Detailed Methods

Phylogenetic Analysis

To generate a phylogeny to serve as a basis for comparative analysis, we began with the character matrix of Turner and Sertich, 2010. The original character matrix includes 81 taxa and 301 discrete characters. The total dataset contains approximately 39% missing data, which is well within the threshold for returning an accurate phylogeny (Wiens, 2003).

We used a Bayesian phylogenetic analysis to infer suchian relationships. This analysis was performed using the software MrBayes v. 3.2.2 (Ronquist et al., 2011). We followed the general protocols outlined by recent paleontological studies for deriving topologies from a morphological dataset (Müller and Reisz, 2006; Clarke and Middleton, 2008; Prieto-Marquez, 2010; Kear and Barrett, 2011; Lee and Worthy, 2012; Lee et al., 2014; Gorscak et al., 2014). We first used an Mk likelihood model of morphological evolution (Lewis, 2001). We then performed an analysis using a variable rates character evolution model. All characters were treated as unordered, and minimum age constraints (relaxed clock) were applied to each taxon using data from the Fossilworks Database (see Fossilworks References for first-appearance datum/last-appearance datum [FAD/LAD] below), which we also cross-checked against the original references. Under the variable rates model character rate variation was drawn from a gamma distribution. The Markov chain Monte Carlo setting ran for 20,000,000 generations, with sampling occurring every 1,000 generations using two heated chains. Our 25% burn-in was sufficient as
convergence was reached early in the run. The majority-rule consensus tree was generated from the combined post-burn-in samples (Supplemental Fig. S1).

This analysis is intended to provide meaningful branch lengths calibrated by both time and character change. We recovered > 90% of the topological relationships in the source tree (Turner and Sertich, 2010), with large polytomies resolved. For careful consideration of interspecies relationships, we refer the reader to Turner and Sertich (2010), Pol et al. (2014), and Turner (2015).

**Morphological Data Collection**

Due to variable preservation quality, four techniques were used to measure head width (HW). (1) as trans-quadratic width, for specimens with complete post-orbital skulls; (2) twice the distance between the midsagittal plane (as defined by an anteroposterior line passing through the midpoint of the occipital condyle) and the lateral margin of the quadrate, for distorted or incomplete cranial specimens; (3) trans-articular width for specimens lacking complete skulls but possessing lower jaws; and (4) or as twice the distance between the midsagittal plane (as defined by the anteroposterior midline passing through a fully articulated mandibular symphysis) and the lateral margins of the articular, for distorted or incomplete lower-jaw specimens.

Retroarticular processes (RAPs) were measured as the anteroposterior length of the articular bone from the midpoint of the quadrate articular joint (i.e., center of rotation) to the posterior-most margin of the articular bone, perpendicular to an imaginary line passing through the center of rotation of the jaw joints. Values for *Metriorhynchus casamequelai* were substituted with values for *Metriorhynchus brachyrhynchus*
(Supplemental Table S3) in the analysis of trait history as they are congeners. RAP length was measured directly on fossil skulls and was measured following manual palpation on living specimens, which were restrained to ensure measurement accuracy.

**Preliminary Evolutionary Model Fitting**

Prior to the evolutionary analysis described in the main text, we first fit a series of standard models of trait evolution and evaluated the location and probability of evolutionary regime shifts on the pruned phylogeny. Evolutionary models of continuous trait evolution were fitted using the ‘geiger,’ ‘phytools,’ and ‘evomap’ R packages (Harmon *et al*., 2008; Revell, 2012; Smaers, 2016). Lambda (Pagel, 1999), delta (time dependent model; Pagel, 1999), kappa (punctuational model; Pagel, 1999), early burst (Harmon *et al*., 2010; similar to the accelerating-decelerating model of Blomberg *et al*., 2003), Brownian motion (Felsenstein, 1973), Ornstein-Uhlenbeck (random walk with central tendency; Butler and King, 2004; with variance-covariance matrix transformation of Slater, 2014), and independent evolution (adaptive peak of Smaers and Vinicius, 2009; implemented in evomap) were fit to the pruned phylogeny and values of natural-logged retroarticular process lengths (as ln mm). The phylogeny was independently scaled to each model and the posterior distribution of traits was calculated using a Bayesian Markov Chain Monte Carlo (MCMC) ancestral character estimation (2,000,000 generations). The relative goodness-of-fit of each model was compared using log likelihood and the small-sample-corrected Akaike information criterion (AICc). The best fit model is one of independent evolution (Supplemental Table S1), which was, therefore, employed in the analysis described in the main text. The worst fit model was Ornstein-
Uhlenbeck (Supplemental Table S1). This may be due to the fact that our pruned phylogeny is both non-ultrametric and contains a sample size fewer than 200 taxa. These issues are described in detail by Slater (2014) and Cooper and colleagues (2016).

