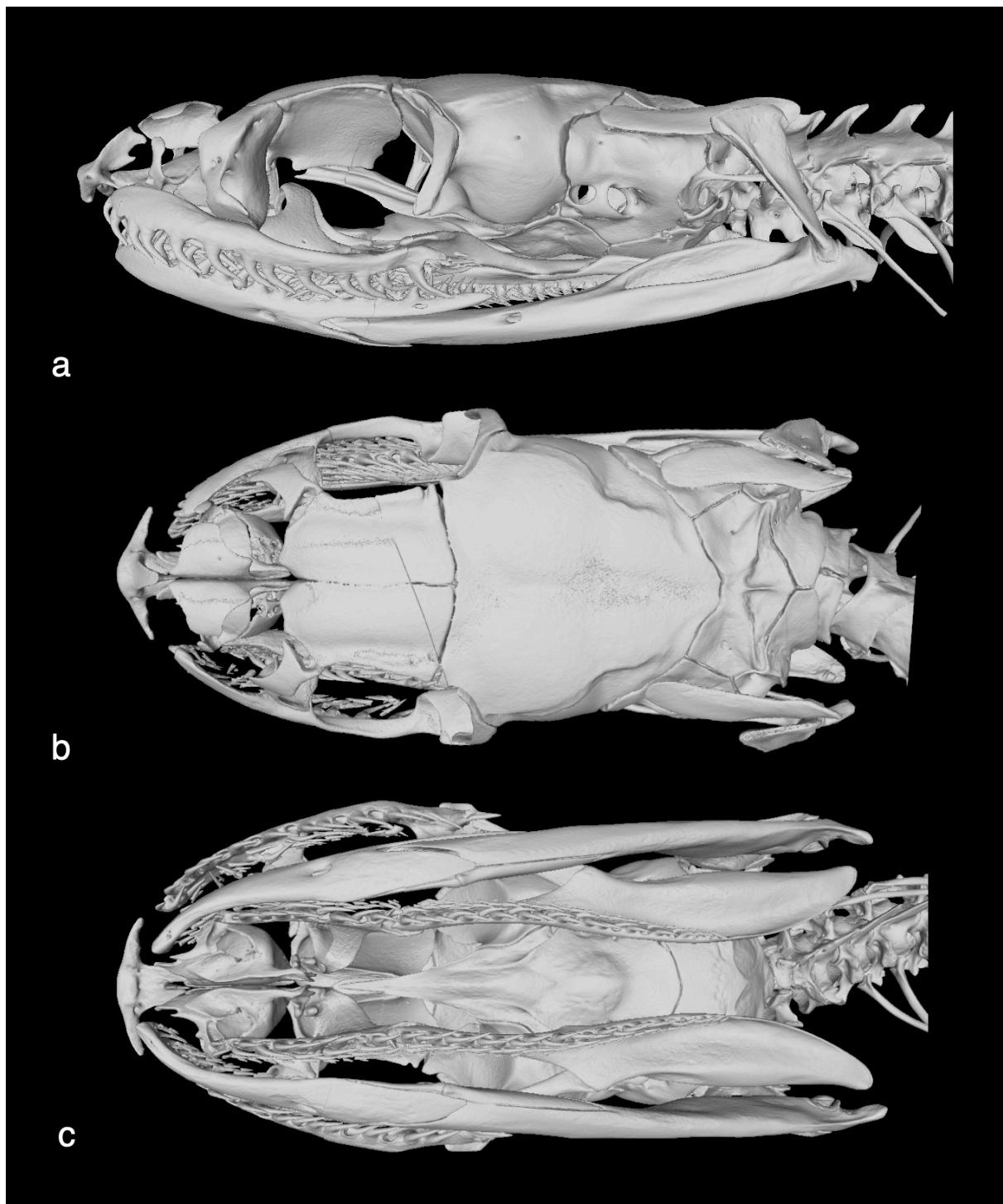


Fig. S28: Lateral (a), dorsal (b) and ventral (c) views of the cranium of *Buhoma procterae* (BEBRINS-VER-REP-18541).

