

## SUPPLEMENTAL TABLES AND FIGURES

**Table S1:** Sample information for newly-collected and previously-collected data. Museums refer to the museum where vouchered specimen is accessioned: AAU (Zoological Museum of Natural History, Addis Ababa University), AMS (Australian Museum), BNHS (Bombay Natural History Society), CAS (California Academy of Sciences), CHUNB (Coleção Herpetológica da Universidade de Brasília), FMNH (Florida Museum of Natural History), LACM (Los Angeles Natural History Museum), MAGNT (Museum and Art Gallery of the Northern Territory), MCZ (Museum of Comparative Zoology, Harvard), MVZ (Museum of Vertebrate Zoology, UC Berkeley), QM (Queensland Museum), SAMA (South Australian Museum), UMMZ (University of Michigan Museum of Zoology), USNM (National Museum of Natural History), WAM (Western Australian Museum).

sample	museum	species	family	source / SRA	#loci	avg. len (bp)
NTMR16167	MAGNT	<i>Acrochordus arafurae</i>	Acrochordidae	SAMN15718166	5071	991
UMFS_11534	UMMZ	<i>Acrochordus granulatus</i>	Acrochordidae	SAMN15718164	4744	520
FMNH230175	FMNH	<i>Gonocephalus doriae</i>	Agamidae	SAMN09221257	5208	1022
CAS_210725	CAS	<i>Leiolepis belliana</i>	Agamidae	Streicher et al. 2016	4526	355
AMSR122474	AMS	<i>Hypsilurus magnus</i>	Agamidae	SAMN15718177	5261	969
CHUNB18599	CHUNB	<i>Alopoglossus angulatus</i>	Alopoglossidae	SAMN15718124	5005	719
UMMZ_245044	UMMZ	<i>Ptychoglossus brevifrontalis</i>	Alopoglossidae	SAMN15718149	5141	841
CHUNB30685	CHUNB	<i>Amphisbaena brasiliiana</i>	Amphisbaenidae	SAMN15718119	5174	738
USNM576222	USNM	<i>Monopeltis guentheri</i>	Amphisbaenidae	SAMN09221386	5185	1264
UMFS_11782	UMMZ	<i>Pseudopus apodus</i>	Anguidae	SAMN15718141	5277	909
MVZ_Herp_177806	MVZ	<i>Abronia fuscolabialis</i>	Anguidae	SAMN09221319	5140	869
CAS_234252	CAS	<i>Anniella grinnelli</i>	Anguidae	SAMN09221162	5203	962
MVZ_Herp_257729	MVZ	<i>Anniella campi</i>	Anguidae	SAMN09221363	5251	1004
CHUNB39981	CHUNB	<i>Anilius scytale</i>	Aniliidae	SAMN15718133	5164	869
CHUNB73453	CHUNB	<i>Anilius scytale</i>	Aniliidae	SAMN15718134	5169	805
GRCOLLI23142	CHUNB	<i>Liotyphlops beui</i>	Anomalepididae	SAMN15718135	5084	976
CHUNB57731	CHUNB	<i>Liotyphlops ternetzii</i>	Anomalepididae	SAMN15718136	5048	762
UMMZ_Bipes_canaliculatus	UMMZ	<i>Bipes canaliculatus</i>	Bipedidae	SAMN15718169	5172	855
MVZ236256	MVZ	<i>Bipes biporus</i>	Bipedidae	Streicher and Wiens 2017	918	281

<b>UMFS_10995</b>	UMMZ	<i>Calabaria reinhardtii</i>	Boidae	SAMN15718162	4773	676
<b>UMFS_9997</b>	UMMZ	<i>Boa constrictor</i>	Boidae	SAMN15718150	5092	781
<b>DWCT_R228</b>		<i>Casarea dussumieri</i>	Bolyeriidae	Streicher and Wiens 2016	4028	381
<b>SAMAR29205</b>	SAM	<i>Saltuarius swaini</i>	Carphodactylidae	SAMN15718145	5207	818
<b>UMMZ_244247</b>	UMMZ	<i>Nephrurus levis</i>	Carphodactylidae	SAMN15718146	5123	765
<b>MVZ_230099</b>	MVZ	<i>Chamaeleo calyptatus</i>	Chamaeleonidae	Streicher et al. 2016	4636	382
<b>CAS_222087</b>	CAS	<i>Xenochrophis bellulus</i>	Colubridae	SAMN09221139	4976	959
<b>UMMZ_242524</b>	UMMZ	<i>Dendrelaphis calligaster</i>	Colubridae	SAMN15718138	4986	893
<b>MVZ_Herp_269290</b>	MVZ	<i>Sibon annulatus</i>	Colubridae	SAMN09221378	5026	911
<b>SDSU4354</b>		<i>Smaug mossambicus</i>	Cordylidae	Streicher and Wiens 2017	2054	288
<b>TJC564</b>	AAU	<i>Cordylus rivae</i>	Cordylidae	SAMN09221241	5228	862
<b>TJC811</b>		<i>Corytophanes hernandesii</i>	Corytophanidae	SAMN09221250	5275	918
<b>TOMH_86-271</b>		<i>Basiliscus basiliscus</i>	Corytophanidae	Streicher et al. 2016	4355	378
<b>UMMZ_201900</b>	UMMZ	<i>Cylindrophis ruffus</i>	Cylindrophiiidae	SAMN15718160	5178	930
<b>RAP0448</b>		<i>Cylindrophis maculatus</i>	Cylindrophiiidae	SAMN09221395	5201	848
<b>CHUNB47014</b>	CHUNB	<i>Anolis punctatus</i>	Dactyloidae	SAMN15718123	5159	683
<b>MVZ_Herp_263594</b>	MVZ	<i>Anolis petersii</i>	Dactyloidae	SAMN09221368	5324	796
<b>LSUMZH9546</b>	LSUMZ	<i>Dibamus novaeguineae</i>	Dibamidae	Streicher and Wiens 2017	2608	282
<b>UMMZ_244237</b>	UMMZ	<i>Lucasium squarrosom</i>	Diplodactylidae	SAMN15718117	5142	819
<b>QMJ57120</b>	QM	<i>Pseudothecadactylus australis</i>	Diplodactylidae	SAMN15718158	4532	632
<b>MCZ_Herp_R190692</b>	MCZ	<i>Celestus costatus</i>	Diploglossidae	SAMN09221295	5240	935
<b>MVZ_Herp_204069</b>	MCZ	<i>Celestus cyanochloris</i>	Diploglossidae	SAMN09221326	5158	967
<b>UMFS_10680</b>	UMMZ	<i>Calliophis bivirgatus</i>	Elapidae	SAMN15718157	5027	965
<b>FK_3102</b>	UMMZ	<i>Hydrophis platurus</i>	Elapidae	SAMN15718156	4939	912
<b>MVZ_Herp_189994</b>	MVZ	<i>Coleonyx switaki</i>	Eublepharidae	SAMN09221320	5128	992
<b>UMMZ_200325</b>	UMMZ	<i>Coleonyx variegatus</i>	Eublepharidae	SAMN15718144	5302	896
<b>WAMR176289</b>	WAM	<i>Gehyra nana</i>	Gekkonidae	SAMN15718155	5159	844
<b>CHUNB56575</b>	CHUNB	<i>Lygodactylus klugei</i>	Gekkonidae	SAMN15718120	5145	806