SUPPLEMENTAL TABLE S1. Support for each model fit based on log-likelihood and AICc values. The best fit model is one of independent evolution (the adaptive peak model of Smaers and Vinicius, 2009). Abbreviations: BM, Brownian Motion; EB, Early Burst; IE, Independent Evolution; OU, Ornstein Uhlenbeck.

| Model | Log Likelihood | AICc  |
|-------|----------------|-------|
| BM    | -68.5          | 139.1 |
| lambda| -58.7          | 121.8 |
| delta | -67.1          | 138.5 |
| kappa | -72.9          | 150.2 |
| EB    | -67.6          | 139.6 |
| OU    | -123.8         | 251.9 |
| IE    | -29.2          | 62.8  |

Evolutionary Model Support

Although the independent evolution model is the best fit and was used to calculate evolutionary rates and ancestral character estimations, a series of exploratory analyses was conducted to (1) estimate and (2) test hypotheses regarding the strength, directionality and probability of regime change within the tree. To identify shifts without a priori hypotheses, the SURFACE model of Ingram and Mahler (2013) was implemented in the R package ‘surface’ (Ingram and Mahler, 2013). SURFACE uses stepwise algorithms to locate regime shifts on a tree with the performance of each model
tested using sequential, iterative changes in AICc values (a model initially conceived of by Hansen, 1997; Ingram and Mahler, 2013). This model involves forward and backward passes, with the forward pass establishing the number of regime shifts and the backward pass identifying instances of convergence in trait evolution (Ingram and Mahler, 2013). Model output includes estimations of the parameters $K$ (number of regime shifts), $\alpha$ (evolutionary rate), $\sigma^2$ (magnitude of uncorrelated diffusion), and $n$ optima of $\theta$ (optimum trait values). Our SURFACE models accounted for both HW and RAP (in ln mm), and identified four regimes in RAP evolutionary rates: (1) early Suchia + Noto- suchia (excluding hypercarnivorous Notosuchia), (2) hypercarnivorous Notosuchia, (3) Neosuchia, and (4) the clade of stem Neosuchians comprised of *Rugosuchus* + *Shamosuchus*. SURFACE estimated parameters are presented in Supplemental Table S2.

**SUPPLEMENTAL TABLE S2.** Regime shift parameters for suchian head width (HW) and retroarticular process (RAP) evolution (in ln mm), calculated using the Hansen method as implemented in the R package ‘SURFACE’ (Ingram and Mahler, 2013). Abbreviations: $\alpha$, evolutionary rate; $\sigma^2$, magnitude of uncorrelated diffusion; HW, head width; $K$, number of regime shifts; $\theta_n$, optimum trait values; RAP, retroarticular process length.

| Parameter | HW    | RAP   |
|-----------|-------|-------|
| $\alpha$  | 0.045 | 0.038 |
| $\sigma^2$| 0.017 | 0.028 |
| $K$       | 6     | 4     |
| $\theta_1$| 3.995 | 2.033 |
| $\theta_2$| 5.683 | 4.649 |
| $\theta_3$| 4.895 | 3.515 |