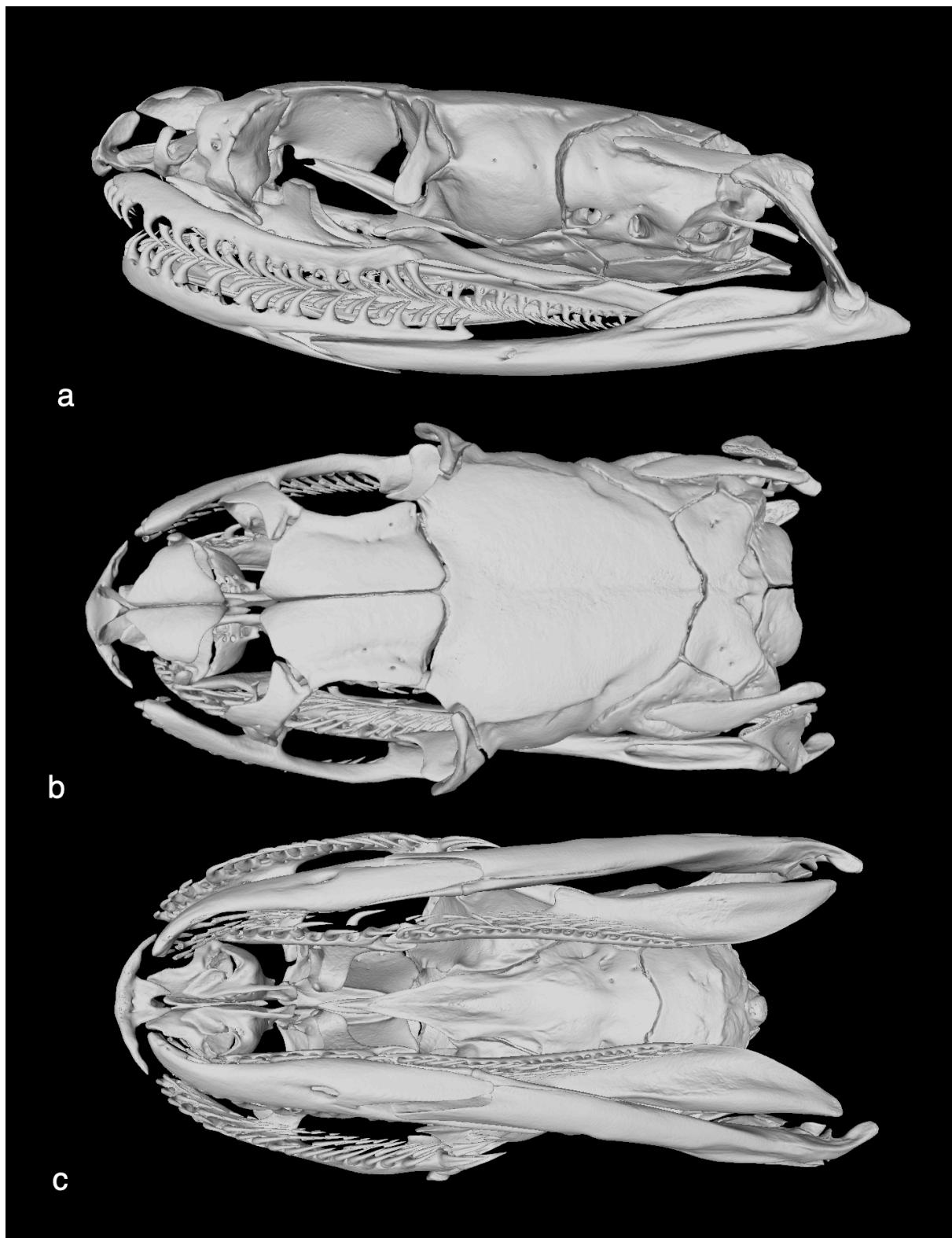


Fig. S29: Lateral (a), dorsal (b) and ventral (c) views of the cranium of *Buhoma vauerocegae* (BE-RBINS-VER-REP-18542).

