Electronic Supplementary information for:

Olfactory Receptor Repertoire Size in Dinosaurs

Graham M. Hughes*[1], John A. Finarelli[1,2].

*Corresponding author: g.hughes@ucd.ie

[1] *School of Biology and Environmental Science, University College Dublin, Belfield, Dublin 4, Ireland*

[2] *Earth Institute, University College Dublin, Belfield, Dublin 4, Ireland*

Supplementary Methods

Olfactory receptor gene sequences

OR genes were mined from raw genome files for each extant target avian taxon. OR sequences were initially mined by mapping all RefSeq query genes to a target reference with blastx [1]. Blast best-hit regions were extended 500bp up and downstream, investigated for OR sequences and assigned to specific gene subfamilies using Hidden Markov Models (HMMs) via the Olfactory Receptor Assigner (ORA [2]). Putative pseudogenes less than 150bp in length were excluded. OR sequences from a number of non-avian sauropsid taxa, (hereafter: 'sauropsids'; *Alligator sinensis*, *Alligator mississippiensis*, *Chrysemys picta*, *Anolis carolinensis*, *Python molurus*) were also downloaded [3-7]. Additionally, the genome of the American alligator, *Alligator mississippiensis*, was mined for OR sequences.

Estimation of ancestral ORs using shared identity

To estimate the minimum number of ancestral OR gene numbers in the dinosaurs, OR sequences from the five sauropsid species mapped to avian ORs using tblastx [1]. Given that the same OR genes may be present in all five, only representative orthologs were used, determined by clustering sequences with 80% shared identity (cd-hit [8]) and choosing one template per cluster, based on the longest sequence. To account for more than 200 MY [9] since the divergence of Aves, subsequent operational thresholds of 65% shared identity and 50% gene coverage were used to infer orthology across both lineages and thus presence in the ancestral dinosaur genome. We further explored OR gene families whose binding odorant ligands are known, and have been verified in human and mouse (de-orphaned), to identify the potential odorant-space [10-12] that was perceivable by extinct dinosaur taxa.

Olfactory bulb ratio correlations

Correlations of the OB ratio with dietary niche and log body mass were investigated across taxa (n = 74, diet data not available for both *Lithornis* sp., no body mass available for *Viavenator* or *Pawpawsaurus*) using Phylogenetic Generalized Least Squares (PGLS), with a null Brownian motion (BM) model of trait evolution in the R packages '*ape*' [13] and '*nlme*' [14]. Correlation between body mass and OB ratio was investigated using PGLS for five groups, specifically 'all taxa', 'non-avian dinosaurs', 'non-avian dinosaurs+stem birds' (that is, members of the Avialae (*Archaeopteryx*, *Confuciusornis*, *Hesperornis*, *Ichthyornis*) outside of Aves), 'Avialae' and 'Aves', with correlation coefficients determined by computing the phylogenetic trait variance-covariance matrix via *phytools* [15], and the *cov2cor* function in R.

We investigated correlations of OB ratio with total OR repertoire and individual gene family sizes for Aves species using a phylogenetically corrected Pearson's correlation coefficient, with Benjamini–Hochberg false discovery rate (FDR [16]), using the *p.adjust* function in R. Three taxa (chicken, *Gallus gallus*; zebra finch, *Taeniopygia guttata*; and budgerigar, *Melopsittacus undulatus*) show a highly expanded OR family 14 relative to other extant birds. These outliers show similar OB ratios to their respective sister taxon, but have a far greater repertoire size (with each sister taxon closer to the mean), suggesting some extreme expansion event post-divergence. This analysis was therefore conducted with and without these outlier taxa. Correlations of OB ratios with trait data were done with Phylogenetic

Generalized Least Squares (PGLS), using a composite phylogeny of all 76 species (see below: *Phylogenetic tree topology*, and Main Text Figure 1).

Phylogenetic tree topology

A composite phylogeny of all 76 species was generated for all comparative analyses. An initial cladogram of extant avian taxa was generated based on the topology of Prum *et al.* [17], with *Lithornis* added as basal to extant birds, and Avialae basal to Aves. The topologies of dinosaur taxa within families/superfamilies were based on various studies (Abelisauridae [18], Allosauroidea [19], Ankylosauridae [20], Dromaeosauridae [21], Ornithomimosauria [22], Tyrannosauroidea [23]), with Ornithischia as sister group to Saurischia, Dinosauria basal to Aves. The location of Therizinosauria was based on Zanno [24], with the Saurichian topology from Cau *et al.* [21], Zanno [24] and Chinzorig *et al* [22] used. *A. mississippiensis* was added as outgroup to all other taxa. The final phylogeny was then created based on the method devised by Grafen [25], where internal nodes are assigned a 'height' based on the number of branching events, with branch lengths scaled based on nodal differences. Grafen transformation was carried out in R using *ape* [13].

Ancestral state reconstruction of OR repertoire and OB ratio

We estimated ancestral OB ratios at internal nodes using both the all-taxon phylogeny (i.e., including fossil taxa) and a tree limited to extant birds. We performed the analyses both with and without the three outlier taxa discussed above, to determine if their inclusion biased the ancestral reconstructions. Additional sauropsid taxa were excluded due to a lack of reported OB ratios. *Alligator mississippiensis* was used as the outgroup for all analyses. A number of methods for reconstructing the ancestral states of internal nodes across the phylogeny were employed. Ancestral state reconstruction was carried out using the '*ape*' package in R, focusing on: 1) Maximum Likelihood (ML), reconstructing ancestral states by maximizing the likelihood under a BM model; 2) Phylogenetic Independent Contrasts (PIC), reconstructing ancestral states recursively with branch-dependent weighting [26] and 3) Generalized Least Squares (GLS), reconstructing ancestral states as a linear combination of extant leaves, based on the variance-covariance matrix and a BM model of evolution. These ancestral OB ratio estimates were compared across methods using a Kruskal-Wallis test.

Modeling OR gene repertoire as a function of OB ratio

PGLS was used to model OR gene repertoire size (functional + non-functional) as a function of OB ratio using data from extant birds ($n = 42$), extant birds with the three outlier species above excluded ($n = 39$) and both with and without *A. mississippiensis* ($n = 43$; $n = 40$, respectively). These models were used to predict OR gene numbers across all extinct taxa. Given the paucity of literature on whether or not an OB-ratio/OR repertoire size correlation exists in the crocodilian or testudine lineages, and the general lack of OB ratios for taxa for which genome sequences are available, we only included the American alligator as an outgroup. For the PGLS modeling, we make the assumption that theropod dinosaurs reflect scaling patterns more similar to the avian lineage rather than crocodilian/testudine lineages.

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Supplementary Table S1. The list of extinct and extant taxa included in this study. OR repertoire sizes OB ratio, Diet and Body mass are displayed. Where multiple OB ratios are available, the mean ratio was used (denoted by *). PGLS corrected repertoire sizes are inferred for extinct taxa. † indicates extinct taxon.

Species	**Common name**	**OR Repertoire**	**OB ratio (%)**	**Inferred OR Repertoire**	**Diet**	**Body mass (kg)**
Alligator mississippiensis	Alligator	1077	49.8	-	Carnivore	150
			54.3	-		
			55.1	-		
			53*	-		
Tinamus guttatus	White-throated tinamou	388	19.5	-	Omnivore	0.8
Struthio camelus	Ostrich	318	19.2	-	Omnivore	111
Taeniopygia guttata	Zebra finch	688	9.7	-	Herbivore	0.0122
Geospiza fortis	Medium ground finch	182	9.7	-	Herbivore	0.0183
Corvus brachyrhynchos	American crow	229	5	-	Omnivore	0.506
Manacus vitellinus	Golden-collared manakin	227	9.7	-	Frugivore	0.0193
Acanthisitta chloris	Rifleman	222	9.7	-	Insectivore	0.007
Melopsittacus undulatus	Budgerigar	484	6.2	-	Herbivore	0.029
Nestor notabilis	Kea	239	8	-	Omnivore	0.956
Falco peregrinus	Peregrine falcon	460	20	-	Carnivore	0.815
Cariama cristata	Red-legged seriema	293	22.2	-	Carnivore	1.4
Picoides pubescens	Downy woodpecker	252	10	-	Omnivore	0.028
Merops nubicus	Northern carmine bee-eater	252	14.5	-	Insectivore	0.051
Colius striatus	Speckled mousebird	292	9.7	-	Frugivore	0.055
Tyto alba	Barn owl	321	18.5	-	Carnivore	0.392
Haliaeetus leucocephalus	Bald eagle	262	18	-	Piscivore	5.35
Haliaeetus albicilla	White-tailed eagle	283	18	-	Carnivore	5.572
Cathartes aura	Turkey vulture	400	28.7	-	Carnivore	2.006
Pelecanus crispus	Dalmatian pelican	330	9.7	-	Piscivore	10
Egretta garzetta	Little egret	491	21.7	-	Omnivore	0.55
Nipponia nippon	Crested ibis	371	21.7	-	Carnivore	1.9
Phalacrocorax carbo	Great cormorant	270	14.5	-	Piscivore	2.4
Pygoscelis adeliae	Adélie penguin	320	17	-	Carnivore	4.85
Aptenodytes forsteri	Emperor penguin	355	17	-	Carnivore	38.2
Fulmarus glacialis	Northern fulmar	370	27.1	-	Carnivore	0.613
Gavia stellata	Red-throated loon	369	20	-	Piscivore	1.729
Phaethon lepturus	White-tailed tropicbird	306	20	-	Carnivore	0.33
Balearica regulorum	Grey crowned crane	369	22.2	-	Omnivore	3.777
Charadrius vociferus	Killdeer	393	16.1	-	Omnivore	0.101
Ophisthocomus hoazin	Hoatzin	467	24.2	-	Herbivore	0.696
Calypte anna	Anna’s hummingbird	324	14	-	Nectivore	0.0045

Chaetura pelagica	Chimney swift	355	18.8	-	Carnivore	0.024
Antrostomus carolinensis	Chuck-will's-widow	353	23.8	-	Insectivore	0.188
Cuculus canorus	Common cuckoo	266	19.5	-	Insectivore	0.117
Mesitornis unicolor	Brown mesite	343	22.2	-	Omnivore	0.148
Pterocles gutturalis	Yellow-throated sandgrouse	280	20.7	-	Herbivore	0.342
Columba livia	Rock dove	437	21.2	-	Herbivore	0.355
Phoenicopterus ruber	American flamingo	363	21.7	-	Carnivore	3.579
Podiceps cristatus	Great crested glebe	319	24.5	-	Carnivore	0.92
Meleagris gallopavo	Wild turkey	313	13.5	-	Omnivore	6.05
Gallus gallus	Chicken	674	15.4	-	Omnivore	0.904
Anas platyrhynchos	Mallard duck	344	19	-	Omnivore	1.082
†*Allosaurus fragilis*		-	51.6	540	Carnivore	2545.13
			50	531		
			50.8*	536		
†*Acrocanthosaurus atokensis*		-	58.1	575	Carnivore	3777.58
†*Carcharodontosaurus saharicus*		-	56	564	Carnivore	7905.47
†*Giganotosaurus carolinii*		-	57.7	573	Carnivore	7559.49
†*Ceratosaurus magnicornis*		-	48.1	521	Carnivore	538.86
†*Majungasaurus crenatissimus*		-	48.3	522	Carnivore	1130
†*Dilong paradoxus*		-	27	407	Carnivore	9.69
†*Albertosaurus sarcophagus*		-	71	645	Carnivore	2545.13
†*Gorgosaurus libratus*		-	68.5	631	Carnivore	2709.45
†*Tarbosaurus bataar*		-	65.1	613	Carnivore	2164.6
†*Tyrannosaurus rex*		-	66.5	621	Carnivore	5855.3
			71	645		
			68.3	630		
			68.7*	632		
†*Garudimimus brevipes*		-	28.8	417	Omnivore	97.84
†*Ornithomimus edmontonensis*		-	31.4	431	Omnivore	152.74
†*Dromiceiomimus brevitertius*		-	29.4	420	Omnivore	206.79
†*Struthiomimus altus*		-	32.5	437	Omnivore	277.97
†*Citipati osmolskae*		-	31.5	431	Omnivore	129.78
†*Saurornitholestes langstoni*		-	34.8	449	Carnivore	16.62
†*Bambiraptor feinbergi*		-	28.5	415	Carnivore	2.44
†*Velociraptor mongoliensis*		-	35.7	454	Carnivore	13.36
†*Troodon formosus*		-	33.2	440	Carnivore	60.76
			33.5	442		
			32.6	437		

			33	439		
			33.1*	440		
†*Archaeopteryx lithographica*		-	17.1	353	Carnivore	0.28
†*Confuciusornis sanctus*		-	17.9	358	Piscivore	0.277
†*Hesperornis regalis*		-	15.3	344	Piscivore	10.608
			21.3	376		
			18.3*	360		
†*Ichthyornis dispar*		-	18.1	359	Piscivore	0.35
†*Lithornis plebius*		-	36.5	458	-	0.48
†*Lithornis promiscuus*		-	37.7	465	-	0.908
†*Deinonychus antirrhopus*		-	41	483	Carnivore	56.7
†*Tsaagan mangas*		-	36	456	Carnivore	13.36
†*Viavenator exxoni*		-	57	569	Carnivore	-
†*Erlikosaurus andrewsi*		-	40	477	Herbivore	173.7
†*Euoplocephalus sp*		-	52	542	Herbivore	2675.90
†*Pawpawsaurus campbelli*		-	46.2	511	Herbivore	-
†*Panoplosaurus mirus*		-	44	499	Herbivore	1600

Supplementary Table S2. Correlations between OB ratio and OR repertoire size in birds were investigated using phylogenetically uncorrected and corrected Pearson's correlation coefficient (r). Correlations for individual OR gene families, OR gene class and total OR repertoire size are given. The p-values were adjusted for multiple comparisons using the Benjamini-Hochberg false discovery rate (FDR, [40]). Significant p-values are highlighted in bold. Correlations with and without outlier species (*Gallus gallus*, *Melopsittacus undulates* and *Taeniopygia guttata*) are displayed.

Family	**Aves (n = 39)**				**Aves (n = 42)**			
	Phylogenetically uncorrected r	**Adjusted p-value**	**Phylogenetically corrected r**	**Adjusted p-value**	**Phylogenetically uncorrected r**	**Adjusted p-value**	**Phylogenetically corrected r**	**Adjusted p-value**
OR 1/3/7	0.2261	0.1791	-0.1555	0.4019	0.1816	0.2496	-0.0788	0.6677
OR 2/13	0.4750	**0.0045**	0.4446	**0.0206**	0.3751	**0.0267**	-0.0878	0.6677
OR 4	0.3952	**0.0179**	0.4061	**0.0206**	0.3212	**0.04845**	0.32448	0.0841
OR 5/8/9	0.5556	**0.0008**	0.1830	0.3369	0.4410	**0.0154**	0.195§	0.3775
OR 6	0.6278	**9.193e-05**	0.4172	**0.0206**	0.6321	**9.96e-05**	0.5317	**0.0041**
OR 10	0.4762	**0.0045**	0.4113	**0.0206**	0.3815	**0.0251**	0.3631	0.0632
OR 11	0.5485	**0.0009**	0.5096	**0.0129**	0.4847	**0.0080**	0.4873	**0.0074**
OR 12	0.2094	0.2008	0.0180	0.9133	0.2625	0.1085	0.3875	0.0524
OR 14	0.3995	**0.0179**	0.2349	0.2624	0.2280	0.1578	-0.03695	0.8163
OR 51	0.4140	**0.0154**	0.1351	0.4438	0.3788	**0.0251**	0.1341	0.5156
OR 52	0.3267	0.0494	0.2069	0.3206	0.3561	**0.0289**	0.3392	0.0783
Alpha (Class I)	0.3868	**0.0191**	0.1943	0.3301	0.3668	**0.0262**	0.1595	0.4870
Gamma (Class II)	0.6267	**9.193e-05**	0.4133	**0.0206**	0.4208	**0.0154**	0.2474	0.2284
Total OR	0.6516	**9.193e-05**	0.4289	**0.0206**	0.4208	**0.0154**	0.1319	0.5156

Supplementary Table S3. Internal ancestral node estimates of OB ratios and OR gene repertoires using three different methods are displayed. All extant taxa, including alligator, is included. Information pertaining to what each ancestral node represents is also given. Node numbers correspond to Supplementary Figure 4.

