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A PRELIMINARY ANALYSIS OF ARCHOSAUROMORPH BARAMINOLOGY

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ABSTRACT

Triassic rocks around the world preserve the remains of fascinating reptile groups like phytosaurs, rhynchosaurs, and tanystropheids that appear in the stratigraphic record as suddenly as they disappear. These animals—along with the more famous archosaurs (e.g., dinosaurs, pterosaurs, and crocodilians)—belong to a large taxonomic group called Archosauromorpha. Although there have been multiple statistical baraminological analyses conducted on various archosaurian taxa, non-archosaur archosauromorphs remain largely unstudied from a creationist perspective. In order to understand the baraminic relationships of these creatures known exclusively from the fossil record, we applied statistical baraminological methods to a recent morphological dataset. We analyzed the dataset with baraminic distance correlation, multidimensional scaling, partition around medoids, and fuzzy analysis via BARCLAY. Recognizing that the dataset contained many disparate taxonomic groups, we reanalyzed the results in subset analyses. As a result of this study, we find multiple non-archosaur archosauromorph holobaramins including: Rhynchosauria, Allokotosauria, Tanystropheidae + Dinocephalosauridae, Proterosuchidae, Erythrosuchidae, Proterochampsidae, Erpetosuchidae, and Phytosauria. These results are consistent with our expectations that 1) there would be different created kinds of non-archosaur archosauromorphs, and 2) statistical baraminological methods would result in groups traditionally recognized in taxonomies and near the level of family.

KEYWORDS

Baraminology, Archosauromorpha, Archosauria, created kinds, Triassic, Rhynchosauria, Proterochampsia, Phytosauria

INTRODUCTION

Traditionally, many of the animals we are analyzing in this article were thrown into a wastebasket group called "Thecodontia" (Owen 1859) named because their teeth were set in sockets (as is the case with crocodilians, dinosaurs, and mammals). The thecodonts were thought to form an ancestral stock out of which came more "derived" taxa such as dinosaurs, crocodilians, pterosaurs, and birds. It was only later with more detailed studies that relationships between the various "thecodont" taxa were teased out. By 1956, Alfred Romer in his classic *The Osteology of Reptiles* recognized various subtaxa within Thecodontia including Proterosuchia (Proterosuchidae and Erythrosuchidae), Pseudosuchia (some modern non-crocodilian pseudosuchians, Euparkeriidae, and Scleromochlidae), and Parasuchia (Phytosauria). He also did not recognize some groups currently considered archosauromorphs to be close relatives of archosaurs as evidenced by his placement of rhynchosaurs within Rhynchocephalia (tuataras and their extinct relatives) and protorosaurs (including tanystropheids) within Euryapsida (an old grouping for sauropterygians and their supposed relatives). Later, Jacques Gauthier (1986) wrote, "From a phylogenetic perspective, "Thecodontia" and Archosauria are diagnosed by the same synapomorphies. Thus, these taxa are redundant…" (p. 2).

The term Archosauromorpha was coined by German paleontologist Friedrich von Huene in 1946. With the advent of cladistics, the name Archosauromorpha was applied to Archosauria and those taxa on the line to it and not on the line to the lepidosaurs (lizards, snakes, and sphenodontians). There have been multiple definitions for the clade Archosauromorpha. Michel Laurin (1991) defined it as the clade containing the most recent common ancestor of *Prolacerta*, *Trilophosaurus*, *Hyperodapedon* and all of its descendants, which is

a node-based definition. David Dilkes (1998) instead defined it as, "*Protorosaurus* and all other saurians that are related more closely to *Protorosaurus* than to Lepidosauria" (p. 528). Dilkes intended his definition to replace Laurin (1991) because Laurin's definition would exclude *Protorosaurus*, Drepanosauridae, and Tanystropheidae. Additionally, this newer definition is stem-based, which matches the stem-based definition for Lepidosauromorpha (Gauthier et al. 1988). Laurin's more exclusive form of Archosauromorpha corresponds closely to the group Crocopoda named by Ezcurra (2016) to include all archosauriforms, rhynchosaurs, and allokotosaurs to the exclusion of tanystropheids.

The first definitive archosauromorphs in the fossil record are found in the Middle-Upper Permian, with Ezcurra et al. (2014) only recognizing four definite species: *Protorosaurus speneri*, *Archosaurus rossicus*, *Eorasaurus olsoni*, and *Aenigmastropheus parringtoni*. Additional Permian archosauromorph remains include a distal humerus reminiscent of tanystropheids from Brazil (Martinelli et al. 2017). However, in the overlying Triassic layers, archosauromorphs are incredibly common and make up the majority of terrestrial tetrapods by the Upper Triassic.

Archosauromorphs are characterized by several features including a premaxilla extending dorsally to the external naris, excluding the maxilla from the narial margin (Laurin 1991), and a lack of an entepicondylar foramen on the humerus (Ezcurra 2016). The major archosauromorph taxa are shown on a cladogram in Figure 1. Excluding the "protorosaurs", all archosauromorphs are in the group Crocopoda. Most crocopods are also in the more exclusive group Archosauriformes (to the exclusion of rhynchosaurs, allokotosaurs, and a few others). Archosauriforms–including Archosauria and a few smaller groups (e.g., proterosuchids, erythrosuchids, protero-

champsians, and phytosaurs)–possess an antorbital fenestra in the skull. Archosauria contains two subgroups: Pseudosuchia (the "crocodile-line" archosaurs) and Avemetatarsalia (the "bird-line" archosaurs) differentiated by unique ankle constructions. Pseudosuchia, despite meaning "false crocodiles," contains the true crocodilians and assorted fascinating extinct groups like the armored aetosaurs, the sail-backed ctenosauriscids, and the ornithomimosaur-mimicking shuvosaurids. Avemetatarsalia contains the aphanosaurs and the large group Ornithodira, which splits into Pterosauromorpha and Dinosauromorpha. Pterosauromorpha contains the pterosaurs and (possibly) the lagerpetids (small, lightly-built, Triassic archosaurs). Dinosauromorpha contains dinosaurs and some non-dinosaur dinosauromorphs like silesaurids. Phylogenetic analyses consistently recover birds (Aves) within the Dinosauria, specifically the theropod dinosaurs, whereas traditional Linnaean taxonomy recognizes Aves (or possibly Avialae) as a Class distinct from Class Reptilia, which contains all of the rest of the archosaurs. Regardless of whether birds actually evolved from dinosaurs or other archosaurs–and they certainly did not–comparative anatomy shows numerous similarities between theropod dinosaurs and birds (e.g., O'Connor and Claessens 2006; Ostrom 1974; Pittman et al. 2022). Indeed, phylogenetic studies using molecular data from extant animals consistently recover crocodiles to be the sister taxa of Aves (e.g., Cotton and Page 2002; Fong and Fujita 2011; Zardoya and Meyer 1998). The relationship of birds to other archosauromorphs is outside the scope of this paper, but has been discussed and debated in other creationist publications
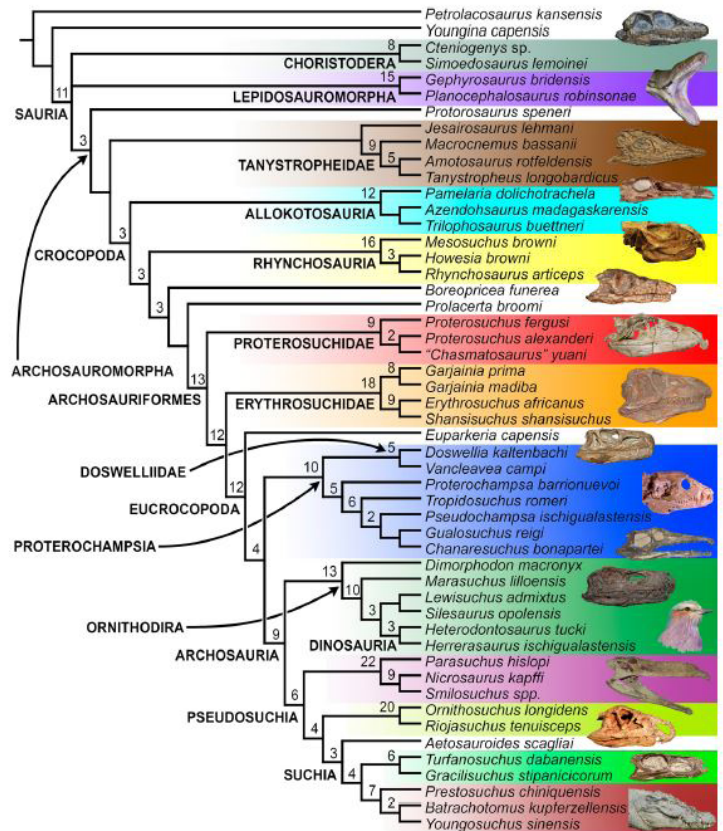
(see, for example, some recent publications on the topic: Cserhati et al. 2020; McLain 2020; McLain et al. 2018; Surtees 2021; Thomas and Sarfati 2018).

A. Recognizable Archosauromorph Group

There are distinct, recognizable groups within Archosauromorpha that creationists might expect to be created kinds. Concerning archosauromorphs, vertebrate paleontologist Hans Sues wrote, "Whereas the individual clades can be readily diagnosed, there are relatively few features that unambiguously relate them to each other" (Sues 2019, p.159). These morphologically distinct groups are characterized by sudden appearances and disappearances in the fossil record. Figure 57 of Ezcurra (2016), reprinted here as Figure 2, illustrates these archosauromorph groups well. The first archosauromorph group on the phylogeny is Tanystropheidae (brown), followed by Allokotosauria (light blue), then Rhynchosauria (yellow), Proterosuchidae (red), Erythrosuchidae (orange), Proterochampsia (blue), Ornithodira (green), Phytosauria (purple), Ornithosuchidae (yellow-green), Gracilisuchidae (lime green), and Paracrocodylomorpha (maroon). Most of these groups are the equivalents of taxonomic families (hence the -idae ending), although some are larger (e.g., Rhynchosauria, Allokotosauria). Many archosauromorph taxa are not present in Figure 2, as the phylogeny and article (Ezcurra 2016) focus on "basal" archosauromorphs. Thus, enormous clades like Ornithodira (which phylogenetically includes all pterosaurs, dinosaurs, and birds) and Paracrocodylomorpha (which includes poposauroids, "rauisuchians," and crocodyliforms) certainly contain many creat-
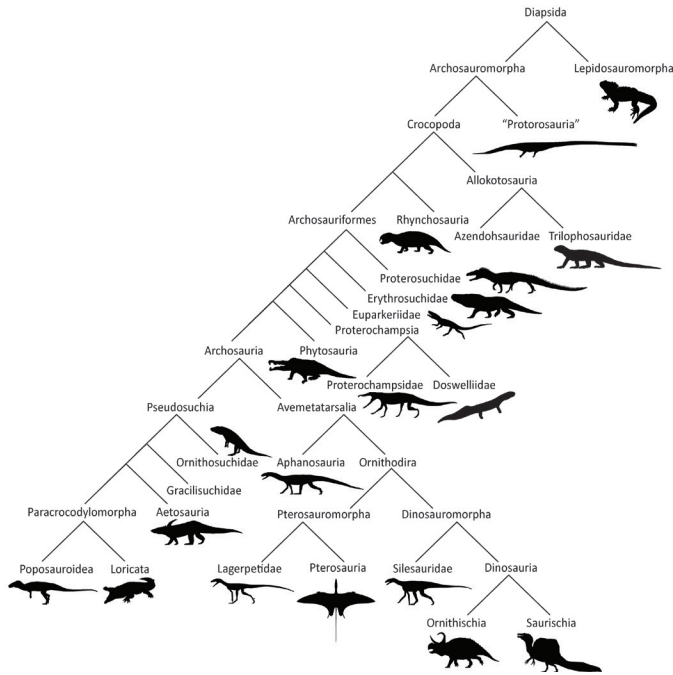
Figure 1. A simplified cladogram of archosauromorphs based on Ezcurra (2016), except in the placement of phytosaurs outside Archosauria, which follows Nesbitt (2011). All silhouette images from PhyloPic (https://phylopic.org) except *Vancleavea* and *Trilophosaurus*, which were made by Matthew McLain from NPS images. All PhyloPic images are public domain except the following: 1) *Garjainia* by Mark Witton (CC BY 3.0), 2) *Euparkeria* by Taenadoman CC BY-SA 3.0, 3) *Chanaresuchus* by Smokeybjb (CC BY-SA 3.0), 4) *Ornithosuchus* by Dmitry Bogdanov (CC BY-SA 3.0), 5) *Smilosuchus* by Robert Gay (CC BY-SA 3.0), and 6) *Teleocrater*, *Ixalerpeton*, and *Asilisaurus* by Scott Hartman (CC BY 3.0). Image licenses: CC BY 3.0 - https://creativecommons.org/licenses/by/3.0/; CC BY-SA 3.0 - https://creativecommons.org/licenses/by-sa/3.0/.

Figure 2. A reprint of Figure 57 from Ezcurra (2016) showing various clades of archosauromorphs color-coded, which correspond to morphologically distinct and recognizable groups. CC BY 4.0 - https://creativecommons.org/licenses/by/4.0/.

ed kinds (see, for example, Doran et al. 2018; Frederico and Mc-Lain 2019; McLain et al. 2018; Wood 2005). It should also be noted that there are some species that do not fall within any of the colored clades (e.g., *Prolacerta broomi* and *Euparkeria capensis*).

If we predict that these recognizable, non-archosaur archosauromorph units on Figure 1 represent distinct baramins, then we can hypothesize 6-10 created kinds (the higher number including the taxa falling outside of the colored clades). If, instead, we estimate the number of non-archosaur archosauromorph baramins as at the family level, then the number would be closer to ~12-15 created kinds. In this article, we will use statistical baraminological methods to test these hypotheses. However, before we address previous baraminology work on archosauromorphs, a brief survey of the various archosauromorph taxa is required.

1. "Protorosauria"

Protorosauria is a likely polyphyletic grouping of archosauromorph reptiles known from Permian and Triassic rocks. The distinctive feature of "protorosaurs" is their long necks, which are made up of lengthened cervical vertebrae with ribs that extend backward to the vertebrae behind them. The name "Protorosauria" was given by English anatomist and palentologist Thomas Henry Huxley in 1871 for the animal *Protorosaurus*.

In 1886, Francesco Bassani described a fossil of a reptile from the Middle Triassic Besano Formation along the border between Italy and Switzerland as a peculiar pterosaur, which he named *Tribelesodon longobardicus*. Later discoveries revealed that what were thought to be the elongated phalanges of a pterosaur were actually elongated neck vertebrae, which compared well with some from Germany that had been assigned to *Tanystropheus conspicuus* (Spiekman et al. 2021). Thus, *Tribelesodon longobardicus* was renamed *Tanystropheus longobardicus*. Tanystropheids are now a well-known group from Lower to Upper Triassic beds from Europe, Asia, North America (Pritchard et al. 2015), and South America (De Oliveira et al. 2018; De Oliveira et al. 2020).

Dinocephalosaurus, a long-necked, fully aquatic "protorosaur" from the Middle Triassic rocks of southwest China (Li et al. 2004), is the stratigraphically lowest example of live birth in archosauromorphs (Liu et al. 2017). Among "protorosaurs", *Dinocephalosaurus* has a neck that is noticeably longer due to an increase in the number of cervical vertebrae, unlike the condition in tanystropheids, where the neck is lengthened mainly by elongation of the cervical vertebrae (Li et al. 2004). Phylogenetic analyses place *Dinocephalosaurus* and *Pectodens* in Dinocephalosauridae, the sister taxon to Tanystropheidae (Spiekman et al. 2021).

As if tanystropheids and dinocephalosaurids were not strange enough, the most bizarre flavor of "protorosaur" comes in the form of the sharovipterygids. *Sharovipteryx mirabilis* is known from a single fossil from Kyrgyzstan that shows evidence of a membrane stretched between its long legs. Unfortunately, the arms are not well preserved, so it is unclear if there was a membrane there, too. Dyke et al. (2006) modeled the gliding ability of *Sharovipteryx* and concluded it was a delta-wing glider, but that it would have needed some kind of small anterior canard wing, attached to the forelimbs or the neck for stability. In 2016, Dzik and Sulej announced the discovery of a close relative to *Sharovipteryx* from Poland, which they named *Ozimek volans*. They suspect it was also a glider, although no evidence of a membrane was discovered on the fossil. Surprisingly, recent phylogenetic work has recovered *Ozimek* (and thus Sharovipterygidae) within Tanystropheidae (e.g., Spiekman et al. 2021).

