Electronic Supplementary information for:

Olfactory Receptor Repertoire Size in Dinosaurs

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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 Pawpawasaurus) 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], Allosauroidae [19], Ankylosauridae [20], Dromaeosauridae [21], Ornithomimosauria [22], Tyrannosauridae [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            |
| *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          |
| *Ophisthocome hoazin*        | Hoatzin                      | 467           | 24.2         | -                      | Herbivore     | 0.696          |
| *Calypte anna*               | Anna’s hummingbird           | 324           | 14           | -                      | Nectivore     | 0.0045         |
| Species                          | Common Name                  | Length | Width | Height | Mass  | Diet            | Mass*  |
|---------------------------------|-------------------------------|--------|-------|--------|-------|-----------------|--------|
| 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 crested grousse     | 363    | 21.7  | -      | -     | Carnivore       | 3.579  |
| Podiceps cristatus              | Great crested grousse        | 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    | 19.1  | -      | -     | Omnivore        | 1.082  |
| †Allosaurus fragilis            |                               | -      | 51.6  | 540    | 50    | Carnivore       | 2545.13|
| †Acrocanthosaurus atokensis    |                               | -      | 50.8* | 536    | 50.8  | Carnivore       | 2545.13|
| †Carcharodontosaurus saharicus |                               | -      | 56    | 564    | 56    | Carnivore       | 7905.47|
| †Giganotosaurus carolinii      |                               | -      | 57.7  | 573    | 57.7  | Carnivore       | 7559.49|
| †Ceratosaurus magnicornis       |                               | -      | 48.1  | 521    | 48.1  | Carnivore       | 538.86 |
| †Majungasaurus crenatissimus   |                               | -      | 48.3  | 522    | 48.3  | Carnivore       | 1130   |
| †Dilong paradoxus              |                               | -      | 27    | 407    | 27    | Carnivore       | 9.69   |
| †Albertosaurus sarcophagus     |                               | -      | 71    | 645    | 71    | Carnivore       | 2545.13|
| †Gorgosaurus libratus          |                               | -      | 68.5  | 631    | 68.5  | Carnivore       | 2709.45|
| †Tarbosaurus bataar            |                               | -      | 65.1  | 613    | 65.1  | Carnivore       | 2164.6 |
| †Tyrannosaurus rex             |                               | -      | 66.5  | 621    | 66.5  | Carnivore       | 5855.3 |
| †Garudimimus brevipes          |                               | -      | 71    | 645    | 71    | Carnivore       | 206.79 |
| †Ornithomimus edmontonensis    |                               | -      | 31.4  | 431    | 31.4  | Omnivore        | 152.74 |
| †Dromiceiominus brevitertiis   |                               | -      | 29.4  | 420    | 29.4  | Omnivore        | 206.79 |
| †Struthiornis altus             |                               | -      | 32.5  | 437    | 32.5  | Omnivore        | 277.97 |
| †Citipati osmolskæ              |                               | -      | 31.5  | 431    | 31.5  | Omnivore        | 129.78 |
| †Saurornitholestes langstoni   |                               | -      | 34.8  | 449    | 34.8  | Carnivore       | 16.62  |
| †Bambiraptor feinbergi         |                               | -      | 28.5  | 415    | 28.5  | Carnivore       | 2.44   |
| †Velociraptor mongoliensis     |                               | -      | 35.7  | 454    | 35.7  | Carnivore       | 13.36  |
| †Troodon formosus              |                               | -      | 33.2  | 440    | 33.2  | Carnivore       | 60.76  |
| Species                        | Mass (kg) | Length (cm) | Diet     | Body Mass Adjusted (Kg) |
|-------------------------------|-----------|-------------|----------|------------------------|
| †Archaeopteryx lithographica  | 33.1*     | 439         | Carnivore| 0.28                   |
| †Confuciusornis sanctus       | 33         | 440         | Carnivore| 0.277                  |
| †Hesperornis regalis          | 17.1       | 353         | Piscivore| 10.608                 |
| †Ichthyornis dispar           | 18.1       | 359         | Piscivore| 0.35                   |
| †Lithornis pleius             | 36.5       | 458         | -        | 0.48                   |
| †Lithornis promiscuus         | 37.7       | 465         | -        | 0.908                  |
| †Deinonychus antirrhopus      | 41         | 483         | Carnivore| 56.7                   |
| †Tsagaan 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 undulatus* 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          | 0.1958           | 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+ Strisosores+Columbaves+Neoaves (Neognathae)                        | 3    | 30.52   | 19.19  | 23.8  | 349        | 353   | 355   |
| Columbaves+Neoaves                                                               | 4    | 28.03   | 20.2   | 22.13 | 436        | 368   | 462   |
| Aequorlitornithes+Afroaves+Opisthocomus+Balearica (Neoaves)                     | 5    | 24.59   | 20.04  | 21.4  | 418        | 429   | 430   |
| Aequornithes+Phaethon+Mirandornithes+Charadrius (Aequorlitornithes)              | 6    | 19.59   | 19.69  | 19.94 | 393        | 349   | 433   |
| Aequornithes+Phaethon                                                             | 7    | 17.74   | 19.46  | 19.67 | 349        | 345   | 347   |
| Palaeognathae+Neoaves+Gavia (Aequornithes)                                       | 8    | 18.24   | 19.25  | 19.54 | 342        | 340   | 342   |
| Galliformes+Phalacrocorax+Neoaves+Gavia (Aequornithes)                           | 9    | 18.75   | 18.9   | 19.34 | 364        | 350   | 411   |