<b>AMB6860</b>		<i>Cordylosaurus subtessellatus</i>	Gerrhosauridae	Streicher and Wiens 2017	2836	280
<b>UMMZ_237560</b>	UMMZ	<i>Zonosaurus laticaudatus</i>	Gerrhosauridae	SAMN15718142	5275	883
<b>CHUNB52077</b>	CHUNB	<i>Micrablepharus maximiliani</i>	Gymnophthalmidae	SAMN06705339	5080	1086
<b>CHUNB56842</b>	CHUNB	<i>Loxopholis osvaldoi</i>	Gymnophthalmidae	SAMN15718125	4185	545
<b>UMFS_10133</b>	UMMZ	<i>Heloderma suspectum</i>	Helodermatidae	SAMN15718151	5021	626
<b>NTMR10697</b>	MAGNT	<i>Fordonia leucobalia</i>	Homalopsidae	SAMN15718174	4952	897
<b>UMMZ_227683</b>	UMMZ	<i>Homalopsis buccata</i>	Homalopsidae	SAMN15718173	4905	900
<b>MVZ_163062</b>	MVZ	<i>Morunasaurus annularis</i>	Hoplocercidae	Streicher et al. 2016	4152	364
<b>CHUNB74034</b>	CHUNB	<i>Hoplocercus spinosus</i>	Hoplocercidae	SAMN15718126	5314	885
<b>MVZ149849</b>	MVZ	<i>Iguana iguana</i>	Iguanidae	SAMN15718170	5274	1027
<b>MVZ_Herp_162071</b>	MVZ	<i>Ctenosaura clarki</i>	Iguanidae	SAMN09221314	5265	895
<b>CAS_228522</b>	CAS	<i>Eremias kavirensis</i>	Lacertidae	SAMN09221148	5062	572
<b>UMFS_12515</b>	UMMZ	<i>Podarcis erhardii</i>	Lacertidae	SAMN15718168	5045	731
<b>CAS_232085</b>	CAS	<i>Psammophis leithii</i>	Lamprophiidae	SAMN09221156	5049	970
<b>UMMZ_200061</b>	UMMZ	<i>Pseudoxyrhopus ambreensis</i>	Lamprophiidae	SAMN15718172	5061	1117
<b>ISIS_393113</b>		<i>Lanthanotus borneensis</i>	Lanthanotidae	Streicher and Wiens 2016	4819	337
<b>MCZ_Herp_R190725</b>	MCZ	<i>Leiocephalus melanochlorus</i>	Leiocephalidae	SAMN09221298	5320	852
<b>MCZ_Herp_R189884</b>	MCZ	<i>Leiocephalus macropus</i>	Leiocephalidae	SAMN09221291	5323	1009
<b>CHUNB62191</b>	CHUNB	<i>Enyalius bilineatus</i>	Leiosauridae	SAMN15718128	5295	878
<b>CHUNB64577</b>	CHUNB	<i>Enyalius bibronii</i>	Leiosauridae	SAMN15718127	5282	909
<b>CHUNB52064</b>	CHUNB	<i>Trilepida brasiliensis</i>	Leptotyphlopidae	SAMN06705334	4600	673
<b>CAS_223962</b>	CAS	<i>Namibiana labialis</i>	Leptotyphlopidae	SAMN09221141	4842	789
<b>MVZ_Herp_240678</b>	MVZ	<i>Liolaemus tregenzai</i>	Liolaemidae	SAMN09221344	5275	994
<b>MVZ_Herp_196648</b>	MVZ	<i>Liolaemus valdesianus</i>	Liolaemidae	SAMN09221324	5228	1000
<b>ZA_46400</b>		<i>Loxocemus bicolor</i>	Loxocemidae	Streicher and Wiens 2016	3666	369
<b>UMMZ_228595</b>	UMMZ	<i>Oplurus cyclurus</i>	Opluridae	Streicher et al. 2016	4775	373
<b>UMMZ_201904</b>	UMMZ	<i>Aplopeltura boa</i>	Pareidae	SAMN15718167	4984	857
<b>FK_2626</b>	UMMZ	<i>Pareas nuchalis</i>	Pareidae	SAMN15718165	5055	953

<b>MVZ161183</b>	MVZ	<i>Petrosaurus thalassinus</i>	Phrynosomatidae	Leache et al. 2015	520	495
<b>TWR_1745</b>		<i>Uta stansburiana</i>	Phrynosomatidae	Streicher et al. 2016	4981	277
<b>MCZ_Herp_R189902</b>	MCZ	<i>Tarentola crombiei</i>	Phyllodactylidae	SAMN09221293	5130	845
<b>CHUNB56581</b>	CHUNB	<i>Phyllopezus periosus</i>	Phyllodactylidae	SAMN15718121	5175	982
<b>CHUNB68997</b>	CHUNB	<i>Polychrus marmoratus</i>	Polychrotidae	SAMN15718130	5234	1151
<b>CHUNB11470</b>	CHUNB	<i>Polychrus acutirostris</i>	Polychrotidae	SAMN15718129	5254	996
<b>UMMZ_242601</b>	UMMZ	<i>Delma tincta</i>	Pygopodidae	SAMN15718175	5106	1137
<b>WAMR168645</b>	WAM	<i>Aprasia repens</i>	Pygopodidae	SAMN15718176	5128	1037
<b>UMFS_5617</b>	UMMZ	<i>Python regius</i>	Pythonidae	SAMN15718163	4785	624
<b>UMFS_11002</b>	UMMZ	<i>Aspidites melanocephalus</i>	Pythonidae	SAMN15718154	5031	642
<b>CAS195955</b>	CAS	<i>Rhineura floridana</i>	Rhineuridae	Streicher and Wiens 2017	3232	291
<b>SEW6684</b>		<i>Saproscincus lewisi</i>	Scincidae	SAMN15718152	5150	829
<b>UMMZ_242646</b>	UMMZ	<i>Ctenotus quattuordecimlineatus</i>	Scincidae	SAMN15718118	5190	968
<b>RAN_64845</b>	UMMZ	<i>Pygomeles sp.</i>	Scincidae	SAMN15718153	5043	622
<b>UMFS_10293</b>	UMMZ	<i>Shinisaurus crocodilurus</i>	Shinisauridae	SAMN15718139	4629	438
<b>MVZ_Herp_193268</b>	MVZ	<i>Aristelliger hechti</i>	Sphaerodactylidae	SAMN09221323	5236	837
<b>CHUNB74119</b>	CHUNB	<i>Gonatodes humeralis</i>	Sphaerodactylidae	SAMN15718122	5221	894
<b>MVZ247605</b>	MVZ	<i>Tupinambis teguixin</i>	Teiidae	SAMN15718148	5261	837
<b>CHUNB51969</b>	CHUNB	<i>Kentropyx calcarata</i>	Teiidae	SAMN06705324	5159	1145
<b>UMMZ_229268</b>	UMMZ	<i>Trachyboa boulengeri</i>	Tropidophiidae	SAMN15718161	5151	1052
<b>CHUNB37546</b>	CHUNB	<i>Uranoscodon superciliosus</i>	Tropiduridae	SAMN15718132	5295	923
<b>CHUNB62385</b>	CHUNB	<i>Stenocercus squarrosus</i>	Tropiduridae	SAMN15718131	5261	1125
<b>UMMZ_242536</b>	UMMZ	<i>Indotyphlops madgemintonae</i>	Typhlopidae	SAMN15718171	4906	990
<b>UMMZ_244201</b>	UMMZ	<i>Anilios waitii</i>	Typhlopidae	SAMN15718116	4671	746
<b>RAP0431</b>		<i>Rhinophis erangaviraji</i>	Uropeltidae	SAMN09221391	5104	1060
<b>ID_7603</b>	BNHS 3221	<i>Uropeltis macrolepis</i>	Uropeltidae	SAMN09221435	5210	879
<b>UMMZ_240786</b>	UMMZ	<i>Varanus griseus</i>	Varanidae	SAMN15718147	5201	643
<b>UMMZ_242696</b>	UMMZ	<i>Varanus eremius</i>	Varanidae	SAMN15718143	5242	894