Support for the SURFACE hypothesized regime shifts was quantified using a Bayesian reversible-jump MCMC, multiple-peak Ornstein-Uhlenbeck model,
implemented using the ‘bayou’ package in R (Uyeda and Harmon, 2014). Whereas SURFACE treats $\alpha$ and $\sigma^2$ as constant throughout the tree, the multi-peak OU model allows these values to change. We ran two models for retroarticular process evolution in ‘bayou’. In the first, all prior parameters were unconstrained (‘heuristic priors’ below). In the second, we set our priors to be roughly equivalent to the results of our SURFACE models (‘four-shift’ below). We identified four branches on which a priori regime shifts were expected, introduced three values for $\theta$ (2.033, 3.515, and 4.649 ln mm), and established initial evolutionary rates and the magnitude of uncorrelated diffusion ($\alpha = 0.038$, $\sigma^2 = 0.028$). Both of our ‘bayou’ models ran for 2,000,000 generations, allowed for a maximum of one regime shift per branch, and all prior distributions were assumed to be normal (with the exception of the distribution of shifts, for which the prior distribution was assumed as conditional Poisson).

Our four-shift model marginally out-performed the ‘heuristic’/unconstrained priors model (lnl = -46.76 and -49.6, respectively; summary statistics in Supplemental Table S3), with both returning high probabilities of regime shift on branches leading to (1) Metasuchia, (2) small-bodied notosuchians, (3) Neosuchia, and (4) Eusuchia (Fig. S3). The four-shift ‘bayou’ model returned a bimodal set of trait optima (Supplemental Table S4): small RAP length (below 2.5 ln mm) and large RAP length (approximately 4 to 5.5 ln mm). Trait optima, along with regime-shift posterior probabilities, are visualized in Supplemental Fig. S3. The density distribution of RAP length values is further visualized in Supplemental Fig. S4, alongside color-coded phylogenetic regime shifts with a posterior probability higher than 0.2. A regime shift toward small-size optima is moderately well-supported for Notosuchia (to the exclusion of the carnivorous taxa
*Montealtosuchus, Uberabasuchus, and Kaprosuchus*, which exhibits a shift toward increasing size. The backbone of the tree leading directly to extant Crocodylia exhibits high posterior probability shifts toward increased RAP length at three nodes: the node demarcating Metasuchia, the base of Neosuchia, and the branch leading to stem and extant Eusuchia. Within the neosuchian ancestors of modern taxa, there is a series of low prior probability (but regular) shifts toward extant Crocodylia (Supplemental Fig. S3, Supplemental Table S4). Further, there is also a secondary regime shift toward increasing trait values elsewhere within Neosuchia, at the branch leading toward largely pelagic and marine forms (e.g. *Pelagosaurus* and *Metriorhynchus*) + hypercarnivorous forms (*Sarcosuchus* and *Terminonaris*). Ultimately, the SURFACE and ‘bayou’ models show strong support for gradual optimization of bite force within Neosuchia, with large shifts toward longer length optima at the bases of first Neosuchia and then either Eusuchia or Crocodylia (e.g., node no. 68 of Supplemental Figure S2). It is possible to implicate either of these locations as the onset of ontogenetic inertia (and, thus, adult over-performance); however, modern data can be most directly extended to shifts within Crocodylia.
SUPPLEMENTAL TABLE S3. Summary statistics for parameters from both ‘bayou’ models. Abbreviations: $\alpha$, evolutionary rate; $\sigma^2$, magnitude of uncorrelated diffusion; $K$, mean number of regime shifts; $N\theta$, mean number of optimum trait values; $\theta_o$, predicted RAP length (ln mm) at the base of the tree; $\theta_{all}$, mean RAP length (ln mm) for all optima.

|                    | Four-Shift | Heuristic Priors |
|--------------------|------------|------------------|
| Log likelihood     | -46.76     | -49.6            |
| Prior              | -32.12     | -29.36           |
| $\alpha$           | 0.01       | 0.01             |
| $\sigma^2$         | 0.03       | 0.04             |
| $K$                | 5.23       | 4.8              |
| $N\theta$          | 6.23       | 5.8              |
| $\theta_o$         | 2.17       | 2.36             |
| $\theta_{all}$     | 3.39       | 3.41             |