Node description	**Node**	**Olfactory bulb ratio**			**Olfactory receptor gene repertoire**		
		ML	**PIC**	**GLS**	**ML**	**PIC**	**GLS**
Alligator+Aves	1	32.09	25.49	25.49	488	497	497
Palaeognathae+ Neognathae	2	32.15	19.22	24.84	470	365	483
Galloanserae+ Strisores+Columbaves+Neoaves (Neognathae)	3	30.52	19.19	23.8	349	353	355
Columbaves+Neoaves	5	28.03	20.2	22.13	436	368	462
Aequorlitornithes+Afroaves+Opisthocomus+Balearica (Neoaves)	6	24.59	20.04	21.4	418	429	430
Aequorlitornithes+ Afroaves + Opisthocomus	7	23.65	19.29	21.19	471	494	472
Aequornithes+Phaethon+Mirandornithes+Charadrius (Aequorlitornithes)	8	19.59	19.69	19.94	393	349	433
Aequornithes+Phaethon	9	17.74	19.46	19.67	349	345	347
Pelecaniformes+Phalacrocorax+Austrodyptornithes+Gavia (Aequornithes)	10	18.24	19.25	19.54	342	340	342
Pelecaniformes+Phalacrocorax+Austrodyptornithes	11	18.75	18.9	19.34	364	350	411
Pelecaniformes+Phalacrocorax	12	17.43	16.83	17.52	325	327	330
Pelecanus+Nipponia+Egretta (Pelecaniformes)	13	17.94	18.27	17.93	342	365	349
Pelecanus+Nipponia	14	17.89	15.7	16.44	325	312	324
Spheniscidae +Fulmarus (Austrodyptornithes)	15	21.64	21.33	20.98	365	359	393
Aptenodytes+Pygocelis (Spheniscidae)	16	18.4	17	18.33	365	355	389
Mirandornithes+Charadrius	17	20.6	20.1	20.09	366	359	367
Podiceps+Phoenicopterus (Mirandornithes)	18	22.08	23.1	22.1	353	321	359
Afroaves+Opisthocomus	19	16.93	18.98	19.54	334	327	329
Inopinaves+Coraciimorphae+Tyto+Acciptrimorphae (Afroaves)	20	17.93	17.15	19.12	291	273	291
Inopinaves+Coraciimorphae+Tyto	21	22.2	14.45	17.08	311	319	341
Psittacopasserae+Falco+Cariama (Inopinaves)	22	18.63	14.76	15.6	288	289	295
Psittacopasserae+Falco	23	16.98	11.83	14.4	274	269	281
Psittaciformes+Passeriformes (Psittacopasserae)	24	15.61	8.21	12.4	266	252	262
Passeroidea+Corvus+Manacus+Acanthisitta (Passeriformes)	25	10.37	8.89	10.33	281	337	338
Passeroidea+Corvus+Manacus	26	9.19	8.46	9.46	302	354	343
Passeroidea+Corvus	27	8.32	7.69	8.5	295	307	332
Geospiza+Taeniopygia (Passeroidea)	28	9.13	9.7	9.3	358	362	359

Melopsittacus+Nestor (Psittaciformes)	29	6.89	7.1	7.58	252	273	297
Coraciimorphae+Tyto	30	15.84	13.96	14.32	286	301	299
Picoides+Merops+Colius (Coraciimorphae)	31	15.37	11.16	12.62	319	347	325
Picoides+Merops	32	13.7	12.25	12.37	400	435	398
Haliaeetus+Cathartes (Acciptrimorphae)	33	21.65	22.59	22.37	337	351	357
Haliaeetus	34	19.19	18	19.46	361	363	363
Strisores+Columbaves+Neoaves	35	29.36	20.04	22.82	347	341	348
Mesitornis+Pterocles+Columba+Cuculus (Columbaves)	35	22.39	20.64	20.69	332	344	350
Mesitornis+Pterocles+Columba	36	21.35	21.34	21.04	338	359	353
Mesitornis+Pterocles	37	21.97	21.45	21.31	341	354	353
Apodiformes+Antrostomus (Strisores)	38	19.31	19.57	19.65	348	351	352
Chaetura+Calypte (Apodiformes)	39	17.46	16.4	17.48	340	338	342
Galliformes+Anas (Galloanserae)	40	17.64	16.4	16.57	352	357	356
Gallus+Meleagris (Galliformes)	41	15.96	14.45	15.16	379	411	385
Tinamus+Struthio (Palaeognathae)	42	20.22	19.35	19.42	361	351	362

Supplementary Table S4. Internal ancestral node estimates of OB ratios and OR gene repertoires for extant taxa, with anomalous species (*Gallus gallus*, *Taeniopygia guttata*, *Melopsittacus undulates*) removed. Information pertaining to what each ancestral node represents is also given. Node numbers correspond to Supplementary Figure 5.

Node description	**Node**	**Olfactory bulb ratio**			**Olfactory receptor gene repertoire**		
		ML	**PIC**	**GLS**	**ML**	**PIC**	**GLS**
Gallus+Meleagris (Galliformes)	1	27.12	25.48	25.48	413	480	480
Melopsittacus+Nestor (Psittaciformes)	2	25.66	19.21	24.82	399	344	466
Geospiza+Taeniopygia (Passeroidea)	3	25.30	19.17	23.78	379	342	443
Alligator+Aves	4	24.02	20.06	22.82	362	346	418
Palaeognathae+ Neognathae	5	22.74	20.22	22.13	352	347	399
Galloanserae+ Strisores+Columbaves+Neoaves (Neognathae)	6	20.97	20.07	21.41	351	354	383
Strisores+Columbaves+Neoaves	7	21.01	19.33	21.20	351	349	380
Columbaves+Neoaves	8	18.70	19.69	19.94	351	351	356
Aequorlitornithes+Afroaves+Opisthocomus+Balearica (Neoaves)	9	18.36	19.46	19.67	346	344	349
Aequorlitornithes+ Afroaves + Opisthocomus	10	17.72	19.25	19.54	351	359	352
Aequornithes+Phaethon+Mirandornithes+Charadrius (Aequorlitornithes)	11	17.59	18.90	19.34	352	354	353
Aequornithes+Phaethon	12	18.26	16.83	17.52	356	357	356
Pelecaniformes+Phalacrocorax+Austrodyptornithes+Gavia (Aequornithes)	13	16.76	18.27	17.93	385	411	385
Pelecaniformes+Phalacrocorax+Austrodyptornithes	14	15.34	15.70	16.44	364	351	362
Pelecaniformes+Phalacrocorax	15	20.40	21.33	20.98	352	351	352
Pelecanus+Nipponia+Egretta (Pelecaniformes)	16	18.42	17.00	18.33	342	338	342
Pelecanus+Nipponia	17	20.15	20.10	20.09	363	363	363
Spheniscidae +Fulmarus (Austrodyptornithes)	18	22.46	23.10	22.10	349	341	348
Aptenodytes+Pygocelis (Spheniscidae)	19	23.54	19.04	19.60	356	347	355
Mirandornithes+Charadrius	20	24.71	17.24	19.18	348	305	346
Podiceps+Phoenicopterus (Mirandornithes)	21	23.79	14.59	17.17	321	294	323
Afroaves+Opisthocomus	22	20.10	14.97	15.77	299	297	306
Inopinaves+Coraciimorphae+Tyto+Acciptrimorphae (Afroaves)	23	16.88	12.09	14.62	295	298	304
Inopinaves+Coraciimorphae+Tyto	24	13.62	8.50	12.69	275	225	279
Psittacopasserae+Falco+Cariama (Inopinaves)	25	10.94	8.79	10.41	238	217	243
Psittacopasserae+Falco	26	8.88	8.29	9.45	228	214	230
Psittaciformes (Nestor)+Passeriformes (Psittacopasserae)	27	8.28	7.35	8.40	219	206	218

Passeroidea+Corvus+Manacus+Acanthisitta (Passeriformes)	28	16.82	13.96	14.33	295	289	293
Passeroidea+Corvus+Manacus	29	14.77	11.16	12.62	281	269	280
Passeroidea (Geospiza)+Corvus	30	13.21	12.25	12.37	261	252	261
Coraciimorphae+Tyto	31	23.34	22.59	22.37	326	327	328
Picoides+Merops+Colius (Coraciimorphae)	32	19.74	18.00	19.46	289	273	291
Picoides+Merops	33	21.46	20.64	20.69	328	327	330
Haliaeetus+Cathartes (Acciptrimorphae)	34	20.79	21.34	21.04	349	365	349
Haliaeetus	35	20.93	21.45	21.31	323	312	324
Mesitornis+Pterocles+Columba+Cuculus (Columbaves)	36	19.86	19.57	19.65	346	345	347
Mesitornis+Pterocles+Columba	37	17.37	16.40	17.48	342	340	342
Mesitornis+Pterocles	38	15.94	16.25	16.45	329	329	332
Apodiformes+Antrostomus (Strisores)	39	19.55	19.35	19.42	353	353	354

Supplementary Table S5. Internal ancestral node repertoire estimates for both extant and extinct taxa using three different methods. Node labels corresponding to the phylogenies displayed in Supplementary Figures S6–8 are also given.

Node label	ML	PIC	GLS
1	31.82	43.21	43.21
2	31.83	41.36	43.08
3	31.98	39.88	42.48
4	32.05	37.38	41.53
5	31.68	33.05	39.46
6	30.53	27.91	35.73
7	29.33	27.36	33.12
8	29.06	24.94	32.35
9	28.8	23.53	31.59
10	26.81	20.57	26.67
11	26.66	21.23	26.06
12	26.62	21.91	25.62
13	26.74	22.78	25.08
14	26.3	19.22	23.97
15	25.88	19.19	23.09
16	25.75	20.04	22.3
17	25.73	20.2	21.75
18	25.53	20.04	21.15
19	25.27	19.29	20.96
20	19.61	19.69	19.9
21	19.31	19.46	19.65
22	19.01	19.25	19.53
23	18.75	18.9	19.33
24	17.34	16.83	17.52
25	17.95	18.27	17.93
26	16.5	15.7	16.44
27	20.99	21.33	20.98
28	18.39	17	18.33
29	20.04	20.1	20.08
30	22.08	23.1	22.09
31	22.27	18.98	19.49
32	21.46	17.15	19.07
33	17.76	14.45	17.05
34	14.5	14.76	15.59
35	13.03	11.83	14.39
36	11.19	8.21	12.4
37	9.71	8.89	10.33
38	9.19	8.46	9.46
39	8.72	7.69	8.5
40	9.56	9.7	9.3
41	7.42	7.1	7.58
42	14.71	13.96	14.31
43	12.89	11.16	12.61
44	12.5	12.25	12.37
45	22.52	22.59	22.37
46	19.5	18	19.46
47	21.05	20.64	20.68
48	21.25	21.34	21.04
49	21.4	21.45	21.31
50	19.66	19.57	19.64
51	17.46	16.4	17.48
52	16.53	16.4	16.55

53	15.11	14.45	15.15
54	19.44	19.35	19.41
55	36.97	37.1	36.96
56	18.3	18.2	18.28
57	34.81	34.47	34.37
58	35.09	35.18	34.69
59	36.92	38.06	37.05
60	36.06	35.85	36.25
61	32.07	31.65	32.08
62	30.26	30.34	30.45
63	30.8	31.3	30.91
64	30.53	30.4	30.57
65	52.9	53.45	53.12
66	59.83	68.33	59.88
67	67.8	69.75	67.78
68	65.58	66.9	65.5
69	53.61	54.87	54.64
70	55.48	57.39	56.12
71	56.32	56.85	56.61
72	50.65	50.7	50.6
73	52.04	52.65	51.97
74	48.02	48.06	48
75	46.12	45.1	46.07

Supplementary Table S6. Inferred repertoire sizes for extinct taxa using various PGLS models and using non-phylogenetically corrected linear regression Mean OB ratios are indicated with '*'. Models with and without the alligator are displayed.

Species	OB ratio	PGLS alligator+Aves, rep= 6.87*OB+305.20	PGLS Aves rep= 5.63*OB+236.38	PGLS alligator+Aves rep= 6.61*OB+328.33	Linear Regression		
		Outlier taxa removed		Outlier taxa included	Fit	Lower	Upper
Allosaurus fragilis	51.6	660.0319	526.7173	669.5696615	753.7345	455.48464	1051.9843
Allosaurus fragilis	50	649.0294	517.7147	658.9884881	735.1643	441.04301	1029.2856
*Allosaurus fragilis**	50.8	654.5306	522.2160	664.2790748	744.4494	448.2818	1040.617
Acrocanthosaurus atokensis	58.1	704.7297	563.2902	712.5556786	829.1758	512.765	1145.5866
Carcharodontosaurus saharicus	56	690.2889	551.4743	698.6678884	804.8025	494.4898	1115.1151
Giganotosaurus carolinii	57.7	701.9791	561.0396	709.9103852	824.5333	509.3	1139.7665
Ceratosaurus magnicornis	48.1	635.9638	507.0242	646.4233446	713.1122	423.7022	1002.5223
Majungasaurus crenatissimus	48.3	637.3392	508.1495	647.7459913	715.4335	425.5376	1005.3294
Dilong paradoxus	27	490.8678	388.3028	506.88412	468.218	214.1662	722.2699
Albertosaurus sarcophagus	71	793.4378	635.8734	797.8663893	978.8978	620.9812	1336.8144
Gorgosaurus libratus	68.5	776.2463	621.8069	781.3333059	949.8819	600.491	1299.2729
Tarbosaurus bataar	65.1	752.8659	602.6764	758.8483123	910.4203	572.2776	1248.563
Tyrannosaurus rex	66.5	762.4931	610.5537	768.1068391	926.6692	583.94542	1269.393
Tyrannosaurus rex	71	793.4378	635.8734	797.8663893	978.8978	620.98125	1336.8144
Tyrannosaurus rex	68.3	774.871	620.6816	780.0106592	947.5607	598.84277	1296.2786
*Tyrannosaurus rex**	68.7	777.6216	622.9322	782.6559525	952.2032	602.1379	1302.2685
Garudimimus brevipes	28.8	503.2456	398.4307	518.7879401	489.1095	233.4306	744.7884
Ornithomimus edmontonensis	31.4	521.1248	413.0599	535.9823469	519.286	260.7588	777.8133
Dromiceiomimus brevitertius	29.4	507.3716	401.8067	522.7558801	496.0733	239.7889	752.3578
Struthiomimus altus	32.5	528.689	419.2491	543.2569037	532.053	272.1475	791.9586
Citipati osmolskae	31.5	521.8124	413.6225	536.6436703	520.4467	261.7983	779.095
Saurornitholestes langstoni	34.8	544.5052	432.1903	558.4673405	558.7476	295.6369	821.8584
Bambiraptor feinbergi	28.5	501.1827	396.7427	516.8039701	485.6276	230.2397	741.0155
Velociraptor mongoliensis	35.7	550.6941	437.2543	564.4192505	569.1934	304.712	833.6747
Troodon formosus	33.2	533.5026	423.1878	547.886167	540.1775	279.34231	801.0126
Troodon formosus	33.5	535.5656	424.8757	549.8701371	543.6594	282.41344	804.9053
Troodon formosus	32.6	529.3767	419.8118	543.918227	533.2137	273.17779	793.2495
Troodon formosus	33	532.1273	422.0624	546.5635204	537.8562	277.29078	798.4216
*Troodon formosus**	33.1	532.815	422.6251	547.2248437	539.0168	278.317	799.7167
Archaeopteryx lithographica	17.1	422.7895	332.5994	441.4131094	353.3151	102.9525	603.6776
Confuciusornis sanctus	17.9	428.2908	337.1007	446.7036961	362.6002	112.2763	612.9241
Hesperornis regalis	15.3	410.4117	322.4715	429.5092893	332.4236	81.75645	583.0908