| Pelecaniformes+Phalaenopterus                                                    | 10   | 18.42   | 19.25  | 19.54 | 342        | 340   | 342   |
| Pelecaniformes+Phalaenopterus                                                    | 11   | 17.43   | 16.83  | 17.52 | 325        | 327   | 330   |
| Pelecanus+Nipponia+Egretta (Pelecaniformes)                                      | 12   | 17.94   | 18.27  | 17.93 | 342        | 365   | 349   |
| Pelecanus+Nipponia                                                               | 13   | 17.89   | 15.7   | 16.44 | 325        | 312   | 324   |
| Spheniscidae+Fulmarus (Austrodyptornithes)                                      | 14   | 21.64   | 21.33  | 20.98 | 365        | 359   | 393   |
| Aptenodytes+Pygocelis (Spheniscidae)                                            | 15   | 18.4    | 17     | 18.33 | 365        | 355   | 389   |
| Mirandornithes+Charadrius                                                       | 16   | 20.6    | 20.1   | 20.09 | 366        | 359   | 367   |
| Podiceps+Phoenicopterus (Mirandornithes)                                       | 17   | 22.08   | 23.1   | 22.1  | 353        | 321   | 359   |
| Afroaves+Ostriches (Mirandornithes)                                            | 18   | 16.93   | 18.98  | 19.54 | 334        | 327   | 329   |
| Inopinaves+Coraciiformes+Tyto+Accipitriformes (Afroaves)                        | 19   | 17.93   | 17.15  | 19.12 | 291        | 273   | 291   |
| Inopinaves+Coraciiformes+Tyto                                                    | 20   | 22.2    | 14.45  | 17.08 | 311        | 319   | 341   |
| Psittacopasserae+Falco+Cariama (Inopinaves)                                      | 21   | 18.63   | 14.76  | 15.6  | 288        | 289   | 295   |
| Psittacopasserae+Falco                                                           | 22   | 16.98   | 11.83  | 14.4  | 274        | 269   | 281   |
| Psittaciformes+Passeriformes (Psittacopasserae)                                  | 23   | 15.61   | 8.21   | 12.4  | 266        | 252   | 262   |
| Passeroidea+Corvus+Manacus+Acanthisitta (Passeriformes)                          | 24   | 10.37   | 8.89   | 10.33 | 281        | 337   | 338   |
| Passeroidea+Corvus+Manacus                                                        | 25   | 9.19    | 8.46   | 9.46  | 302        | 354   | 343   |
| Geospiza+Taeniopygia (Passeroidea)                                              | 26   | 8.32    | 7.69   | 8.5   | 295        | 307   | 332   |
|                                                                                   | 27   | 9.13    | 9.7    | 9.3   | 358        | 362   | 359   |
|                             | 29 | 30  | 31  | 32  | 33  | 34  | 35  | 36  | 37  | 38  | 39  | 40  | 41  | 42  |
|-----------------------------|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Melopsittacus+Nestor (Psittaciformes) | 6.89 | 7.1 | 7.58 | 252 | 273 | 297 |
| Coraciimorphae+Tyto         | 15.84 | 13.96 | 14.32 | 286 | 301 | 299 |
| Picoides+Merops+Colius (Coraciimorphae) | 15.37 | 11.16 | 12.62 | 319 | 347 | 325 |
| Picooides+Merops            | 13.7 | 12.25 | 12.37 | 400 | 435 | 398 |
| Haliaetus+Cathartes (Acciprimorphae) | 21.65 | 22.59 | 22.37 | 337 | 351 | 357 |
| Haliaetus                   | 19.19 | 18   | 19.46 | 361 | 363 | 363 |
| Strisores+Columbaves+Neoaves | 29.36 | 20.04 | 22.82 | 347 | 341 | 348 |
| Mesitornis+Pterocles+Columba+Cuculus (Columbaves) | 22.39 | 20.64 | 20.69 | 332 | 344 | 350 |
| Mesitornis+Pterocles+Columba | 21.35 | 21.34 | 21.04 | 338 | 359 | 353 |
| Mesitornis+Pterocles        | 21.97 | 21.45 | 21.31 | 341 | 354 | 353 |
| Apodiformes+Antrostomus (Strisores) | 19.31 | 19.57 | 19.65 | 348 | 351 | 352 |
| Chaetura+Calypte (Apodiformes) | 17.46 | 16.4  | 17.48 | 340 | 338 | 342 |
| Galliformes+Anas (Galloanserae) | 17.64 | 16.4  | 16.57 | 352 | 357 | 356 |
| Gallus+Meleagris (Galliformes) | 15.96 | 14.45 | 15.16 | 379 | 411 | 385 |
| Tinamus+Struthio (Palaeognathae) | 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+Balearia (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+Accipitriformes (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 |
| Taxon                                                                 | Node | R1  | R2  | R3  | R4  | R5  | R6  | R7  | R8  |
|----------------------------------------------------------------------|------|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 |
| Coraciiformes + Tyto                                                | 31   | 23.34 | 22.59 | 22.37 | 326 | 327 | 328 |
| Picoides + Merops + Colius (Coraciiformes)                          | 32   | 19.74 | 18.00 | 19.46 | 289 | 273 | 291 |
| Picoides + Merops                                                    | 33   | 21.46 | 20.64 | 20.69 | 328 | 327 | 330 |
| Haliaeetus + Cathartes (Accipitriformes)                            | 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–S8 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 removed           | Outlier taxa removed                     |                  |
|                              |          |                                          |                                |                                          |                  |
| Allosaurus fragilis          | 51.6     | 660.0319                                 | 526.7173                      | 669.5696615                             | 753.7345         |
| Allosaurus fragilis          | 50       | 649.0294                                 | 517.7147                      | 658.988481                              | 735.1643         |
| Allosaurus fragilis*         | 50.8     | 654.5306                                 | 522.2160                      | 664.2790748                             | 744.4494         |
| Acrocanthosaurus atokensis  | 58.1     | 704.7297                                 | 563.2902                      | 712.5556786                             | 829.1758         |
| Ceratotholosa saharicus     | 56       | 690.2889                                 | 551.4743                      | 698.6678844                             | 804.8025         |