SUPPLEMENTAL TABLE S4. Posterior probabilities (PP) and magnitude of regime shifts within suchian retroarticular process length evolution based on a four-shift model.

| Branch | PP      | Clade            | Magnitude of $\theta$ | SE $\theta^2$ |
|--------|---------|------------------|-----------------------|---------------|
| 60     | 0.4245  | Metasuchia       | 4.166                 | 0.0124        |
| 56     | 0.3413  | Neosuchia (base) | 4.711                 | 0.0144        |
| 33     | 0.2549  | Neosuchia (marine) | 5.387                | 0.0165        |
| 54     | 0.2195  | Notosuchia (small-bodied) | 2.496        | 0.0114        |
| 53     | 0.1755  | Notosuchia (hypercarnivores) | 3.922        | 0.0197        |
| 12     | 0.1425  | Crocodylia (base) | 4.52                  | 0.023         |
| 55     | 0.1366  | Notosuchia (all)  | 3.138                 | 0.0155        |
| 34     | 0.111   | Eusuchia         | 4.043                 | 0.0214        |
| 51     | 0.1089  | Kaprosuchus      | 4.065                 | 0.0379        |
| 59     | 0.1039  | Shantungosuchus + Zosuchus | 1.399        | 0.0263        |
SUPPLEMENTAL FIGURE S1. Complete time-calibrated, majority-rule consensus tree of Suchia, generated from the combined post-burn-in samples. The phylogeny was derived from the character matrix of Turner and Sertich (2010). (Higher resolution version available at: https://dx.doi.org/10.6084/m9.figshare.3413596)
SUPPLEMENTAL FIGURE S2. Phylogeny of Suchia pruned for fossil taxa with complete retroarticular process (RAP) and head width (HW) data (n = 36) and with nodes labelled numerically (see Supplemental Table S9 for node values).
SUPPLEMENTAL FIGURE S3. Phylogeny of Suchia with retroarticular process length (bite force proxy) evolutionary regime shifts. Blue indicates shifts toward a decreasing trait value, and pink indicates shifts toward an increasing trait value. Circle sizes on branches indicate relative posterior probabilities of regime shift (larger = higher probability).
SUPPLEMENTAL FIGURE S4. Phylogeny of Suchia with tips matched to density of phenotypic trait values. Each color within the phylogeny represents a regime shift with a posterior probability of greater than 0.2. Phenotypic trait values are approximately bimodally distributed with a peak for small trait values (shorter retroarticular process [RAP] lengths and, thus, low bite forces) and a peak for higher trait values (longer RAP lengths and, thus, relatively higher bite forces). Black = early Suchia; purple = Notosuchia; green = Neosuchia (inclusive of modern Crocodylia); red = Neosuchia (e.g. marine and pelagic forms).
SUPPLEMENTAL TABLE S5. Retroarticular process (RAP) length (mm) and bite forces (Newtons; N); experimentally measured at the most prominent molariform tooth position; protocol reported in Gignac and Erickson, 2015) for a developmental series of wild *Alligator mississippiensis* (Pearson’s product moment correlation = 0.97 on best-fit power regression, n = 28).

| RAP | Bite Forces |
|-----|-------------|
| 4   | 15          |
| 5   | 14          |
| 9   | 31          |
| 10  | 41          |
| 20  | 260         |
| 24  | 170         |
| 25  | 198         |
| 27  | 275         |
| 28  | 347         |
| 35  | 1,076       |
| 46  | 1,052       |
| 50  | 2,323       |
| 53  | 2,274       |
| 55  | 1,780       |
| 60  | 2,326       |
| 62  | 3,512       |
| 65  | 3,521       |
| 66  | 1,884       |
| 80  | 4,630       |
| 80  | 5,900       |
| 85  | 8,120       |
| 90  | 5,840       |
| 90  | 5,998       |
| 95  | 9,618       |
| 100 | 10,058      |
| 110 | 8,833       |
| 125 | 11,127      |
| 126 | 10,057      |
SUPPLEMENTAL TABLE S6. Head width (HW; mm) and body-mass (kg) measurements for a developmental series of wild *Alligator mississippiensis* (Pearson’s product moment correlation = 0.99 on best-fit power regression, n = 35).