<b>CHUNB71688</b>	CHUNB	<i>Bothrops moojeni</i>	Viperidae	SAMN15718137	5049	888
<b>MVZ_Herp_249821</b>	MVZ	<i>Causus maculatus</i>	Viperidae	SAMN09221351	4977	1057
<b>MVZ241283</b>	MVZ	<i>Cricosaura typica</i>	Xantusiidae	Streicher and Wiens 2017	2874	280
<b>LACM128548</b>	LACM	<i>Lepidophyma flavimaculatum</i>	Xantusiidae	Streicher and Wiens 2017	2078	283
<b>FK_3026</b>	UMMZ	<i>Xenopeltis unicolor</i>	Xenopeltidae	SAMN15718159	5182	1013
<b>UMFS_11796</b>	UMMZ	<i>Xenosaurus platyceps</i>	Xenosauridae	SAMN15718140	5256	1009
<b>taeGut2</b>		<i>Taeniopygia guttata</i>	outgroup	genome	5207	1098
<b>galGal5</b>		<i>Gallus gallus</i>	outgroup	genome	5241	1184
<b>hg38</b>		<i>Homo sapiens</i>	outgroup	genome	4500	1042
<b>allMis1</b>		<i>Alligator mississippiensis</i>	outgroup	genome	5245	1040
<b>chrPic1</b>		<i>Chrysemys picta</i>	outgroup	genome	5050	1030

**Table S2:** The 17 focal relationships tested, along with their possible topologies; numbering of relationships follows Figures 3 & 4 and Table 1. Topologies are ranked by their summed  $D_{LNL}$  support, and asterisks mark topologies recovered in the concatenated phylogeny (Fig. 2). Figure 2 also includes labels indicating family and higher-level names. Reported are the number of gene trees whose topology contained the given node, the sum of  $D_{LNL}$  values across all loci for which this topology had the highest likelihood, and the number of loci for which  $D_{LNL} > 2$  for that given topology.

Uncertain relationship	possible topologies	# supporting loci	summed $D_{LNL}$	# loci $D_{LNL} > 2$
<b>1. position of Anniellidae</b>	*sister to Anguidae	1444	6205.3	857
	sister to Anguidae & Diploglossidae	1016	3905.8	540
	sister to Diploglossidae	1071	3871.3	540
<b>2. position of Anomalepididae</b>	sister to Leptotyphlopidae & Typhlopidae	732	16273.4	1116
	*sister to all non-blind snakes	1210	6375.3	978
	sister to all other snakes	494	3405.3	364
<b>3. position of Bolyeriidae</b>	sister to Boidae	397	5242.2	749
	*sister to Pythonidae, Loxocemidae & Xenopeltidae	349	5032.1	807
<b>4. position of Cyliodactylidae &amp; Uropeltidae</b>	*sister to Bolyeriidae, Boidae, Pythonidae, Loxocemidae & Xenopeltidae	309	6878.2	797
	sister to Acrochordidae, Bolyeriidae, Boidae, Colubridae, Elapidae, Homalopsidae, Pythonidae, Lamprophiidae, Pareidae, Viperidae, Loxocemidae & Xenopeltidae	213	6864.0	805
	sister to Pythonidae, Loxocemidae & Xenopeltidae	170	1948.8	269
<b>5. position of Dibamidae</b>	sister to all other squamates	22	1381.45	84
	*sister to all non-geckos	56	614.2	123
	sister to Gekkota	502	415.9	90
<b>6. position of Diplodactylidae</b>	*sister to Carphodactylidae & Pygopodidae	1444	4761.7	721
	sister to Carphodactylidae	1000	4473.4	561
	sister to Pygopodidae	1026	3806.6	500
<b>7. position of Eublepharidae</b>	sister to Carphodactylidae, Pygopodidae & Diplodactylidae	1617	10059.7	1241
	*sister to Phyllodactylidae, Gekkonidae & Sphaerodactylidae	1388	7595.3	1095
<b>8. position of Gymnophthalmidae</b>	*sister to Teiidae & Alopoglossidae	1060	10313.8	1290
	sister to Alopoglossidae	958	6023.9	915
	sister to Teiidae	586	4391.1	627
<b>9. position of Homalopsidae</b>	*sister to Elapidae, Lamprophiidae & Colubridae	1166	10008.9	1185
	sister to Colubridae	766	5033.0	725
	sister to Elapidae & Lamprophiidae	474	3038.6	375
	sister to Elapidae	63	593.1	96
<b>10. position of Iguania</b>	*sister to Anguimorpha	1915	144533.3	4193
	sister to all other squamates	33	9844.0	572