We hypothesize that Tanystropheidae is either a holobaramin or

monobaramin within a larger holobaramin that also contains Dinocephalosauridae. However, we are unsure of how other "protorosaurs" might be related to this group.

2. Allokotosauria

The name Allokotosauria was derived from Greek meaning "strange reptiles," which suits them well. Allokotosaurs are a group of archosauromorph reptiles known from Middle to Upper Triassic rocks. Allokotosauria consists of two families: Azendohsauridae and Trilophosauridae. Trilophosauridae was named for *Trilophosaurus buettneri* by E.C Case in 1928. *Trilophosaurus* was named for its peculiar tricuspid teeth that are unknown in other archosauromorphs. It is an herbivore, possessing a keratinous beak in addition to its teeth, and it also has a long tail and grasping claws, allowing it to live an arboreal lifestyle probably reminiscent of an iguana (Spielmann et al. 2008). A very peculiar animal with a long snout named *Teraterpeton*, which was originally placed in its own family called Teraterpetidae (Sues 2003), has been included in Trilophosauridae because it is similar in having chisel-like cheek teeth and a toothless beak (Pritchard and Sues 2019).

Azendohsauridae was more recently named than Trilophosauridae (Nesbitt et al. 2015), and it includes animals like *Azendohsaurus* and *Shringasaurus,* a peculiar reptile with *Triceratops*-like brow horns (Sengupta et al. 2017). Azendohsaurids often have very short and robust limbs, with digits that are short and stout, possessing noticeably broad, curved claws on all four feet (Nesbitt et al. 2015). They also possess a single midline narial opening on the skull (Nesbitt et al. 2022). Many azendohsaurids were herbivorous, although there are some carnivorous forms known (e.g., *Malerisaurus* and *Puercosuchus*) (Marsh et al. 2022).

Azendohsauridae and Trilophosauridae have been recovered as sister taxa within Allokotosauria in recent phylogenies (e.g., Ezcurra et al. 2016; Nesbitt et al. 2022). Synapomorphies for Allokotosauria include a distinct morphology of the distal condyles of the humerus, a prominent tubercle distal to the glenoid fossa of the scapula, and a rugose surface of the frontal near the orbit margin (Nesbitt et al. 2015).

Due to their peculiarities when compared to other archosauromorphs and similarities that allokotosaurs share, we hypothesize that Allokotosauria (Azendohsauridae + Trilophosauridae) is either a holobaramin composed of two monobaramins or two separate holobaramins.

3. Rhynchosauria

Rhynchosaurs all possess two long, curved teeth that grow from the premaxilla right at the front of the face. The beak-like structure to these paired teeth makes them perfect for holding and tearing into soft foods (Mukherjee and Ray 2022). This unique feature inspired Richard Owen in 1842a to give the first discovered form the name *Rhynchosaurus*, meaning "beaked lizard." Because of their unique teeth and wide heads that seem too broad for the rest of their body, rhynchosaurs are easy to distinguish from other archosauromorphs. Rhynchosaur fossils have been found in South Africa, South America, Europe, India, Tanzania, Madagascar, and North America. The genus *Hyperodapedon* is one of the most commonly found tetrapods in Triassic beds that contain dinosaurs, making this genus a biostratigraphic index fossil (Ezcurra et al. 2016).

The species that are considered "basal" rhynchosaurs generally have smaller heads (~90 mm) than most of the others (~140 mm, with the exception of *Isalorhynchus genovefae*). This leads Ezcurra et al. (2016) to conclude that there were two distinct increases in skull

size, first in the clade Stenaulorhynchinae and then in the clade Hyperodapedontinae.

The stratigraphically lowest known species of rhynchosaur is *Noteosuchus colletti*, currently found in Lower Triassic strata in South Africa. When it was first discovered, *Noteosuchus* was thought to be an "eosuchian" (Watson 1917) and was later believed to be an ancestor to multiple different species, including phytosaurs (Broom 1925). It was not until 1928 that Franz Nopcsa first identified it as a rhynchosaur, which was later affirmed in 1976 by Robert Carroll. Still, this species tends to be problematic for phylogenetic trees since it lacks a cranium.

Due to the distinct qualities of Rhynchosauria as a whole, namely their edentulous premaxillae, unique maxillary dentition, and broad heads, we expect to see continuity within the group Rhynchosauria and discontinuity from the other groups within Archosauromorpha.

4. Proterosuchidae, Erythrosuchidae, and Euparkeriidae

Proterosuchidae, Erythrosuchidae, and Euparkeriidae are families within the group Archosauriformes. There have been 30 species placed in Proterosuchia (Ezcurra et al. 2013). Although proterosuchids and erythrosuchids are near each other cladistically (along with Euparkeriidae) and have previously been placed within Proterosuchia, they are very different morphologically (Ezcurra et al. 2013).

Proterosuchids are the stratigraphically first appearing archosauriforms, with the species *Archosaurus rossicus* found in the uppermost Permian deposits of Russia. It is only known from one specimen, which includes fragmentary bones from the skull and cervical vertebrae. Although common in Lower Triassic layers, it has been claimed that proterosuchids were found in Middle Triassic strata, but these examples are questionable (Ezcurra et al. 2013). It may be that these specimens are not even from proterosuchids at all. Proterosuchids from the Lower Triassic include *Proterosuchus fergusi*, from the Induan stage of South Africa, and *Chasmatosaurus yuani,* from the Induan stage of China. Proterosuchids are characterized by an overhanging premaxilla, sprawling gait, and elongated low skulls. It has been proposed that they had palatal and pterygoidal teeth, however, most fossil samples are not well preserved enough to tell. The largest members of the group could reach up to 4 meters long, and the longest skull length recorded was 47.7 centimeters. They were believed to be semi-terrestrial, living mostly on land but taking to the water when needed, possibly to feed. Their pelvic girdle allowed for powerful locomotion forward, and the structure of the zygapophyses allowed for lateral flexure of the tail (Ezcurra et al. 2013). According to Ezcurra et al. (2013), they were the most abundant predator found in the Lower Triassic of the Karoo Basin.

Erythrosuchids were large predators (4.75-5 meters long) that had less of a sprawling gait than proterosuchids. They are thought to have been the top carnivores of their ecosystems (Ezcurra et al. 2013). Although most erythrosuchids lacked palatal teeth (Butler et al. 2019b; Ezcurra et al. 2018), erythrosuchids possessed massive skulls in proportion to their bodies with sharp teeth, resulting in erythrosuchids sometimes being described as "prehistoric bulldogs." It has been suggested that the disproportionately large heads of erythrosuchids and large theropods indicate that enormous heads are prerequisites for hypercarnivory in archosauriforms, but Bestwick et al. (2022) concluded that phylogeny, rather than factors like diet, largely determined the enormous skull size in the two groups.

It has been debated whether or not erythrosuchids were terrestrial or semi-aquatic based on their enormous skull size. The consensus is that they probably lived in marshy, swamp environments (Ezcurra et

al. 2013). Fossil samples have been found in the uppermost Lower Triassic and Middle Triassic (up to the Ladinian) layers. The histology in the limb bones of erythrosuchids and proterosuchids shows that there was rapid growth in their bodies before they reached sexual maturity (Ezcurra et al. 2013).

Euparkeria is another non-archosaurian archosauriform, but it is a much smaller animal than the proterosuchids or erythrosuchids, reaching about 1 m in length. It and its closest relatives (*Osmolskina* and *Halazhaisuchus*) form the family Euparkeriidae, although there are no definite synapomorphies that define this family, making it possible that this is an artificial grouping (Borsuk−Białynicka and Evans 2009). Dilkes and Sues (2009) concluded that *Euparkeria capensis* was stem-ward of *Erythrosuchus africanus*, whereas Ezcurra et al. (2010) recognized it as more crownward. Ezcurra (2016) recovered *Euparkeria* as the sister taxon to the group that includes proterochampsians and archosaurs. It has been suggested that euparkeriids might be bipedal, but Sookias and Butler (2013) argue that the head would have been too large for the animal to stand on its hind legs. Based on the size of the scerlotic ring in *Euparkeria*, Schmitz and Motani (2011) concluded that it may have been nocturnal. Euparkeriids were carnivorous, and based on their size, would have hunted smaller prey. Fossil samples for *Euparkeria* are very sparse, limited to only the lower portion of the Middle Triassic in South Africa.

Our prediction in conducting baraminology research is that we will find discontinuity between these three groups. While there are similarities between them morphologically, our suspicion is that there will be distinct created kinds.

5. Proterochampsia

The proterochampsians are a group of semi-aquatic archosauriforms found in Middle to Upper Triassic rocks of Brazil and Argentina. Superficially similar to crocodylians, proterochampsians have elongated snouts with the nostrils on the tip, semi-round orbits, ornamented armor, and conical, curved, thecodont teeth (Trotteyn et al. 2013). However, proterochampsians had other features unlike crocodylians, including longer legs and a ridge that runs underneath the eyes. Although sometimes included within the group Archosauria (Parrish 1993), Proterochampsia is most commonly recovered within non-archosaurian Archosauriformes (Ezcurra 2016; Nesbitt 2011).

Rhadinosuchus gracilis was the first proterochampsian to be discovered, and throughout the mid-1900s, more proterochampsian fossils were found in the Santa Maria, Chañares, and Ischigualasto Formations (Trotteyn et al. 2013). Proterochampsia was named by Bonaparte in 1971 to include Proterochampsidae and Cerritosauridae (although now *Cerritosaurus* is just seen as a member of Proterochampsidae).

According to Ezcurra (2016), Proterochampsidae is one of the two groups within Proterochampsia, with the second being Doswelliidae, although this clade is not considered to be a part of Proterochampsia by all researchers (e.g., Benton and Clark 1988). The Doswelliidae are also crocodylian-like archosauriforms, but often have flatter, longer snouts and longer bodies than other proterochampsids. While the Proterochampsidae are found mainly in South America, a few doswelliid species have been found in Europe and in North America. Doswelliids have morphological similarities to proterochampsids, such as the conical thecodont teeth, ornamented armor, and long snouts (Weems 1980). *Vancleavea campi* is a peculiar short-snouted, heavily armored, semi-aquatic archosauromorph from the Chinle Formation (Nesbitt et al. 2009) that has been considered as a possible doswelliid (Ezcurra 2016).

With these thoughts in mind, we predict that there will be evidence of continuity within each of the families Doswelliidae and Proterochampsidae, but there may be discontinuity between the two groups themselves, as they are sometimes recovered separately in the phylogenetic trees. We expect to see evidence of discontinuity between Proterochampsia and other non-archosaur archosauromorphs.

6. Phytosauria

Phytosauria is a group of extinct crocodile-like archosauriforms with at least 30 valid species and one of the richest fossil records of all Triassic archosauromorphs (Stocker and Butler 2013; Stocker et al. 2017). The first phytosaur was named by Georg Friedrich Jaeger in 1828. He named the creature "plant lizard" because he mistook sediment-filled alveoli in the jaw as herbivore teeth. Since then, many specimens have been found possessing two kinds of teeth: conical, crocodile-like teeth in the front of the jaws and sometimes serrated carnivorous teeth similar to those of theropod dinosaurs farther back in the jaws. Phytosaurs could grow to be up to six meters long. They possessed unique triangular osteoderms that are exclusive to phytosaurs which allow them to be easily distinguished. The placement of the nostrils above or close to the eyes is another distinctive feature of phytosaurs. Numerous phytosaur fossils have been discovered worldwide in what have been recognized as lacustrine and fluvial paleoenvironments, but more recently, it has been shown that some of them may have also existed in marine habitats (Butler et al. 2019a). Many scientists have utilized phytosaurs as index taxa for biostratigraphic and biochronological correlation since they are widely distributed and easy to differentiate (e.g., Lucas and Hunt 1993; Martz and Parker 2017).

The phylogenetic position of phytosaurs within Archosauriformes has been debated over time. Many scientists have recognized phytosaurs within Archosauria (e.g., Ezcurra 2016), which matches their possession of the "crocodile-normal ankle joint", a complex ankle joint where the hinge line zig-zags between the calcaneum and astragalus rather than the simple hinge line between the proximal and distal tarsals found in avemetatarsalians (see below). This feature was believed to show that phytosaurs were pseudosuchians. However, other studies suggest that phytosaurs are a sister taxon of Archosauria, reinterpreting the crocodile-normal ankle joint as plesiomorphic for Phytosauria and Archosauria (Nesbitt 2011). The origin of phytosaurs was shrouded in mystery from an evolutionary perspective as they seemed to suddenly pop onto the scene in the Late Triassic fully formed, like aetosaurs, rauisuchians, and many other archosauromorphs. However, reinterpretation of a Chinese Middle Triassic archosauriform called *Diandongosuchus* resulted in its recognition as the basalmost phytosaur (Stocker et al. 2017). *Diandongosuchus* lacks many classic phytosaur traits (e.g., elongated rostrum), but it does share several features in common with phytosaurs (e.g., shape of the scapular blade).

Given the uniqueness of the phytosaur bauplan and the clear distinction between phytosaurs and non-phytosaurs, we expect Phytosauria to be a holobaramin. Additionally, we anticipate that *Diandongosuchus* will be discontinuous with other phytosaurs and will therefore be in a different holobaramin.

7. Pseudosuchia

The name Pseudosuchia means "false crocodiles," which is ironic given that the group includes true crocodiles! The name originated with Karl Alfred von Zittel who coined it to group together *Aetosaurus*, *Typothorax*, and *Dyoplax*. Later authors removed aetosaurs from the group, but made it a suborder of Thecodontia containing animals like *Ornithosuchus* (e.g., Romer 1956). With the use of phy-

logenetics in paleontology, Pseudosuchia became the group containing all archosaurs more closely related to crocodilians than to birds (Gauthier 1986). It has a confusing history with another term—Crurotarsi—which Sereno defined to replace Pseudosuchia as the clade containing phytosaurs, ornithosuchids, *Prestosuchus*, Suchia, and all descendants of their common ancestor. However, Nesbitt (2011) found phytosaurs outside of Archosauria, which means Crurotarsi is a clade that includes phytosaurs and all archosaurs (including avemetatarsalians).

Pseudosuchia is a group with immense diversity and disparity. Modern crocodilians look relatively similar to each other, mainly differing in skull shapes and proportions. However, fossil pseudosuchians have radically different appearances from modern crocodilians and from each other. The group includes the armored, shovel-snouted aetosaurs; the hypercarnivorous "rauisuchians;" the agile, ostrich-mimic mimicking shuvosaurids; the sail-backed ctenosauriscids; the marine metriorhynchids; the pug-nosed *Simosuchus*; and many, many other forms. As such, we predict that the group will contain multiple holobaramins. However, this analysis will not be able to truly investigate the baraminic relationships of pseudosuchians as the list of taxa are mainly focused on non-archosaur Archosauromorpha.

8. Avemetatarsalia

Benton (1999) defined Avemetatarsalia as all crown-group archosaurs closer to Dinosauria than to Crocodylia. He erected the group because of his work on *Scleromochlus*, which he saw as outside the clade containing pterosaurs and dinosaurs (Ornithodira). *Scleromochlus* has been a difficult animal to classify, and for many years it seemed like Avemetatarsalia may be identical in composition to Ornithodira. However, the description of *Teleocrater* and recognition of its position along with other taxa in Aphanosauria just outside Ornithodira have confirmed that Ornithodira and Avemetatarsalia are not the same (Nesbitt et al. 2017). We anticipate aphanosaurs to share continuity and to be discontinuous from all other taxa.

Ornithodirans can be readily distinguished from pseudosuchians in the anatomy of their ankles (except among some dinosauriforms such as the silesaurid *Asilisaurus* (Nesbitt et al. 2017), which possess more pseudosuchian-like ankle joints). Ornithodirans possess simple hinge joints between the proximal and distal tarsals, whereas pseudosuchians have a more complex joint that goes between the two proximal tarsals (calcaneum and astragalus) called the "crocodile-normal" ankle. Nesbitt et al. (2017) proposed that the "crocodile-normal" ankle is plesiomorphic for Archosauria.