| HW | Body Mass |
|----|-----------|
| 23 | 0.06      |
| 23 | 0.06      |
| 33 | 0.22      |
| 34 | 0.25      |
| 68 | 2.20      |
| 70 | 2.45      |
| 70 | 2.60      |
| 75 | 3.60      |
| 78 | 3.15      |
| 95 | 4.50      |
| 123| 17.20     |
| 125| 16.30     |
| 130| 15.50     |
| 130| 20.00     |
| 140| 18.00     |
| 160| 32.10     |
| 170| 42.60     |
| 170| 41.00     |
| 175| 47.60     |
| 207| 128.00    |
| 215| 56.00     |
| 220| 87.50     |
| 225| 77.10     |
| 225| 104.50    |
| 240| 116.00    |
| 250| 106.20    |
| 270| 132.00    |
| 275| 129.50    |
| 280| 158.00    |
| 280| 190.50    |
| 290| 155.00    |
| 300| 225.00    |
| 305| 198.00    |
| 330| 230.20    |
SUPPLEMENTAL TABLE S7. Retroarticular process (RAP) lengths (mm), head widths (HWs; mm), and specimen details for fossil taxa used in this study that were sourced from museum collections. Institutional abbreviations: AMNH—American Museum of Natural History, New York, USA; FSU-VC—Florida State University Vertebrate Collection, Florida, USA; IGM—Mongolian Institute of Geology, Ulaan Bataar, Mongolia; MBR—Museum für Naturkunde der Humboldt Universität, Berlin, Germany; MCZ—Museum of Comparative Zoology, Massachusetts, USA; MVZ—Museum of Vertebrate Zoology, California, USA; NHM UK—Natural History Museum, London, United Kingdom; UA, Université d’Antananarivo, Antananarivo, Madagascar; UCRC—University of Chicago Research Collection, Illinois, USA; UFRJ—Universidade Federal do Rio de Janeiro, Brazil.

| Taxon                        | Specimen No.       | HW  | RAP  |
|------------------------------|--------------------|-----|------|
| *Alligator mississippiensis* | FSUVC 082405-1     | 340 | 125  |
| *Crocodylus niloticus*       | MVZ 81487          | 343 | 106  |
| *Diplocynodon hantaniensis*  | AMNH 27632         | 224 | 74   |
| *Gavialis gangeticus*        | NHMUK 61.4.1.2     | 202 | 87   |
| *Goniopholis simus*          | NHMUK 5259–61      | 276 | 90   |
| *Gracilisuchus stipanicorum* | MCZ 4118           | 101 | 14   |
| *Kaprosuchus saharicus*      | UCRC PVC8          | 227 | 117  |
| *Malawisuchus amarali*       | UFRJ DG 106-R e    | 67  | 10   |
| *Metriorhynchus brachyrhynchus* | UFRJ DG 105-R     | 273 | 75   |
| *Metriorhynchus superciliosis* | UFRJ DG 5-R     | 190 | 56   |
| *Montealtosuchus arrudacamposi* | NHMUK PV R 3804 | 121 | 34   |
| *Notosuchus*                 | MBR 3981           | 135 | 23   |
| *Pelagosaurus sp.*           | MBR 2883           | 101 | 43   |
| *Pholidosaurus schwamburgensis* | MBR 1965       | 272 | 99   |
| *Shamosuchus djadochaensis*  | IGM 100/1105       | 83  | 15   |
| *Simosuchus clarki*          | UA 8670            | 83  | 10   |
| *Steneosaurus obtusidens*    | NHMUK PV R 3168    | 358 | 172  |
| *Zosuchus*                   | IGM 100/1304       | 35  | 4    |
SUPPLEMENTAL TABLE S8. Retroarticular process (RAP) lengths (mm), head widths (HWs; mm), and specimen details for fossil taxa used in this study that were sourced from figures available in the literature. Institutional abbreviations: **BMNH**—British Museum of Natural History; **CMNH**—Carnegie Museum of Natural History; **FC-DVP**—Facultad de Ciencias, Colección de Vertebrados Fósiles, Montevideo, Uruguay; **CPPLIP**—Centro de Pesquisas Paleontológicas Llewellyn Ivor Price; **IGV**—Geological Institute of the Chinese Academy of Geological Sciences Vertebrate Paleontology Collection; **IVPP**—Institute of Vertebrate Paleontology and Paleoanthropology, Academia Sinica, Beijing; **MGB**—Museo de Geología del Ayuntamiento de Barcelona; **MNK-PAL**—Museo ‘Noel Kempff Mercado’; **MNN**—Muséum National du Niger, Niamey, République de Niger; **MOZ**—Museo Profesor J. Olsacher, Zapala, Argentina; **MPMA**—Museu de Paleontologia de Monte Alto, Brazil; **MZSP-PV**—Museu de Zoologia, Universidade de São Paulo; **SMNH**—Royal Saskatchewan Museum (formerly the Saskatchewan Museum of Natural History), Regina, Saskatchewan, Canada; **ZPAL**—Instytut Paleobiologii **PAN**, Warszawa, Poland.