<b>11. position of Lanthanotidae</b>	*sister to Varanidae	943	34384.1	1753
	sister to all other Anguimorpha	485	9090.0	932
<b>12. position of Rhineuridae</b>	sister to Bipedidae, Amphisbaenidae & Lacertidae	136	3438.2	518
	*sister to Lacertidae	276	3174.3	543
<b>13. position of Scincoidea</b>	*sister to Episquamata	2534	68572.7	4645
	sister to Lacertoidea	35	1998.5	210
<b>14. position of Serpentes</b>	*sister to Anguimorpha & Iguania	839	32076.5	1784
	sister to Anguimorpha	346	23858.6	983
<b>15. position of Typhlopidae</b>	*sister to Leptotyphlopidae	1917	21279.1	1882
	sister to all other snakes	460	2690.8	367
	sister to all non-blind snakes	401	2573.2	292
<b>16. position of Xenosauridae</b>	sister to Anniellidae, Anguinae, Diploglossidae & Helodermatidae	754	3589.9	444
	*sister to Helodermatidae	719	3565.7	493
	sister to Anguinae & Diploglossidae	790	2805.2	449
<b>17. relationship between Gekkota &amp; Scincoidea</b>	*Gekkota sister to Scincoidea & all other squamates	1653	14353.1	1779
	Gekkota and Scincoidea sister	1101	8411.0	1257

**Table S3:** Results of non-parametric testing across locus-specific metrics of quality, informativeness, and heterogeneity (Table 2). We compared differences in values for loci that supported the top topological resolution vs. those that supported the second-best resolution. We defined supporting loci as those with  $D_{LNL} > 0$  for the given topology. We calculated two-sided significance by generating 1000 scrambled datasets and counting the fraction of simulations where the real difference was greater than the absolute value of randomized differences. Shown are only those metrics with significance  $< 0.01$ . For most topologies, and most metrics, the best-supported topology is supported by loci with higher quality (e.g., see Iguania).

Uncertain relationship	metric	sig.	1st resolution	2nd resolution	details
Anniellidae	root-tip variance	0	0.0198	0.0696	less-supported topology supported by loci with greater root-tip variance
Anomalepididae	comp. het. RCFV	0	0.0212	0.0226	less-supported topology supported by loci with greater heterogeneity
Anomalepididae	length	0	1020	942	less-supported topology supported by shorter loci
Anomalepididae	missing	0	0.209	0.214	less-supported topology supported by loci with greater missingness
Anomalepididae	SH	0.001	79.2	78.5	less-supported topology supported by loci with less support
Anomalepididae	when max PI	0.001	121	117	less-supported topology supported by less informative loci
Dibamidae	heterozygosity	0.001	0.0012	0.000901	more-supported topology supported by loci with greater heterozygosity
Dibamidae	max PI	0.004	1.2	1.06	less-supported topology supported by less informative loci
Dibamidae	mean residuals	0.002	0.0755	0.059	more-supported topology supported by loci with greater root-tip variance
Dibamidae	missing	0.006	0.216	0.208	more-supported topology supported by loci with greater missingness
Dibamidae	tree length	0.008	7.15	6.46	more-supported topology supported by faster loci
Dibamidae	when max PI	0.002	114	123	more-supported topology supported by less informative loci
Gekkota & Scincoidea	comp. het. RCFV	0.008	0.0215	0.022	less-supported topology supported by loci with greater heterogeneity
Gekkota & Scincoidea	length	0	983	954	less-supported topology supported by shorter loci
Gekkota & Scincoidea	tree length	0.004	6.68	6.97	less-supported topology supported by faster loci
Gymnophthalmidae	branch outliers	0.003	1.26	1.15	more-supported topology supported by loci with more outliers
Gymnophthalmidae	comp. het. RCFV	0	0.0223	0.0208	less-supported topology supported by loci with greater heterogeneity
Gymnophthalmidae	GC	0	0.3	0.312	less-supported topology supported by loci with greater GC
Gymnophthalmidae	heterozygosity	0	0.00108	0.00096	more-supported topology supported by loci with greater heterozygosity
Gymnophthalmidae	length	0	965	1020	more-supported topology supported by shorter loci
Gymnophthalmidae	max PI	0	1.29	1.1	less-supported topology supported by less informative loci
Gymnophthalmidae	mean residuals	0	0.0674	0.0567	more-supported topology supported by loci with greater root-tip variance
Gymnophthalmidae	missing	0	0.214	0.204	more-supported topology supported by loci with greater missingness
Gymnophthalmidae	saturation C-value	0	11.5	14.9	less-supported topology supported by loci with greater saturation
Gymnophthalmidae	SH	0.002	79.2	78.5	less-supported topology supported by loci with less support