| Giganotosaurus carolinii    | 57.7     | 701.9791                                 | 561.0396                      | 709.9130852                             | 824.5333         |
| Ceratosaurus magnicorns      | 48.1     | 635.9638                                 | 507.0242                      | 646.4234464                             | 713.1122         |
| Majungasaurus crenatissimus | 48.3     | 637.3392                                 | 508.1495                      | 647.7459913                             | 715.4335         |
| Dilong paradoxus            | 27       | 490.8678                                 | 388.3028                      | 506.88412                               | 468.2182         |
| Albertosaurus sarcophagus   | 71       | 793.4378                                 | 635.8734                      | 797.8663893                             | 978.8978         |
| Gorgosaurus libratus        | 68.5     | 776.2463                                 | 621.8069                      | 781.333059                              | 949.8819         |
| Tarbosaurus bataar          | 65.1     | 752.8659                                 | 602.6764                      | 758.843812                              | 910.4203         |
| Tyrannosaurus rex           | 66.5     | 762.4931                                 | 610.5537                      | 768.1068391                             | 926.6692         |
| Tyrannosaurus rex           | 71       | 793.4378                                 | 635.8734                      | 797.8663893                             | 978.8978         |
| Tyrannosaurus rex*          | 68.7     | 777.6216                                 | 622.9322                      | 782.659525                              | 952.2032         |
| Ornithomimus brevipes       | 28.8     | 503.2456                                 | 398.4307                      | 518.7879401                             | 489.1095         |
| Dromiceiomimus breviterius | 29.4     | 507.3716                                 | 401.8067                      | 522.7558801                             | 496.0733         |
| Struthiomimus altus         | 32.5     | 528.689                                 | 419.2491                      | 543.2569037                             | 532.0532         |
| Saurornitholestes langston i | 34.8   | 544.5052                                 | 432.1903                      | 558.4673405                             | 530.4647         |
| Bambiraptor feinbergi       | 28.5     | 501.1827                                 | 396.7427                      | 516.803971                              | 485.6276         |
| Velociraptor mongoliensis   | 35.7     | 550.6941                                 | 437.2543                      | 564.4192505                             | 569.1934         |
| Troodon formosus            | 33.2     | 533.5026                                 | 423.1878                      | 547.886167                              | 540.1775         |
| Troodon formosus            | 33.5     | 535.5656                                 | 424.8757                      | 549.870137                              | 543.6594         |
| Troodon formosus            | 32.6     | 529.3767                                 | 419.8118                      | 543.918227                              | 533.2137         |
| Troodon formosus            | 33       | 532.1273                                 | 422.0624                      | 546.5635204                             | 537.8562         |
| Troodon formosus*           | 33.1     | 532.815                                 | 422.6251                      | 547.224837                              | 539.0168         |
| Archaeopteryx lithographica | 17.1     | 422.7895                                 | 332.5994                      | 441.413094                              | 353.3151         |
| Confuciusornis sanctus      | 17.9     | 428.2908                                 | 337.1007                      | 446.703961                              | 362.6002         |
| Hesperornis regalis         | 15.3     | 410.4117                                 | 322.4715                      | 429.509289                              | 332.4236         |

Upper
| Species                  | Weight (kg) | Length (mm) | Width (mm) | Height (mm) | Mass (g)  | Length (mm) | Width (mm) | Height (mm) | Weight (kg) | Length (mm) | Width (mm) | Height (mm) | Weight (kg) | Length (mm) | Width (mm) | Height (mm) |
|--------------------------|-------------|-------------|------------|-------------|-----------|-------------|------------|-------------|-------------|-------------|------------|-------------|-------------|-------------|------------|-------------|
| Hesperornis regalis     | 21.3        | 451.6712    | 356.2312   | 469.1886897 | 402.0618  | 151.2376    | 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 pleius        | 36.5        | 556.1954    | 441.7555   | 569.7098372 | 578.4785  | 312.7251    | 844.2318   |
| Lithornis promiscuus    | 37.7        | 564.4473    | 448.5075   | 577.5457173 | 592.4061  | 324.6515    | 860.1607   |
| Deinonychus antirrhopus | 41          | 587.14      | 467.0753   | 599.4693875 | 630.7071  | 356.8918    | 904.5223   |
| Tsaagan mangus          | 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 | |
| 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 4E1 | |
| XM_006033996.1 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 10A7 | |
| XM_006037936.1 PREDICTED: Alligator sinensis olfactory receptor 51G2 | |
| XM_006036778.1 PREDICTED: Alligator sinensis olfactory receptor 1020 | |
| XM_014523915.1 PREDICTED: Alligator sinensis olfactory receptor 51G2 | |
| XM_006032221.2 PREDICTED: Alligator sinensis olfactory receptor COR8 | |
| 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_006032247.1 PREDICTED: Alligator sinensis olfactory receptor 1009 | |
| 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 | |

RefSeq [6]
| Accession   | Description                                      |
|-------------|--------------------------------------------------|