Ornithodira splits into Pterosauromorpha and Dinosauromorpha. Pterosauromorpha contains Lagerpetidae and Pterosauria, a group readily distinguished from all other archosauromorphs by numerous characters, especially those related to flight. Triassic pterosaurs are surprisingly diverse, and all currently known forms were flight capable (see, for example, Britt et al. 2018; Dalla Vecchia 2013). Despite the recognition of the similarities between lagerpetids and pterosaurs (hence their inclusion in Pterosauromorpha (Ezcurra et al. 2020)), conventional scientists are no closer to finding a "proto-pterosaur" than when the first Triassic pterosaur was discovered in 1973. Previous baraminology work has found evidence for discontinuity within Pterosauria, even within the non-pterodactyloids (Clausen and McLain, 2021; McLain, 2021; McLain 2022). As such, we anticipate that this study will find discontinuity surrounding Pterosauria, and—given the inclusion of pterosaurs from multiple families in the dataset—discontinuity separating some pterosaurs from others. We also anticipate that Lagerpetidae will be a holobaramin.

Dinosauromorpha contains Dinosauria (and Aves cladistically),

but there are a number of Triassic forms just outside of Dinosauria that have been discovered in the last few decades. The best known non-dinosaur dinosauromorphs are the silesaurids, a group of relatively long-necked, quadrupedal herbivores and omnivores found in Middle Triassic to Upper Triassic rocks of the United States, Brazil, Argentina, Morocco, Zambia, Madagascar, and Poland (Martz and Small 2019). Silesaurids are typically considered to be non-dinosaurian dinosauriforms (e.g., Nesbitt 2011), although some studies recover them as "basal" ornithischians (e.g., Norman et al. 2022) or as the sister taxon to Ornithischia (e.g., Cabreira et al. 2016). *Lagosuchus* is a non-dinosaur dinosauromorph of uncertain placement. We anticipate that Silesauridae will be a holobaramin, but we are not sure how *Lagosuchus* will correlate with the other taxa in the analysis.

Dinosauria (even excluding birds) is an enormous group full of immense diversity and disparity, from tiny bipeds smaller than chickens to enormous beasts weighing in over 60 tons. Richard Owen named Dinosauria in 1842b, and H.G. Seeley later in 1887 recognized what most today see as the two major groups of dinosaurs: Saurischia (including Theropoda and Sauropodomorpha) and Ornithischia. This classic dichotomy was challenged in 2017 by a scheme that would see Theropoda and Ornithischia as sister taxa in the group Ornithoscelida, to the exclusion of Sauropodomorpha and the enigmatic, Triassic group Herrerasauridae (Baron et al. 2017).

Regardless of these higher classification questions, there are some recognizable groups of dinosaurs found in Triassic rocks. Theropods and herrerasaurids both make an appearance as do multiple groups of sauropodomorphs (classic "prosauropods" like *Plateosaurus* as well as guaibasaurids and theropod-like forms such as *Eoraptor*). Assuming silesaurids are not ornithischians, there are no definitive Triassic ornithischians known as of yet (as *Pisanosaurus* may be a silesaurid (Müller and Garcia 2020)). Despite the many classification issues with these Triassic dinosaurs, we suspect that there are multiple holobaramins present, in agreement with Doran et al. (2018).

B. Previous Baraminology Work on Archosauromorphs

All previous baraminology studies on archosauromorphs have focused on archosaur taxa except one on phytosaurs (Grimes and McLain 2017). The majority of archosaur baraminology studies have focused on avemetatarsalians. Only three studies have investigated pseudosuchians: two focused on extant crocodilians (Cserháti 2023; Hennigan 2014) and the other on both fossil and extant eusuchians (Frederico and McLain 2019). As such, there have been no baraminology studies that have looked at the abundant, diverse, and disparate non-eusuchian pseudosuchian taxa (e.g., "rauisuchians", aetosaurs, poposauroids, etc.).

Avemetatarsalians, the group containing dinosaurs and pterosaurs (Fig. 1), have received a great deal more attention than pseudosuchians. Non-ornithodiran avemetatarsalians (e.g., aphanosaurs) have not been analyzed for baraminic status. Among the pterosauromorphs, there have only been a few pterosaur studies (Clausen and McLain 2021; McLain 2021; McLain 2022), although these have mainly focused on non-pterodactyloid pterosaurs. The large majority of baraminology studies in archosaurs have focused on Dinosauria, with non-dinosaurian dinosauromorphs (e.g., silesaurids) currently lacking specific studies (although a manuscript is currently in preparation). Most major non-avian dinosaur taxa have been analyzed except for sauropods (Aaron 2014; Cavanaugh 2011; Cserhati et al. 2020; Doran et al. 2018; McLain et al. 2018; Wood et al. 2011). Mesozoic non-avian avialans were the focus of one study (Garner et al. 2013). Extant birds (Aves) have been the subject of numerous

baraminological studies, both with statistical baraminology (Brophy 2021; Brophy and McConnachie 2021; Matthews et al. 2022; Wood 2005; Wood 2016) and without (Ahlquist and Lightner 2019; Lightner 2010; Lightner 2013; More 1998).

METHODS

We analyzed a dataset from a recent publication on Triassic archosaurs (Kellner et al. 2022) with statistical baraminological methods. We used BARCLAY (Wood 2020) to analyze the dataset with the following methods: 1) Pearson baraminic distance correlation (BDC), 2) Spearman BDC, 3) three-dimensional multidimensional scaling (3D MDS), 4) partition around medoids (PAM), and 5) fuzzy analysis (FANNY). We recognized that this dataset likely contains multiple created kinds, which would necessitate splitting up the taxa into smaller taxonomic groups, following the example of other studies (e.g., McLain et al. 2018; Wood 2005). The dataset and all subset versions were analyzed at a 0.75 character relevance cutoff. Table 1 shows the character and taxa numbers for each of the different analyses we ran on BARCLAY.

RESULTS

A. All Archosauromorpha

Analyzing all of the archosauromorph taxa required excluding 61 poorly known taxa below a 0.2 character relevance cutoff (Supplemental Table 1). Thus, 135 taxa remained along with only 83 characters at a 0.75 character relevance cutoff. As anticipated, the results at this level were not very informative. The Pearson and Spearman BDC plots (Supplemental Fig. 1 and Fig. 2) show positive correlation uniting almost all of the taxa. Only the rhynchosaurs are set apart by some negative correlation from the rest of the taxa, although even they share positive correlation with many of the taxa in the analysis. The highest average silhouette width for PAM was 0.08 at two groups, with a large number of taxa with negative silhouette values in the red group (Supplemental Fig. 3A). FANNY, by contrast, had an average silhouette width value of 0.33 at two groups (Supplemental Fig. 3B), and it would not work correctly at higher group numbers. The red group in FANNY had many taxa with negative silhouette width values. We did not attempt MDS results as the other methods were demonstrating that it was not worth the effort at this scale. In order to resolve the actual patterns of continuity and discontinuity among these archosauromorph taxa, we split up the dataset into recognizable taxonomic groups.

B. "Protorosauria"

The Pearson BDC results for the "Protorosauria" subset dataset (Figure 3A) show four blocks of positive correlation with no shared positive correlation between them. The largest block consists of tanystropheids and dinocephalosaurids. Additionally, the enigmatic *Jesairosaurus* shares positive correlation with the dinocephalosaurid *Pectodens*, which is in turn positively correlated with *Dinocephalosaurus*. The three remaining blocks of positive correlation are all different outgroup taxa. One block contains the rhynchocephalians (tuatara relatives) *Planocephalosaurus* and *Gephyrosaurus*. Another contains the choristoderes *Simoedosaurus* and *Cteniogenys*, a group previously analyzed with statistical baraminology by McLain and Doran (2019). The third outgroup block contains the "basal" diapsids *Petrolacosaurus* (an araeoscelidian), *Youngina* (a youngiform), and *Acerosodontosaurus* (a form of uncertain affinities).

Table 1. List of the number of taxa and characters used in each analysis. An asterisk (*) indicates that the analysis is in the supplemental material.

Dataset	Kellner, et al. (2022)	
Original Characters	823	
Original Taxa	196	
Dataset/Subset	Remaining Characters	Remaining Taxa
All Archosauromorpha	83	135
"Protorosauria"	294	17
Allokotosauria	234	10
Rhynchosauria	167	15
Rhynchosauria lacking problematic taxa	289	12
Proterosuchidae and Erythrosuchidae	95	14
*Proterosuchidae, Erythrosuchidae, *Euparkeria*, and *Osmolskina*	77	15
Proterochampsia (no outgroup)	214	14
Proterochampsia (with outgroup)	191	16
Phytosauria	278	14
Pseudosuchia	138	22
Non-paracrocodylomorph Pseudosuchia	195	13
Paracrocodylomorpha	144	10
*Gracilisuchidae, some Paracrocodylomorpha, and*Ticinosuchus*	213	9
Avemetatarsalia	66	31
Dinosauromorpha	542	13
Pterosauromorpha (0.2 taxic relevance cutoff)	44	16
Pterosauromorpha (0.29 taxic relevance cutoff)	104	12
"Basal" Avemetatarsalia	160	10

Protorosaurus shares no correlation of any kind with any other taxon in the analysis. The Spearman results (Figure 3B) are remarkably different, showing two major blocks of positive correlation mainly separated by negative correlation. One block contains Tanystropheidae and Dinocephalosauridae, whereas the other block contains the outgroup taxa and *Protorosaurus*. *Protorosaurus* is only connected to the outgroup block via the choristodere *Cteniogenys*, and it also shares positive correlation with the tanystropheid + dinocephalosaurid block via the tanystropheid *Macrocnemus*.

The MDS results for "Protorosauria" (Figure 4) shows a cluster of Tanystropheidae + Dinocephalosauridae (purple) separated from the rest of the taxa (blue). *Protorosaurus* falls in between the Tanystropheidae + Dinocephalosauridae cluster and the outgroup cluster. The outgroup cluster is more diffuse, with the choristoderes, rhynchocephalians, and the rest of the outgroup as three separate clusters.

The model with the highest average silhouette value for PAM was at three groups at 0.24; however, two groups was nearly identical in value at 0.23. The two-group model (Figure 5A) shows Tanystropheidae + Dinocephalosauridae in green and the outgroup taxa in red. Strangely, the outgroup taxon *Cteniogenys* is in the green group but with a strongly negative silhouette value, whereas the archo-
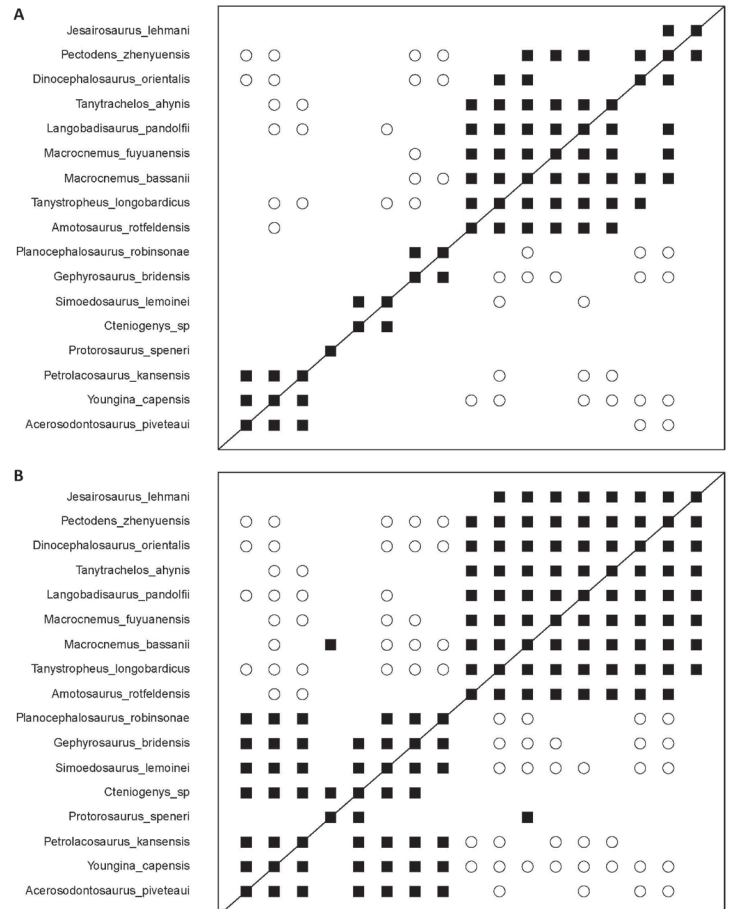
Figure 3. Baraminic distance correlation (BDC) results for the "Protorosauria" subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.

sauromorph *Protorosaurus* is in the red group also with a negative average silhouette value. The three-group model (Figure 5B) splits the outgroup taxa into blue (Rhynchocephalia) and red (the rest of the outgroup) groups. The same unusual situation is retained with *Cteniogenys* and *Protorosaurus*, respectively. Adding a fourth group (Figure 5C) lowers the average silhouette value to 0.16 and results in splitting up the Tanystropheidae from the Dinocephalosauridae, including separating the two *Macrocnemus* species from each other.

FANNY at two groups had an average silhouette value of 0.26 (Figure 6), and the program failed to run the analysis at any higher group number. The groups split into Tanystropheidae + Dinocephalosauridae (green) and the outgroup taxa (red). *Protorosaurus* is in the red group, but it has a negative average silhouette value.

C. Allokotosauria

The Pearson BDC results for the Allokotosauria subset dataset (Figure 7a) show two blocks of positive correlation (Azendohsauridae and Trilophosauridae) and four taxa that do not positively correlate with any other taxa in the analysis (the three outgroup taxa and *Malerisaurus*). The Spearman BDC (Figure 7B) shows the azendohsaurid and trilophosaurid blocks connected by positive correlation between *Spinosuchus* and *Malerisaurus*. The three outgroup taxa still do not positively correlate with any other taxon.

MDS results (Figure 8) for the Allokotosauria subset dataset show two clusters, one tightly clustered in purple (Allokotosauria) and the other diffusely clustered in blue (outgroup). Trilophosaurids and azendohsaurids form their own small clusters, but there is no significant gap between the two.

The PAM results (Figure 9) for the Allokotosauria subset dataset shows the distinction between Allokotosauria and outgroups when analyzing with two groups (average silhouette width = 0.3). At 3 groups (Figure 8B), the outgroup taxa are split into two groups with Allokotosauria still in a single group (average silhouette of 0.28).

The FANNY results for the Allokotosauria subset dataset at two groups (Figure 10A; average silhouette width = 0.2) shows Allokotosauria as one group and the outgroup in the other, except for the azendohsaurid *Pamelaria*, which is in the green group, but with a very large negative silhouette width. FANNY at three groups (Figure 10B) separates Allokotosauria into two groups (Azendohsauridae

and Trilophosauridae) and returns *Pamelaria* to the Azendohsauridae group (average silhouette width = 0.21). The green group contains the outgroup taxa, with *Sarmatosuchus* and *Yarasuchus* both having negative silhouette widths.

D. Rhynchosauria

The Pearson BDC results for the complete rhynchosaur dataset (Figure 11A) show shared positive correlation in a few different places. The rhynchosaurid taxa (including the hyperodapedontines) shared significant positive correlation, and there was only one instance of shared positive correlation with a "basal" rhynchosaur (*Rhynchosaurus articeps* and *Eohyosaurus wolvaardti*). The "basal" rhynchosaurs (*Eohyosaurus, Howesia browni, Mesosuchus browni*) share positive correlation except for *Noteosuchus colletti*, which shares no correlation with any taxon in the analysis. *Mesosuchus* shares positive correlation with the outgroup taxa via *Prolacerta*. The Spearman BDC for the complete rhynchosaur dataset (Figure 11B) has some instances of negative correlation. There are a few gaps in the rhynchosaurid block of positive correlation. *Noteosuchus* still lacks correlation with any other taxa in the analysis. The biggest difference between the Pearson and Spearman BDC plots is the negative correlation between the outgroup taxon *Prolacerta* and the rhynchosaurid species *Teyumbaita sulcognathus* and *Isalorhynchus genovefae*. Additionally, there are more instances of shared positive correlation between the "basal" rhynchosaurs and the outgroup taxa, and no instances of shared positive correlation between the "basal" rhynchosaurs and Rhynchosauridae.