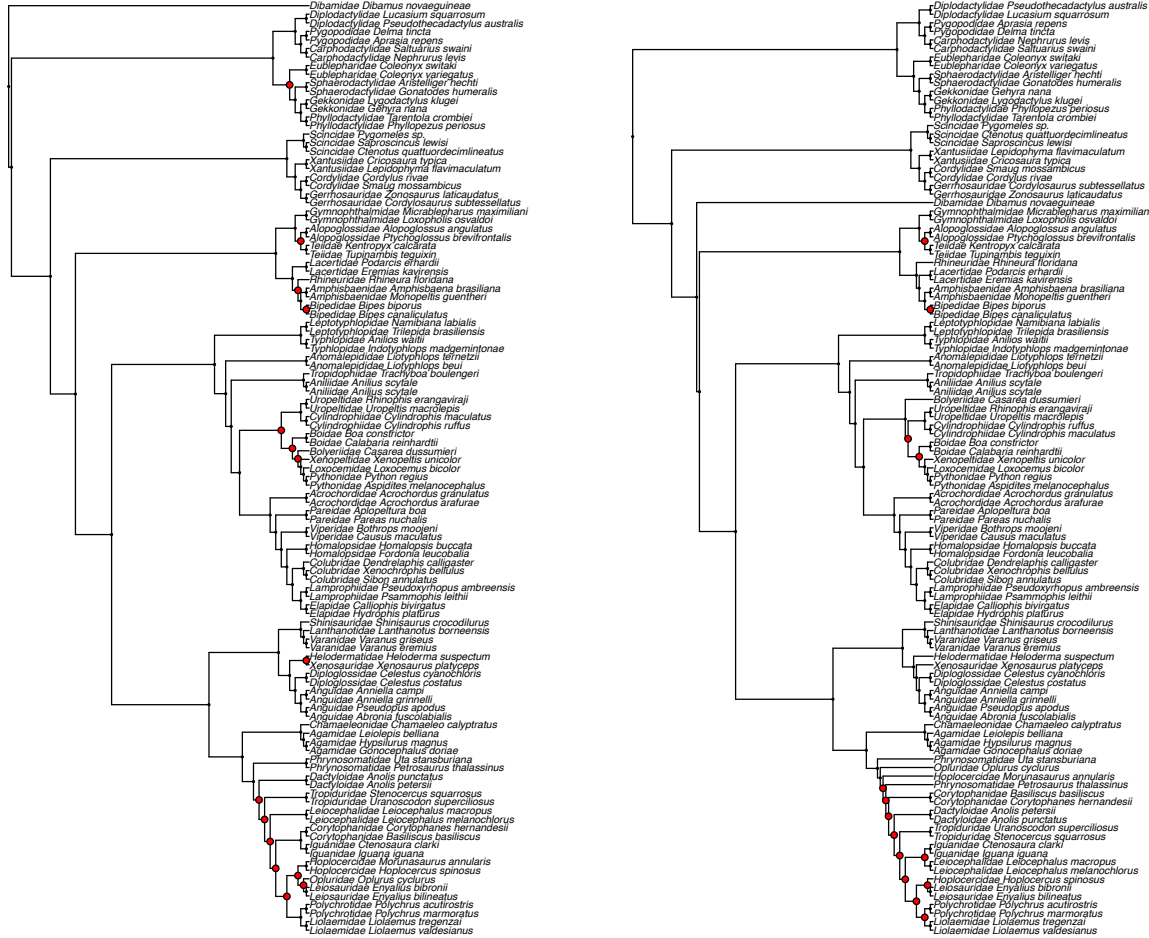


<b>Gymnophthalmidae</b>	tree length	0	7.37	6.14	more-supported topology supported by faster loci
<b>Gymnophthalmidae</b>	when max PI	0	113	128	more-supported topology supported by less informative loci
<b>Homalopsidae</b>	GC	0	0.313	0.303	more-supported topology supported by loci with greater GC
<b>Homalopsidae</b>	length	0	1030	989	less-supported topology supported by shorter loci
<b>Homalopsidae</b>	max PI	0.009	1.24	1.16	less-supported topology supported by less informative loci
<b>Homalopsidae</b>	when max PI	0.007	120	124	more-supported topology supported by less informative loci
<b>Iguania</b>	branch outliers	0.007	1.17	1.27	less-supported topology supported by loci with more outliers
<b>Iguania</b>	comp. het. RCFV	0.007	0.0213	0.0218	less-supported topology supported by loci with greater heterogeneity
<b>Iguania</b>	heterozygosity	0	0.000989	0.00116	less-supported topology supported by loci with greater heterozygosity
<b>Iguania</b>	max PI	0.002	1.18	1.32	more-supported topology supported by less informative loci
<b>Iguania</b>	mean residuals	0	0.0621	0.0721	less-supported topology supported by loci with greater root-tip variance
<b>Iguania</b>	missing	0	0.209	0.219	less-supported topology supported by loci with greater missingness
<b>Iguania</b>	occupancy	0.002	96.9	95.2	less-supported topology supported by loci with greater missingness
<b>Iguania</b>	root-tip variance	0.003	0.0225	0.0699	less-supported topology supported by loci with greater root-tip variance
<b>Iguania</b>	saturation C-value	0	13.3	15.3	less-supported topology supported by loci with greater saturation
<b>Iguania</b>	SH	0	78.6	77.3	less-supported topology supported by loci with less support
<b>Iguania</b>	tree length	0	6.52	7.13	less-supported topology supported by faster loci
<b>Iguania</b>	when max PI	0	122	112	less-supported topology supported by less informative loci
<b>Lanthanotidae</b>	GC	0	0.299	0.307	less-supported topology supported by loci with greater GC
<b>Lanthanotidae</b>	heterozygosity	0	0.00101	0.00118	less-supported topology supported by loci with greater heterozygosity
<b>Rhineuridae</b>	GC	0.005	0.301	0.311	less-supported topology supported by loci with greater GC
<b>Scincoidea</b>	comp. het. RCFV	0.001	0.0213	0.0226	less-supported topology supported by loci with greater heterogeneity
<b>Scincoidea</b>	heterozygosity	0	0.000998	0.00121	less-supported topology supported by loci with greater heterozygosity
<b>Scincoidea</b>	length	0	985	926	less-supported topology supported by shorter loci
<b>Scincoidea</b>	max PI	0	1.18	1.41	more-supported topology supported by less informative loci
<b>Scincoidea</b>	mean residuals	0.001	0.0626	0.0702	less-supported topology supported by loci with greater root-tip variance
<b>Scincoidea</b>	missing	0	0.209	0.225	less-supported topology supported by loci with greater missingness
<b>Scincoidea</b>	occupancy	0	97.3	93.7	less-supported topology supported by loci with greater missingness
<b>Scincoidea</b>	saturation C-value	0.009	13.3	15.1	less-supported topology supported by loci with greater saturation
<b>Scincoidea</b>	SH	0	78.7	77.5	less-supported topology supported by loci with less support
<b>Scincoidea</b>	tree length	0	6.61	7.3	less-supported topology supported by faster loci
<b>Scincoidea</b>	when max PI	0	122	104	less-supported topology supported by less informative loci