| 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_006036686.1 | Predicted: Alligator sinensis olfactory receptor 2AT4 |
| XM_006037243.2 | Predicted: Alligator sinensis olfactory receptor 6X1 |
| XM_014527719.1 | Predicted: Alligator sinensis olfactory receptor 14D9 |
| 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 |
| 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_006271899.2 | 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_014989814.1 | Predicted: Alligator mississippiensis olfactory receptor 6B1 |
| XM_006258018.2 | Predicted: Alligator mississippiensis olfactory receptor 10C1 |
| XM_006262993.2 | Predicted: Alligator mississippiensis olfactory receptor 51C2 |
| XM_006263697.2 | Predicted: Alligator mississippiensis olfactory receptor 51C2 |
| 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_006263191.1 | Predicted: Alligator mississippiensis olfactory receptor 10C1 |
| XM_006265550.1 | Predicted: Alligator mississippiensis olfactory receptor 4S2 |

RefSeq [7]
| 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 |
| XM_008175041.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 4D5 |
| XM_008176388.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 14A16 |
| XM_008175031.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6B1 |
| XM_005302244.2 | PREDICTED: Chrysemys picta bellii olfactory receptor 1468 |
| XM_008174413.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 1411 |
| 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 11A1 |
| 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_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 11A1 |
| XM_005310272.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| 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 10A7 |
| XM_005310439.2 | PREDICTED: Chrysemys picta bellii olfactory receptor 14A16 |
| XM_008174340.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| XM_005290045.2 | 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 51G2 |
| XM_005310292.2 | PREDICTED: Chrysemys picta bellii olfactory receptor 14A16 |
| XM_005310406.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 10A7 |
| XM_005314585.2 | PREDICTED: Chrysemys picta bellii olfactory receptor 14A16 |
| XM_005309641.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 10A7 |
| 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_005309431.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6P1 |
| XM_00530955.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6B1 |

RefSeq [5]
| XM     | Accession Number | Description                                      |
|--------|------------------|--------------------------------------------------|
| 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_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_005312401.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6F1 |
| XM_005309014.1 | 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_005312401.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6F1 |
| XM_005309014.1 | 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_005314254.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| XM_005312282.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 5V1 |
| 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_005312401.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6F1 |
| 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_008177186.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6N1 |
| XM_005314254.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| XM_005312282.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 5V1 |
| 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_008177186.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6N1 |
| XM_005314254.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| XM_005312282.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 5V1 |
| 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_008177186.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6N1 |
| XM_005314254.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| XM_005312282.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 5V1 |
| 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_008177186.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 6N1 |
| XM_005314254.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 11A1 |
| XM_005312282.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 5V1 |
| XM_005309014.1 | PREDICTED: Chrysemys picta bellii olfactory receptor 10A4 |
| XM_005310433.1 | C89 | Pm066 |
| XM_005310433.1 | C89 | Pm091 |
| XM_005310433.1 | C89 | Pm010 |
| XM_005310433.1 | C89 | Pm120 |
| XM_005310433.1 | C89 | Pm047 |
| XM_005310433.1 | C89 | Pm068 |
| XM_005310433.1 | C89 | Pm020 |
| XM_005310433.1 | C89 | Pm046 |
| XM_005310433.1 | C89 | Pm055 |
| XM_005310433.1 | C89 | Pm136 |
| XM_005310433.1 | C89 | Pm045 |
| XM_005310433.1 | C89 | Pm148 |
| XM_005310433.1 | C89 | Pm070 |
| XM_005310433.1 | C89 | Pm119 |
| XM_005310433.1 | C89 | Pm014 |
| XM_005310433.1 | C89 | Pm053 |
| XM_005310433.1 | C89 | Pm030 |
| XM_005310433.1 | C89 | Pm036 |
| XM_005310433.1 | C89 | Pm049 |
| XM_005310433.1 | C89 | Pm088 |
| Pm115 |        |        |
|-------|--------|--------|
| Pm005 |        |        |
| Pm132 |        |        |
| Pm057 |        |        |
| 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 leptopus 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 leptopus OR4 | 201 | 309 | 65% |
| Accession | Species                        | Start | Stop | Identity   |
|-----------|-------------------------------|-------|------|------------|
| XM_006036061.1 | Alligator sinensis olfactory receptor 4S2 | 320   | 392  | 68%        |
| XM_006037726.1 | Alligator sinensis olfactory receptor 4N2 | 320   | 392  | 71%        |
| XM_006038500.1 | Alligator sinensis olfactory receptor 6F1 | 433   | 505  | 66%        |
| XM_006032092.1 | Alligator sinensis olfactory receptor 51E2 | 319   | 391  | 76%        |
| XM_006033957.1 | Alligator sinensis olfactory receptor 4S2 | 319   | 391  | 74%        |
| XM_006034122.1 | Alligator sinensis olfactory receptor 6N1 | 319   | 391  | 84%        |