The 3D MDS results for the complete rhynchosaur dataset clarify and support the BDC results (Figure 12A). The outgroup taxa, colored red in the figure, cluster together at a large distance from the rhynchosaurs. The three basal rhynchosaurs (in green) experience some clustering, but, again, at a distance from the others. *N. colletti* is there in purple, right in the middle, not clustering with either the basal group, the hyperodapedontines, or the non-hyperodapedontine rhynchosaurids. Hyperodapedontinae (dark blue) and the rest of the Rhynchosauridae (light blue) cluster tightly together and also appear closer together than the other groups.

The results of the PAM silhouette plot for the complete rhynchosaur dataset are inconclusive (Figure 13A). No matter how many groups are used (2-5), the average silhouette width is incredibly small, all of which are negative. The highest width occurred when there were two clusters with an average width of -0.07.

The result from FANNY with the highest average silhouette width (0.48) is at four groups. These four groups are the non-hyperodapedontine rhynchosaurs (red), the hyperodapedontines (yellow), the "basal" rhynchosaurs (blue), and the outgroup (green). The average widths of each group are, respectively, 0.31, 0.55, 0.54, and 0.63. *Noteosuchus* is in the hyperodapedontine group, but its silhouette width is nearly 0.

The Pearson BDC results (Figure 11C) for the dataset excluding the poorly known taxa (*Noteosuchus, Eohyosaurus,* and *Langeronyx)* has three groups of positive correlation, which are negatively correlated with the other two groups in most cases (except one instance of shared positive correlation between *Prolacerta* and *Mesosuchus*, as well as some instances of no correlation). One group includes all
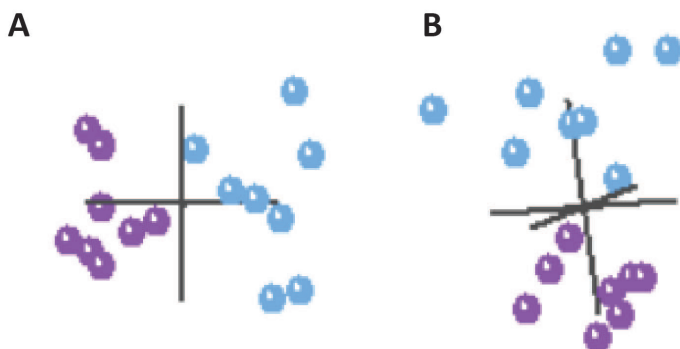
Figure 4. 3D multidimensional scaling (MDS) results for the "Protorosauria" subset dataset in two views: A and B. Blue represents outgroup taxa and *Protorosaurus*, whereas purple represents Tanystropheidae + Dinocephalosauridae.
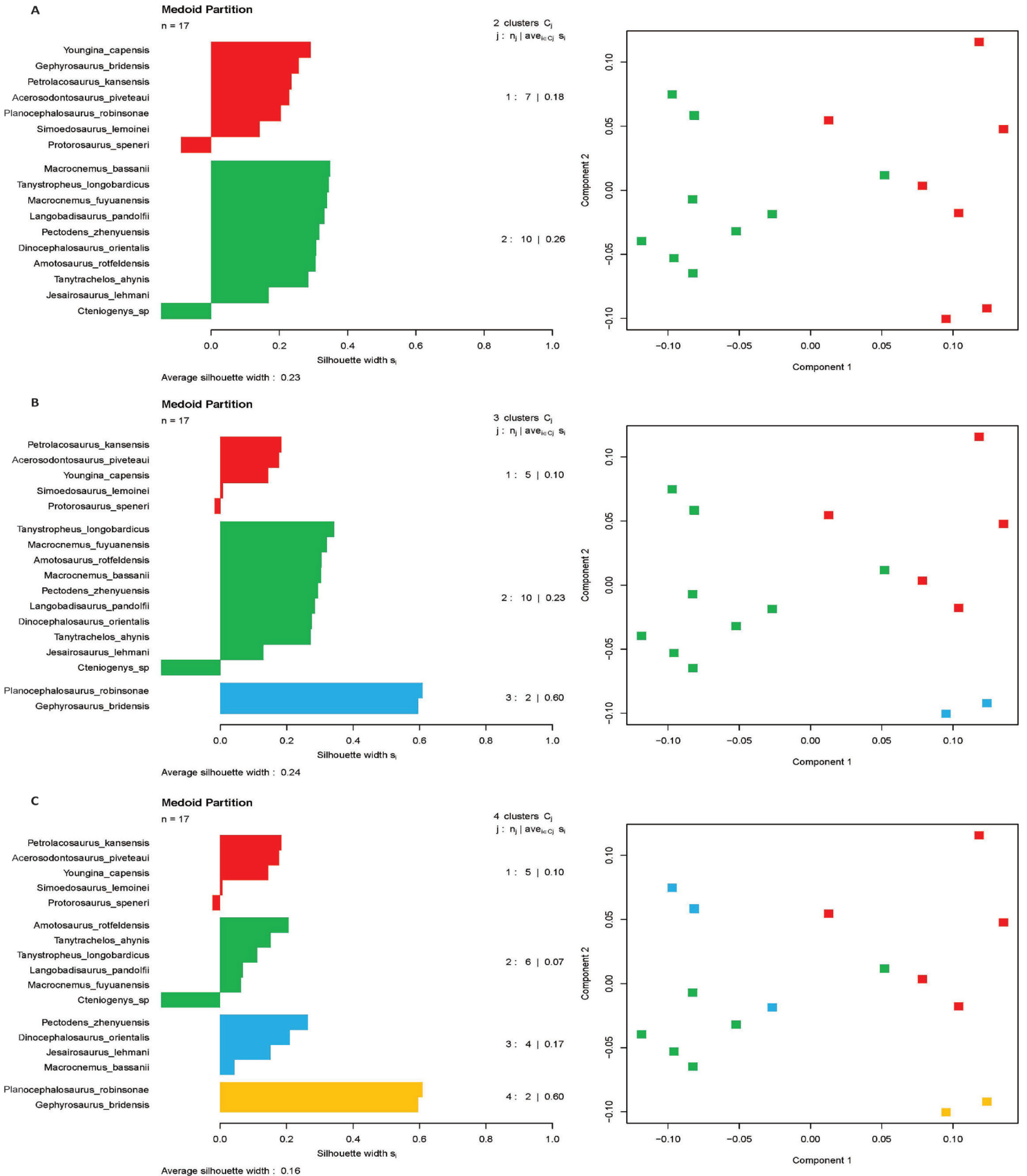
Figure 5. Partitions around medoids (PAM) analysis of the "Protorosauria" subset dataset by: A) 2 groups, B) 3 groups, C) 4 groups.
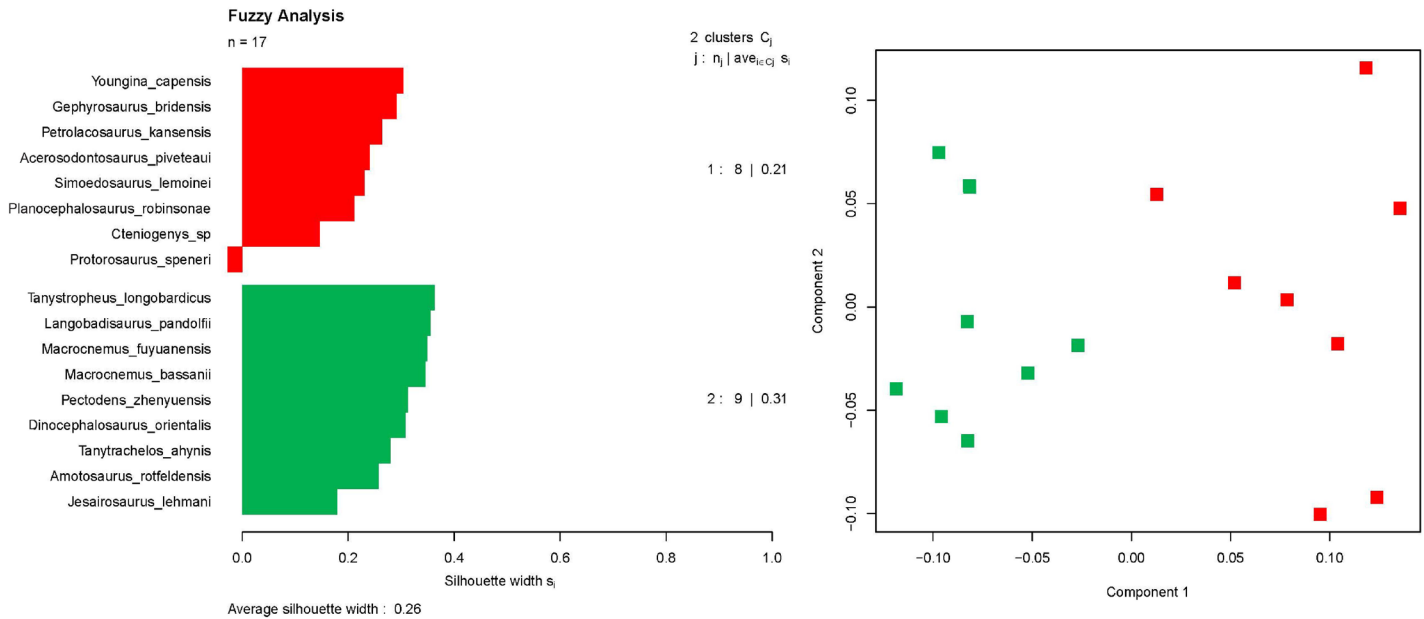
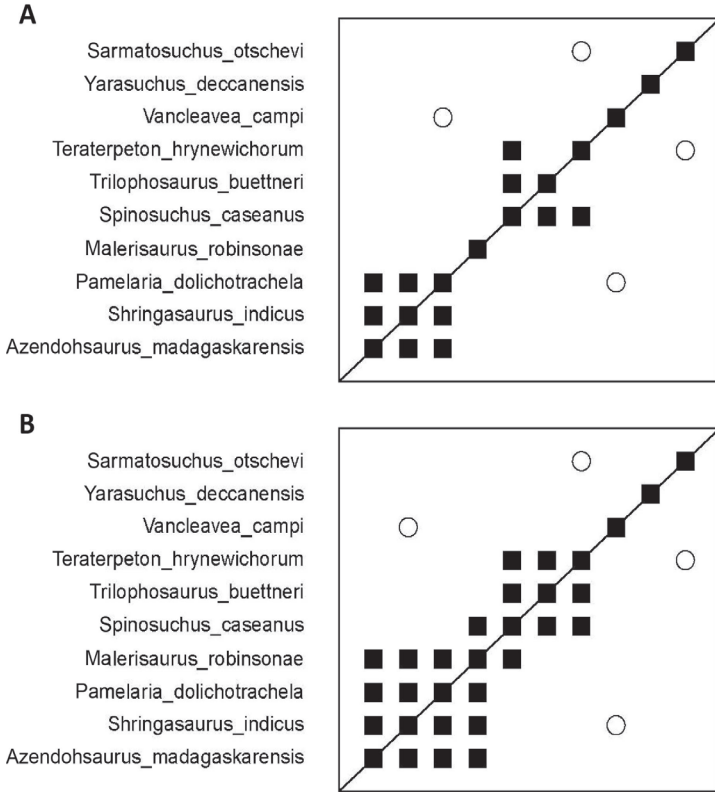**Figure 6.** Fuzzy analysis (FANNY) of the "Protorosauria" subset dataset in 2 groups

Figure 7. Baraminic distance correlation (BDC) results for the Allokotosauria subset dataset analysis using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.

rhynchosaurids, one group includes the outgroup, and the final group includes the "basal" rhynchosaurs. The rhynchosaurid taxa share significant positive correlation. There is negative correlation separating the rhynchosaurids from the outgroup, but there are only instances of negative correlation between the rhynchosaurids and *Mesosuchus* among the "basal" rhynchosaurs.

The Spearman BDC plot for the same taxa (Figure 11D) similarly shows three blocks of positive correlation with negative correlation surrounding the two rhynchosaurid blocks but with no instances of positive or negative correlation between those two blocks. However, two of the blocks this time are made of rhynchosaurid taxa: 1) Hyperodapedontinae and 2) the rest of the rhynchosaurids. The final block of positive correlation consists of the "basal" rhynchosaurs and the outgroup.

The MDS results for the rhynchosaur subset excluding the poorly known taxa give deeper insight into the clustering patterns among these species (Figure 12B). The outgroup is again separated from the other groups, but the "basal rhynchosaurs" do not really cluster with
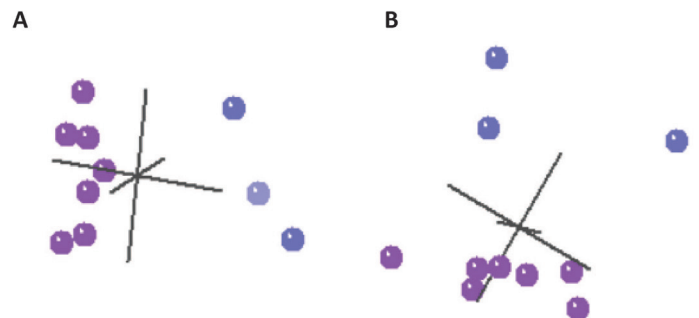
Figure 8. 3D multidimensional scaling (MDS) results for the Allokotosauria subset dataset analysis in two views: A and B. Blue represents outgroup taxa and purple represents Allokotosauria.

the outgroup or with the rhynchosaurids. The hyperodapedontines and the non-hyperodapedontine rhynchosaurids show more distinction between each other in these results than they did when *Noteosuchus, Langeronyx,* and *Eohyosaurus* were included.

The PAM result with the highest average silhouette value (0.48) is at four groups (Figure 13B): 1) non-hyperodapedontine rhynchosaurids (red), 2) outgroup (green), 3) "basal" rhynchosaurs (blue), and 4) Hyperodapedontinae (yellow). Each of these four groups in PAM have medium to high silhouette widths. The non-hyperodapedontine rhynchosaurs have an average width of 0.42, the hyperodapedontines 0.48, the "basal" rhynchosaurs 0.53, and the outgroup 0.55.

When the three problematic taxa were removed, the FANNY result

with the highest average silhouette width (0.43) is at three groups. The three groups are the "basal" rhynchosaurs and outgroup (green), the hyperodapedontines (blue), and the non-hyperodapedontine rhynchosaurids (red).