| Taxon                                    | Specimen No. | HW  | RAP | Reference                                                                 | Figure(s) |
|------------------------------------------|--------------|-----|-----|---------------------------------------------------------------------------|-----------|
| *Alligatorium (Montsecosuchus) depereti* | MGB 512      | 32  | 5   | Buscalioni, AD, Sanz, JL. 1990. J Vert Paleo 10:244–254.                  | 3, 4      |
| *Anatosuchus minor*                      | MNN GAD17    | 60  | 15  | Sereno PC, Larsson HCE. 2009. ZooKeys 28:1–143.                           | 5         |
| *Baurusuchus salgadoensis*               | MPMA-62-0001-02 | 196 | 51  | Vasconcellos FM, Carvalho IS. 2007. Paleontologia 1:319–332.              | 1         |
| Species                          | Catalogue | Locality | Age | Reference                                                                 |
|---------------------------------|-----------|----------|-----|---------------------------------------------------------------------------|
| *Dakosaurus andiniensis*        | MOZ 6146P |          |     | Gasparini Z, Pol D, Spalletti LA. 2005. Science 311:70–73.               |
| *Dibothrosuchus elaphros*       | IVPP V 7907 |          | 93  | Wu X-C, Chatterjee S. 1993. J Vert Paleo 13:58–89.                         |
| *Gobiosuchus kielanae*          | ZPAL MgR-II 69 |          | 31  | Osmólska H, Hua S, Buffetaut E. 1997. Act Paleo Pol 42:257–289.             |
| *Leidyosuchus canadensis*       | ROM 1903 |          | 258 | Wu X-C, et al. 2001. Can J Earth Sci 38:1665–1687.                        |
| *Protosuchus haughtoni*         | BP/1/4770 |          | 46  | Gow CE. 2000. J Vert Paleo 20:49–56.                                      |
| *Rugosuchus nonganensis*        | IGV 33 |          | 133 | Wu X-C, et al. 2001. Can J Earth Sci 38:1653–1663. Sereno P, et al. 2001. |
| *Sarcosuchus imperator*         | MNN 604 |          | 840 | Science 294:1516–1519.                                                    |
| *Shantungosuchus hangjinensis*  | IVPP V 10097 |          | 31  | Wu X-C, et al. 1994. J Vert Paleo 14:210–229. Buffetaut E, Ingavat R. 1980. |
| *Sunosuchus miaoi*              | CMNH 8028 |          | 154 | Shantungosuchus hangjinensis                                                |
| *Sphagesaurus huenei*           | MZSP-PV 139 |          | 70  | Pol D, et al. 2014. PLOS ONE 9:e93105.                                   |
| *(Caipirasuchus stenognathus)*  | SMNH P2411.1 |          | 409 | Wu X-C, Russell AP, Cumbaa SL. 2001. J Vert Paleo. 21:492–514.             |
| *Terminonaris robusta*          | BMNH R 7557 |          | 37  | Crush PJ. 1984. Palaeontology 27:131-157.                                 |
| *Terrestrisuchus gracilis*      | CPPLIP 630 |          | 141 | Carvalho I, et al. 2004. Gond Res 7:975–1002.                             |
| *Uberabasuchus terrificus*      | CPPLIP 630 |          | 141 | Carvalho I, et al. 2004. Gond Res 7:975–1002.                             |
**Supplemental Table S9.** Trait histories for ratios between retroarticular process (RAP) lengths (ln mm) and head widths (HWs) (ln mm), reconstructed for each direct ancestral node between *Alligator* and the origin of Suchia (node no. 37; Supplemental Figure S1).