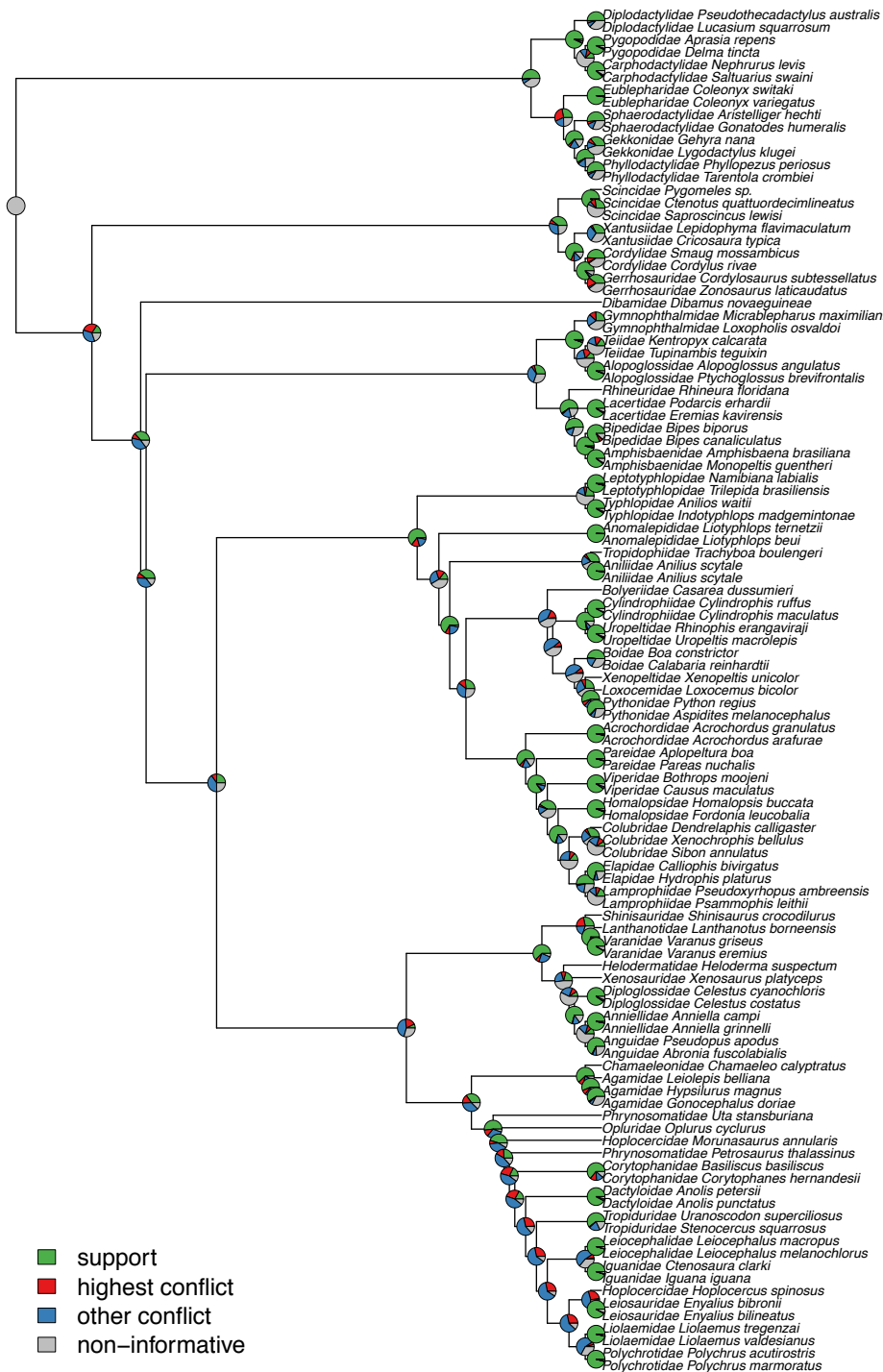
<b>Serpentes</b>	root-tip variance	0	0.0248	0.0611	less-supported topology supported by loci with greater root-tip variance
<b>Typhlopidae</b>	GC	0.008	0.31	0.304	more-supported topology supported by loci with greater GC
<b>Typhlopidae</b>	mean residuals	0.005	0.0603	0.068	less-supported topology supported by loci with greater root-tip variance
<b>Typhlopidae</b>	missing	0.006	0.208	0.214	less-supported topology supported by loci with greater missingness
<b>Typhlopidae</b>	tree length	0.002	6.67	7.18	less-supported topology supported by faster loci
<b>Typhlopidae</b>	when max PI	0.005	123	116	less-supported topology supported by less informative loci
<b>Xenosauridae</b>	heterozygosity	0.001	0.00113	0.00095	more-supported topology supported by loci with greater heterozygosity
<b>Xenosauridae</b>	max PI	0.001	1.3	1.17	less-supported topology supported by less informative loci
<b>Xenosauridae</b>	missing	0.002	0.214	0.207	more-supported topology supported by loci with greater missingness
<b>Xenosauridae</b>	saturation C-value	0	11.7	15.1	less-supported topology supported by loci with greater saturation
<b>Xenosauridae</b>	SH	0.004	79.4	78.5	less-supported topology supported by loci with less support
<b>Xenosauridae</b>	tree length	0	7.4	6.68	more-supported topology supported by faster loci
<b>Xenosauridae</b>	when max PI	0.001	115	123	more-supported topology supported by less informative loci

**Table S4:** Summary of results across topologies tested by marker type. Shown is the relationship tested, what topology was best supported by  $D_{LNL}$  analyses (see Table S2), whether this topology was strongly resolved, and if  $D_{LNL}$  analyses done with Anchored Hybrid Enrichment (AHE) markers alone find similar patterns as that done with the whole data set.  $D_{LNL}$  analyses for ultraconserved elements (UCE) markers alone are not shown because results for the UCE-only and full dataset are identical. This is likely because UCE markers comprise the majority of the dataset (>90% by locus).

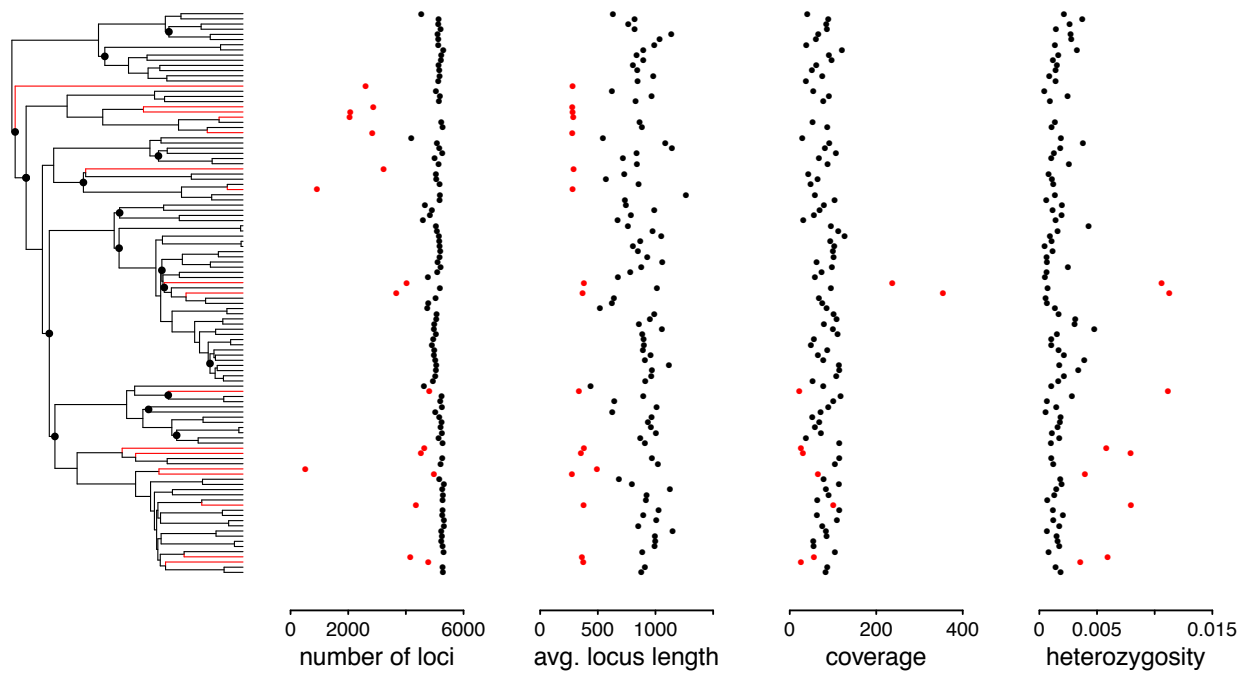
<b>Uncertain relationship</b>	<b>topology best supported by <math>D_{LNL}</math> analysis</b>	<b>strong resolution?</b>	<b>AHE agrees?</b>	<b>AHE resolution strong?</b>
<b>position of Anniellidae</b>	sister to Anguidae	True	True	True
<b>position of Anomalepididae</b>	sister to Leptotyphlopidae & Typhlopidae	True	False	False
<b>position of Bolyeridae</b>	sister to Boidae	False	True	True
<b>position of Cyliodrophiidae &amp; Uropeltidae</b>	sister to Bolyeriidae, Boidae, Pythonidae, Loxocemidae & Xenopeltidae	False	False	True
<b>position of Dibamidae</b>	sister to all other squamates	True	True	True
<b>position of Diplodactylidae</b>	sister to Carphodactylidae & Pygopodidae	False	False	False
<b>position of Eublepharidae</b>	sister to Carphodactylidae, Pygopodidae & Diplodactylidae	False	True	True
<b>position of Gymnophthalmidae</b>	sister to Teiidae & Alopoglossidae	True	False	False
<b>position of Homalopsidae</b>	sister to Elapidae, Lamprophiidae & Colubridae	True	True	True
<b>position of Iguania</b>	sister to Anguimorpha	True	True	True
<b>position of Lanthanotidae</b>	sister to Varanidae	True	True	True
<b>position of Rhineuridae</b>	sister to Bipedidae, Amphisbaenidae & Lacertidae	False	False	False
<b>position of Scincoidea</b>	sister to Episquamata	True	True	True
<b>position of Serpentes</b>	sister to Anguimorpha & Iguania	False	True	True
<b>position of Typhlopidae</b>	sister to Leptotyphlopidae	True	True	True
<b>position of Xenosauridae</b>	sister to Anniellidae, Anguidae, Diploglossidae & Helodermatidae	False	False	False
<b>relationship between Gekkota &amp; Scincoidea</b>	Gekkota sister to Scincoidea & all other squamates	True	True	True