Hesperornis regalis	21.3	451.6712	356.2312	469.1886897	402.0618	151.23762	652.886
*Hesperornis regalis**	18.3	431.0414	339.3513	449.3489895	367.2427	116.9158	617.5697
Ichthyornis dispar	18.1	429.6661	338.226	448.0263428	364.9214	114.5979	615.245
Lithornis plebius	36.5	556.1954	441.7555	569.7098372	578.4785	312.7251	844.2318
Lithornis promiscuus	37.7	564.4473	448.5075	577.6457173	592.4061	324.6515	860.1607
Deinonychus antirrhopus	41	587.14	467.0753	599.4693875	630.7071	356.8918	904.5223
Tsaagan mangas	36	552.7571	438.9422	566.4032206	572.6753	307.7228	837.6277
Viavenator exxoni	57	697.1655	557.1009	705.2811218	816.4088	503.2184	1129.5992
Erlikosaurus andrewsi	40	580.2635	461.4487	592.8561541	619.1007	347.2063	890.9951
Euoplocephalus sp	52	662.7825	528.9679	672.2149549	758.377	459.0728	1057.6813
Pawpawsaurus campbelli	46.2	622.8983	496.3336	633.8582012	691.0601	406.1437	975.9766
Panoplosaurus mirus	44	607.7698	483.9551	619.3090877	665.5261	385.5273	945.525

Supplementary Table S7. Representative reptilian OR genes used to find orthologous sequences in bird genomes, using 65% identity as a threshold.

Olfactory Receptor	**Source**
XM_006035034.1 PREDICTED: Alligator sinensis olfactory receptor 4E1	RefSeq [6]
XM_006039314.1 PREDICTED: Alligator sinensis olfactory receptor 52L1	
XM_006032220.2 PREDICTED: Alligator sinensis olfactory receptor 1052	
XM_006032219.1 PREDICTED: Alligator sinensis olfactory receptor 1052	
XM_014526796.1 PREDICTED: Alligator sinensis olfactory receptor 2AP1	
XM_006038492.1 PREDICTED: Alligator sinensis olfactory receptor 6B1	
XM_014527740.1 PREDICTED: Alligator sinensis olfactory receptor 6C75	
XM_006038961.2 PREDICTED: Alligator sinensis olfactory receptor 10A2	
XM_014527570.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	
XM_006035991.2 PREDICTED: Alligator sinensis olfactory receptor 10A5	
XM_014527671.1 PREDICTED: Alligator sinensis olfactory receptor 10A3	
XM_006034106.2 PREDICTED: Alligator sinensis olfactory receptor 6	
XM_006039013.2 PREDICTED: Alligator sinensis olfactory receptor 14A16	
XM_006034107.1 PREDICTED: Alligator sinensis olfactory receptor 12	
XM_006035018.1 PREDICTED: Alligator sinensis olfactory receptor 6C4	
XM_006036718.1 PREDICTED: Alligator sinensis olfactory receptor 52B2	
XM_006032241.2 PREDICTED: Alligator sinensis olfactory receptor 2G3	
XM_006031572.2 PREDICTED: Alligator sinensis olfactory receptor 5B21	
XM_006032244.1 PREDICTED: Alligator sinensis olfactory receptor 1052	
XM_014524909.1 PREDICTED: Alligator sinensis olfactory receptor 6P1	
XM_006035017.1 PREDICTED: Alligator sinensis olfactory receptor 6C4	
XM_006032228.2 PREDICTED: Alligator sinensis olfactory receptor 5AR1	
XM_006036717.1 PREDICTED: Alligator sinensis olfactory receptor 52D1	
XM_006032217.1 PREDICTED: Alligator sinensis olfactory receptor 1019	
XM_014526923.1 PREDICTED: Alligator sinensis olfactory receptor 51Q1	
XM_006037936.1 PREDICTED: Alligator sinensis olfactory receptor 51G2	
XM_006036778.1 PREDICTED: Alligator sinensis olfactory receptor 1020	
XM_006032087.1 PREDICTED: Alligator sinensis olfactory receptor 52R1	
XM_014523915.1 PREDICTED: Alligator sinensis olfactory receptor 51S1	
XM_006032091.1 PREDICTED: Alligator sinensis olfactory receptor 51L1	
XM_006035000.1 PREDICTED: Alligator sinensis olfactory receptor 4E1	
XM_006039093.1 PREDICTED: Alligator sinensis olfactory receptor 12D2	
XM_014524856.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	
XM_006036061.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	
XM_006037726.1 PREDICTED: Alligator sinensis olfactory receptor 4N2	
XM_006038500.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	
XM_006032092.1 PREDICTED: Alligator sinensis olfactory receptor 51E2	
XM_006033957.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	
XM_006034122.1 PREDICTED: Alligator sinensis olfactory receptor 6N1	
XM_014526782.1 PREDICTED: Alligator sinensis olfactory receptor 10T2	
XM_006032221.2 PREDICTED: Alligator sinensis olfactory receptor COR8	
XM_006034790.2 PREDICTED: Alligator sinensis olfactory receptor COR4	
XM_014523649.1 PREDICTED: Alligator sinensis olfactory receptor 10A7	
XM_014523977.1 PREDICTED: Alligator sinensis olfactory receptor 1019	
XM_014526594.1 PREDICTED: Alligator sinensis olfactory receptor 52A5	
XM_006032247.1 PREDICTED: Alligator sinensis olfactory receptor 1009	
XM_006020988.2 PREDICTED: Alligator sinensis olfactory receptor 2A5	
XM_006039254.1 PREDICTED: Alligator sinensis olfactory receptor 10A7	
XM_006031595.1 PREDICTED: Alligator sinensis olfactory receptor 6M1	
XM_006039174.1 PREDICTED: Alligator sinensis olfactory receptor 4D9	
XM_006034999.1 PREDICTED: Alligator sinensis olfactory receptor 49	
XM_006031590.2 PREDICTED: Alligator sinensis olfactory receptor 1052	
XM_014527682.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	

XM_006032090.2 PREDICTED: Alligator sinensis olfactory receptor 51G2	
XM_006039094.1 PREDICTED: Alligator sinensis olfactory receptor 12D3	
XM_014524214.1 PREDICTED: Alligator sinensis olfactory receptor 10R2	
XM_006039141.1 PREDICTED: Alligator sinensis olfactory receptor 6X1	
XM_006032222.1 PREDICTED: Alligator sinensis olfactory receptor 1052	
XM_006032242.1 PREDICTED: Alligator sinensis olfactory receptor 1013	
XM_006034789.1 PREDICTED: Alligator sinensis olfactory receptor 1019	
XM_006039298.1 PREDICTED: Alligator sinensis olfactory receptor 12D2	
XM_014525901.1 PREDICTED: Alligator sinensis olfactory receptor 1019	
XM_014526945.1 PREDICTED: Alligator sinensis olfactory receptor 10A7	
XM_006033958.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	
XM_014527719.1 PREDICTED: Alligator sinensis olfactory receptor 4D9	
XM_006036686.1 PREDICTED: Alligator sinensis olfactory receptor 2AT4	
XM_006037243.2 PREDICTED: Alligator sinensis olfactory receptor 6X1	
XM_014526109.1 PREDICTED: Alligator sinensis olfactory receptor 14A16	
XM_006036787.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	
XM_014527787.1 PREDICTED: Alligator sinensis olfactory receptor 52R1	
XM_006039137.2 PREDICTED: Alligator sinensis olfactory receptor 5V1	
XM_006035034.1 PREDICTED: Alligator sinensis olfactory receptor 4E1	
XM_014604867.2 PREDICTED: Alligator mississippiensis olfactory receptor COR4	RefSeq [7]
XM_019478665.1 PREDICTED: Alligator mississippiensis olfactory receptor 9G4	
XM_019488518.1 PREDICTED: Alligator mississippiensis olfactory receptor 2A12	
XM_014597746.1 PREDICTED: Alligator mississippiensis olfactory receptor 11A1	
XM_006269294.2 PREDICTED: Alligator mississippiensis olfactory receptor 1009	
XM_014611427.1 PREDICTED: Alligator mississippiensis olfactory receptor 49	
XM_019499955.1 PREDICTED: Alligator mississippiensis olfactory receptor 10AC1	
XM_006278564.2 PREDICTED: Alligator mississippiensis olfactory receptor 2A5	
XM_006274969.2 PREDICTED: Alligator mississippiensis olfactory receptor 10T2	
XM_014594828.1 PREDICTED: Alligator mississippiensis olfactory receptor 10A4	
XM_014597745.1 PREDICTED: Alligator mississippiensis olfactory receptor 1440	
XM_019482376.1 PREDICTED: Alligator mississippiensis olfactory receptor 52A5	
XM_006260764.3 PREDICTED: Alligator mississippiensis olfactory receptor 1052	
XM_006269293.1 PREDICTED: Alligator mississippiensis olfactory receptor 11A1	
XM_006271879.2 PREDICTED: Alligator mississippiensis olfactory receptor 10H1	
XM_006262992.2 PREDICTED: Alligator mississippiensis olfactory receptor 51G2	
XM_006267750.2 PREDICTED: Alligator mississippiensis olfactory receptor 2G3	
XM_006268318.2 PREDICTED: Alligator mississippiensis olfactory receptor 10C1	
XM_014609974.2 PREDICTED: Alligator mississippiensis olfactory receptor 4N2	
XM_019489818.1 PREDICTED: Alligator mississippiensis olfactory receptor 6F1	
XM_006262994.2 PREDICTED: Alligator mississippiensis olfactory receptor 51Q1	
XM_014597747.1 PREDICTED: Alligator mississippiensis olfactory receptor 6A2	
XM_014611430.1 PREDICTED: Alligator mississippiensis olfactory receptor 6M1	
XM_019489814.1 PREDICTED: Alligator mississippiensis olfactory receptor 6B1	
XM_006258018.2 PREDICTED: Alligator mississippiensis olfactory receptor 4M1	
XM_006262993.2 PREDICTED: Alligator mississippiensis olfactory receptor 51I2	
XM_006263697.2 PREDICTED: Alligator mississippiensis olfactory receptor 51I2	
XM_006268307.3 PREDICTED: Alligator mississippiensis olfactory receptor 10A4	
XM_006263040.1 PREDICTED: Alligator mississippiensis olfactory receptor 1038	
XM_006259095.1 PREDICTED: Alligator mississippiensis olfactory receptor 4D9	
XM_006260759.1 PREDICTED: Alligator mississippiensis olfactory receptor 1019	
XM_006267538.1 PREDICTED: Alligator mississippiensis olfactory receptor 1019	
XM_006268320.1 PREDICTED: Alligator mississippiensis olfactory receptor 10A7	
XM_014595168.1 PREDICTED: Alligator mississippiensis olfactory receptor 2A12	
XM_006278509.1 PREDICTED: Alligator mississippiensis olfactory receptor 4N5	
XM_014594485.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	
XM_006268319.1 PREDICTED: Alligator mississippiensis olfactory receptor 10C1	
XM_006265550.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	

XM_006278498.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	
XM_006278500.2 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	
XM_019486358.1 PREDICTED: Alligator mississippiensis olfactory receptor 12D1	
XM_019496768.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	
XM_019496752.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	
XM_005311793.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	RefSeq [5]
XM_008175041.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4D5	
XM_008176388.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	
XM_008175039.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	
XM_008175031.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_005309244.2 PREDICTED: Chrysemys picta bellii olfactory receptor 1468	
XM_008174413.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14I1	
XM_005289441.2 PREDICTED: Chrysemys picta bellii olfactory receptor 2AT4	
XM_008175033.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A4	
XM_005309234.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_008175027.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5	
XM_005314359.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52E4	
XM_008178121.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1019	
XM_008174412.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4D2	
XM_008168738.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	
XM_005310841.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5V1	
XM_005310413.1 PREDICTED: Chrysemys picta bellii olfactory receptor 12D2	
XM_008168730.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	
XM_008178018.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52K1	
XM_008175965.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1009	
XM_005311801.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	
XM_008177963.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1019	
XM_005312774.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4N2	
XM_008175572.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	
XM_005309056.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_008177588.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	
XM_008175561.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	
XM_005313796.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6C75	
XM_008174336.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_008174338.1 PREDICTED: Chrysemys picta bellii olfactory receptor 12D2	
XM_005310393.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_005310272.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_005310292.2 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	
XM_005310408.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_008171713.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1019	
XM_005310400.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10C1	
XM_008177751.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_005309045.2 PREDICTED: Chrysemys picta bellii olfactory receptor 12	
XM_008175036.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_008176638.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4Q2	
XM_005309255.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	
XM_005310439.2 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	
XM_008174340.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_005290034.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	
XM_005310406.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A7	
XM_005314585.2 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	
XM_005309064.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10AG1	
XM_005314320.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_005311899.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_005290011.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	
XM_005309043.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6P1	
XM_005309055.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	

XM_005310422.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_008174332.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_008177992.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A7	
XM_005309019.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1020	
XM_005313885.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52K2	
XM_005310280.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	
XM_008174321.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_005309024.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10C1	
XM_005311817.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	
XM_005312282.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5V1	
XM_005290052.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	
XM_005313248.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52R1	
XM_008178061.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52P1	
XM_005314254.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_008174690.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_005310270.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_005309010.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A4	
XM_005313793.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6C4	
XM_005284256.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_008177186.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_005290036.2 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	
XM_008177901.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51E2	
XM_005309014.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A4	
XM_005310433.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5V1	
XM_005312401.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	
XM_008174396.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4M1	
XM_005311794.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	
XM_005310423.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	
XM_008174324.1 PREDICTED: Chrysemys picta bellii olfactory receptor 476	
XM_008177669.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B6	
XM_008174403.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4D9	
XM_008177073.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	
XM_005309054.2 PREDICTED: Chrysemys picta bellii olfactory receptor 1038	
XM_005309062.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11L1	
XM_008177845.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52K1	
XM_005309038.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	
XM_005310284.2 PREDICTED: Chrysemys picta bellii olfactory receptor 1038	
Pm066	[3]
Pm091	
Pm010	
Pm120	
Pm047	
Pm068	
Pm020	
Pm046	
Pm055	
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Pm148	
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Pm036	
Pm049	
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Pm005	
Pm132	
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Pm123	
Pm004	
Pm096	
Pm023	
Pm054	
Pm155_P	
Pm171_T	
Pm207_T	
Pm213_T	
Pm223_T	
Pm222_T	
Pm209_T	
Pm248_T	
Pm250_T	
Pm271_T	
Pm275_T	
Pm277_T	
Pm184_T	
Pm195_T	
Pm188_T	
Pm243_T	
Pm219_T	
Pm279_T	
Pm178_T	
Pm252_T	
Pm204_T	
Ac93	
Ac89	
Ac75	
Ac109	
Ac110	
Ac52	
Ac98	
Ac106	
Ac131	
Ac59	
Ac3	
Ac91	
Ac125	
Ac112	
Ac119	
Ac44	
Ac103	
Ac27	
Ac20	
Ac37	
Ac87	
Ac81	

Supplementary Table S8. Query reptilian OR genes were used to find orthologs in birds with 65% shared amino acid identity. The query, orthologs, sequence lengths and shared identities for all sequences used are displayed.