E. Proterosuchidae, Erythrosuchidae, and Euparkeriidae

The Pearson BDC of the Proterosuchidae and Erythrosuchidae subset (Figure 15A) shows two blocks of positive correlation: Erythrosuchidae and Proterosuchidae, although the Panchet proterosuchid and *Fugusuchus hejiapanensis* only shared positive correlation with *Proterosuchus fergusi*. *Garjainia madiba* only shared positive correlation with *Garjainia prima* in the erythrosuchid block. *Sarmatosuchus otschevi* did not share correlation of any kind with any other
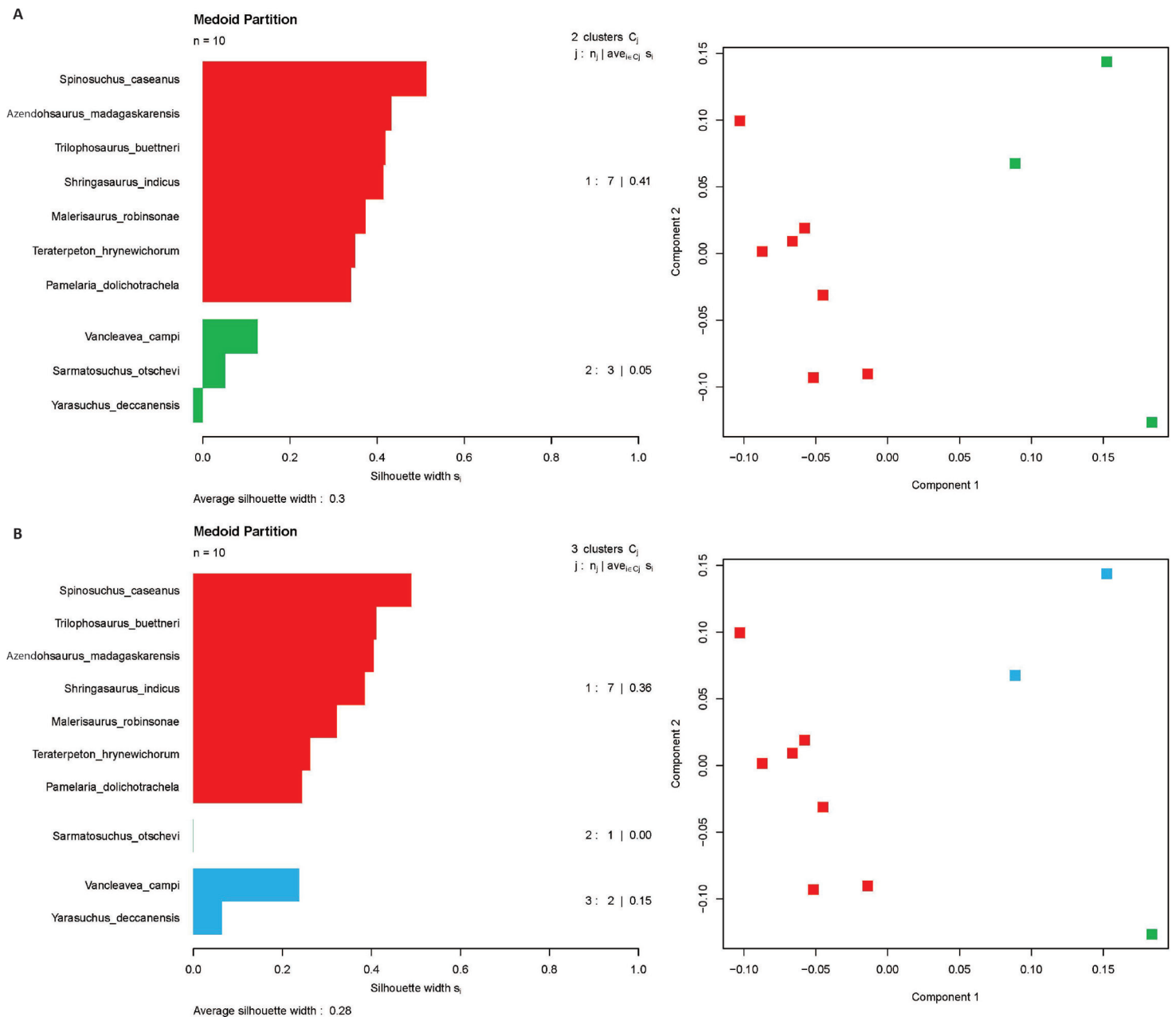
Figure 9. Partitions around medoids (PAM) analysis of the Allokotosauria subset dataset in: A) 2 groups and B) 3 groups. The two groups correspond to Allokotosauria (red) and outgroup (green). The three groups correspond to Allokotosauria (red), *Sarmatosuchus* (green), and other outgroup taxa (blue).

taxon in the analysis. In the Spearman BDC (Figure 15B), there was a clear division between the two groups Erythrosuchidae and Proterosuchidae, but *Sarmatosuchus ostchevi* again correlated with only itself. The two blocks of positive correlation shared only negative correlation or no correlation between them. When we added the euparkeriid *Euparkeria capensis* and the possible euparkeriid *Osmolskina czatkowicensis,* the two blocks were still clear (Supplemental Figure 4). *Euparkeria* did not share positive correlation with any other taxon, but it shared negative correlation with most erythrosuchids and the Panchet proterosuchid. Surprisingly, *Osmolskina* showed positive correlation with some erythrosuchids and not *Euparkeria*.

In the MDS results (Figure 16), both groups were clearly separated, with *Sarmatosuchus ostchevi* grouping with the proterosuchids. We also ran it with *Euparkeria capensis* and *Osmolskina czatkoviensis,* which made the proterosuchid and erythrosuchid clustered less clear (Supplemental Figure 5). As with the BDC results (Supplemental Figure 4), *Euparkeria* did not cluster with any other taxa, whereas *Osmolskina* clusters with the erythrosuchids.

When we put the data through PAM (Figure 17), the highest average silhouette values were at two groups (0.41) and three groups (0.33). At two groups (Figure 17A), proterosuchids (red) and erythrosuchids
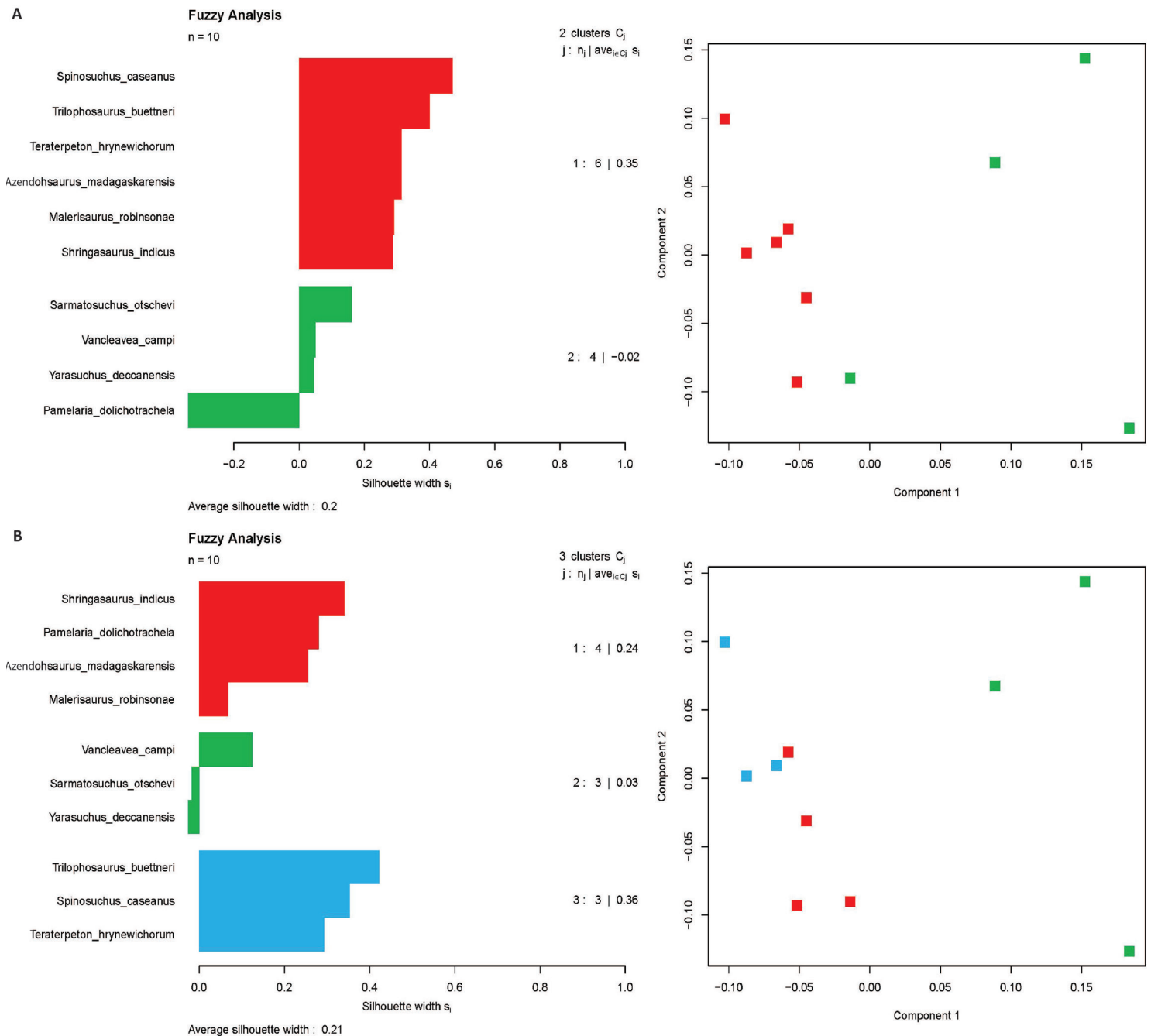
Figure 10. Fuzzy analysis (FANNY) of the Allokotosauria subset dataset in: A) 2 groups and B) 3 groups. The two groups correspond to Allokotosauria (red) and outgroup + *Pamelaria* (green). The three groups correspond to Azendohsauridae (red), outgroup (green), and Trilophosauridae (blue).
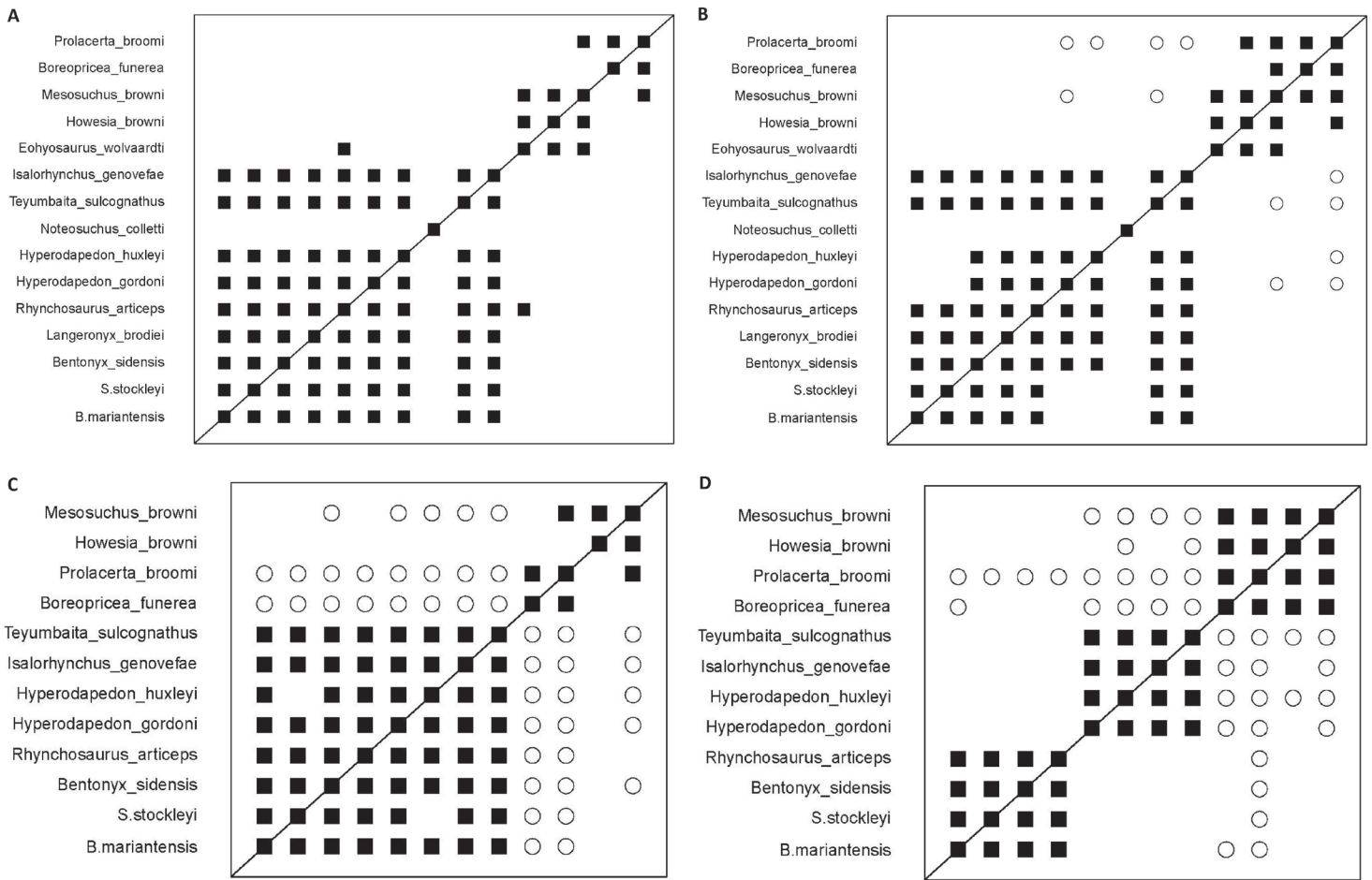
Figure 11. Baraminic distance correlation (BDC) results for the Rhynchosauria subset dataset. Four plots were generated: A) Pearson BDC plot at 167 characters including problematic taxa (*Noteosuchus, Langeronyx, and Eohyosaurus)*, B) Spearman BDC plot at 167 characters including problematic taxa, C) Pearson BDC plot at 429 characters excluding problematic taxa, and D) Spearman BDC plot at 429 characters excluding problematic taxa. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation. *Stenaulorhynchus stockleyi* and *Brasinorhynchus mariantensis* shortened to *S. stockleyi* and *B. mariantensis.*

(green) were separated with *Sarmatosuchus* in the proterosuchid group, although with a negative silhouette value. At three groups (Figure 17B), the proterosuchids and erythrosuchids were separated, but three proterosuchids were separated into a third group: *Fugusuchus, Sarmatosuchus,* and the Panchet proterosuchid. While those species were grouped together, *Sarmatosuchus* and the Panchet proterosuchid had negative silhouette widths.

When we ran the subset dataset through FANNY (Figure 18), the highest average silhouette value was at two groups (0.43), followed by three groups (0.32). At two groups (Figure 18A), all of the species in both groups had silhouette values over 0.2, except for *Sarmatosuchus*. *Sarmatosuchus* was also grouped with erythrosuchids, instead of proterosuchids. At three groups (Figure 18B), four species grouped together (shown in blue: *Fugusuchus,* the Panchet proterosuchid*, Garjainia mandiba,* and *Sarmatosuchus.*) *Garjania* and the Panchet proterosuchid had negative silhouette values, and most of the erythrosuchid group had silhouette values less than 0.4.

F. Proterochampsia

The data collected from Kellner et al. (2022) were analyzed for proterochampsian relationships by creating two subset datasets of pro-

terochampsian taxa. The first one included an outgroup (*Euparkeria capensis* and *Osmolskina czatkowicensis* (based on multiple specimens and not just the holotype), resulting in the inclusion of 17 taxa and 153 of the 823 possible characters. The second group excluded the outgroup, making the total taxa 15 and the total characters used 214.

The Pearson BDC results that included the outgroup taxa (Figure 19A) show four blocks of positive correlation (Proterochampsidae, Doswelliidae, Erpetosuchidae, and the outgroup), as well as two taxa that do not share positive correlation with any other taxa (*Vancleavea* and *Litorosuchus*). The only instances of negative correlation are between the erpetosuchid block and *Vancleavea* and *Litorosuchus*, as well as one instance of negative correlation between *Euparkeria* and *Doswellia*. The Spearman BDC results that included the outgroup taxa (Figure 19B) show three main blocks of positive correlation. The Proterochampsidae block shows positive correlation amongst its members and one example of positive correlation between *Proterochampsa barrionuevoi* and *Vancleavea campi*, but no negative correlation with the other taxa except between *Pr. barrionuevoi* and the outgroup taxa. The species within Doswelliidae (*sensu* Ezcurra 2016) were much more broken up. One block of positive correlation con-

tained the three erpetosuchid taxa, *Erpetosuchus granti, Pagosvenator candelariensis*, and *Tarjadia ruthae*, which were positively correlated with the outgroup taxa. *Vancleavea campi* positively correlated with *Litorosuchus somnii* (as well as the aforementioned *Proterochampsa barrionuevoi*). The final two doswelliids did not positively correlate with any other taxa in the analysis, although *Doswellia kaltenbachi* did negatively correlate with the outgroup taxa. *Vancleavea* and *Litorosuchus* also shared negative correlation with the erpetosuchids.