Supplementary tables

Table S1 (next page): Accession number of traditional nuclear and mitochondrial loci. The accession numbers in blue are the sequences generated in this study; ‘Reference genome’ means the sequence of the traditional nuclear marker has been harvested from the reference genome; ‘mitochondrion’ means the sequence of the mitochondrial marker has been harvested from a complete mitochondrial genome; ‘Alignment issue’ means sequence for the particular locus is available for the species in question but it does not align with most of the other sequences that were used; the first column lists the names of the species in the UCE dataset (e.g., *Heteroliodon lava* contributes the UCE sequences whereas some of the traditional marker sequences are of *H. occipitalis*; in such cases, however, an overwhelming majority of sequence data is contributed by the former); the last column lists the names used for composites in the – traditional nuclear marker dataset (traditional mito-nuclear marker dataset) [traditional mitochondrial marker datasets]; composite names are formed from the first letter of the specific epithet (e.g., *Daboia* PSR = *Daboia palaestinae* + *siamensis* + *russelii*).

Family/subfamily	Species (named as in the UCE data)	<i>12s</i>	<i>16s</i>	<i>ND4</i>	<i>CYTB</i>	<i>BDNF</i>	<i>RAG1</i>	<i>RAG2</i>	<i>C-MOS</i>	Renaming of composites
Atractaspidinae	<i>Atractaspis reticulata</i>	NA	MK621470	MK621528	MK621586	NA	MK621501	NA	MK621643	
	<i>Atractaspis irregularis</i>	NA	MK621473	MK621570	MK621629	JN614212	MK621517	NA	MK621648	
	<i>Aparallactus modestus</i>	FJ404130	MG746954	MG775975	AY612007	EU402626 (<i>A. werneri</i>)	MG775761	FJ404405	MG775861	<i>Aparallactus MW</i>
	<i>Homoroselaps lacteus</i>	KX694590	MK621499	MK621583	MK621641	JQ599029	MK621524	FJ404411	MK621677	
	<i>Polemon collaris</i>	FJ404139	MG746931	MG775943	AY612029	NA	MG775736	FJ404414	MG775829	
	<i>Polemon fulvicollis</i>	NA	MG746942	MG775949	MG746837	NA	NA	NA	MG775837	
	<i>Polemon graueri</i>	NA	MG746939	MG775948	MG746835	NA	MG775742	NA	MG775836	
	<i>Polemon robustus</i>	NA	MG746937	MG775946	MG746831	NA	MG775739	NA	MG775832	
	<i>Xenocalamus bicolor</i>	FJ404141 (<i>X. transvaalensis</i>)	MG746906	MG775913	MG746796	NA	MG775716	NA	AY611934 (<i>X. transvaalensis</i>)	<i>Xenocalamus BT</i>
Buhoma	<i>Buhoma procterae</i>	FJ404148	AY611818	DQ486328	DQ486353	NA	NA	FJ404423	DQ486177	
	<i>Buhoma depressiceps</i>	FJ404147	OR295386	OR296691	OR296690	OR296686	OR296692	FJ404422	OR296688	
	<i>Buhoma marlieri</i>	NA	OR295387	Discarded	Discarded	OR296687	OR296693	NA	OR296689	
Cyclocoridae	<i>Cyclocorus lineatus</i>	NA	NA	NA	MG458749	NA	NA	NA	MG458759	
	<i>Oxyrhabdium leporinum</i>	NA	NA	NA	MN166286	NA	NA	FJ404466	MN166283	
	<i>Oxyrhabdium modestum</i>	NA	NA	NA	MG458756	NA	NA	NA	NA	