| XM_014526782.1 | Alligator sinensis olfactory receptor 10T2 | 430   | 502  | 70%        |
| XM_006032221.2 | Alligator sinensis olfactory receptor COR8 | 318   | 390  | 73%        |
| XM_006034790.2 | Alligator sinensis olfactory receptor COR4 | 318   | 390  | 70%        |
| XM_014523649.1 | Alligator sinensis olfactory receptor 10A7 | 318   | 390  | 66%        |
| XM_014523977.1 | Alligator sinensis olfactory receptor 1019 | 318   | 390  | 65%        |
| XM_014526594.1 | Alligator sinensis olfactory receptor 52A5 | 318   | 390  | 67%        |
| XM_006032247.1 | Alligator sinensis olfactory receptor 1009 | 317   | 389  | 66%        |
| XM_006032098.2 | Alligator sinensis olfactory receptor 2A5 | 316   | 388  | 79%        |
| XM_006039254.1 | Alligator sinensis olfactory receptor 10A7 | 421   | 503  | 65%        |
| XM_006031595.1 | Alligator sinensis olfactory receptor 6M1 | 316   | 388  | 66%        |
| XM_006039174.1 | Alligator sinensis olfactory receptor 4D9 | 316   | 388  | 66%        |
| XM_006034999.1 | Alligator sinensis olfactory receptor 49 | 316   | 388  | 70%        |
| XM_006031590.2 | Alligator sinensis olfactory receptor 1052 | 316   | 388  | 67%        |
| XM_014527682.1 | Alligator sinensis olfactory receptor 6F1 | 315   | 387  | 73%        |
| XM_006032090.2 | Alligator sinensis olfactory receptor 51G2 | 314   | 386  | 82%        |
| XM_006039094.1 | Alligator sinensis olfactory receptor 12D3 | 314   | 386  | 73%        |
| XM_014524214.1 | Alligator sinensis olfactory receptor 10R2 | 314   | 386  | 71%        |
| XM_006039141.1 | Alligator sinensis olfactory receptor 6X1 | 409   | 491  | 66%        |
| XM_006032222.1 | Alligator sinensis olfactory receptor 1052 | 313   | 385  | 72%        |
| XM_006032222.1 | Alligator sinensis olfactory receptor 1013 | 313   | 385  | 71%        |
| XM_006034789.1 | Alligator sinensis olfactory receptor 1019 | 313   | 385  | 70%        |
| XM_006039298.1 | Alligator sinensis olfactory receptor 12D2 | 313   | 385  | 68%        |
| XM_014525901.1 | Alligator sinensis olfactory receptor 1019 | 313   | 385  | 75%        |
| XM_014526945.1 | Alligator sinensis olfactory receptor 10A7 | 313   | 385  | 74%        |
| XM_006033958.1 | Alligator sinensis olfactory receptor 4S2 | 403   | 485  | 84%        |
| XM_014527719.1 | Alligator sinensis olfactory receptor 4D9 | 400   | 482  | 67%        |
| XM_006036686.1 | Alligator sinensis olfactory receptor 2AT4 | 396   | 478  | 74%        |
| XM_006037243.2 | Alligator sinensis olfactory receptor 6X1 | 311   | 393  | 70%        |
| XM_014526109.1 | Alligator sinensis olfactory receptor 14A16 | 307   | 389  | 66%        |
| XM_006036787.1 | Alligator sinensis olfactory receptor 6F1 | 298   | 380  | 65%        |
| XM_014527787.1 | Alligator sinensis olfactory receptor 52R1 | 277   | 359  | 73%        |
| XM_006039137.2 | Alligator sinensis olfactory receptor 5V1 | 261   | 343  | 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 | 66% |
| 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 006269922.2 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% |
| Accession   | Description                                                                 | Confidence | Specificity |
|-------------|------------------------------------------------------------------------------|------------|-------------|
| XM_014594485.1 | Alligator mississippiensis olfactory receptor 4S2                       | 312        | 70%         |
| XM_006268319.1 | Alligator mississippiensis olfactory receptor 10C1                       | 311        | 72%         |
| XM_006265550.1 | Alligator mississippiensis olfactory receptor 4S2                       | 310        | 71%         |
| XM_006278498.1 | Alligator mississippiensis olfactory receptor 4S2                       | 310        | 73%         |
| XM_006278500.2 | Alligator mississippiensis olfactory receptor 4S2                       | 310        | 75%         |
| XM_019486358.1 | Alligator mississippiensis olfactory receptor 12D1                      | 308        | 66%         |
| XM_019496768.1 | Alligator mississippiensis olfactory receptor 4S2                       | 302        | 65%         |
| XM_019496762.1 | Alligator mississippiensis olfactory receptor 4S2                       | 292        | 75%         |
| XM_005311793.2 | Chrysemys picta bellii olfactory receptor 51G2                           | 596        | 74%         |
| XM_008175041.1 | Chrysemys picta bellii olfactory receptor 4D5                           | 229        | 68%         |
| XM_008176388.1 | Chrysemys picta bellii olfactory receptor 14A16                         | 226        | 65%         |
| XM_008175039.1 | Chrysemys picta bellii olfactory receptor 6F1                           | 376        | 68%         |
| XM_008175031.1 | Chrysemys picta bellii olfactory receptor 6B1                           | 201        | 65%         |
| XM_005309244.2 | Chrysemys picta bellii olfactory receptor 1468                         | 199        | 66%         |
| XM_008174413.1 | Chrysemys picta bellii olfactory receptor 14I                            | 188        | 70%         |
| XM_005289441.2 | Chrysemys picta bellii olfactory receptor 2A14                          | 372        | 81%         |
| XM_008175033.1 | Chrysemys picta bellii olfactory receptor 10A4                          | 175        | 71%         |
| XM_005309234.1 | Chrysemys picta bellii olfactory receptor 6B1                           | 169        | 69%         |
| XM_008175027.1 | Chrysemys picta bellii olfactory receptor 5                              | 169        | 69%         |
| XM_005314359.1 | Chrysemys picta bellii olfactory receptor 52E4                         | 108        | 66%         |
| XM_008178121.1 | Chrysemys picta bellii olfactory receptor 1019                          | 584        | 74%         |
| XM_008174412.1 | Chrysemys picta bellii olfactory receptor 4D2                          | 360        | 71%         |
| XM_008168738.1 | Chrysemys picta bellii olfactory receptor 14A16                         | 356        | 67%         |