Query Reptile sequence	Length (amino acids)	Bird orthologs	Shared amino acids	Bird OR length	% identity
XM_006035034.1 PREDICTED: Alligator sinensis olfactory receptor 4E1	377	Struthio camelus OR4	207	300	69%
XM_006039314.1 PREDICTED: Alligator sinensis olfactory receptor 52L1	229	Struthio camelus OR52	130	178	73%
XM_006032220.2 PREDICTED: Alligator sinensis olfactory receptor 1052	375	Anas platyrhynchos OR5	221	305	72%
XM_006032219.1 PREDICTED: Alligator sinensis olfactory receptor 1052	370	Anas platyrhynchos OR5	201	305	66%
XM_014526796.1 PREDICTED: Alligator sinensis olfactory receptor 2AP1	367	Aptenodytes forsteri OR10	200	307	65%
XM_006038492.1 PREDICTED: Alligator sinensis olfactory receptor 6B1	364	Cathartes aura OR6	249	307	81%
XM_014527740.1 PREDICTED: Alligator sinensis olfactory receptor 6C75	360	Fulmarus glacialis OR6	210	300	70%
XM_006038961.2 PREDICTED: Alligator sinensis olfactory receptor 10A2	562	Pterocles gutturalis OR10	212	294	72%
XM_014527570.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	355	Nestor notabilis OR6	212	306	69%
XM_006035991.2 PREDICTED: Alligator sinensis olfactory receptor 10A5	348	Tinamus guttatus OR10	184	270	68%
XM_014527671.1 PREDICTED: Alligator sinensis olfactory receptor 10A3	346	Charadrius vociferus OR10	189	270	70%
XM_006034106.2 PREDICTED: Alligator sinensis olfactory receptor 6	344	Antrostomus carolinensis OR6 Pseudogene	139	215	65%
XM_006039013.2 PREDICTED: Alligator sinensis olfactory receptor 14A16	344	Nipponia nippon OR14	200	307	65%
XM_006034107.1 PREDICTED: Alligator sinensis olfactory receptor 12	342	Balearica regulorum OR14	223	308	72%
XM_006035018.1 PREDICTED: Alligator sinensis olfactory receptor 6C4	342	Charadrius vociferus OR6	217	308	70%
XM_006036718.1 PREDICTED: Alligator sinensis olfactory receptor 52B2	342	Meleagris gallopavo OR52	213	304	70%
XM_006032241.2 PREDICTED: Alligator sinensis olfactory receptor 2G3	337	Cathartes aura OR13	228	309	74%
XM_006031572.2 PREDICTED: Alligator sinensis olfactory receptor 5B21	510	Phoenicopterus ruber OR13	197	304	65%
XM_006032244.1 PREDICTED: Alligator sinensis olfactory receptor 1052	336	Charadrius vociferus OR5	208	311	67%
XM_014524909.1 PREDICTED: Alligator sinensis olfactory receptor 6P1	336	Aptenodytes forsteri OR5	187	273	68%
XM_006035017.1 PREDICTED: Alligator sinensis olfactory receptor 6C4	334	Nipponia nippon OR6	205	300	68%
XM_006032228.2 PREDICTED: Alligator sinensis olfactory receptor 5AR1	333	Cathartes aura OR5	241	313	77%
XM_006036717.1 PREDICTED: Alligator sinensis olfactory receptor 52D1	333	Struthio camelus OR52	217	303	72%
XM_006032217.1 PREDICTED: Alligator sinensis olfactory receptor 1019	332	Fulmarus glacialis OR5	221	307	72%
XM_014526923.1 PREDICTED: Alligator sinensis olfactory receptor 51Q1	330	Columba livia OR51	203	305	67%
XM_006037936.1 PREDICTED: Alligator sinensis olfactory receptor 51G2	328	Tinamus guttatus OR51	171	225	76%
XM_006036778.1 PREDICTED: Alligator sinensis olfactory receptor 1020	477	Phaeton lepturus OR10	209	313	67%
XM_006032087.1 PREDICTED: Alligator sinensis olfactory receptor 52R1	325	Gavia stellata OR52	224	308	73%
XM_014523915.1 PREDICTED: Alligator sinensis olfactory receptor 51S1	325	Struthio camelus OR51 Pseudogene	142	200	71%
XM_006032091.1 PREDICTED: Alligator sinensis olfactory receptor 51L1	324	Struthio camelus OR51	195	298	65%
XM_006035000.1 PREDICTED: Alligator sinensis olfactory receptor 4E1	459	Struthio camelus OR4	243	301	81%
XM_006039093.1 PREDICTED: Alligator sinensis olfactory receptor 12D2	322	Cariama cristata OR12	230	309	74%
XM_014524856.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	321	Phaeton lepturus OR4	201	309	65%

XM_006036061.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	320	Gavia stellata OR4	211	312	68%
XM_006037726.1 PREDICTED: Alligator sinensis olfactory receptor 4N2	320	Cathartes aura OR4	227	320	71%
XM_006038500.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	433	Cuculus canorus OR5	206	310	66%
XM_006032092.1 PREDICTED: Alligator sinensis olfactory receptor 51E2	319	Phaeton lepturus OR51	241	319	76%
XM_006033957.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	319	Struthio camelus OR4	226	307	74%
XM_006034122.1 PREDICTED: Alligator sinensis olfactory receptor 6N1	319	Gavia stellata OR10	259	307	84%
XM_014526782.1 PREDICTED: Alligator sinensis olfactory receptor 10T2	430	Charadrius vociferus OR10	215	307	70%
XM_006032221.2 PREDICTED: Alligator sinensis olfactory receptor COR8	318	Gallus gallus OR5	230	315	73%
XM_006034790.2 PREDICTED: Alligator sinensis olfactory receptor COR4	318	Phaeton lepturus OR5	215	308	70%
XM_014523649.1 PREDICTED: Alligator sinensis olfactory receptor 10A7	318	Nipponia nippon OR5	201	306	66%
XM_014523977.1 PREDICTED: Alligator sinensis olfactory receptor 1019	318	Anas platyrhynchos OR5	200	309	65%
XM_014526594.1 PREDICTED: Alligator sinensis olfactory receptor 52A5	318	Struthio camelus OR52	212	316	67%
XM_006032247.1 PREDICTED: Alligator sinensis olfactory receptor 1009	317	Tyto alba OR5	202	308	66%
XM_006020988.2 PREDICTED: Alligator sinensis olfactory receptor 2A5	316	Struthio camelus OR2	238	303	79%
XM_006039254.1 PREDICTED: Alligator sinensis olfactory receptor 10A7	421	Tinamus guttatus OR10	196	301	65%
XM_006031595.1 PREDICTED: Alligator sinensis olfactory receptor 6M1	316	Opisthocomus hoazin OR6	208	316	66%
XM_006039174.1 PREDICTED: Alligator sinensis olfactory receptor 4D9	316	Pterocles gutturalis OR4	206	314	66%
XM_006034999.1 PREDICTED: Alligator sinensis olfactory receptor 49	316	Nipponia nippon OR6	214	307	70%
XM_006031590.2 PREDICTED: Alligator sinensis olfactory receptor 1052	419	Balearica regulorum OR13	189	283	67%
XM_014527682.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	315	Tinamus guttatus OR6	227	310	73%
XM_006032090.2 PREDICTED: Alligator sinensis olfactory receptor 51G2	314	Struthio camelus OR51	249	303	82%
XM_006039094.1 PREDICTED: Alligator sinensis olfactory receptor 12D3	314	Cariama cristata OR12	230	314	73%
XM_014524214.1 PREDICTED: Alligator sinensis olfactory receptor 10R2	314	Balearica regulorum OR10	211	298	71%
XM_006039141.1 PREDICTED: Alligator sinensis olfactory receptor 6X1	409	Fulmarus glacialis OR6	153	231	66%
XM_006032222.1 PREDICTED: Alligator sinensis olfactory receptor 1052	313	Struthio camelus OR5	225	311	72%
XM_006032242.1 PREDICTED: Alligator sinensis olfactory receptor 1013	313	Gavia stellata OR9	222	312	71%
XM_006034789.1 PREDICTED: Alligator sinensis olfactory receptor 1019	313	Fulmarus glacialis OR5	218	311	70%
XM_006039298.1 PREDICTED: Alligator sinensis olfactory receptor 12D2	313	Cariama cristata OR12	210	309	68%
XM_014525901.1 PREDICTED: Alligator sinensis olfactory receptor 1019	313	Struthio camelus OR5	234	311	75%
XM_014526945.1 PREDICTED: Alligator sinensis olfactory receptor 10A7	313	Tinamus guttatus OR10	223	301	74%
XM_006033958.1 PREDICTED: Alligator sinensis olfactory receptor 4S2	403	Gavia stellata OR4	262	312	84%
XM_014527719.1 PREDICTED: Alligator sinensis olfactory receptor 4D9	400	Geospiza fortis OR4	203	303	67%
XM_006036686.1 PREDICTED: Alligator sinensis olfactory receptor 2AT4	396	Nipponia nippon OR2	231	312	74%
XM_006037243.2 PREDICTED: Alligator sinensis olfactory receptor 6X1	311	Aptenodytes forsteri OR2	217	309	70%
XM_014526109.1 PREDICTED: Alligator sinensis olfactory receptor 14A16	307	Columba livia OR14	203	306	66%
XM_006036787.1 PREDICTED: Alligator sinensis olfactory receptor 6F1	298	Cathartes aura OR6	195	299	65%
XM_014527787.1 PREDICTED: Alligator sinensis olfactory receptor 52R1	277	Gavia stellata OR52	164	224	73%
XM_006039137.2 PREDICTED: Alligator sinensis olfactory receptor 5V1	261	Aptenodytes forsteri OR10	131	203	65%

XM_006035034.1 PREDICTED: Alligator sinensis olfactory receptor 4E1	377	Struthio camelus OR4	207	300	69%
XM_014604867.2 PREDICTED: Alligator mississippiensis olfactory receptor COR4	334	Gallus gallus OR5	201	305	66%
XM_019478665.1 PREDICTED: Alligator mississippiensis olfactory receptor 9G4	160	Phoenicopterus ruber OR6	68	93	73%
XM_019488518.1 PREDICTED: Alligator mississippiensis olfactory receptor 2A12	363	Fulmarus glacialis OR2	200	305	66%
XM_014597746.1 PREDICTED: Alligator mississippiensis olfactory receptor 11A1	357	Phoenicopterus ruber OR6	205	306	67%
XM_006269294.2 PREDICTED: Alligator mississippiensis olfactory receptor 1009	353	Nipponia nippon OR5	200	310	65%
XM_014611427.1 PREDICTED: Alligator mississippiensis olfactory receptor 49	331	Fulmarus glacialis OR6	215	324	66%
XM_019499955.1 PREDICTED: Alligator mississippiensis olfactory receptor 10AC1	331	Podiceps cristatus OR10	245	326	75%
XM_006278564.2 PREDICTED: Alligator mississippiensis olfactory receptor 2A5	328	Charadrius vociferus OR2	205	306	67%
XM_006274969.2 PREDICTED: Alligator mississippiensis olfactory receptor 10T2	326	Charadrius vociferus OR10	229	303	76%
XM_006274969.2 PREDICTED: Alligator mississippiensis olfactory receptor 10T2	326	Charadrius vociferus OR10	229	303	76%
XM_014594828.1 PREDICTED: Alligator mississippiensis olfactory receptor 10A4	326	Charadrius vociferus OR10	216	308	70%
XM_014597745.1 PREDICTED: Alligator mississippiensis olfactory receptor 1440	325	Phoenicopterus ruber OR10	164	247	66%
XM_019482376.1 PREDICTED: Alligator mississippiensis olfactory receptor 52A5	469	Struthio camelus OR52	195	279	70%
XM_006260764.3 PREDICTED: Alligator mississippiensis olfactory receptor 1052	324	Anas platyrhynchos OR5	205	305	67%
XM_006269293.1 PREDICTED: Alligator mississippiensis olfactory receptor 11A1	324	Fulmarus glacialis OR10	146	226	65%
XM_006271879.2 PREDICTED: Alligator mississippiensis olfactory receptor 10H1	324	Haliaeetus leucocephalus OR10	200	308	65%
XM_006262992.2 PREDICTED: Alligator mississippiensis olfactory receptor 51G2	322	Tinamus guttatus OR51	231	318	73%
XM_006267750.2 PREDICTED: Alligator mississippiensis olfactory receptor 2G3	321	Melopsittacus undulatus OR10	197	303	65%
XM_006268318.2 PREDICTED: Alligator mississippiensis olfactory receptor 10C1	321	Cathartes aura OR10	237	316	75%
XM_014609974.2 PREDICTED: Alligator mississippiensis olfactory receptor 4N2	320	Cathartes aura OR4	235	312	75%
XM_019489818.1 PREDICTED: Alligator mississippiensis olfactory receptor 6F1	320	Aptenodytes forsteri OR4	208	303	69%
XM_006262994.2 PREDICTED: Alligator mississippiensis olfactory receptor 51Q1	318	Columba livia OR51	226	303	75%
XM_014597747.1 PREDICTED: Alligator mississippiensis olfactory receptor 6A2	318	Nipponia nippon OR6	209	318	66%
XM_014611430.1 PREDICTED: Alligator mississippiensis olfactory receptor 6M1	318	Pygoscelis adeliae OR6	227	313	73%
XM_019489814.1 PREDICTED: Alligator mississippiensis olfactory receptor 6B1	318	Fulmarus glacialis OR10	148	227	65%
XM_006258018.2 PREDICTED: Alligator mississippiensis olfactory receptor 4M1	315	Pterocles gutturalis OR4	215	309	70%
XM_006262993.2 PREDICTED: Alligator mississippiensis olfactory receptor 51I2	315	Struthio camelus OR51	242	309	78%
XM_006263697.2 PREDICTED: Alligator mississippiensis olfactory receptor 51I2	315	Struthio camelus OR51	214	309	69%
XM_006268307.3 PREDICTED: Alligator mississippiensis olfactory receptor 10A4	315	Tinamus guttatus OR10	189	270	70%
XM_006263040.1 PREDICTED: Alligator mississippiensis olfactory receptor 1038	314	Struthio camelus OR5	234	307	76%
XM_006259095.1 PREDICTED: Alligator mississippiensis olfactory receptor 4D9	313	Gavia stellata OR4	203	312	65%
XM_006260759.1 PREDICTED: Alligator mississippiensis olfactory receptor 1019	310	Fulmarus glacialis OR5	221	307	72%
XM_006260759.1 PREDICTED: Alligator mississippiensis olfactory receptor 1019	313	Fulmarus glacialis OR5	220	305	72%
XM_006267538.1 PREDICTED: Alligator mississippiensis olfactory receptor 1019	313	Struthio camelus OR5	224	310	72%
XM_006268320.1 PREDICTED: Alligator mississippiensis olfactory receptor 10A7	313	Tinamus guttatus OR10	213	303	70%
XM_014595168.1 PREDICTED: Alligator mississippiensis olfactory receptor 2A12	313	Nipponia nippon OR2	212	313	68%
XM_006278509.1 PREDICTED: Alligator mississippiensis olfactory receptor 4N5	312	Pygoscelis adeliae OR4	207	304	68%