| Node Number | HW     | RAP     | Stage Assignment |
|-------------|--------|---------|------------------|
| 37          | 4.589067 | 2.812592 | 1                |
| 38          | 4.582657 | 2.840437 | 1                |
| 40          | 4.529138 | 2.876542 | 2                |
| 41          | 4.424912 | 2.990188 | 2                |
| 42          | 4.427167 | 2.991335 | 3                |
| 44          | 4.465903 | 3.025687 | 4                |
| 55          | 4.833527 | 3.286161 | 5                |
| 63          | 4.911033 | 3.287499 | 6                |
| 65          | 4.739929 | 3.058593 | 7                |
| 66          | 4.64784  | 2.968581 | 8                |
| 68          | 5.204641 | 3.306364 | 9                |
| 69          | 5.294412 | 4.312054 | 9                |
| 70          | 5.191259 | 4.314440 | 10               |
| 71          | 5.198303 | 4.314237 | 10               |
| *Alligator* | 5.828946 | 4.828314 | 10               |

**Supplemental Table S10.** Values for ratios between retroarticular process (RAP) lengths (ln mm) and head widths (HWs) (ln mm) for *Alligator mississippiensis*, averaged within each of ten developmental stages between hatchlings (28 cm total length [TL]) and the largest adult (364 cm TL) in our sample (n = 34).
| HW     | RAP    | Stage Assignment |
|--------|--------|------------------|
| 3.135494 | 1.386294 | 1                |
| 3.135494 | 1.609438 | 1                |
| 3.496508 | 2.197225 | 2                |
| 3.526361 | 2.397895 | 2                |
| 4.248495 | 2.995732 | 3                |
| 4.248495 | 3.178054 | 3                |
| 4.553877 | 3.218876 | 3                |
| 4.219508 | 3.218876 | 3                |
| 4.356709 | 3.295837 | 4                |
| 4.317488 | 3.332205 | 4                |
| 4.867534 | 3.367296 | 4                |
| 4.867534 | 3.555348 | 5                |
| 4.828314 | 3.688879 | 5                |
| 4.941642 | 3.806662 | 5                |
| 4.812184 | 3.828641 | 5                |
| 5.135798 | 3.912023 | 6                |
| 5.164786 | 3.951244 | 6                |
| 5.075174 | 4.007333 | 6                |
| 5.135798 | 4.094345 | 7                |
| 5.370638 | 4.127134 | 7                |
| 5.416100 | 4.174387 | 7                |
| 5.416100 | 4.248495 | 7                |
| 5.393628 | 4.290459 | 7                |
| 5.332719 | 4.382027 | 8                |
| 5.480639 | 4.382027 | 8                |
| 5.616771 | 4.382027 | 8                |
| 5.669881 | 4.442651 | 8                |
| 5.598422 | 4.499810 | 9                |
| 5.634790 | 4.499810 | 9                |
| 5.703782 | 4.553877 | 9                |
| 5.799093 | 4.653960 | 10               |
| 5.768321 | 4.700480 | 10               |
| 5.828946 | 4.828314 | 10               |
| 5.720312 | 4.836282 | 10               |
| 5.828946 | 4.828314 | 10               |
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