Psammodynastidae new family	<i>Psammodynastes pulverulentus</i>	MK065545	MK194116	KX660600 (<i>P. pictus</i>)	AF471031	Reference genome	Reference genome	Reference genome	Reference genome	<i>Psammodynastes PP</i> (<i>Psammodynastes pulverulentus</i>)
Elapidae	<i>Emydocephalus ijimae</i>	NC_066234	NC_066234	NC_066234	NC_066234	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Elapoidea boulengeri</i>	AF544745 (<i>E. semiannulata</i>)	JF357946 (<i>E. semiannulata</i>)	JF357928 (<i>E. semiannulata</i>)	AF039260 (<i>E. semiannulata</i>)	FJ433987 (<i>E. semiannulata</i>)	Alignment issue	EF144098 (<i>E. semiannulata</i>)	AF544678 (<i>E. semiannulata</i>)	<i>Elapoidea semiannulata</i>
	<i>Bungarus multicinctus</i>	MK065561	MK194133	MN165167	AJ565002	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Laticauda laticaudata</i>	KX239655	KX239663	FJ606538	AB701328	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Laticauda colubrina</i>	KX239654	MK193892	EU546998	KX239643	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Laticauda saintgironsi</i>	NA	NA	FJ606507	NA	NA	NA	NA	NA	
	<i>Hydrophis cyanocinctus</i>	KX239648	MK194271	FJ593215	KX239640	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Hydrophis curtus</i>	KX239653	KJ653939	KJ653856	KJ653904	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Hydrophis melanocephalus</i>	MK775532	MK775532	MK775532	MK775532	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Notechis scutatus</i>	U96802	KU323981	EU547034 (<i>N. ater</i>)	LC640464	Reference genome	Reference genome	Reference genome	Reference genome	<i>Notechis SA</i> (<i>Notechis scutatus</i>)
	<i>Naja naja</i>	EU547088	GQ359756	MT346908	MT346712	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Naja melanoleuca</i>	U96801	MF497427	MH337394	MH337588	NA	MT347390	NA	AY611904	
	<i>Ophiophagus hannah</i>	JN687930	JN687931	MZ343823	MZ343887	Reference genome	Reference genome	Reference genome	Reference genome	
	<i>Suta gouldii</i>	NA	NA	MT151759	NA	NA	EU546889 (<i>Suta spectabilis</i>)	NA	EU546928 (<i>Suta spectabilis</i>)	<i>Suta GS</i> (<i>Suta spectabilis</i>)
	<i>Walterinnesia aegyptia</i>	U96807	HQ267785	MT346955	MT346782	NA	MT347441	NA	MT347033	
Lamprophiinae	<i>Boaedon fuliginosus</i>	FJ404165	AY611881	KM519696	KM519716	EU402646	KM519732	FJ404438	FJ404266	
	<i>Boaedon olivaceus</i>	FJ404170	KX277253	KM519697	KM519717	NA	KM519731	FJ404443	FJ404271	
	<i>Boaedon perisilvestris</i>	NA	KX249794	NA	NA	NA	NA	NA	NA	
	<i>Boaedon radfordi</i>	NA	NA	KM519694	KM519713	NA	KM519728	NA	KM519748	
	<i>Bothropthalmus lineatus</i>	FJ404146	FJ404198	FJ404349	LC640409	NA	NA	FJ404421	FJ404251	
	<i>Hormonotus modestus</i>	FJ404159	FJ404195	FJ404360	FJ404296	NA	NA	FJ404433	FJ404261	
	<i>Gracililima nyassae</i>	FJ404182	AY611896	HQ207150	MF804432	NA	NA	NA	MF804462	