XM_014594485.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	312	Phaeton lepturus OR4	218	312	70%
XM_006268319.1 PREDICTED: Alligator mississippiensis olfactory receptor 10C1	311	Columba livia OR10	219	305	72%
XM_006265550.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	310	Struthio camelus OR4	220	308	71%
XM_006278498.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	310	Phaeton lepturus OR4	227	310	73%
XM_006278500.2 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	310	Phaeton lepturus OR4	231	310	75%
XM_019486358.1 PREDICTED: Alligator mississippiensis olfactory receptor 12D1	308	Pterocles gutturalis OR12	171	259	66%
XM_019496768.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	302	Podiceps cristatus OR4	195	300	65%
XM_019496752.1 PREDICTED: Alligator mississippiensis olfactory receptor 4S2	292	Struthio camelus OR4	186	249	75%
XM_005311793.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	596	Tinamus guttatus OR51	224	301	74%
XM_008175041.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4D5	229	Pterocles gutturalis OR4	142	209	68%
XM_008176388.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	226	Columba livia OR14	125	192	65%
XM_008175039.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	376	Nestor notabilis OR6	206	303	68%
XM_008175031.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	201	Picoides pubescens OR10	124	191	65%
XM_005309244.2 PREDICTED: Chrysemys picta bellii olfactory receptor 1468	199	Melopsittacus undulatus OR10	129	195	66%
XM_008174413.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14I1	188	Nipponia nippon OR14	96	138	70%
XM_005289441.2 PREDICTED: Chrysemys picta bellii olfactory receptor 2AT4	372	Nipponia nippon OR2	251	308	81%
XM_008175033.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A4	175	Fulmarus glacialis OR10	123	174	71%
XM_005309234.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	169	Fulmarus glacialis OR10	117	169	69%
XM_008175027.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5	169	Fulmarus glacialis OR10	118	169	70%
XM_005314359.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52E4	108	Phoenicopterus ruber OR52	62	94	66%
XM_008178121.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1019	584	Gavia stellata OR5	230	311	74%
XM_008174412.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4D2	360	Corvus brachyrhynchos OR5	217	307	71%
XM_008168738.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	356	Columba livia OR14	206	307	67%
XM_005310841.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5V1	356	Egretta garzetta OR13	220	322	68%
XM_005310413.1 PREDICTED: Chrysemys picta bellii olfactory receptor 12D2	355	Cariama cristata OR12	223	311	72%
XM_008168730.1 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	355	Podiceps cristatus OR14	195	302	65%
XM_008178018.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52K1	543	Struthio camelus OR51	211	280	75%
XM_008175965.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1009	351	Fulmarus glacialis OR8	177	270	66%
XM_005311801.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	538	Tinamus guttatus OR51	222	301	74%
XM_008177963.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1019	348	Balearica regulorum OR5	172	253	68%
XM_005312774.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4N2	528	Cathartes aura OR4	230	313	73%
XM_008175572.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	346	Tyto alba OR51	174	253	69%
XM_005309056.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	345	Phoenicopterus ruber OR10	158	243	65%
XM_008177588.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	345	Charadrius vociferus OR52	242	307	79%
XM_008175561.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	517	Tinamus guttatus OR51	218	299	73%
XM_005313796.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6C75	341	Fulmarus glacialis OR6	208	311	67%
XM_008174336.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	339	Fulmarus glacialis OR10	150	226	66%
XM_008174338.1 PREDICTED: Chrysemys picta bellii olfactory receptor 12D2	338	Charadrius vociferus OR12	218	310	70%

XM_005310393.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	336	Phaeton lepturus OR10	204	310	66%
XM_005310272.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	503	Haliaeetus leucocephalus OR5	211	320	66%
XM_005310292.2 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	334	Tinamus guttatus OR14	189	292	65%
XM_005310408.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	333	Opisthocomus hoazin OR6	239	315	76%
XM_008171713.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1019	333	Cathartes aura OR5	209	307	68%
XM_005310400.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10C1	332	Cathartes aura OR10	210	309	68%
XM_008177751.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	490	Charadrius vociferus OR5	201	310	65%
XM_005309045.2 PREDICTED: Chrysemys picta bellii olfactory receptor 12	330	Balearica regulorum OR5	222	306	73%
XM_008175036.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	330	Fulmarus glacialis OR6	229	312	73%
XM_008176638.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4Q2	487	Nestor notabilis OR4	193	297	65%
XM_005309255.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	484	Cathartes aura OR6	203	307	66%
XM_005310439.2 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	483	Gavia stellata OR14	157	242	65%
XM_008174340.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	326	Phoenicopterus ruber OR6	209	309	68%
XM_005290034.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	325	Anas platyrhynchos OR52	272	323	84%
XM_005310406.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A7	324	Pelecanus crispus OR10	206	303	68%
XM_005314585.2 PREDICTED: Chrysemys picta bellii olfactory receptor 14A16	324	Columba livia OR14	195	290	67%
XM_005309064.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10AG1	323	Balearica regulorum OR14	198	305	65%
XM_005314320.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	323	Fulmarus glacialis OR10	148	227	65%
XM_005311899.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	323	Phoenicopterus ruber OR6	207	309	67%
XM_005290011.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	322	Phaeton lepturus OR52	203	305	67%
XM_005309043.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6P1	322	Opisthocomus hoazin OR6	200	310	65%
XM_005309055.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	322	Podiceps cristatus OR10	164	249	66%
XM_005310422.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	322	Aptenodytes forsteri OR10	197	303	65%
XM_008174332.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	322	Phoenicopterus ruber OR6	203	312	65%
XM_008177992.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A7	438	Phoenicopterus ruber OR6	202	306	66%
XM_005309019.1 PREDICTED: Chrysemys picta bellii olfactory receptor 1020	321	Aptenodytes forsteri OR5	224	314	71%
XM_005313885.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52K2	321	Cathartes aura OR52	233	316	74%
XM_005310280.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	320	Mesitornis unicolor OR6	229	304	75%
XM_008174321.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	320	Phoenicopterus ruber OR10	160	246	65%
XM_005309024.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10C1	319	Gavia stellata OR10	242	310	78%
XM_005311817.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	319	Struthio camelus OR51	235	295	80%
XM_005312282.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5V1	317	Charadrius vociferus OR5	235	316	74%
XM_005290052.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	316	Tinamus guttatus OR51	215	308	70%
XM_005313248.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52R1	316	Gavia stellata OR52	224	307	73%
XM_008178061.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52P1	628	Haliaeetus leucocephalus OR52	215	316	68%
XM_005314254.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	316	Aptenodytes forsteri OR10	206	317	65%
XM_008174690.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	316	Cuculus canorus OR5	203	310	65%
XM_005310270.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	418	Charadrius vociferus OR5	200	310	65%

XM_005309010.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A4	315	Tinamus guttatus OR10	195	301	65%
XM_005313793.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6C4	315	Charadrius vociferus OR6	194	300	65%
XM_005284256.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	417	Phoenicopterus ruber OR6	203	306	66%
XM_008177186.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	414	Melopsittacus undulatus OR10	206	319	65%
XM_005290036.2 PREDICTED: Chrysemys picta bellii olfactory receptor 52B2	313	Struthio camelus OR52	222	310	72%
XM_008177901.1 PREDICTED: Chrysemys picta bellii olfactory receptor 51E2	313	Phaeton lepturus OR51	230	300	77%
XM_005309014.1 PREDICTED: Chrysemys picta bellii olfactory receptor 10A4	312	Chaetura pelagica OR10	214	309	69%
XM_005310433.1 PREDICTED: Chrysemys picta bellii olfactory receptor 5V1	312	Phoenicopterus ruber OR13	209	308	68%
XM_005312401.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6F1	309	Tinamus guttatus OR6	195	302	65%
XM_008174396.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4M1	309	Pelecanus crispus OR4	199	308	65%
XM_005311794.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2	391	Tinamus guttatus OR51	211	299	71%
XM_005310423.1 PREDICTED: Chrysemys picta bellii olfactory receptor 6N1	305	Fulmarus glacialis OR10	145	203	71%
XM_008174324.1 PREDICTED: Chrysemys picta bellii olfactory receptor 476	303	Fulmarus glacialis OR10	120	184	65%
XM_008177669.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52B6	303	Pelecanus crispus OR52	195	302	65%
XM_008174403.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4D9	387	Geospiza fortis OR4	203	289	70%
XM_008177073.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11A1	287	Charadrius vociferus OR5	184	272	68%
XM_005309054.2 PREDICTED: Chrysemys picta bellii olfactory receptor 1038	281	Picoides pubescens OR10	160	236	68%
XM_005309062.1 PREDICTED: Chrysemys picta bellii olfactory receptor 11L1	281	Melopsittacus undulatus OR10	170	256	66%
XM_008177845.1 PREDICTED: Chrysemys picta bellii olfactory receptor 52K1	270	Struthio camelus OR51	146	211	69%
XM_005309038.2 PREDICTED: Chrysemys picta bellii olfactory receptor 6B1	379	Fulmarus glacialis OR10	146	226	65%
XM_005310284.2 PREDICTED: Chrysemys picta bellii olfactory receptor 1038	245	Charadrius vociferus OR5	129	196	66%
Pm066	349	Cathartes aura OR4	210	298	70%
Pm091	343	Opisthocomus hoazin OR6	242	310	78%
Pm010	334	Charadrius vociferus OR4	240	306	78%
Pm120	333	Struthio camelus OR51	226	303	75%
Pm047	331	Tinamus guttatus OR5	212	309	69%
Pm068	331	Podiceps cristatus OR2	209	318	66%
Pm020	328	Cuculus canorus OR5	201	310	65%
Pm046	328	Fulmarus glacialis OR10	227	311	73%
Pm055	328	Struthio camelus OR6	213	297	72%
Pm136	324	Antrostomus carolinensis OR9 Pseudogene	142	215	66%
Pm045	322	Struthio camelus OR5	197	303	65%
Pm148	322	Opisthocomus hoazin OR52	228	301	76%
Pm070	320	Tinamus guttatus OR52	221	303	73%
Pm119	318	Falco peregrinus OR52	251	314	80%
Pm014	316	Tinamus guttatus OR5	207	312	66%
Pm053	316	Struthio camelus OR5	205	308	67%
Pm030	314	Cariama cristata OR12	208	314	66%

Pm036	314	Anas platyrhynchos OR4 Pseudogene	127	190	67%
Pm049	314	Falco peregrinus OR4	206	309	67%
Pm088	313	Antrostomus carolinensis OR11	207	313	66%
Pm115	313	Cathartes aura OR4	199	305	65%
Pm005	310	Pterocles gutturalis OR5	219	302	73%
Pm132	310	Gallus gallus OR5	215	309	70%
Pm057	309	Balearica regulorum OR5	205	305	67%
Pm123	308	Tyto alba OR9	215	297	72%
Pm004	300	Phoenicopterus ruber OR5	194	300	65%
Pm096	296	Fulmarus glacialis OR6	207	271	76%
Pm023	385	Struthio camelus OR4	226	301	75%
Pm054	280	Struthio camelus OR6	222	269	83%
Pm155_P	196	Gavia stellata OR10	93	142	65%
Pm171_T	226	Struthio camelus OR4	142	212	67%
Pm207_T	209	Opisthocomus hoazin OR6	142	195	73%
Pm213_T	207	Fulmarus glacialis OR6	133	193	69%
Pm223_T	199	Fulmarus glacialis OR4	136	197	69%
Pm222_T	198	Antrostomus carolinensis OR12 Pseudogene	128	185	69%
Pm209_T	195	Gallus gallus OR5	125	189	66%
Pm248_T	194	Struthio camelus OR2	130	186	70%
Pm250_T	190	Anas platyrhynchos OR12	129	190	68%
Pm271_T	180	Gavia stellata OR10	134	180	74%
Pm275_T	179	Fulmarus glacialis OR10	103	159	65%
Pm277_T	174	Cariama cristata OR12	106	159	67%
Pm184_T	169	Fulmarus glacialis OR2	110	169	65%
Pm195_T	155	Phoenicopterus ruber OR10	63	97	65%
Pm188_T	148	Nestor notabilis OR5	101	145	70%
Pm243_T	144	Aptenodytes forsteri OR5	96	142	68%
Pm219_T	141	Cathartes aura OR10	82	126	65%
Pm279_T	141	Opisthocomus hoazin OR9	85	131	65%
Pm178_T	140	Nestor notabilis OR5	93	140	66%
Pm252_T	132	Antrostomus carolinensis OR12 Pseudogene	91	132	69%
Pm204_T	261	Nestor notabilis OR6	177	260	68%
Ac93	331	Podiceps cristatus OR10	225	322	70%
Ac89	324	Struthio camelus OR6	235	319	74%
Ac75	323	Pterocles gutturalis OR6	205	310	66%
Ac109	323	Tinamus guttatus OR13	198	303	65%
Ac110	314	Tinamus guttatus OR5	164	237	69%