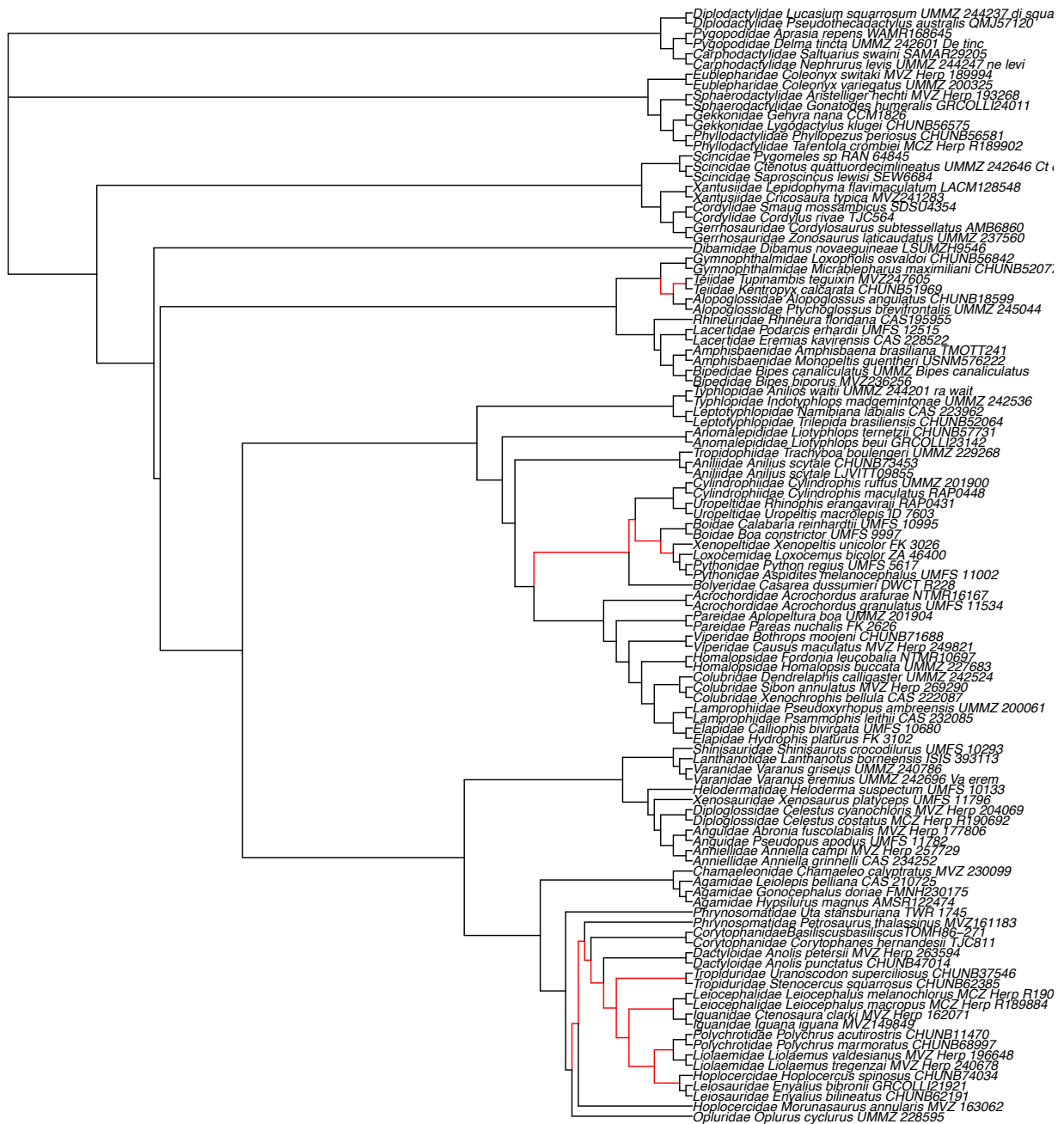
**Figure S1:** Comparison of phylogenies inferred with AHE ( $N=372$ ) vs. UCE data ( $N=5052$ ) only. (Left) ExaML-inferred phylogenies and (Right) ASTRAL-inferred phylogenies. Shown are the topologies based on UCE loci only; nodes that conflict with the topologies built with AHE loci shown in red. We do not compare these topologies to the topology inferred with the full data set because the full data set is 87% UCE loci by sequence. Many of the nodes that are discordant between the two locus sets have been previously identified as nodes of interest (see Table 1).