The MDS results including the outgroup taxa (Figure 20A) show similar clustering patterns to the BDC results. The outgroup taxa, which are colored pink, are relatively distinct from the other species. However, *Litorosuchus + Vancleavea* cluster together (purple) with an even farther distance from the rest of the proterochampsians. The erpetosuchids (in yellow) cluster together. *Doswellia kaltenbachi* (red) and *Jaxtasuchus salomoni* (black) do not cluster together and neither clusters with any of the other species. Each of these four previous clusters are approximately equal distances away from the proterochampsids (blue).
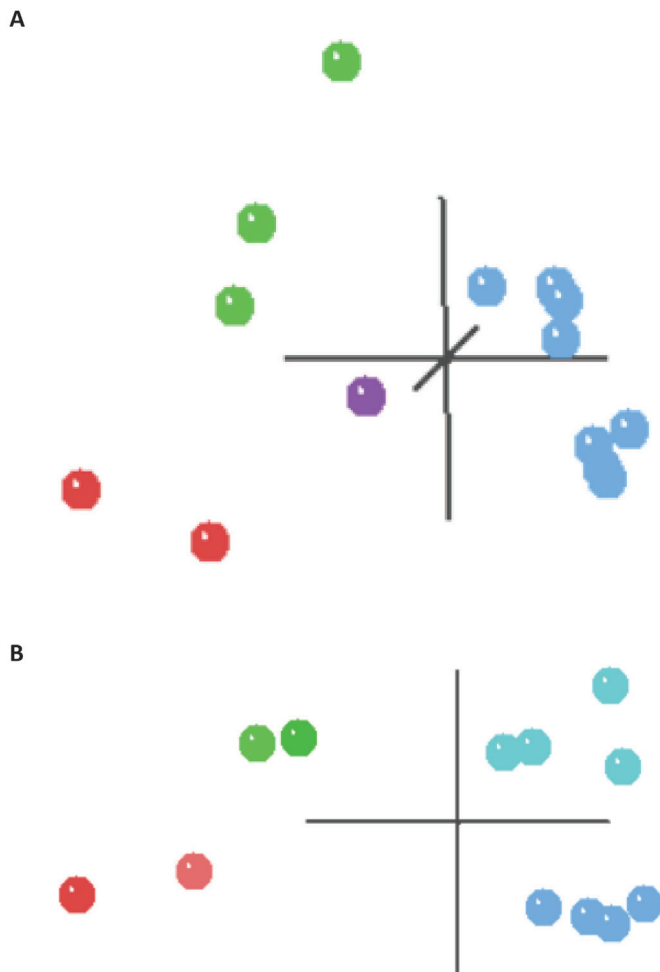
Figure 12. 3D multidimensional scaling (MDS) results for the Rhynchosauria subset dataset: A) MDS plot at 167 characters including problematic taxa. B) MDS plot at 429 characters excluding problematic taxa. Colors: Red - outgroup; green - "basal" rhynchosaurs; purple - *Noteosuchus*; blue - Hyperodapedontinae; light blue - non-hyperodapedontine Rhynchosauridae.

The PAM results (Figure 21A) group best when given groups of five with an average silhouette width of 0.32. *Vancleavea* (purple) is by itself, so it has a width of 0.0. *Pr. nodosa + Pr. barrionuevoi* group with *Doswellia + Jaxtasuchus* (green) and have a very small average silhouette width of 0.08, with *Pr. barrionuevoi* possessing a negative silhouette width. The outgroup taxa group with *Litorosuchus* (yellow) and have an average width of 0.21, although *Litorosuchus* has a value of nearly 0. The erpetosuchids (blue) have the highest average silhouette width at 0.62, with the proterochampsids (red) as next highest having an average width of 0.46.

The FANNY results (Figure 22A) also have the highest silhouette value (0.36) at five groups. *Pr. nodosa + Pr. barrionuevoi* group together with *Vancleavea* (purple). Because *Vancleavea* has little similarity to the other two taxa, the average silhouette width is at a low at 0.11. The outgroup and *Litorosuchus* (yellow) have an average silhouette width of 0.24. *Doswelliia + Jaxtasuchus* (green) have the next lowest width at 0.33. The proterochampsids (red) have a silhouette width of 0.44. The group with the highest average silhouette width are again the erpetosuchids (blue) with a width of 0.66.

Removing the outgroup and running the data through the same process again did not change much about the results. *Jaxtasuchus, Litorosuchus, Vancleavea,* and *Doswelliia* all showed no correlation with any other proterochampsian species in the Pearson BDC (Figure 19C). There was negative correlation between *Vancleavea* and a few of the other species and negative correlation between *Doswelliia* and the proterochampsid *Tropidosuchus*. Again, there were fewer instances of positive correlation between species within the Proterochampsidae block in Pearson versus Spearman (Figure 19D). The Spearman BDC recovered positive correlation between *Vancleavea + Litorosuchus*, same as when the outgroup was present. The Erpetosuchidae were a clear block of positive correlation in both Pearson and Spearman BDC plots.

The MDS results (Figure 20B) without the outgroup taxa were also similar to the plot with the outgroup. The proterochampsids clustered together, as did the erpetosuchids. The same four that were not showing correlation in the Pearson BDC were not clustering with any other species in the MDS and were instead standing almost equally separate from the protereochampsids.

These results from PAM (Figure 21B) are generally similar to the PAM results that included outgroup taxa (Figure 21A), but the average silhouette size is larger at 0.39. However, there are some notable differences. *Vancleavea* and *Litorosuchus* are grouped together (although with an average silhouette value of 0.08), and the two problematic proterochampsids in PAM/FANNY (*Pr. barrionuevoi* and *Pr. nodosa*) now form their own group together with an average silhouette value of 0.70.

Once the outgroup is removed and the resulting dataset is put into FANNY (with a suggestion of four groups), the results are essentially the same (Figure 22B). The average silhouette width is 0.34. *Vancleavea*, *Litorosuchus*, and the two *Proterochampsa* species are groupted together with an average silhouette value of 0.02.

G. Phytosauria

The Pearson BDC results for the Phytosauria subset (Figure 23A) show a large block of positive correlation containing all of the para-

suchids (true phytosaurs). The possible "basal" phytosaur *Diandon-gosuchus fuyuanensis* does not correlate with any other taxa in the analysis. The two outgroup taxa do not share any correlation with each other, and have many examples of shared negative correlation with the parasuchids.

Spearman BDC results for the Phytosauria subset (Figure 23B) reveal weaker positive correlations within Parasuchidae. There are two main blocks of positive correlation: "basal" phytosaurs (*Wannia, Parasuchus hislopi, Parasuchus (Paleorhinus) angustifrons, Ebrachosuchus neukami*, and *Paleorhinus sawini*) and "more derived" phytosaurs (*Smilosuchus, Redondasaurus, Machaeroprosopus pristinus, Angistorhinus talainti, Nicrosaurus kapffi*, and *Mystriosuchus planirostris*). *Paleorhinus sawini* positively correlates with

Nicrosaurus and *Angistorhinus*, linking the two blocks of positive correlation. Additionally, *Wannia* positively correlates with *Diandongosuchus*, which is itself positively correlated with the outgroup taxa.

The 3D MDS results (Figure 24) shows similar results. There is a gap in character space between *Lotosaurus adentus, Prestosuchus chiniquensis*, and *Diandongosuchus* (shown in red) and the tightly clustered parasuchids (shown in green). The parasuchid cluster is made of three smaller clusters: 1) *Wannia, Par. angustifrons, Par. hislopi, Ebrachosuchus*, and *Pal. sawini*. 2) *Angistorhinus, Nicrosaurus*, and *Smilosuchus*; and 3) *Machaeroprosopus, Redondasaurus*, and *Mystriosuchus*.

Two- and three-group models were used in the PAM analysis (Fig-
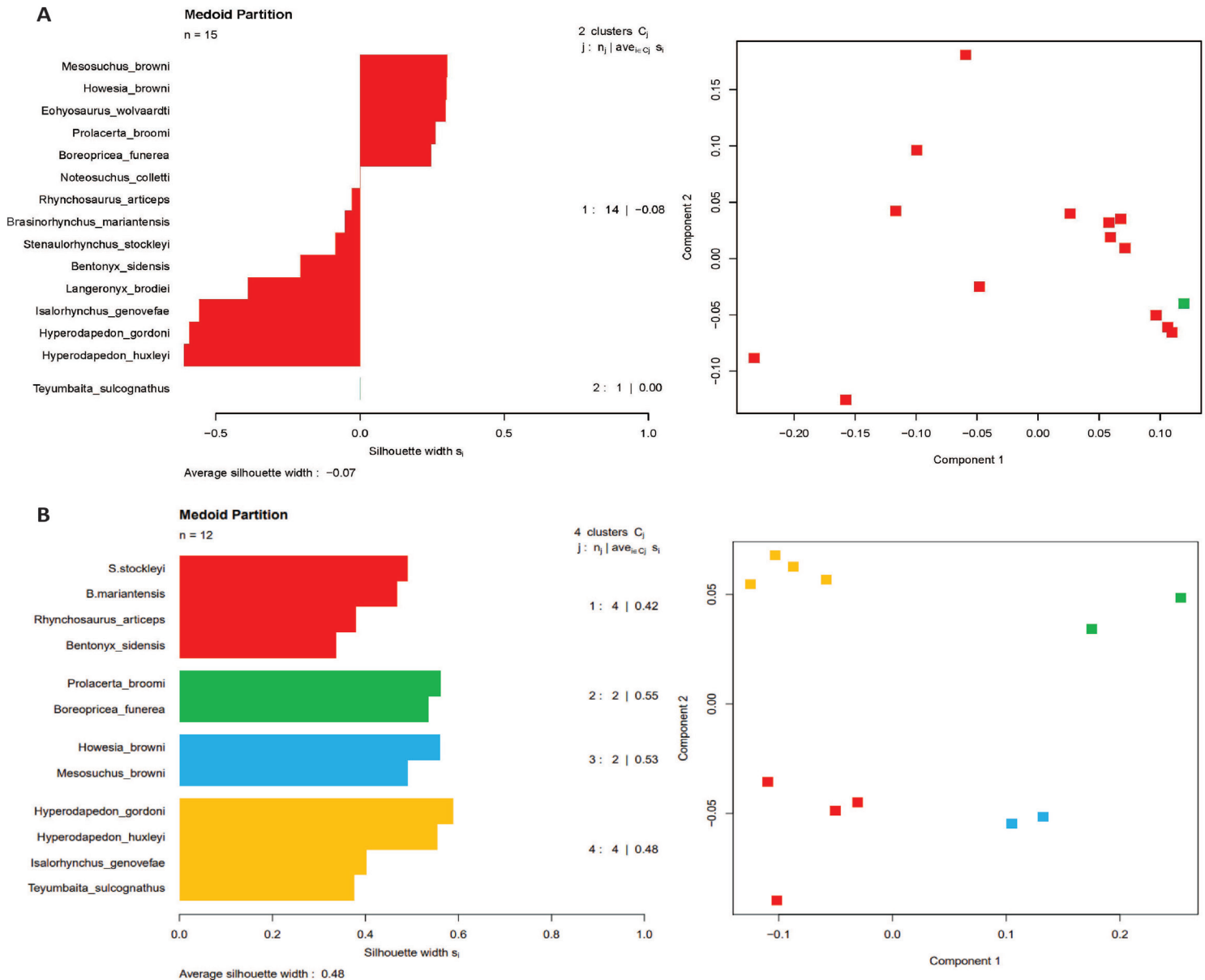
Figure 13. Partitions around medoids (PAM) analysis of the Rhynchosauria subset dataset: A) PAM Plot at four groups including problematic taxa, 4 groups and B) PAM Plot at four groups excluding problematic taxa.
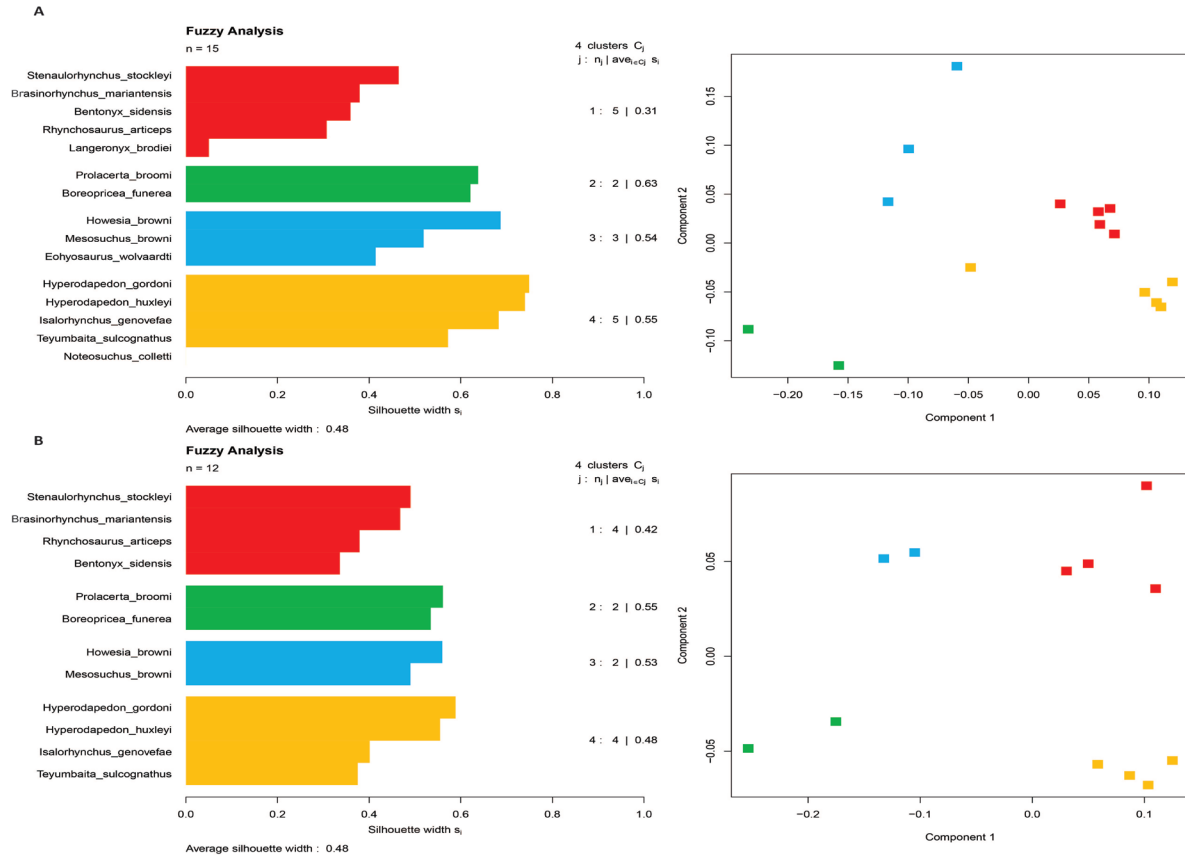
Figure 14: Fuzzy analysis (FANNY) of the Rhynchosauria subset dataset: A) FANNY analysis at four groups including problematic taxa. (b) FANNY analysis at four groups excluding problematic taxa.

ure 25) because they had the highest average silhouette values (0.51 and 0.45, respectively). In the PAM analysis for two groups (Figure 25A), all of the phytosaurs (including *Diandongosuchus*) are grouped together (red), whereas the two outgroup taxa are in green. In the PAM analysis for three groups (Figure 25B), *Diandongosuchus* was grouped with the parasuchids (red), although it has a negative silhouette value. *Lotosaurus* (green) and *Prestosuchus* (blue) were placed in their own separate groups.

In the FANNY analysis we ran the dataset in three, four, and five clusters (Figure 26). The average silhouette width for each analysis is as follows: three groups (0.26), four groups (0.21), and five groups (0.24). The FANNY analysis for three groups (Figure 26A) splits up the phytosaurs into two groups (red and blue), with the outgroup and *Diandongosuchus* forming their own group (green), although *Diandongosuchus* has a negative silhouette width. The FANNY analysis for four groups (Figure 26B) splits up the larger phytosaur group into two (red and yellow). The FANNY analysis for five groups (Figure 26C) places the outgroup taxon *Lotosaurus* in its own group, and puts together *Diandongosuchus* and *Prestosuchus* (although *Diandongosuchus* has a negative silhouette width). Additionally, *Pal. sawini* has a negative silhouette width in its phytosaur group (red).

H. Pseudosuchia

The Pearson and Spearman BDC results (Figure 27) for the Pseudosuchia subset analysis were uninformative except that they showed

Lotosaurus as very distinct, sharing no positive correlation with any other taxon. We suspected that evidence for discontinuity was masked by these results, given that Pseudosuchia is almost certainly made up of many created kinds. As such, we decided to split up the taxa according to the major division of Paracrocodylomorpha vs. non-paracrocodylomorph Pseudosuchia. As *Ticinosuchus* is difficult to classify and falls right between the two groups, we included it in both subset analyses.

I. Non-paracrocodylomorph Pseudosuchia

The Pearson and Spearman BDC results for the non-paracrocodylomorph pseudosuchian subset analysis are almost identical (Figure 28), both showing three blocks of positive correlation: Aetosauria (3 taxa), Ornithosuchidae (4 taxa), and Gracilisuchidae + *Nundasuchus* + *Ticinosuchus*. The Spearman results include *Parringtonia* with the gracilisuchid block of positive correlation (Figure 28B), whereas the Pearson BDC shows it on its own (Figure 28A). Both Pearson and Spearman BDC plots show negative correlation between Aetosauria and Ornithosuchidae.