| XM_005310841.1 | Chrysemys picta bellii olfactory receptor 5V1                           | 356        | 68%         |
| XM_005310413.1 | Chrysemys picta bellii olfactory receptor 12D2                          | 355        | 72%         |
| XM_008168730.1 | Chrysemys picta bellii olfactory receptor 14A16                         | 355        | 65%         |
| XM_008178018.1 | Chrysemys picta bellii olfactory receptor 52K1                          | 543        | 75%         |
| XM_008175965.1 | Chrysemys picta bellii olfactory receptor 1009                          | 351        | 66%         |
| XM_005311801.1 | Chrysemys picta bellii olfactory receptor 51G2                          | 538        | 74%         |
| XM_008177963.1 | Chrysemys picta bellii olfactory receptor 1019                          | 348        | 68%         |
| XM_005312774.1 | Chrysemys picta bellii olfactory receptor 4N2                           | 528        | 73%         |
| XM_008175572.1 | Chrysemys picta bellii olfactory receptor 51G2                          | 346        | 69%         |
| XM_005309056.2 | Chrysemys picta bellii olfactory receptor 6B1                           | 345        | 65%         |
| XM_008177588.1 | Chrysemys picta bellii olfactory receptor 52B2                          | 345        | 79%         |
| XM_008175561.1 | Chrysemys picta bellii olfactory receptor 51G2                          | 517        | 73%         |
| XM_005313796.2 | Chrysemys picta bellii olfactory receptor 6C75                         | 341        | 67%         |
| XM_008174336.1 | Chrysemys picta bellii olfactory receptor 6N1                           | 339        | 66%         |
| XM_008174338.1 | Chrysemys picta bellii olfactory receptor 12D2                          | 338        | 70%         |
| Accession     | Predicted            | Species                        | OR10  | OR14  | OR51  |
|--------------|----------------------|--------------------------------|-------|-------|-------|
| XM_005310393.1 | Chrysemys picta bellii olfactory receptor 6N1 | Phaeon lepturus | 204   | 310   | 66%   |
| XM_005310272.1 | Chrysemys picta bellii olfactory receptor 11A1 | Haliaeetus leucocephalus | 211   | 320   | 66%   |
| XM_005310292.2 | Chrysemys picta bellii olfactory receptor 14A16 | Tinamus guttatus | 189   | 292   | 65%   |
| XM_005310408.1 | Chrysemys picta bellii olfactory receptor 6B1 | Opisthocomus hoazin | 239   | 315   | 76%   |
| XM_008171713.1 | Chrysemys picta bellii olfactory receptor 1019 | Cathartes aura | 209   | 307   | 68%   |
| XM_005310401.1 | Chrysemys picta bellii olfactory receptor 10C1 | Cathartes aura | 210   | 309   | 68%   |
| XM_008177751.1 | Chrysemys picta bellii olfactory receptor 11A1 | Charadrius vociferus | 201   | 310   | 65%   |
| XM_005309045.2 | Chrysemys picta bellii olfactory receptor 12 | Baleafrica regulorum | 222   | 306   | 73%   |
| XM_008175036.1 | Chrysemys picta bellii olfactory receptor 6B1 | Fulmarus glacialis | 229   | 312   | 73%   |
| XM_008176638.1 | Chrysemys picta bellii olfactory receptor 4Q2 | Nester notabilis | 193   | 297   | 65%   |
| XM_005309255.1 | Chrysemys picta bellii olfactory receptor 6F1 | Cathartes aura | 203   | 307   | 66%   |
| XM_005310439.2 | Chrysemys picta bellii olfactory receptor 14A16 | Gavia stellata | 157   | 242   | 65%   |
| XM_008174340.1 | Chrysemys picta bellii olfactory receptor 11A1 | Phoenicopterus ruber | 209   | 309   | 68%   |
| XM_005290034.1 | Chrysemys picta bellii olfactory receptor 52B2 | Anas platyrhynchos | 272   | 323   | 84%   |
| XM_005310406.1 | Chrysemys picta bellii olfactory receptor 10A7 | Pelecanus crispus | 206   | 303   | 68%   |
| XM_005314585.2 | Chrysemys picta bellii olfactory receptor 14A16 | Columba livia | 195   | 290   | 67%   |
| XM_005309064.1 | Chrysemys picta bellii olfactory receptor 10AG1 | Baleafrica regulorum | 198   | 305   | 65%   |
| XM_005313202.1 | Chrysemys picta bellii olfactory receptor 11A1 | Fulmarus glacialis | 148   | 227   | 65%   |
| XM_005311899.1 | Chrysemys picta bellii olfactory receptor 6N1 | Phoenicopterus ruber | 207   | 309   | 67%   |
| XM_005290011.1 | Chrysemys picta bellii olfactory receptor 52B2 | Phaethon lepturus | 203   | 305   | 67%   |
| XM_005309043.1 | Chrysemys picta bellii olfactory receptor 6P1 | Opisthocomus hoazin | 200   | 310   | 65%   |
| XM_005309055.1 | Chrysemys picta bellii olfactory receptor 6B1 | Podiceps cristatus | 164   | 249   | 66%   |
| XM_005310422.1 | Chrysemys picta bellii olfactory receptor 6N1 | Aptenodytes forsteri | 197   | 303   | 65%   |
| XM_008174332.1 | Chrysemys picta bellii olfactory receptor 6B1 | Phoenicopterus ruber | 203   | 312   | 65%   |
| XM_008177992.1 | Chrysemys picta bellii olfactory receptor 10A7 | Phoenicopterus ruber | 202   | 306   | 66%   |
| XM_005309019.1 | Chrysemys picta bellii olfactory receptor 1020 | Aptenodytes forsteri | 224   | 314   | 71%   |
| XM_005313885.1 | Chrysemys picta bellii olfactory receptor 52K2 | Cathartes aura | 233   | 316   | 74%   |
| XM_005310280.2 | Chrysemys picta bellii olfactory receptor 6F1 | Mesitornis unicolor | 229   | 304   | 75%   |
| XM_008174321.1 | Chrysemys picta bellii olfactory receptor 6N1 | Phoenicopterus ruber | 230   | 246   | 65%   |
| XM_005309024.1 | Chrysemys picta bellii olfactory receptor 10C1 | Gavia stellata | 242   | 310   | 78%   |
| XM_005311817.2 | Chrysemys picta bellii olfactory receptor 51G2 | Struthio camelus | 235   | 295   | 80%   |
| XM_005312282.1 | Chrysemys picta bellii olfactory receptor 5V1 | Charadrius vociferus | 235   | 316   | 74%   |
| XM_005290052.1 | Chrysemys picta bellii olfactory receptor 51G2 | Tinamus guttatus | 215   | 308   | 70%   |
| XM_005313248.1 | Chrysemys picta bellii olfactory receptor 52R | Gavia stellata | 224   | 307   | 73%   |
| XM_008178061.1 | Chrysemys picta bellii olfactory receptor 52P1 | Haliaeetus leucocephalus | 215   | 316   | 68%   |
| XM_005314254.1 | Chrysemys picta bellii olfactory receptor 11A1 | Aptenodytes forsteri | 206   | 317   | 65%   |
| XM_008174690.1 | Chrysemys picta bellii olfactory receptor 11A1 | Cuculus canorus | 203   | 310   | 65%   |