	<i>Limaformosa chanleri</i>	NA	NA	NA	MF804439	NA	NA	NA	MF804469	
	<i>Lycopodium capense</i>	FJ404178	AY611838	FJ404376	MT433521	EU402652	Alignment issue	FJ404450	AY611930	
	<i>Mehelya poensis</i>	FJ404183	AY611863	FJ404380	AY612045	NA	NA	FJ404454	AY611954	
Micrelapidae	<i>Micrelaps muelleri</i>	NA	NA	MG776013	MW075289	NA	NA	NA	MW075300	
Prosymninae	<i>Prosymna frontalis</i>	KR814630	KR814655	KR814707	MT482414	NA	MT460640	NA	MT460582	
	<i>Prosymna sundevalli</i>	NA	NA	NA	MT482424	NA	MT460650	NA	MT460590	
	<i>Prosymna visseri</i>	FJ404192	AY188072	NA	MT482427	NA	MT460652	FJ404463	FJ404292	
Psammophiinae	<i>Dipsina multimaculata</i>	NA	NA	DQ486332	DQ486357	NA	NA	NA	DQ486181	
	<i>Hemirhagerrhis viperina</i>	FJ404134 (<i>H. hildebrandtii</i>)	FJ404214 (<i>H. hildebrandtii</i>)	DQ486289	DQ486453	NA	NA	FJ404409 (<i>H. hildebrandtii</i>)	FJ404239 (<i>H. hildebrandtii</i>)	<i>Hemirhagerrhis HV (Hemirhagerrhis hildebrandtii)</i>
	<i>Malpolon insignitus</i>	DQ451951	AY611851	FJ404320 (<i>M. monspessulanus</i>)	AY612033	OL547595 (<i>M. monspessulanus</i>)	KY762208 (<i>M. monspessulanus</i>)	FJ404390 (<i>M. monspessulanus</i>)	AY611942	<i>Malpolon IM</i>
	<i>Rhamphiophis rostratus</i>	FJ404126	AY611897	FJ404329	DQ486394	JQ599049 (<i>R. oxyrhynchus</i>)	NA	FJ404401	DQ486187	<i>Rhamphiophis RO</i>
	<i>Psammophis phillipsii</i>	FJ404120	MK005716	MK032669	LC640454	NA	NA	FJ404395	AY611970	
	<i>Psammophis schokari</i>	HQ658448	HQ658453	MG003080	MG003028	NA	NA	FJ404396	MG002958	
Pseudaspidinae	<i>Pseudaspis cana</i>	FJ404187	AY611898	FJ404384	AY612080	NA	NA	FJ404458	AY058942	
	<i>Pythonodipsas carinata</i>	FJ404189	AY188075	FJ404386	AY188036	NA	NA	FJ404460	AY187997	
Pseudoxyrhophiinae	<i>Duberria shirana</i>	FJ404154 (<i>D. lutrix</i>)	KX694640 (<i>D. lutrix</i>)	LR798686 (<i>D. lutrix</i>)	LR798605	NA	KX695083 (<i>D. lutrix</i>)	FJ404428 (<i>D. lutrix</i>)	AF471138 (<i>D. lutrix</i>)	<i>Duberria SL (Duberria lutrix)</i>
	<i>Heteroliodon lava</i>	FJ404158 (<i>H. occipitalis</i>)	FJ404211 (<i>H. occipitalis</i>)	NA	FJ404308 (<i>H. occipitalis</i>)	NA	NA	FJ404432 (<i>H. occipitalis</i>)	FJ387211 (<i>H. occipitalis</i>)	<i>Heteroliodon occipitalis</i>
	<i>Langaha madagascariensis</i>	FJ404172	AY188059	FJ404370	AY188020	NA	NA	FJ404445	AY187981	
	<i>Leioheterodon madagascariensis</i>	KX694599	AF544797	FJ404371	KX694881	FJ433992	Alignment issue	EF144103	KX694824	
	<i>Madagascarophis colubrinus</i>	FJ404181 (<i>M. meridionalis</i>)	MG189475	MCU49313	AY586253	JQ073077 (<i>M. meridionalis</i>)	NA	KU925301	AY586226	<i>Madagascarophis CM</i>
Colubridae (outgroup)	<i>Dolichophis jugularis</i>	AY039152	AY376769	AY487046	AY486917	NA	NA	NA	AY486941	
	<i>Spalerosophis diadema</i>	AY039148	MG700257	AY487059	AY486926	NA	Alignment issue	NA	AY486950	
Homalopsidae (outgroup)	<i>Myanophis thanlyinensis</i>	NC_060375 (mitochondrion)	NC_060375 (mitochondrion)	NC_060375 (mitochondrion)	NC_060375 (mitochondrion)	Reference genome	Reference genome	Reference genome	Reference genome	
Viperidae (outgroup)	<i>Daboia palaestinae</i>	JN870183	AJ275775	DQ305477 (<i>D. russelii</i>)	MF140586	LC519947 (<i>D. siamensis</i>)	Reference genome	MK194871 (<i>D. siamensis</i>)	Reference genome	<i>Daboia PSR (Daboia siamensis) [Daboia PR]</i>