The MDS results (Figure 29) agree well with the BDC plots, showing three different clusters: Aetosauria, Ornithosuchidae, and Gracilisuchidae. *Nundasuchus* clusters closely with the gracilisuchids in a single linear trajectory. *Parringtonia* and *Ticinosuchus* are closest to the Gracilisuchidae + *Nundasuchus* cluster, but they are in a different trajectory, one on each side of the gracilisuchid *Yonghesuchus*.

The PAM and FANNY results agree with the BDC and MDS results

(Figures 30 and 31). At three groups (average silhouette width: 0.49 (PAM); 0.49 (FANNY)), *Ticinosuchus*, *Parringtonia*, and *Nundasuchus* are grouped with the gracilisuchids, with *Ticinosuchus* and *Parringtonia* possessing silhouette values less than 0.2. Interestingly, *Nundasuchus* has a silhouette value higher than two gracilisuchids (~0.5). Changing PAM to four groups (average silhouette width = 0.47) simply separates out *Parringtonia* as its own group. However, changing FANNY to four groups (average silhouette width = 0.41) causes *Nundasuchus* and *Ticinosuchus* to group together and *Parringtonia* to group with the gracilisuchids making a group that has very low silhouette values (<0.3) with the gracilisuchid *Turfanosuchus* possessing a negative silhouette value.

J. Paracrocodylomorpha

The Pearson and Spearman BDC plots (Figure 32) for the Paracrocodylomorpha subset analysis show *Lotosaurus* separate from all other taxa by either negative correlation or no correlation. The poposauroids *Arizonasaurus*, *Xilousuchus*, and *Qianosuchus* share positive correlation with each other and not with any other taxon in the Spearman BDC (Figure 32B), although in the Pearson BDC *Qianosuchus* shares positive correlation with *Ticinosuchus* and *Decuriasuchus* (Figure 32A). The remaining taxa form a block of positive correlation with more positive correlation connections in the Pearson BDC

than the Spearman BDC.

The MDS results for this subset (Figure 33) agree with the BDC plots in the position of *Lotosaurus*: far from everything. The three other poposauroid taxa form a cluster separate from the remaining paracrocodylomorphs.

PAM results (Figure 34) were analyzed with two, three, and four groups (average silhouette widths: 0.29, 0.26, 0.26, respectively). Two groups clustered *Lotosaurus*, *Arizonasaurus*, and *Xilousuchus* together, although *Xilousuchus* had a negative silhouette value. The rest of the taxa fell into the other cluster with *Qianosuchus* possessing a silhouette value of less than 0.2. Three groups seemed to agree well with the BDC results: *Lotosaurus* by itself, the three other poposauroids, and the rest of the paracrocodylomorphs. Four groups resulted in the same pattern except that *Prestosuchus nyassicus* was pulled out of the larger group, surprisingly separated from *Prestosuchus chiniquensis*.

We also analyzed the dataset with FANNY (Figure 35) at two, three, and four groups (average silhouette widths: 0.26, 0.13, 0.23, respectively). Two groups put all of the poposauroids (including *Lotosaurus*) together, although *Qianosuchus* had a negative silhouette value. Strangely, three groups retained this poposauroid group and instead split up the remaining taxa into two groups: 1) *Prestosuchus chiniquensis* + *Batrachotomus* + *Decuriasuchus* and 2) *Prestosuchus nyassicus* + *Mandasuchus* + *Ticinosuchus*. Both *Mandasuchus* and *Ticinosuchus* had negative silhouette values. It was only at four groups that *Lotosaurus* finally separated out as its own group. The rest of the groups remained the same, although the silhouette values for the poposauroid group increased substantially.

K. Avemetatarsalia

The BDC results for the Avemetatarsalia subset analysis for both Pearson and Spearman correlations showed two groups of positive correlation: Pterosauromorpha and Dinosauromorpha + Aphanosauria (Figure 36). The Spearman results revealed no instances of shared positive correlation between the two blocks, whereas the Pearson BDC shows the pterosaurs *Preondactylus* and *Cacibupteryx* sharing positive correlation with several dinosaur taxa. Additionally, the lagerpetids *Lagerpeton* and *Ixalerpeton* are only positively correlated with one pterosaur (*Seazzadactylus*), whereas the lagerpetid *Dromomeron* shares positive correlation with both *Lagerpeton* and
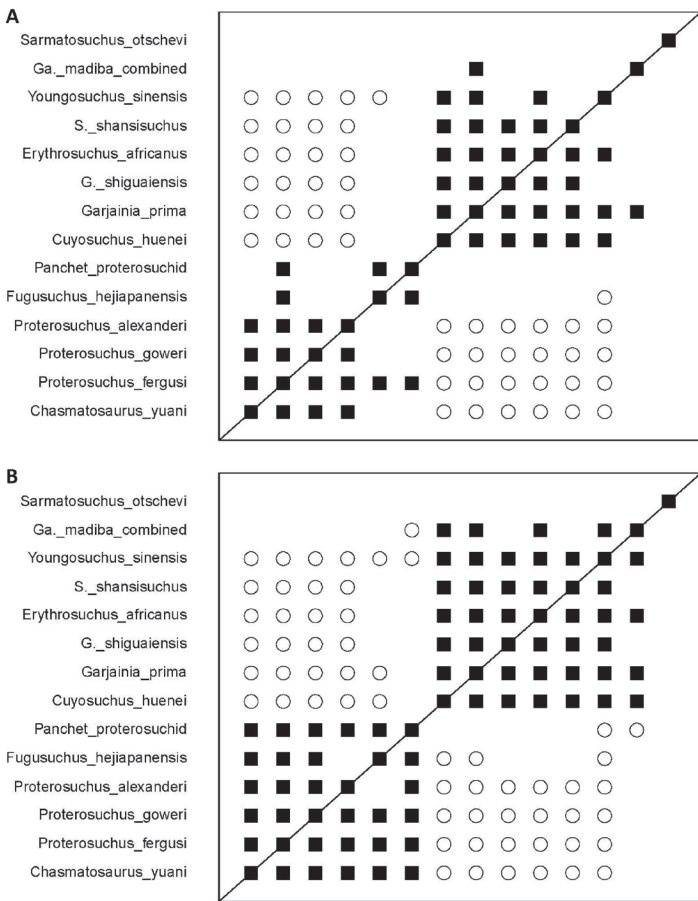
Figure 15. Baraminic distance correlation (BDC) results for the Proterosuchidae and Erythrosuchidae subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
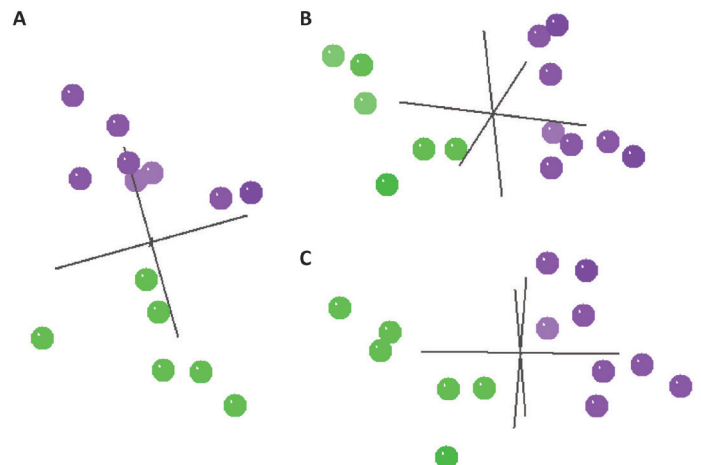
Figure 16. 3D multidimensional scaling (MDS) results for the Proterosuchidae and Erythrosuchidae subset dataset in two views: A and B. Erythrosuchids are represented by green and proterosuchids by purple.

*Ixalerpeton* and with many pterosaurs.

As expected with a dataset containing taxa from multiple created kinds, the MDS results are quite confusing (Figure 37). The pterosaurs are one side, not mixed with the dinosauromorphs and *Teleocrater*, but there is not as clear a gap in character space between the Pterosauromorpha and Dinosauromorpha as one might predict from the BDC results. The aphanosaur *Yarasuchus* and the lagerpetid *Lagerpeton* do not cluster with any other taxa.

We determined to split the avemetatarsalian subset into three subset analyses: 1) Dinosauromorpha (Dinosauria + Silesauridae + *Lagosuchus*), 2) Pterosauromorpha (Pterosauria + Lagerpetidae), and 3) "basal" Avemetatarsalia (Aphanosauria + Lagerpetidae + Silesauridae + *Lagosuchus*).

L. Dinosauromorpha

Both the Pearson and Spearman BDC plots for the dinosauromorph subset analysis revealed three groups of positive correlation: Ornithischia, Saurischia, and Silesauridae + *Lagosuchus* (Figure 38). The Spearman BDC plot (Figure 38B) did show positive correlation linking the ornithischian *Lesothosaurus* to two theropods: *Coelophysis* and *Megapnosaurus*. The Pearson BDC plot (Figure 38A) had the silesaurid *Silesaurus* sharing positive correlation only with the silesaurid *Asilisaurus*, and there were fewer instances of shared positive correlation within Saurischia. The MDS results for the dinosauromorpha subset match the BDC results perfectly with three easily
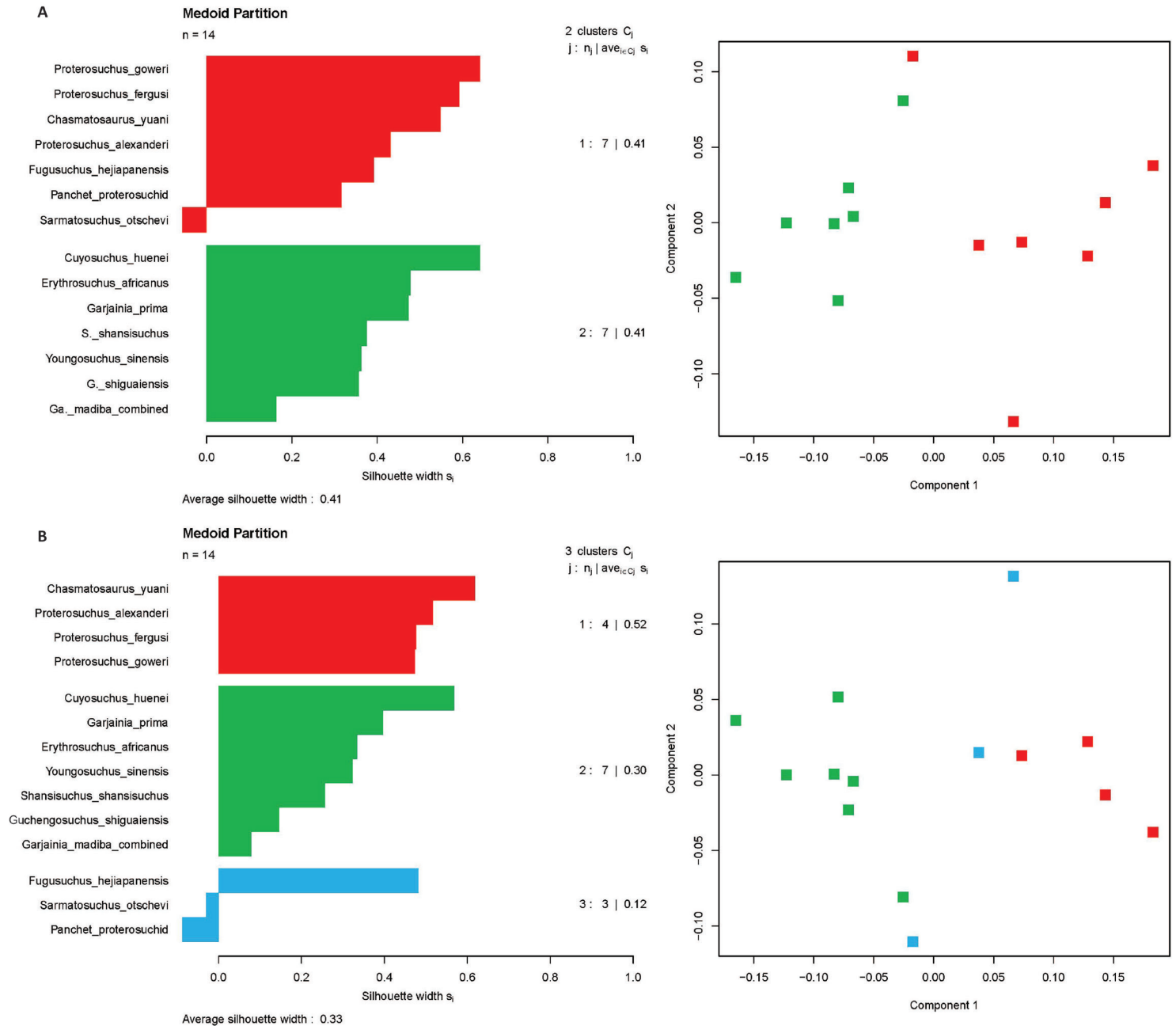
Figure 17. Partitions around medoids (PAM) analysis of the Proterosuchidae and Erythrosuchidae subset dataset in: A) two groups and B) three groups. With two groups, red is Proterosuchidae + *Sarmatosuchus* and green is Erythrosuchidae. With three groups, red is some proterosuchids, green is Erythrosuchidae, and blue is other proterosuchids + *Sarmatosuchus*.

recognizable clusters of taxa separated from each other: Ornithischia, Saurischia, and Silesauridae + *Lagosuchus* (Figure 39).

Interestingly, the highest average silhouette values were at two groups (0.33) and four groups (0.28) when using both PAM and FANNY to analyze this subset dataset (Figure 40). The two-group model split up the silesaurids + *Lagosuchus* from the rest of the taxa (Dinosauria). The four-group model retained the silesaurid + *Lagosuchus* group, but it then created three groups of dinosaurs: Ornithischia, Theropoda, and Sauropodomorpha. *Herrerasaurus* was included with the sauropodomorph group, but with a negative silhouette width.