| XM_005310270.2 | Chrysemys picta bellii olfactory receptor 6N1 | Charadrius vociferus | 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_005311794.2 PREDICTED: Chrysemys picta bellii olfactory receptor 51G2 | 391 | Tinamus guttatus OR51 | 211 | 299 | 71% |
| XM_008174396.1 PREDICTED: Chrysemys picta bellii olfactory receptor 4M1 | 305 | Fulmarus glacialis OR10 | 145 | 203 | 71% |
| XM_008174324.1 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 11L1 | 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 | 379 | Fulmarus glacialis OR10 | 146 | 226 | 65% |
| XM_005310838.2 PREDICTED: Chrysemys picta bellii olfactory receptor 52B6 | 245 | Charadrius vociferus OR5 | 129 | 196 | 66% |
| Pm066 | 349 | Cathartes aura OR4 | 210 | 298 | 70% |
| Pm091 | 343 | Opisthocomus hoazin OR6 | 242 | 310 | 78% |
| Pm100 | 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 | Anstrocomus 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 | Baleaecia 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 | 196 | Gavia stellata OR10             | 93  | 142 | 65% |
| Pm171 | 226 | Struthio camelus OR4            | 142 | 212 | 67% |
| Pm207 | 209 | Opisthocomus hoazin OR6         | 142 | 195 | 73% |
| Pm213 | 207 | Fulmarus glacialis OR6          | 133 | 193 | 69% |
| Pm223 | 199 | Fulmarus glacialis OR4          | 136 | 197 | 69% |
| Pm222 | 198 | Antrostomus carolinensis OR12 Pseudogene | 128 | 185 | 69% |
| Pm209 | 195 | Gallus gallus OR5               | 125 | 189 | 66% |
| Pm248 | 194 | Struthio camelus OR2            | 130 | 186 | 70% |
| Pm250 | 190 | Anas platyrhynchos OR12         | 129 | 190 | 68% |
| Pm271 | 180 | Gavia stellata OR10             | 134 | 180 | 74% |
| Pm275 | 179 | Fulmarus glacialis OR10         | 103 | 159 | 65% |
| Pm277 | 174 | Cariama cristata OR12           | 106 | 159 | 67% |
| Pm184 | 169 | Fulmarus glacialis OR2          | 110 | 169 | 65% |
| Pm195 | 155 | Phoenicopterus ruber OR10       | 63  | 97  | 65% |
| Pm188 | 148 | Nestor notabilis OR5            | 101 | 145 | 70% |
| Pm243 | 144 | Aptenodytes forsteri OR5        | 96  | 142 | 68% |
| Pm219 | 141 | Cathartes aura OR10             | 82  | 126 | 65% |
| Pm279 | 141 | Opisthocomus hoazin OR9         | 85  | 131 | 65% |
| Pm178 | 140 | Nestor notabilis OR5            | 93  | 140 | 66% |
| Pm252 | 132 | Antrostomus carolinensis OR12 Pseudogene | 91  | 132 | 69% |
| Pm204 | 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 | 66% |
| Ac125 | 312 | Fulmarus glacialis OR10 | 148 | 226 | 65% |
| Ac112 | 312 | Phaeton lepturus OR5 | 118 | 179 | 66% |
| Ac119 | 311 | 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 OR10/PSEUDOGENE | 60       | Gavia stellata OR8 Pseudogene       | 42 | 60 | 70% |
| Alligator mississippiensis predicted OR10/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 OR12/PSEUDOGENE | 63       | Eretta 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       | Haliaetus 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 mississippiensi predicted OR14/PSEUDOGENE  | 36       | Balearica regulorum OR14           | 23 | 35 | 66% |
| Alligator mississippiensi predicted OR6/PSEUDOGENE   | 28       | Phoenicopterus ruber OR13           | 19 | 28 | 68% |
| Alligator mississippiensi predicted OR51             | 350      | Struthio camelus OR51              | 245| 317| 77% |
| Alligator mississippiensi predicted OR10             | 344      | Fulmarus glacialis OR10            | 153| 226| 68% |
| Alligator mississippiensi predicted OR10             | 343      | Phoenicopterus ruber OR10          | 209| 294| 71% |
| Alligator mississippiensi predicted OR55             | 332      | Struthio camelus OR55              | 195| 285| 68% |
| Alligator mississippiensi predicted OR52             | 331      | Cathartes aura OR52               | 235| 310| 76% |
| Alligator mississippiensi predicted OR6              | 331      | Podiceps cristatus OR10            | 164| 250| 66% |
| Alligator mississippiensi predicted OR10             | 328      | Aptenodytes forsteri OR5           | 216| 323| 67% |
| Alligator mississippiensi predicted OR6              | 326      | Struthio camelus OR6               | 257| 313| 82% |
| Alligator mississippiensi predicted OR10             | 325      | Phoenicopterus ruber OR10          | 160| 246| 65% |
| Alligator mississippiensi predicted OR10             | 321      | Fulmarus glacialis OR10            | 147| 226| 65% |
| Alligator mississippiensi predicted OR52             | 321      | Merops nubicus OR52               | 210| 303| 69% |
| Alligator mississippiensi predicted OR5              | 321      | Aptenodytes forsteri OR5           | 201| 310| 65% |
| Alligator mississippiensi predicted OR6              | 320      | Opisthocomus hoazin OR6            | 241| 303| 80% |
| Alligator mississippiensi predicted OR10             | 320      | Charadrius vociferus OR10          | 218| 319| 68% |
| Alligator mississippiensi predicted OR5              | 319      | Phoenicopterus ruber OR5           | 221| 311| 71% |
| Alligator mississippiensi predicted OR6              | 319      | Anas platyrhynchos OR6             | 224| 312| 72% |
| Alligator mississippiensi predicted OR10             | 317      | Pelecanus crispus OR10             | 220| 308| 71% |
| Species predicted | OR | Length | Species predicted | OR | Length | Similarity |
|-------------------|----|--------|-------------------|----|--------|------------|
| Alligator mississippiensis | OR10 | 317 | Balearica regulorum | OR10 | 219 | 69% |
| Alligator mississippiensis | OR52 | 317 | Tinamus guttatus | OR52 | 231 | 75% |
| Alligator mississippiensis | OR52 | 316 | Cariama cristata | OR52 | 251 | 80% |
| Alligator mississippiensis | OR10 | 316 | Fulmarus glacialis | OR10 | 209 | 70% |
| Alligator mississippiensis | OR6 | 316 | Columba livia | OR6 | 231 | 74% |
| Alligator mississippiensis | OR6 | 316 | Struthio camelus | OR6 | 252 | 81% |
| Alligator mississippiensis | OR5 | 315 | Charadrius vociferus | OR5 | 231 | 74% |
| Alligator mississippiensis | OR52 | 315 | Struthio camelus | OR52 | 225 | 72% |