Table S2–S5: Accession number of query sequences used to perform BLAST search against a reference genome to locate and extract a particular nuclear gene.

Table S2

Query	Subject genome	Gene targeted
EU402646	<i>Psammodynastes pulverulentus</i>	<i>BDNF</i>
FJ433986	<i>Myanophis thalyinensis</i>	<i>BDNF</i>
FJ433990	<i>Hydrophis curtus</i>	<i>BDNF</i>
FJ433990	<i>Hydrophis melanocephalus</i>	<i>BDNF</i>
FJ433990	<i>Hydrophis cyanocinctus</i>	<i>BDNF</i>
FJ433990	<i>Emydocephalus ijimae</i>	<i>BDNF</i>
FJ433990	<i>Laticauda colubrina</i>	<i>BDNF</i>
FJ433990	<i>Laticauda laticaudata</i>	<i>BDNF</i>
EU402656	<i>Notechis scutatus</i>	<i>BDNF</i>
LC519961	<i>Ophiophagus hannah</i>	<i>BDNF</i>
FJ433990	<i>Bungarus multicinctus</i>	<i>BDNF</i>
LC533897	<i>Naja naja</i>	<i>BDNF</i>

Table S3

Query	Subject genome	Gene targeted
MG458761	<i>Psammodynastes pulverulentus</i>	<i>C-MOS</i>
JX463013	<i>Myanophis thanlyinensis</i>	<i>C-MOS</i>
KT965865	<i>Hydrophis curtus</i>	<i>C-MOS</i>
KT965865	<i>Hydrophis melanocephalus</i>	<i>C-MOS</i>
KT965865	<i>Hydrophis cyanocinctus</i>	<i>C-MOS</i>

KT965865	<i>Emydocephalus ijimae</i>	<i>C-MOS</i>
AF544702	<i>Laticauda colubrina</i>	<i>C-MOS</i>
AF544702	<i>Laticauda laticaudata</i>	<i>C-MOS</i>
EU546944	<i>Notechis scutatus</i>	<i>C-MOS</i>
KX694798	<i>Ophiophagus hannah</i>	<i>C-MOS</i>
AY058924	<i>Bungarus multicinctus</i>	<i>C-MOS</i>
EU366445	<i>Naja naja</i>	<i>C-MOS</i>
AF471156	<i>Daboia siamensis</i>	<i>C-MOS</i>

Table S4

Query	Subject genome	Gene targeted
MT347390	<i>Psammodynastes pulverulentus</i>	<i>RAG1</i>
EU546908	<i>Myanophis thanlyinensis</i>	<i>RAG1</i>
EU546889	<i>Hydrophis curtus</i>	<i>RAG1</i>
EU546889	<i>Hydrophis melanocephalus</i>	<i>RAG1</i>
EU546889	<i>Hydrophis cyanocinctus</i>	<i>RAG1</i>
EU546908	<i>Emydocephalus ijimae</i>	<i>RAG1</i>
EU546908	<i>Laticauda colubrina</i>	<i>RAG1</i>
EU546908	<i>Laticauda laticaudata</i>	<i>RAG1</i>
EU546905	<i>Notechis scutatus</i>	<i>RAG1</i>
MZ753612	<i>Ophiophagus hannah</i>	<i>RAG1</i>
JF357954	<i>Bungarus multicinctus</i>	<i>RAG1</i>
MT347390	<i>Naja naja</i>	<i>RAG1</i>
EU546908	<i>Daboia siamensis</i>	<i>RAG1</i>

Table S5

Query	Subject genome	Gene targeted
MK194960	<i>Psammodynastes pulverulentus</i>	<i>RAG2</i>
EF144097	<i>Myanophis thanlyinensis</i>	<i>RAG2</i>
MK195117	<i>Hydrophis curtus</i>	<i>RAG2</i>
MK195117	<i>Hydrophis melanocephalus</i>	<i>RAG2</i>
MK195117	<i>Hydrophis cyanocinctus</i>	<i>RAG2</i>
MK195117	<i>Emydocephalus ijimae</i>	<i>RAG2</i>
MK194731	<i>Laticauda colubrina</i>	<i>RAG2</i>
MK194731	<i>Laticauda laticaudata</i>	<i>RAG2</i>
MK195117	<i>Notechis scutatus</i>	<i>RAG2</i>
MK194875	<i>Ophiophagus hannah</i>	<i>RAG2</i>
MK195078	<i>Bungarus multicinctus</i>	<i>RAG2</i>
MK195061	<i>Naja naja</i>	<i>RAG2</i>