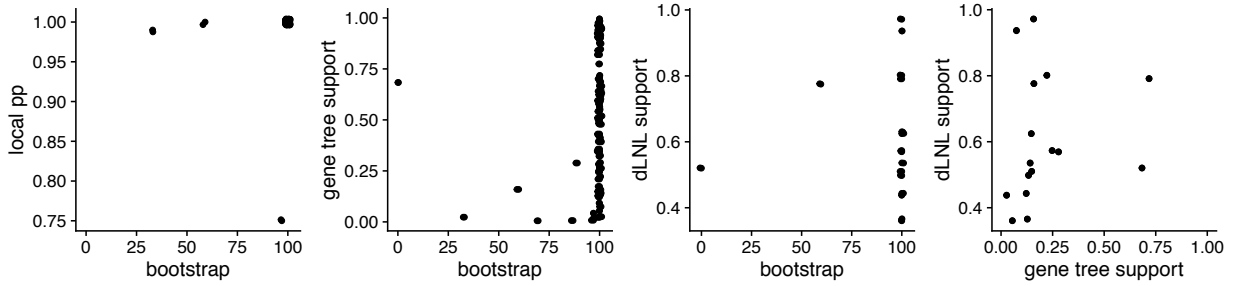
**Figure S2:** ASTRAL-inferred tree with levels of conflict shown at each node. Pie proportions represent the number of gene trees that either support a node, support the most common conflicting relationship, support other less common conflicting relationships, or are non-informative. Branches in gene trees with <80 SH-like support were collapsed before measuring levels of support. Some nodes are supported by very few gene trees.



**Figure S3:** Data quality metrics for the 109 ingroup taxa included in this study. Metrics are the total number of loci >300 bp, average locus length, average coverage of captured loci, and heterozygosity for sites with >10× coverage. Putatively contentious nodes marked with black circles (Table 1); tips and points shown in red indicate previously-published data. Some previously-published samples are missing data on coverage and heterozygosity because we only had access to assembled data. Data quality is high across included tips, although quality was generally lower for previously-published data.

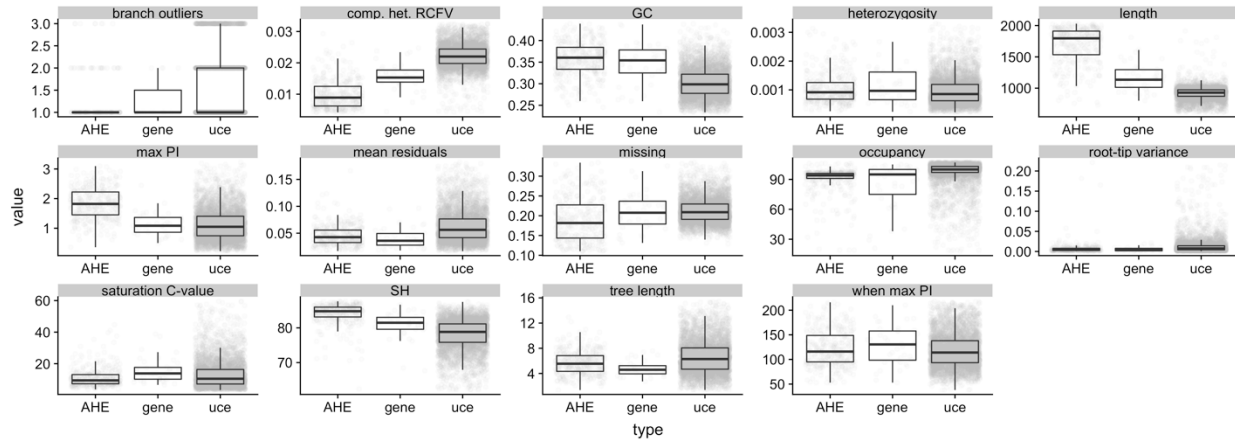


**Figure S4:** Coalescent-based topology of ingroup taxa with edges falling into the anomaly zone marked in red. Overall, few edges fall into the anomaly zone, and the majority of these are within the rapid radiation of Iguania.

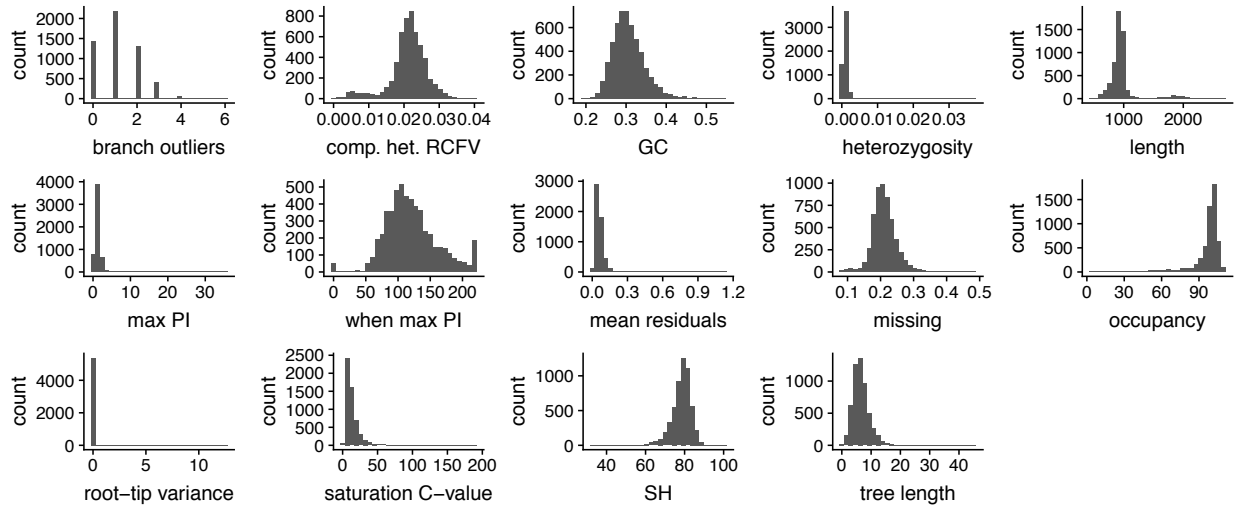


**Figure S5:** Correlations among the four different types of support values measured in this study: bootstrap values as inferred with the maximum-likelihood tree, local posterior probability as inferred from the coalescent-based tree, percent of supporting gene trees as measured by bp, and percent of supporting gene trees as measured by  $D_{LNL}$ . Some nodes could not be included in comparison of bootstrap and local posterior probability values because they were discordant in the maximum-likelihood and coalescent-based trees. Points shown with jitter to reduce overlap. Nodes that have high statistical support still exhibit extensive conflict.





**Figure S6:** Patterns of locus-level metrics across the three loci types included in this study: AHE, gene, and UCE. As determined by ANOVA, metrics differed significantly across locus types for all metrics but ‘occupancy’ and ‘tree length’. In general, AHE markers showed evidence of being higher quality (i.e., they had lower levels of missingness) and more informative (i.e., trees inferred with AHE markers had higher nodal support as measured by Shimodaira–Hasegawa (SH)-like support).



**Figure S7:** Histograms showing the distribution of the 14 metrics measured for each locus; see Table 2 for more details on these metrics. Most metrics show a fairly normal distribution with a few outliers.