Ac52	314	Pterocles gutturalis OR4	201	306	66%
Ac98	314	Podiceps cristatus OR10	163	248	66%
Ac106	314	Struthio camelus OR4	224	301	74%
Ac131	314	Cariama cristata OR9	124	170	73%
Ac59	313	Struthio camelus OR6	201	305	66%
Ac3	312	Tinamus guttatus OR5	204	306	67%
Ac91	312	Struthio camelus OR6	231	304	76%
Ac125	312	Fulmarus glacialis OR10	148	226	65%
Ac112	312	Phaeton lepturus OR5	118	179	66%
Ac119	312	Cariama cristata OR12	120	186	65%
Ac44	311	Phaeton lepturus OR6	215	311	69%
Ac103	311	Balearica regulorum OR6	205	308	67%
Ac27	310	Cathartes aura OR4	205	298	69%
Ac20	309	Tinamus guttatus OR5	198	305	65%
Ac37	307	Phoenicopterus ruber OR13	198	305	65%
Ac87	307	Opisthocomus hoazin OR6	231	305	76%
Ac81	306	Calypte anna OR10	197	302	65%
Alligator_mississippiensis_predicted OR4	240	Phoenicopterus ruber OR4	102	156	65%
Alligator_mississippiensis_predicted OR10	225	Charadrius vociferus OR10	174	219	79%
Alligator_mississippiensis_predicted OR51|PSEUDOGENE	212	Tinamus guttatus OR51	76	114	67%
Alligator_mississippiensis_predicted OR13|PSEUDOGENE	201	Pelecanus crispus OR13	130	198	66%
Alligator_mississippiensis_predicted OR6|PSEUDOGENE	197	Columba livia OR6	98	131	75%
Alligator_mississippiensis_predicted OR12|PSEUDOGENE	77	Podiceps cristatus OR12	53	76	70%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	94	Haliaeetus leucophalus OR12	59	91	65%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	35	Podiceps cristatus OR10	23	34	68%
Alligator_mississippiensis_predicted OR6|PSEUDOGENE	144	Cathartes aura OR5	71	110	65%
Alligator_mississippiensis_predicted OR2|PSEUDOGENE	109	Gavia stellata OR10	68	105	65%
Alligator_mississippiensis_predicted OR2|PSEUDOGENE	83	Phoenicopterus ruber OR13	56	82	68%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	122	Phaeton lepturus OR13	79	117	68%
Alligator_mississippiensis_predicted OR2|PSEUDOGENE	28	Anas platyrhynchos OR12	20	28	71%
Alligator_mississippiensis_predicted OR11|PSEUDOGENE	53	Picoides pubescens OR10	35	53	66%
Alligator_mississippiensis_predicted OR9|PSEUDOGENE	103	Pygoscelis adeliae OR10	71	102	70%
Alligator_mississippiensis_predicted OR2|PSEUDOGENE	43	Struthio camelus OR6	20	31	65%
Alligator_mississippiensis_predicted OR5|PSEUDOGENE	50	Phaeton lepturus OR10	29	44	66%
Alligator_mississippiensis_predicted OR12|PSEUDOGENE	97	Cariama cristata OR12	63	95	66%
Alligator_mississippiensis_predicted OR5|PSEUDOGENE	97	Phoenicopterus ruber OR6	61	89	69%
Alligator_mississippiensis_predicted OR8|PSEUDOGENE	52	Anas platyrhynchos OR5	38	52	73%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	77	Fulmarus glacialis OR5	44	66	67%

Alligator_mississippiensis_predicted OR10|PSEUDOGENE	40	Aptenodytes forsteri OR5 Pseudogene	15	22	68%
Alligator_mississippiensis_predicted OR13|PSEUDOGENE	73	Phoenicopterus ruber OR10 Pseudogene	32	48	67%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	71	Charadrius vociferus OR10	29	40	73%
Alligator_mississippiensis_predicted OR12|PSEUDOGENE	70	Manacus vitellinus OR12	43	66	65%
Alligator_mississippiensis_predicted OR12|PSEUDOGENE	53	Anas platyrhynchos OR12	36	52	69%
Alligator_mississippiensis_predicted OR2|PSEUDOGENE	69	Nipponia nippon OR5	42	61	69%
Alligator_mississippiensis_predicted OR13|PSEUDOGENE	65	Phoenicopterus ruber OR13	31	47	66%
Alligator_mississippiensis_predicted OR13|PSEUDOGENE	60	Gavia stellata OR8 Pseudogene	42	60	70%
Alligator_mississippiensis_predicted OR13|PSEUDOGENE	35	Aptenodytes forsteri OR6 Pseudogene	26	35	74%
Alligator_mississippiensis_predicted OR2|PSEUDOGENE	64	Antrostomus carolinensis OR2 Pseudogene	28	39	72%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	64	Phoenicopterus ruber OR10	29	43	67%
Alligator_mississippiensis_predicted OR14|PSEUDOGENE	63	Egretta garzetta OR14	40	59	68%
Alligator_mississippiensis_predicted OR12|PSEUDOGENE	62	Struthio camelus OR2	41	61	67%
Alligator_mississippiensis_predicted OR10	361	Fulmarus glacialis OR10	148	227	65%
Alligator_mississippiensis_predicted OR13|PSEUDOGENE	57	Struthio camelus OR5	33	50	66%
Alligator_mississippiensis_predicted OR1|PSEUDOGENE	50	Haliaeetus albicilla OR12 Pseudogene	31	47	66%
Alligator_mississippiensis_predicted OR1|PSEUDOGENE	40	Struthio camelus OR5	26	40	65%
Alligator_mississippiensis_predicted OR10|PSEUDOGENE	45	Gavia stellata OR8 Pseudogene	26	36	72%
Alligator_mississippiensis_predicted OR5|PSEUDOGENE	37	Fulmarus glacialis OR8	24	36	67%
Alligator_mississippiensis_predicted OR14|PSEUDOGENE	36	Balearica regulorum OR14	23	35	66%
Alligator_mississippiensis_predicted OR6|PSEUDOGENE	28	Phoenicopterus ruber OR13	19	28	68%
Alligator_mississippiensis_predicted OR51	350	Struthio camelus OR51	245	317	77%
Alligator_mississippiensis_predicted OR10	344	Fulmarus glacialis OR10	153	226	68%
Alligator_mississippiensis_predicted OR10	343	Phoenicopterus ruber OR10	209	294	71%
Alligator_mississippiensis_predicted OR55	332	Struthio camelus OR55	195	285	68%
Alligator_mississippiensis_predicted OR52	331	Cathartes aura OR52	235	310	76%
Alligator_mississippiensis_predicted OR6	331	Podiceps cristatus OR10	164	250	66%
Alligator_mississippiensis_predicted OR10	328	Aptenodytes forsteri OR5	216	323	67%
Alligator_mississippiensis_predicted OR6	326	Struthio camelus OR6	257	313	82%
Alligator_mississippiensis_predicted OR10	325	Phoenicopterus ruber OR10	160	246	65%
Alligator_mississippiensis_predicted OR10	321	Fulmarus glacialis OR10	147	226	65%
Alligator_mississippiensis_predicted OR52	321	Merops nubicus OR52	210	303	69%
Alligator_mississippiensis_predicted OR5	321	Aptenodytes forsteri OR10	201	310	65%
Alligator_mississippiensis_predicted OR6	320	Opisthocomus hoazin OR6	241	303	80%
Alligator_mississippiensis_predicted OR10	320	Charadrius vociferus OR10	218	319	68%
Alligator_mississippiensis_predicted OR5	319	Phoenicopterus ruber OR5	221	311	71%
Alligator_mississippiensis_predicted OR6	319	Anas platyrhynchos OR6	224	312	72%
Alligator_mississippiensis_predicted OR10	317	Pelecanus crispus OR10	220	308	71%

Alligator_mississippiensis_predicted OR10	317	Balearica regulorum OR10	219	317	69%
Alligator_mississippiensis_predicted OR52	317	Tinamus guttatus OR52	231	310	75%
Alligator_mississippiensis_predicted OR52	317	Cariama cristata OR52	251	314	80%
Alligator_mississippiensis_predicted OR10	316	Fulmarus glacialis OR10	209	300	70%
Alligator_mississippiensis_predicted OR6	316	Columba livia OR6	231	311	74%
Alligator_mississippiensis_predicted OR6	316	Struthio camelus OR6	252	310	81%
Alligator_mississippiensis_predicted OR5	315	Charadrius vociferus OR5	231	313	74%
Alligator_mississippiensis_predicted OR52	315	Struthio camelus OR52	225	313	72%
Alligator_mississippiensis_predicted OR10	315	Tinamus guttatus OR10	204	301	68%
Alligator_mississippiensis_predicted OR4	315	Pterocles gutturalis OR4	231	306	75%
Alligator_mississippiensis_predicted OR6	315	Nipponia nippon OR6	200	310	65%
Alligator_mississippiensis_predicted OR5	314	Phaeton lepturus OR5	205	308	67%
Alligator_mississippiensis_predicted OR12	314	Cariama cristata OR12	223	309	72%
Alligator_mississippiensis_predicted OR5	314	Struthio camelus OR5	219	308	71%
Alligator_mississippiensis_predicted OR5	313	Fulmarus glacialis OR5	226	307	74%
Alligator_mississippiensis_predicted OR5	313	Tinamus guttatus OR5	244	313	78%
Alligator_mississippiensis_predicted OR10	313	Aptenodytes forsteri OR10	192	284	68%
Alligator_mississippiensis_predicted OR10	313	Tinamus guttatus OR10	203	275	74%
Alligator_mississippiensis_predicted OR2	313	Nipponia nippon OR2	213	313	68%
Alligator_mississippiensis_predicted OR5	311	Haliaeetus leucocephalus OR5	211	306	69%
Alligator_mississippiensis_predicted OR11	311	Struthio camelus OR6	218	310	70%
Alligator_mississippiensis_predicted OR14	310	Egretta garzetta OR14	173	268	65%
Alligator_mississippiensis_predicted OR10	301	Anas platyrhynchos OR2	207	295	70%
Alligator_mississippiensis_predicted OR2	301	Charadrius vociferus OR2	213	300	71%
Alligator_mississippiensis_predicted OR6	298	Taeniopygia guttata OR2	190	262	73%
Alligator_mississippiensis_predicted OR10	381	Anas platyrhynchos OR10	203	286	71%
Alligator_mississippiensis_predicted OR8	265	Phoenicopterus ruber OR13	131	200	66%
Alligator_mississippiensis_predicted OR4	250	Podiceps cristatus OR4	115	163	71%

Supplementary Table S9. OR genes showing at least 65% shared identity between reptiles and birds were considered present in extinct dinosaur taxa. Shared ORs that have had their odorant ligand de-orphaned in humans and mice, as well as their human odorant 'descriptions', are displayed.

Receptor 65% identity between reptiles and birds	Ligands	Odor	PubChem CID	Ref
OR51E2	Propanoic acid	Sharp, rancid	1032	[10]
OR51L1	Hexanoic acid	Goat-like, Barn-yard animal	8892	
	Allyl phenylacetate	-		
OR51G2	Vanillic acid	Pleasant, creamy	8468	[10]
OR51Q1	Heptanoic acid	Rancid	8094	
OR52B2	Heptanoic acid	Rancid	8094	
	Pentanal	Strong, acrid, pungent	8063	
	Pentanoic acid	Very unpleasant	7991	
	3-Methylbutanoic acid	Disagreeable, rancid-cheese		
OR52E4	Octanoic acid	Fruity, unpleasant, irritating	379	
	Nonanoic acid	Fatty, coconut	8158	
	Decanoic acid	Unpleasant, rancid	2969	
OR52D1	Octanoic acid, methyl ester	Powerful, fruity	8091	
	Heptanoic acid	Rancid	8094	[11]
	Octanoic acid	Fruity, unpleasant, irritating	379	[10]
OR52R1	Decanoic acid	Unpleasant, rancid	2969	
	Nonanoic acid	Fatty, coconut	8158	
OR2A5	Nonanoic acid	Fatty, coconut	8158	[10]
	1-Octanol	Orange rose	957	[10,11]
	1-Nonanol	Floral	8914	[10]
	1-Decanol	Sweet, floral, fruity	8174	
	1-Heptanol	Fragrant	8129	
OR4E2	(Methylthio)-methanethiol	-	122370	
	(Methylthio)-ethanthiol	-	525462	
	Bis(Methyl-thiomethyl) disulphide	-	158825	
OR5AR1 (Olfr1019)	Prenyl acetate	Fruity, floral	14489	
	R-limonene	Fruity	440917	
OR6A2	Heptanal	Fatty, pungent, fruity, metallic blood	8130	[10,12]
OR6N1	Allyl benzene	-	9309	[10]
OR6P1	Eugenol	Spicy, floral	3314	
OR6X1	(-)-Carvone	-	16724	
OR10A3	1-Nonanethiol	Unpleasant	15077	
	1-Octanol	Orange rose	957	[10,11]
OR11A1	2-Ethyl fenchol	Earthy	106997	[10]
OR11L1	(+)-Camphor	Fragrant, penetrating	159055	
	(-)-Camphor	Fragrant, penetrating	444294	
	(-)-Fenchone	Similar to camphor	82229	
OR12D3	(+)-Carvone	-	16724	
Olfr545	Nonanedioic acid	-	2266	

Supplementary figure legends

Supplementary Figure S1. Boxplot of olfactory bulb (OB) ratios with respect to a piscivorous, insectivorous, omnivorous, herbivorous and carnivorous dietary niches. Data represents taxa with known diet data (n = 74). Median values (black) and mean values (red) are displayed.

Supplementary Figure S2. Body mass vs. OB ratio. The body mass (Kg) and olfactory bulb (OB) ratio for 74 taxa, combining non-avian dinosaurs, crown-clade Aves and stem birds, shows a strong linear relationship, possibly driven by larger theropods (tyrannosaurs labeled in red).

Supplementary Figure S3. Body mass (Kg) vs. size of the olfactory receptor repertoire observed in modern birds. There is no significant correlation between the two variables.

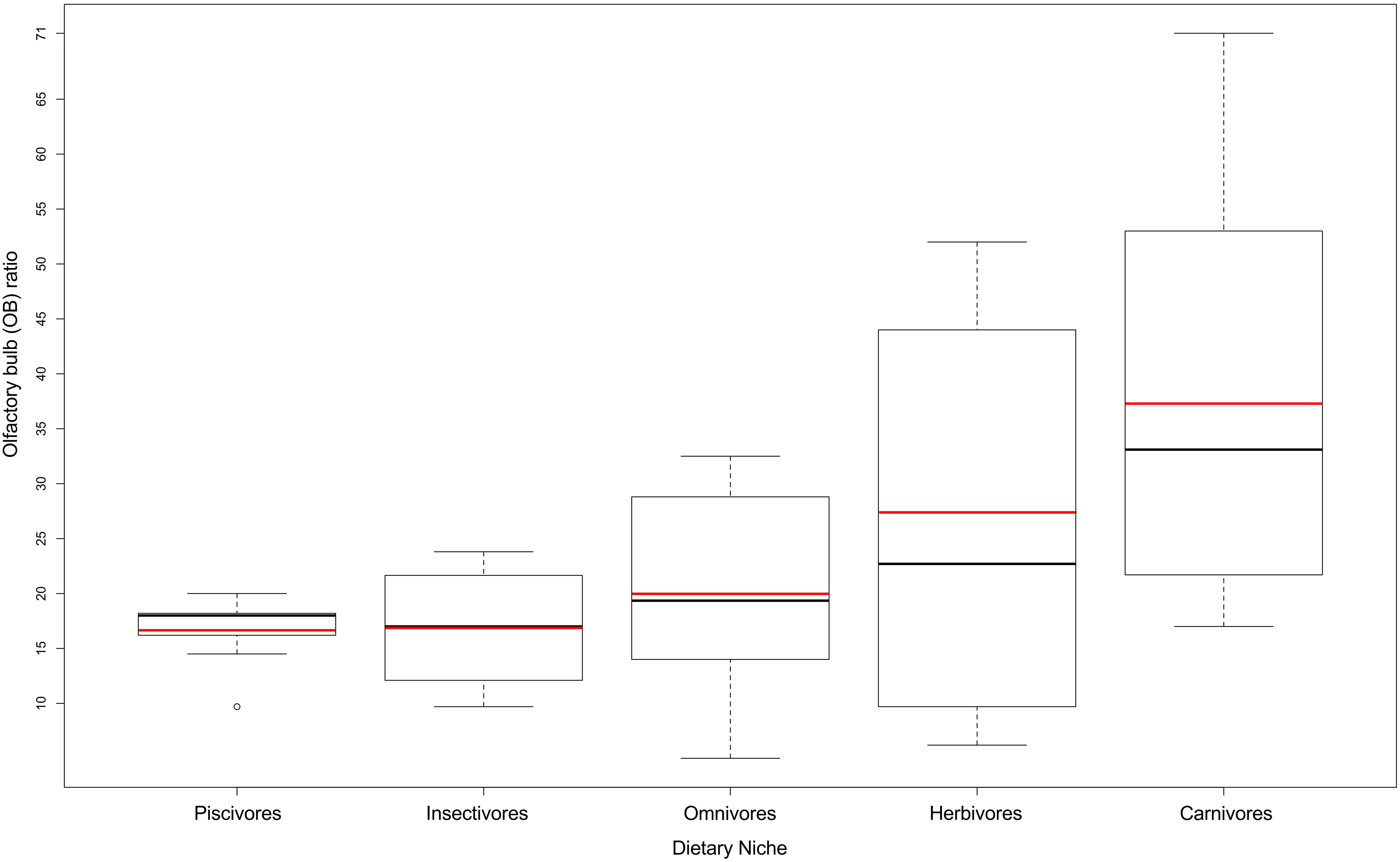
Supplementary Figure S4. Ancestral olfactory bulb ratios estimated using maximum likelihood, with only extant taxa and outliers (*Gallus gallus*, *Taeniopygia guttata* and *Melopsittacus undulatus*) included. Node numbers correspond to Supplemental Table S3.