Table S6: MorphoSource ark number+links to the slices and 3D volumes of the micro-CT

scans generated in this study

Catalogue number	Species	Slices	3DModel
BE-RBINS-VER-REP-43	<i>Ophiophagus hannah</i>	http://n2t.net/ark:/87602/m4/541884	http://n2t.net/ark:/87602/m4/541004
BE-RBINS-VER-REP-19300	<i>Naja melanoleuca</i>	http://n2t.net/ark:/87602/m4/541887	http://n2t.net/ark:/87602/m4/541011
BE-RBINS-VER-REP-19104	<i>Naja annulata</i>	http://n2t.net/ark:/87602/m4/541890	http://n2t.net/ark:/87602/m4/541017

BE-RBINS-VER-TYPES-2612	<i>Elapoidea trapei</i>	http://n2t.net/ark:/87602/m4/541893	http://n2t.net/ark:/87602/m4/541034
BE-RBINS-VER-REP-8408	<i>Pseudaspis cana</i>	http://n2t.net/ark:/87602/m4/541039	http://n2t.net/ark:/87602/m4/541896
BE-RBINS-VER-REP-19125	<i>Mehelya poensis</i>	http://n2t.net/ark:/87602/m4/541899	http://n2t.net/ark:/87602/m4/541043
BE-RMCA-VER-R.30641	<i>Mehelya nyassae</i>	http://n2t.net/ark:/87602/m4/541072	http://n2t.net/ark:/87602/m4/541082
BE-RBINS-VER-REP-18885	<i>Boaedon olivaceus</i>	http://n2t.net/ark:/87602/m4/541052	http://n2t.net/ark:/87602/m4/541054
BE-RMCA-VER-REP-14864	<i>Lycodonomorphus subtaeniatus</i>	http://n2t.net/ark:/87602/m4/541669	http://n2t.net/ark:/87602/m4/541671
BE-RBINS-VER-REP-18542	<i>Buhoma vauerocegae</i>	http://n2t.net/ark:/87602/m4/541059	http://n2t.net/ark:/87602/m4/541061
BE-RMCA-VER-REP 18091	<i>Buhoma marlieri</i> Holotype	http://n2t.net/ark:/87602/m4/543336	http://n2t.net/ark:/87602/m4/543342
BE-RBINS-VER-REP-8620	<i>Buhoma marlieri</i>	http://n2t.net/ark:/87602/m4/541067	http://n2t.net/ark:/87602/m4/541075
BE-RBINS-VER-REP-16404	<i>Buhoma depressiceps</i>	http://n2t.net/ark:/87602/m4/541080	http://n2t.net/ark:/87602/m4/541091
BE-RBINS-VER-REP-18541	<i>Buhoma procterae</i>	http://n2t.net/ark:/87602/m4/541676	http://n2t.net/ark:/87602/m4/541678
RBINS 9284	<i>Psammophis mossambicus</i>	http://n2t.net/ark:/87602/m4/541683	http://n2t.net/ark:/87602/m4/541688
BE-RBINS-VER-REP-561	<i>Malpolon monspessulanus</i>	http://n2t.net/ark:/87602/m4/541692	http://n2t.net/ark:/87602/m4/541694
BE-RBINS-VER-REP-6719	<i>Lycodonomorphus inornatus</i>	http://n2t.net/ark:/87602/m4/541699	http://n2t.net/ark:/87602/m4/541906

BE-RBINS-VER- REP-5069	<i>Rhamphiophis rostratus</i>	http://n2t.net/ark:/87602/m 4/541703	http://n2t.net/ark:/87602/ m4/541908
BE-RBINS-VER- REP-18633	<i>Kladirostratus acutus</i>	http://n2t.net/ark:/87602/m 4/541712	http://n2t.net/ark:/87602/ m4/541910
BE-RMCA-VER- R.11	<i>Prosymna ambigua bocagei</i> Holotype	http://n2t.net/ark:/87602/m 4/541707	http://n2t.net/ark:/87602/ m4/541914
BE-RBINS-VER- REP-11733	<i>Prosymna sundevalli</i>	http://n2t.net/ark:/87602/m 4/541881	http://n2t.net/ark:/87602/ m4/541912