| Alligator mississippiensis | OR10 | 315 | Tinamus guttatus | OR10 | 204 | 68% |
| Alligator mississippiensis | OR4 | 315 | Pterocles gutturalis | OR4 | 231 | 75% |
| Alligator mississippiensis | OR6 | 315 | Nipponia nippon | OR6 | 200 | 65% |
| Alligator mississippiensis | OR5 | 314 | Struthio camelus | OR5 | 219 | 71% |
| Alligator mississippiensis | OR5 | 314 | Tinamus guttatus | OR5 | 226 | 74% |
| Alligator mississippiensis | OR5 | 313 | Fulmarus glacialis | OR5 | 226 | 74% |
| Alligator mississippiensis | OR5 | 313 | Tinamus guttatus | OR5 | 244 | 78% |
| Alligator mississippiensis | OR10 | 313 | Apterodytes forsteri | OR10 | 192 | 68% |
| Alligator mississippiensis | OR10 | 313 | Tinamus guttatus | OR10 | 203 | 75% |
| Alligator mississippiensis | OR2 | 313 | Nipponia nippon | OR2 | 213 | 68% |
| Alligator mississippiensis | OR5 | 311 | Haliaeetus leucocephalus | OR5 | 211 | 69% |
| Alligator mississippiensis | OR11 | 311 | Struthio camelus | OR11 | 218 | 70% |
| Alligator mississippiensis | OR14 | 310 | Egretta garzetta | OR14 | 173 | 65% |
| Alligator mississippiensis | OR10 | 301 | Anas platyrhynchos | OR10 | 207 | 70% |
| Alligator mississippiensis | OR2 | 301 | Charadrius vociferus | OR2 | 213 | 71% |
| Alligator mississippiensis | OR6 | 298 | Taeniopygia guttata | OR6 | 190 | 73% |
| Alligator mississippiensis | OR10 | 381 | Anas platyrhynchos | OR10 | 203 | 71% |
| Alligator mississippiensis | OR8 | 265 | Phoenicopterus ruber | OR8 | 131 | 66% |
| Alligator mississippiensis | OR4 | 250 | Podiceps cristatus | OR4 | 115 | 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        |     |
| OR51L1                                          | Hexanoic acid                                | Goat-like, Barn-yard animal               | 8892        |     |
| OR51G2                                          | Heptanoic acid                               | Rancid                                   | 8094        |     |
| OR51Q1                                          | Hexanoic acid                                | Rancid                                   | 8094        |     |
| OR52B2                                          | Fentanal                                     | Strong, acrid, pungent                    | 8063        | [10]|
| OR52E4                                          | Octanoic acid                                | Fruity, unpleasant, irritating            | 379         |     |
| OR52D1                                          | Octanoic acid, methyl ester                  | Powerful, fruity                          | 8091        |     |
| OR52R1                                          | Octanoic acid                                | Rancid                                   | 8094        | [11]|
| OR52R1                                          | Octanoic acid                                | Fruity, unpleasant, irritating            | 379         | [10]|
| OR2A5                                           | Nonanoic acid                                | Fatty, coconut                            | 8158        | [10]|
| OR2A5                                           | 1-Octanol                                    | Orange rose                              | 957         | [10,11]|
| OR2A5                                           | 1-Nonanol                                    | Floral                                   | 8914        |     |
| OR2A5                                           | 1-Decanol                                    | Sweet, floral, fruity                     | 8174        |     |
| OR2A5                                           | 1-Heptanol                                   | Fragrant                                 | 8129        |     |
| OR4E2                                           | (Methylthio)-methanethiol                    | -                                        | 122370      | [10]|
| OR4E2                                           | (Methylthio)-ethanethiol                     | -                                        | 525462      |     |
| OR4E2                                           | Bis(Methyl-thiomethyl) disulphide             | -                                        | 158825      |     |
| OR5AR1 (Olfr1019)                                | Prenyl acetate                               | Fruity, floral                           | 14489       |     |
| OR5AR1 (Olfr1019)                                | R-limonene                                   | Fruity                                   | 440917      |     |
| OR6A2                                           | Heptanal                                     | Fatty, pungent, fruity, metallic blood    | 8130        | [10,12]|
| OR6N1                                           | Allyl benzene                                | -                                        | 9309        |     |
| OR6P1                                           | Eugenol                                      | Spicy, floral                            | 3314        |     |
| OR6X1                                           | (+)-Carvone                                  | -                                        | 16724       |     |
| OR10A3                                          | 1-Nonanethiol                                | Unpleasant                               | 15077       |     |
| OR10A3                                          | 1-Heptanal                                   | Orange rose                              | 957         | [10,11]|
| OR11A1                                          | 2-Ethyl fenchol                              | Earthy                                   | 106997      |     |
| OR11L1                                          | (+)-Camphor                                  | Fragrant, penetrating                     | 159055      | [10]|
| OR11L1                                          | (-)-Camphor                                  | Fragrant, penetrating                     | 444294      |     |
| OR11L1                                          | (+)-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.