Supplementary Figure S5. Ancestral olfactory bulb ratios estimated using maximum likelihood, with only extant taxa and outliers (*Gallus gallus*, *Taeniopygia guttata* and *Melopsittacus undulatus*) excluded. Node numbers correspond to Supplemental Table S4.

Supplementary Figure S6. Grafen length phylogeny with ancestral olfactory bulb ratios estimated using maximum likelihood. Branches show an increase (red) or decrease (blue) in OB ratio relative to the most recent common ancestor. Node labels correspond to Supplementary Table S5.

Supplementary Figure S7. Grafen phylogeny with ancestral olfactory bulb ratios estimated using phylogenetic independent contrasts (PICs). Branches show increases (red) or decreases (blue) in OB ratio relative to a most recent common ancestor. Node labels correspond to Supplementary Table S5.

Supplementary Figure S8. Grafen length phylogeny with ancestral olfactory bulb ratios estimated using generalized least squares (GLS). Branches show an increase (red) or decrease (blue) in OB ratio relative to the most recent common ancestor. Node labels correspond to Supplementary Table S5.


Olfactory bulb (OB) ratio
71
65
60
55
50
45
40
35
30
25
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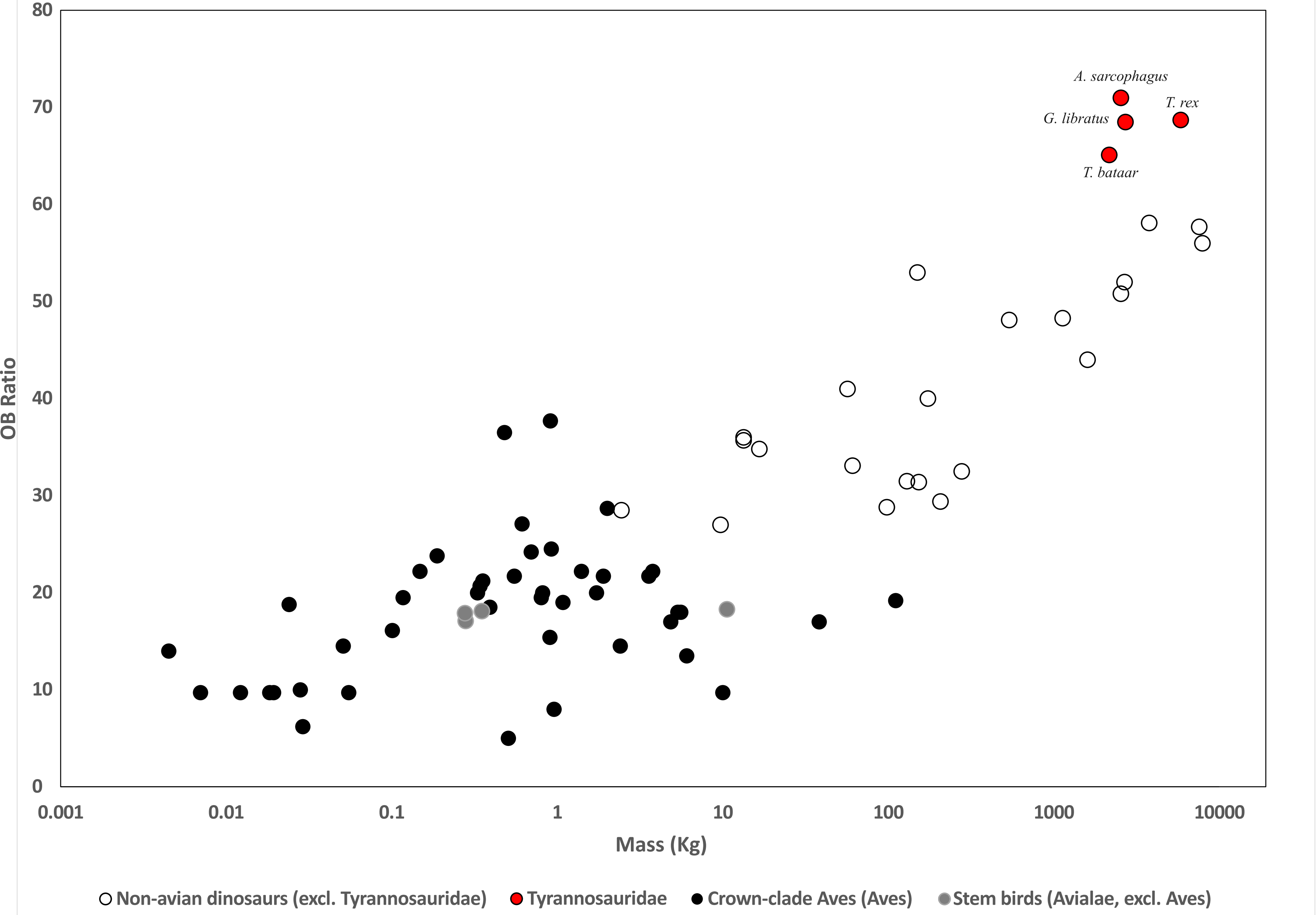
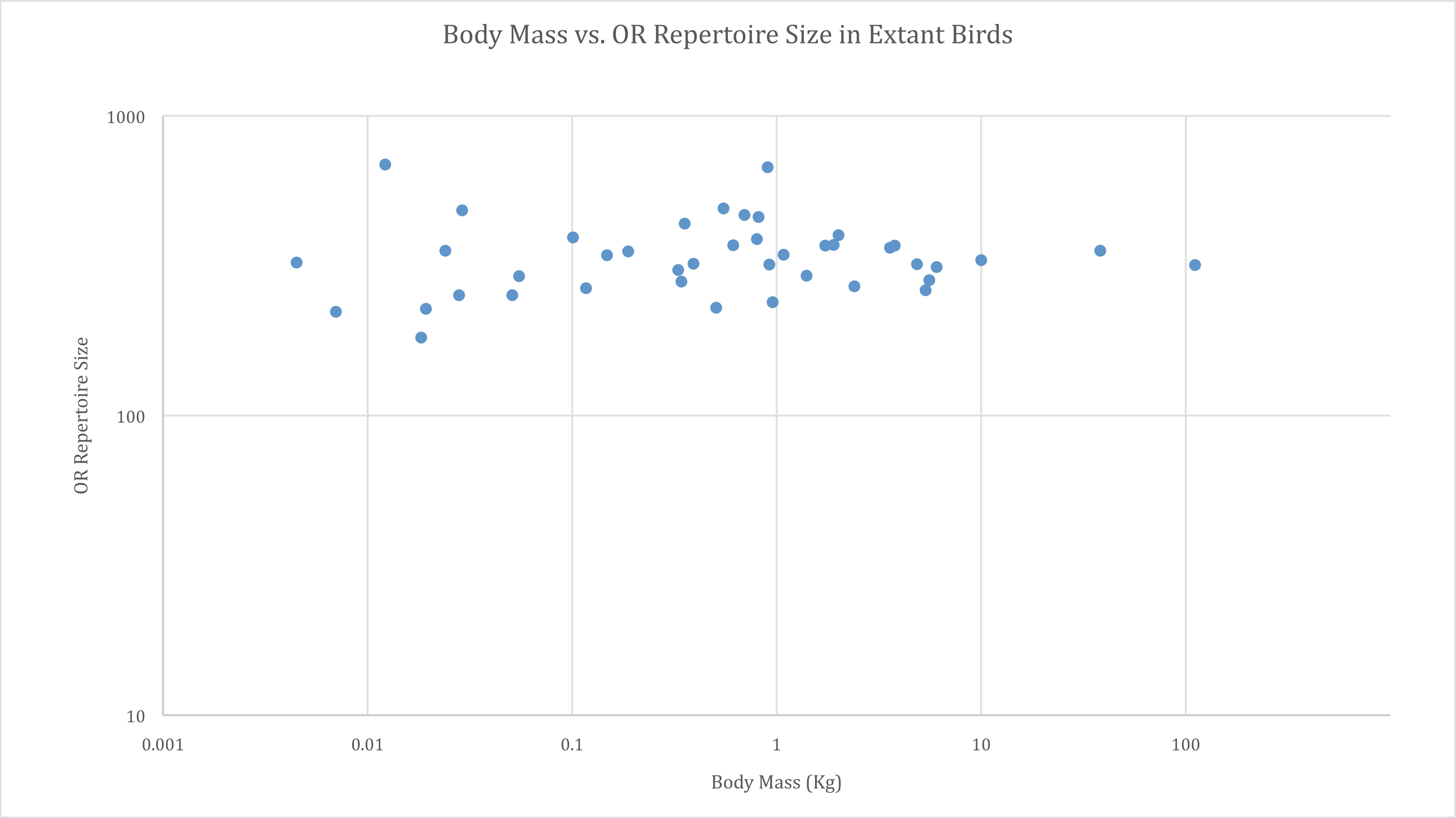
15
10
Piscivores
Insectivores
Omnivores
Herbivores
Carnivores
Dietary Niche


80
70
60
50
40
30
20
10
0
OB Ratio
0.001
0.01
0.1
1
10
100
1000
10000
Mass (Kg)
A. sarcophagus
T. rex
G. libratus
T. bataar
○ Non-avian dinosaurs (excl. Tyrannosauridae)
● Tyrannosauridae
● Crown-clade Aves (Aves)
● Stem birds (Avialae, excl. Aves)


Body Mass vs. OR Repertoire Size in Extant Birds
1000
100
10
0.001
0.01
0.1
1
10
100
OR Repertoire Size
Body Mass (Kg)


14
17.89
Pelecanus crispus
13
17.94
Nipponia nippon
12
17.43
Egretta garzetta
11
18.75
Phalacrocorax carbo
10
18.24
15
21.64
Fulmarus glacialis
16
18.4
Pygoscelis adeliae
9
17.74
Aptenodytes forsteri
Gavia stellata
8
19.59
Phaethon lepturus
17
20.6
Charadrius vociferus
18
22.08
Podiceps cristatus
Phoenicopterus ruber
28
9.13
Geospiza fortis
27
8.32
Taeniopygia guttata
26
9.19
Corvus brachyrhynchos
25
10.37
Manacus vitellinus
24
15.61
Acanthisitta chloris
7
23.65
23
16.98
29
6.89
Melopsittacus undulatus
22
18.63
Nestor notabilis
Falco peregrinus
21
22.2
Cariama cristata
32
13.7
Picoides pubescens
31
15.37
Merops nubicus
6
24.59
30
15.84
Colius striatus
20
17.93
Tyto alba
19
16.93
34
19.19
Haliaeetus albicilla
33
21.65
Haliaeetus leucocephalus
5
28.03
Cathartes aura
Opisthocomus hoazin
Balearica regulorum
4
29.36
37
21.97
Mesitornis unicolor
36
21.35
Pterocles gutturalis
35
22.39
Columba livia
3
30.52
Cuculus canorus
39
17.46
Chaetura pelagica
38
19.31
Calypte anna
2
32.15
Antrostomus carolinensis
41
15.96
Gallus gallus
40
17.64
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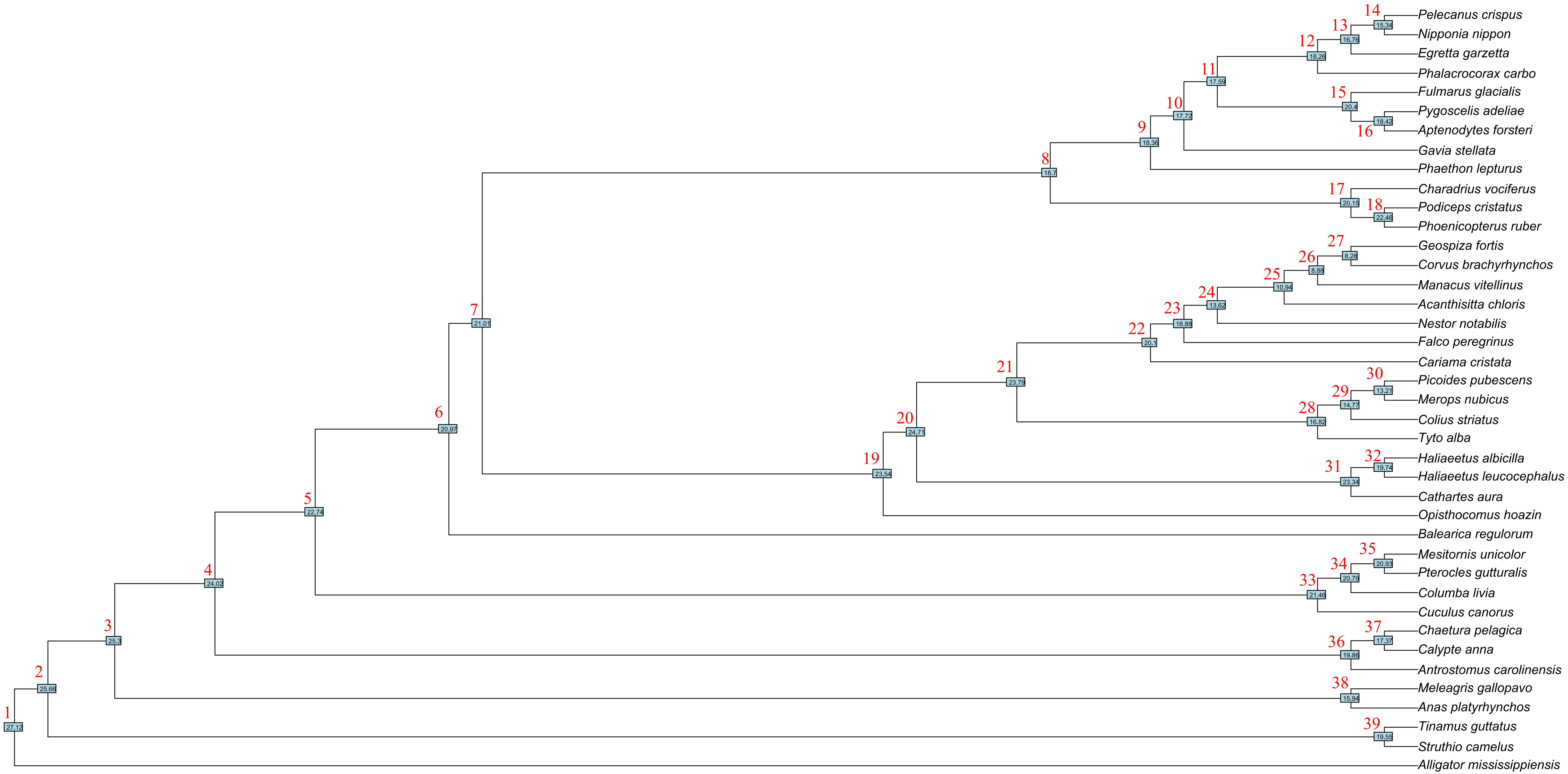
32.09
Anas platyrhynchos
42
20.22
Tinamus guttatus
Struthio camelus
Alligator mississippiensis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15
20.4
Fulmarus glacialis
Pygoscelis adeliae
18.42
16
Aptenodytes forsteri
10
17.72
9
18.36
Gavia stellata
Phaethon lepturus
8
18.7
17
20.15
Charadrius vociferus
18
22.46
Podiceps cristatus
Phoenicopterus ruber
27
8.28
Geospiza fortis
26
8.88
Corvus brachyrhynchos
25
10.94
Manacus vitellinus
24
13.62
Acanthisitta chloris
23
16.88
Nestor notabilis
22
20.1
Falco peregrinus
Cariama cristata
7
21.01
21
23.79
30
13.21
Picoides pubescens
29
14.77
Merops nubicus
28
16.82
Colius striatus
Tyto alba
6
20.97
20
24.71
32
19.74
Haliaeetus albicilla
31
23.34
Haliaeetus leucocephalus
19
23.54
Cathartes aura
Opisthocomus hoazin
5
22.74
Balearica regulorum
35
20.93
Mesitornis unicolor
34
20.79
Pterocles gutturalis
33
21.46
Columba livia
Cuculus canorus
4
24.02
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17.37
Chaetura pelagica
Calypte anna
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19.86
Antrostomus carolinensis
3
25.3
38
15.94
Meleagris gallopavo
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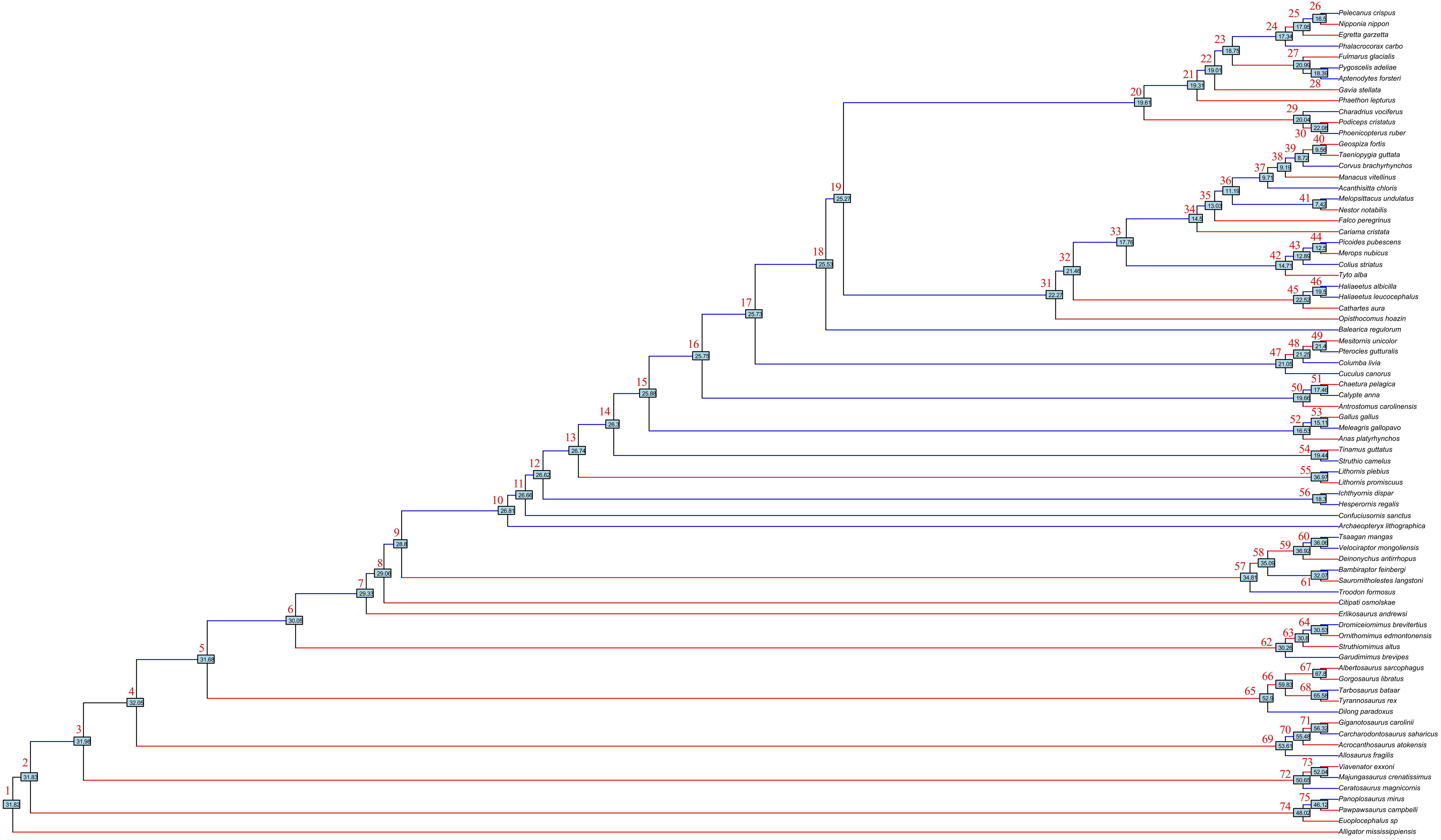
Tinamus guttatus
Struthio camelus
1
27.12
Alligator mississippiensis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Egretta garzetta
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Gavia stellata
Phaethon lepturus
Charadrius vociferus
Podiceps cristatus
Phoenicopterus ruber
Geospiza fortis
Taeniopygia guttata
Corvus brachyrhynchos
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Mesitornis unicolor
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Columba livia
Cuculus canorus
Chaetura pelagica
Calypte anna
Antrostomus carolinensis
Gallus gallus
Meleagris gallopavo
Anas platyrhynchos
Tinamus guttatus
Struthio camelus
Lithornis plebius
Lithornis promiscuus
Ichthyornis dispar
Hesperornis regalis
Confuciusornis sanctus
Archaeopteryx lithographica
Tsaagan mangas
Velociraptor mongoliensis
Deinonychus antirrhopus
Bambiraptor feinbergi
Saurornitholestes langstoni
Troodon formosus
Citipati osmolskae
Erlikosaurus andrewsi
Dromiceiomimus brevitertius
Ornithomimus edmontonensis
Struthiomimus altus
Garudimimus brevipes
Albertosaurus sarcophagus
Gorgosaurus libratus
Tarbosaurus bataar
Tyrannosaurus rex
Dilong paradoxus
Giganotosaurus carolinii
Carcharodontosaurus saharicus
Acrocanthosaurus atokensis
Allosaurus fragilis
Viavenator exxoni
Majungasaurus crenatissimus
Ceratosaurus magnicornis
Panoplosaurus mirus
Pawpawsaurus campbelli
Euoplocephalus sp
Alligator mississippiensis
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23 18.75
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27 20.99
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35 13.03
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64 30.53
65 52.9
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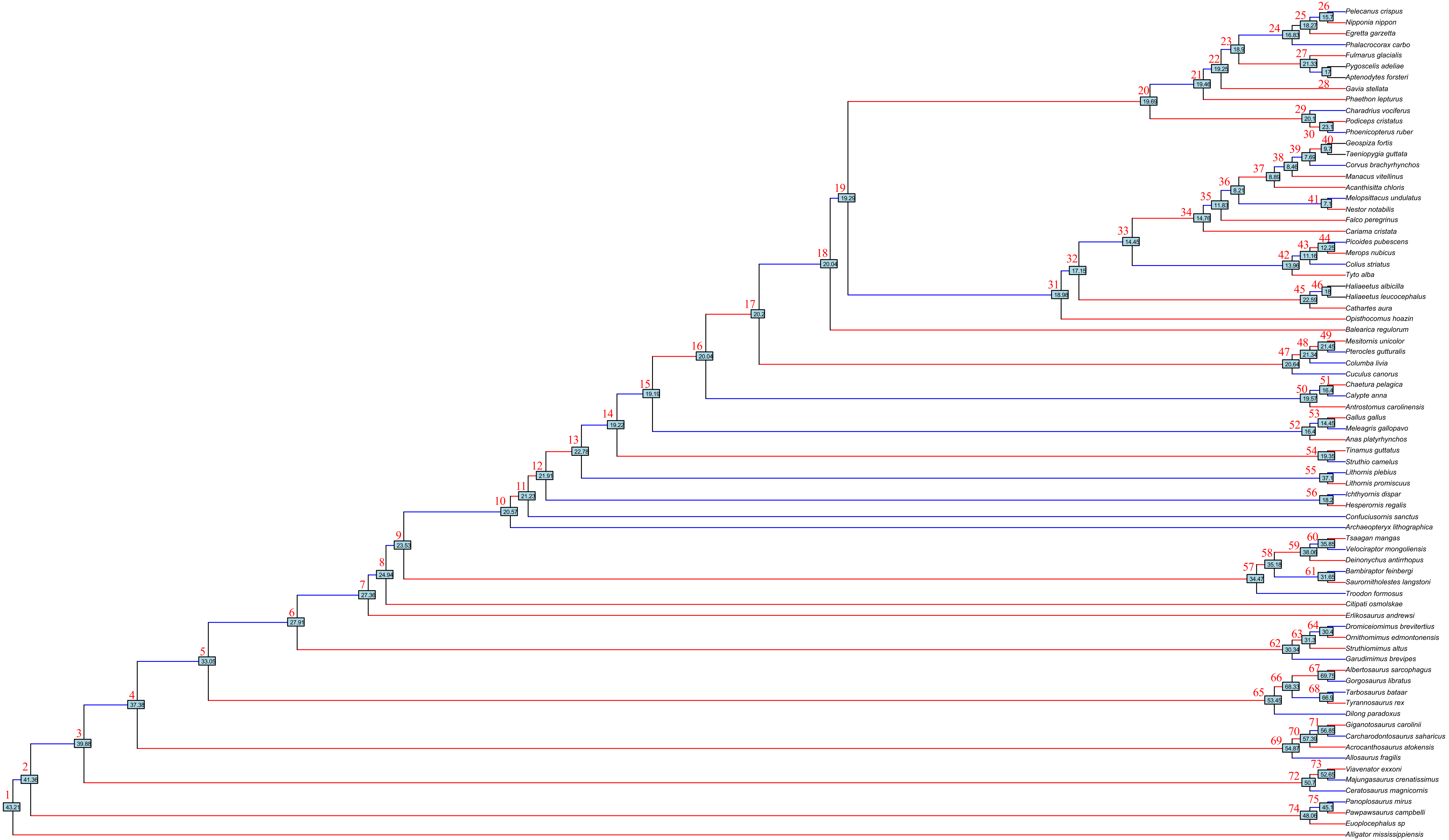
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Phaethon lepturus
Charadrius vociferus
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Saurornitholestes langstoni
Troodon formosus
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Erlikosaurus andrewsi
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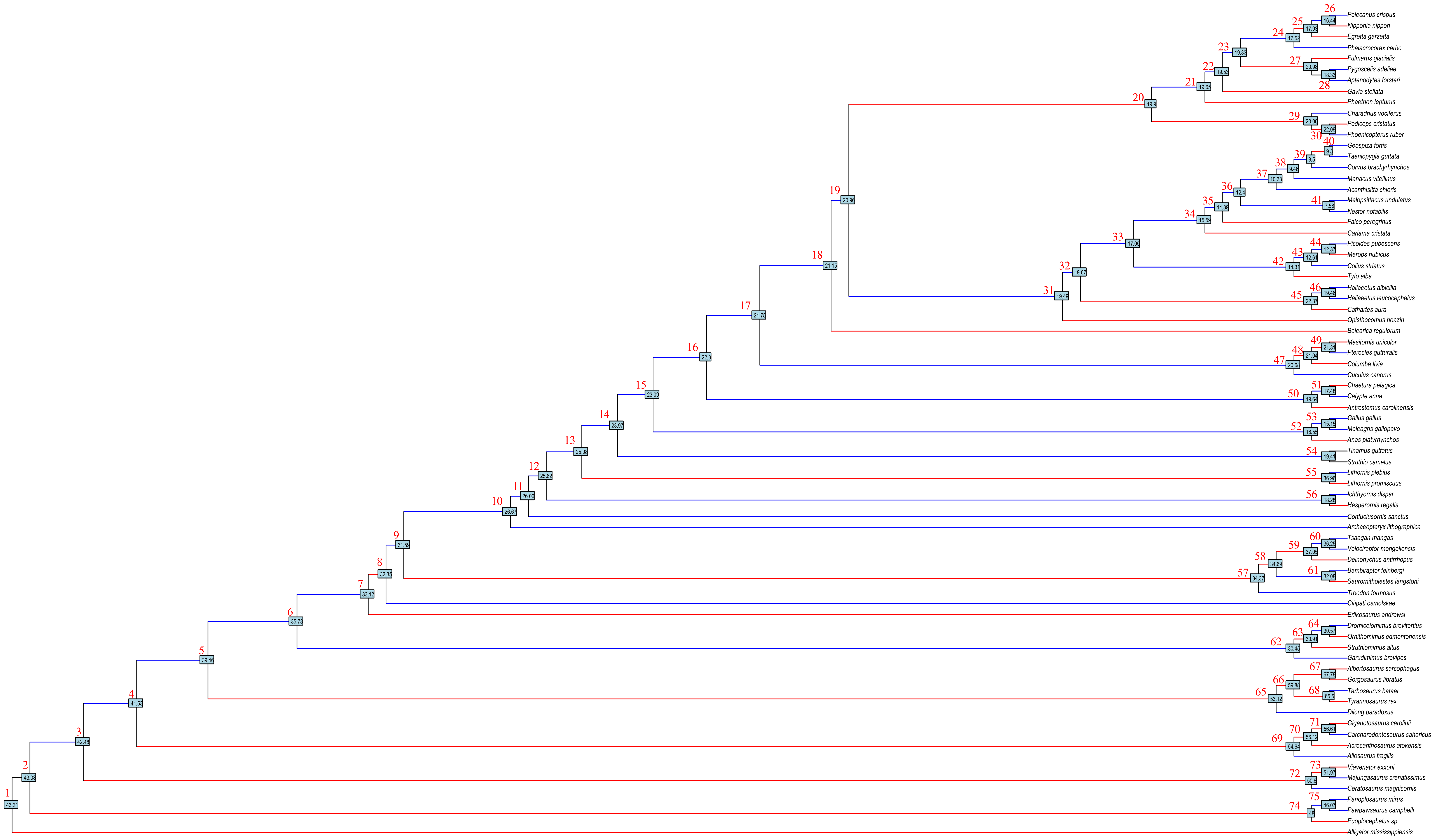
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Velociraptor mongoliensis
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