M. Pterosauromorpha

Unfortunately, both the Pearson and Spearman BDC plots for the pterosauromorph subset analysis are essentially unintelligible (Figure 41). The MDS results (Figure 42) likely reveal one of the reasons why. The four lagerpetids and two pterosaurs (*Austriadraco* and *Peteinosaurus*) form vertices of an unusual polyhedron that encompasses the more tightly clustered Pterosauria within. The other issue with this subset analysis is that a meager 44 of the original 823 characters were used.
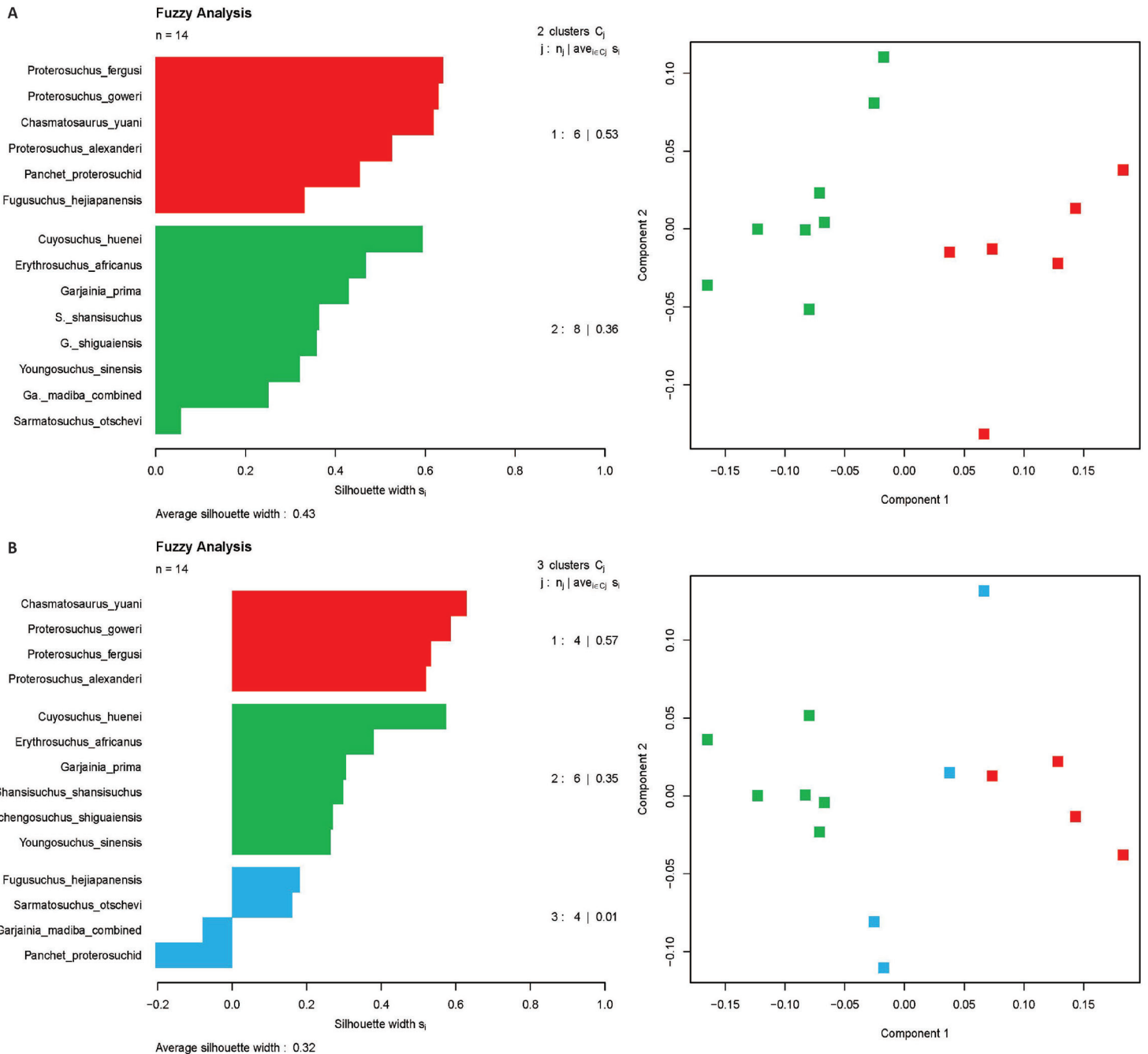
Figure 18. Fuzzy analysis (FANNY) of the Proterosuchidae and Erythrosuchidae subset dataset in: A) two groups and B) three groups. With two groups, red is Proterosuchidae and green is Erythrosuchidae + *Sarmatosuchus*. With three groups, red is some proterosuchids, green is Erythrosuchidae, and blue is some proterosuchids and *Sarmatosuchus*.
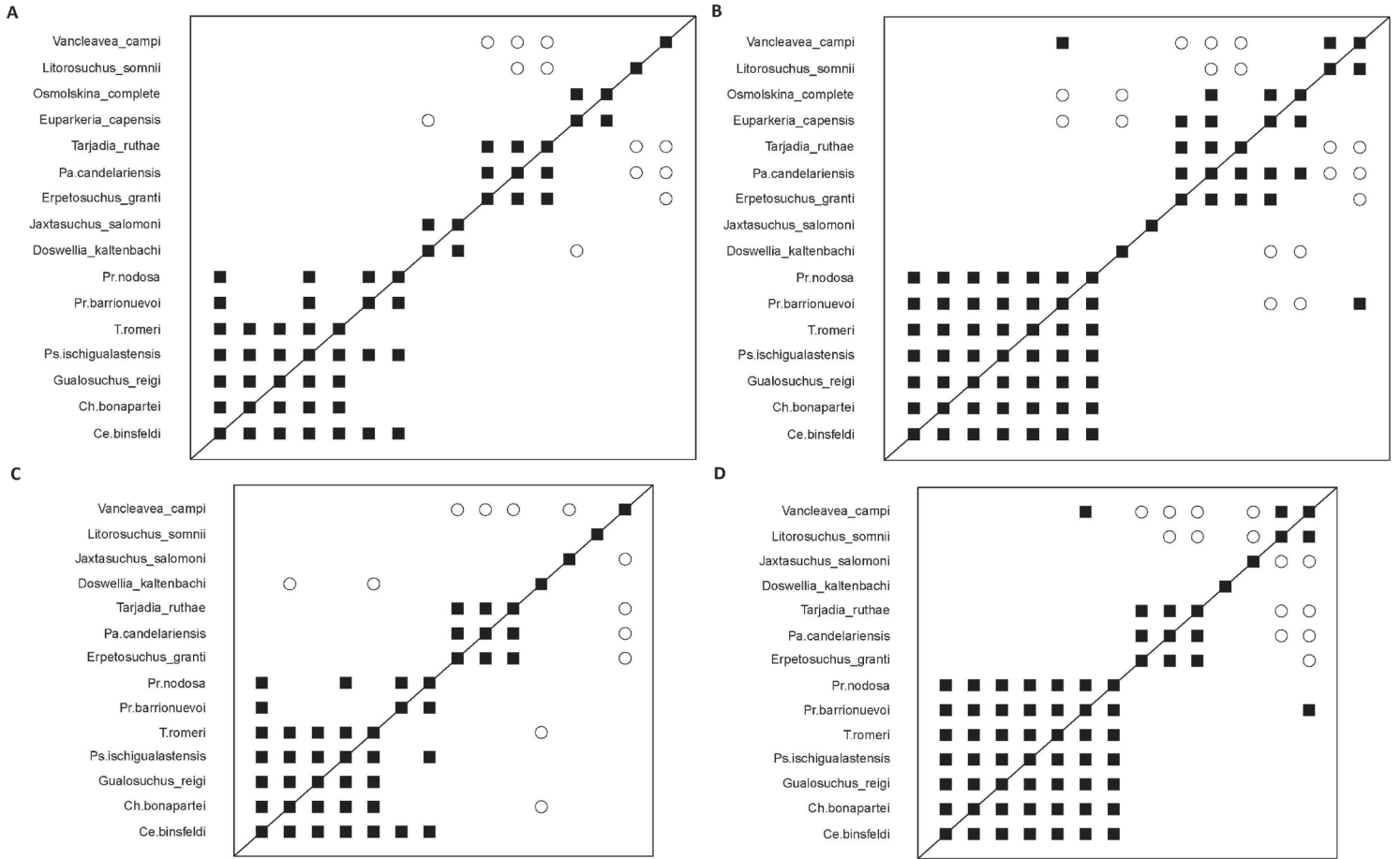
Figure 19. Baraminic distance correlation (BDC) results for the Proterochampsia subset dataset. Four plots were generated: A) Pearson BDC plot at 191 characters including the outgroup, B) Spearman BDC plot at 191 characters including the outgroup, C) Pearson BDC plot at 214 characters excluding the outgroup, and D) Spearman BDC plot at 214 characters excluding the outgroup.
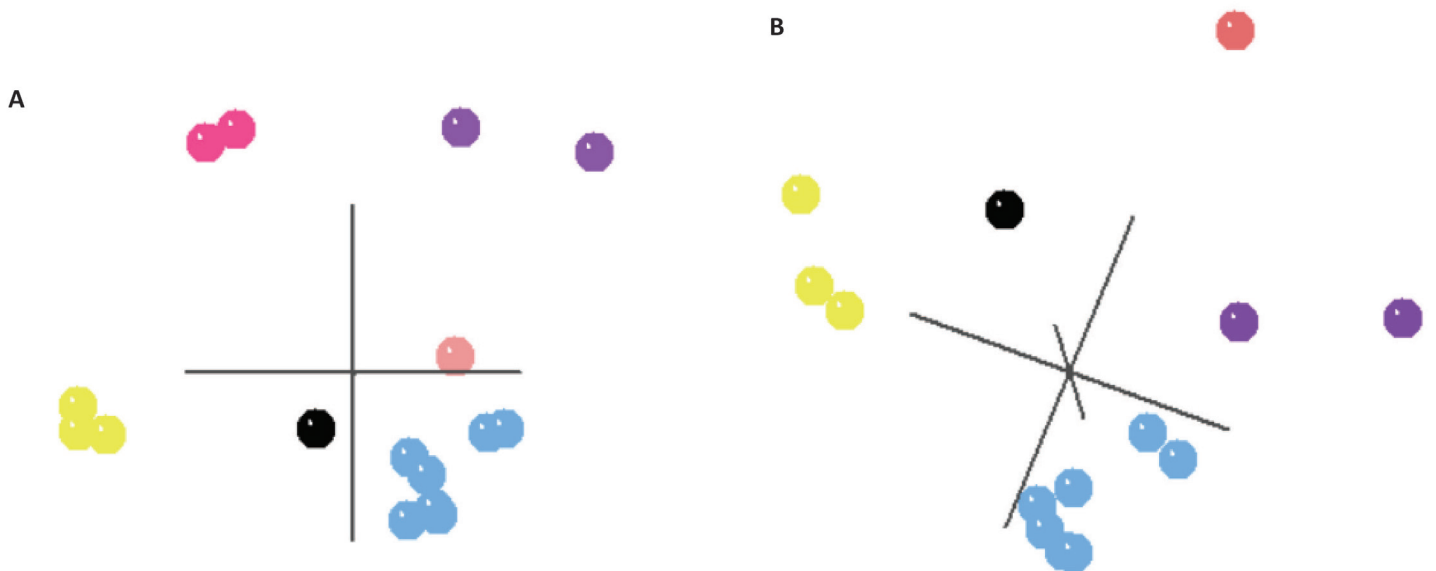
Figure 20. 3D multidimensional scaling (MDS) results for the Proterochampsia subset dataset. Two plots were generated: A) MDS plot at 191 characters including outgroup and B) MDS plot at 214 characters excluding outgroup. Colors: Pink - outgroup; purple - *Vancleavea + Litorosuchus*; yellow - Erpetosuchidae; blue - Proterochampsidae; red - *Doswellia*; black - *Jaxtasuchus*.

In order to see if we could detect discontinuity within these taxa (which is reasonable given that some of them have wings, whereas others do not), we determined to increase the taxic relevance cutoff from 0.20 to 0.29 to run it again. Raising the cutoff increased the number of included characters from 44 to 104, but it resulted in the exclusion of four taxa: the lagerpetid *Dromomeron* and three pterosaurs (*Caelestiventus*, *Cacibupteryx*, and *Austriadraco*). Thankfully, removal of these taxa does not result in the loss of a particular group (e.g., lagerpetids and dimorphodontids are still represented).

The 0.29 Pterosauromorpha analysis BDC results did show actual blocks of positive correlation, although there were few instances of negative correlation (Figure 43). The Spearman BDC plot shows more instances of positive correlation than the Pearson BDC plot. As

a result, three blocks of positive correlation are present on the Spearman plot: 1) Lagerpetidae, 2) Eudimorphodontoidea, and 3) the rest of the pterosaurs (Figure 43B). The Pearson BDC also showed three blocks of positive correlation composed of the same taxa, but the pterosaurs *Rhamphorhynchus* and *Eudimorphodon* and the likely lagerpetid *Scleromochlus* showed no instances of shared positive correlation with any other taxa in the analysis (Figure 43A).

The MDS results for the 0.29 Pterosauromorpha subset analysis show a clear separation between the three lagerpetids and the pterosaur taxa (Figure 44). The lagerpetids form a trajectory in character space with *Scleromochlus* on the end closest to the pterosaurs and *Lagerpeton* on the other end. There are two tight clusters of pterosaur taxa. One contains *Austriadactylus*, *Preondactylus*, and
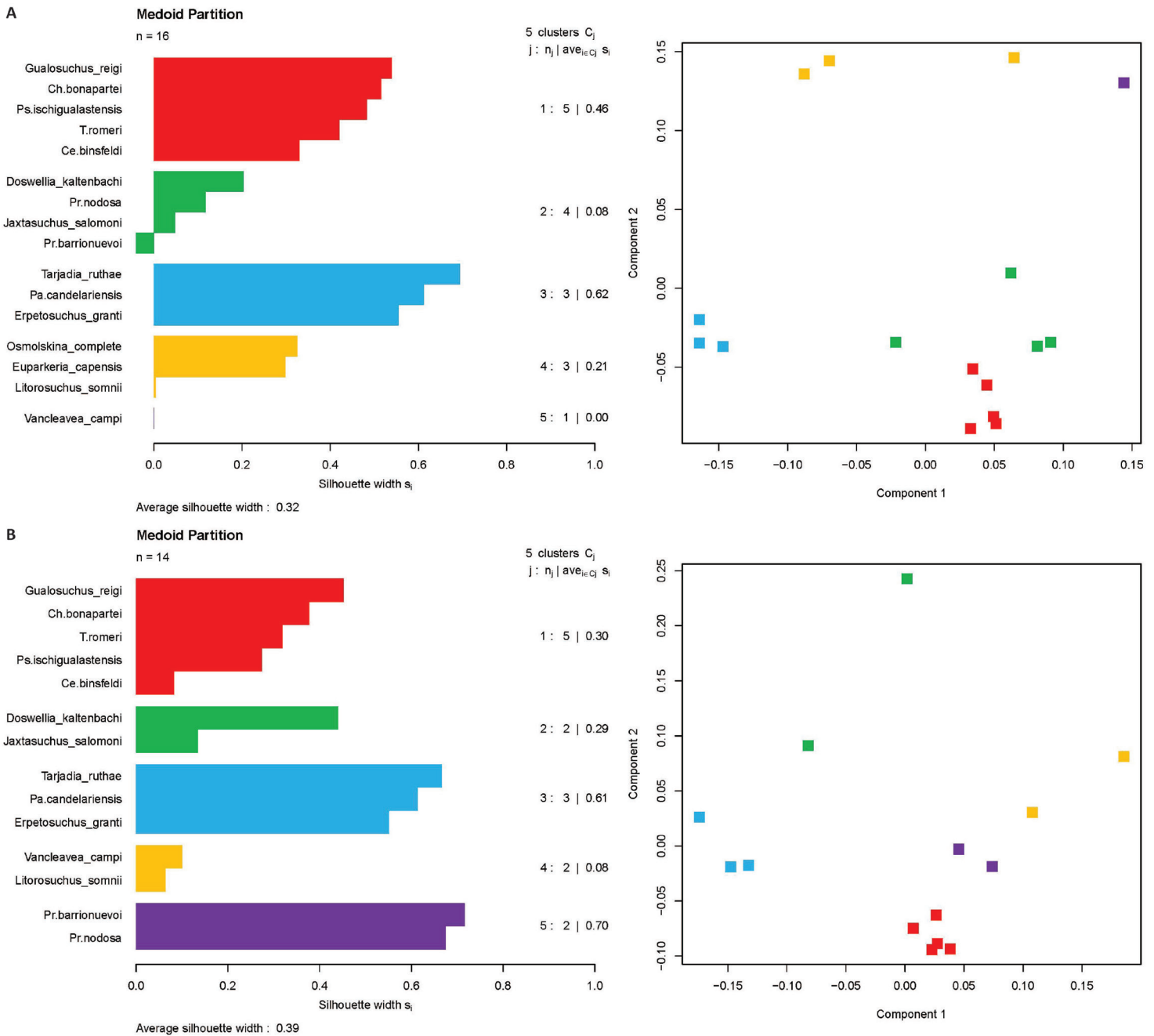
Figure 21. Partitions around medoids (PAM) analysis of the Proterochampsia subset dataset: A) including outgroup at five groups and B) no outgroup at five groups.

Dimorphodon. The other contains *Carniadactylus*, *Eudimorphodon*, and *Seazzadactylus*. *Rhamphorhynchus* is roughly equidistant to both groups, whereas *Peteinosaurus* is closest to the first group and *Raeticodactylus* is far from all of the other taxa. As such, the MDS matches the BDC results in general pattern (i.e., lagerpetids separate from pterosaurs), but some of the positions of pterosaur taxa in MDS are surprising (e.g., *Raeticodactylus*).

The PAM results (Figure 45) were all relatively close in average silhouette width regardless of which model we ran: two groups (0.33), three groups (0.32), four groups (0.31), or five groups (0.34). The two-group model separated the lagerpetids from the pterosaurs, although *Scleromochlus* grouped with the pterosaurs with a silhouette

width of -0.2. The three-group model, rather than separating *Scleromochlus* from the pterosaurs, split up the pterosaurs into Eudimorphodontoidea (green) and the rest of the pterosaurs (red). At four groups, *Rhamphorhynchus* was set apart as its own group. Finally, the five-group model recognized Lagerpetidae (blue), Eudimorphodontoidea (green), *Dimorphodon* + "basal" pterosaurs (red), *Rhamphorhynchus* (yellow), and *Scleromochlus* (purple).

By contrast, the FANNY results (Figure 46) noticeably differed in average silhouette values: two groups (0.16), three groups (0.31), four groups (0.33), and five groups (0.25). Concerning the two highest values, the three-group model recognized a non-pterosaur group, a Eudimorphodontoidea group (including *Rhamphorhynchus*
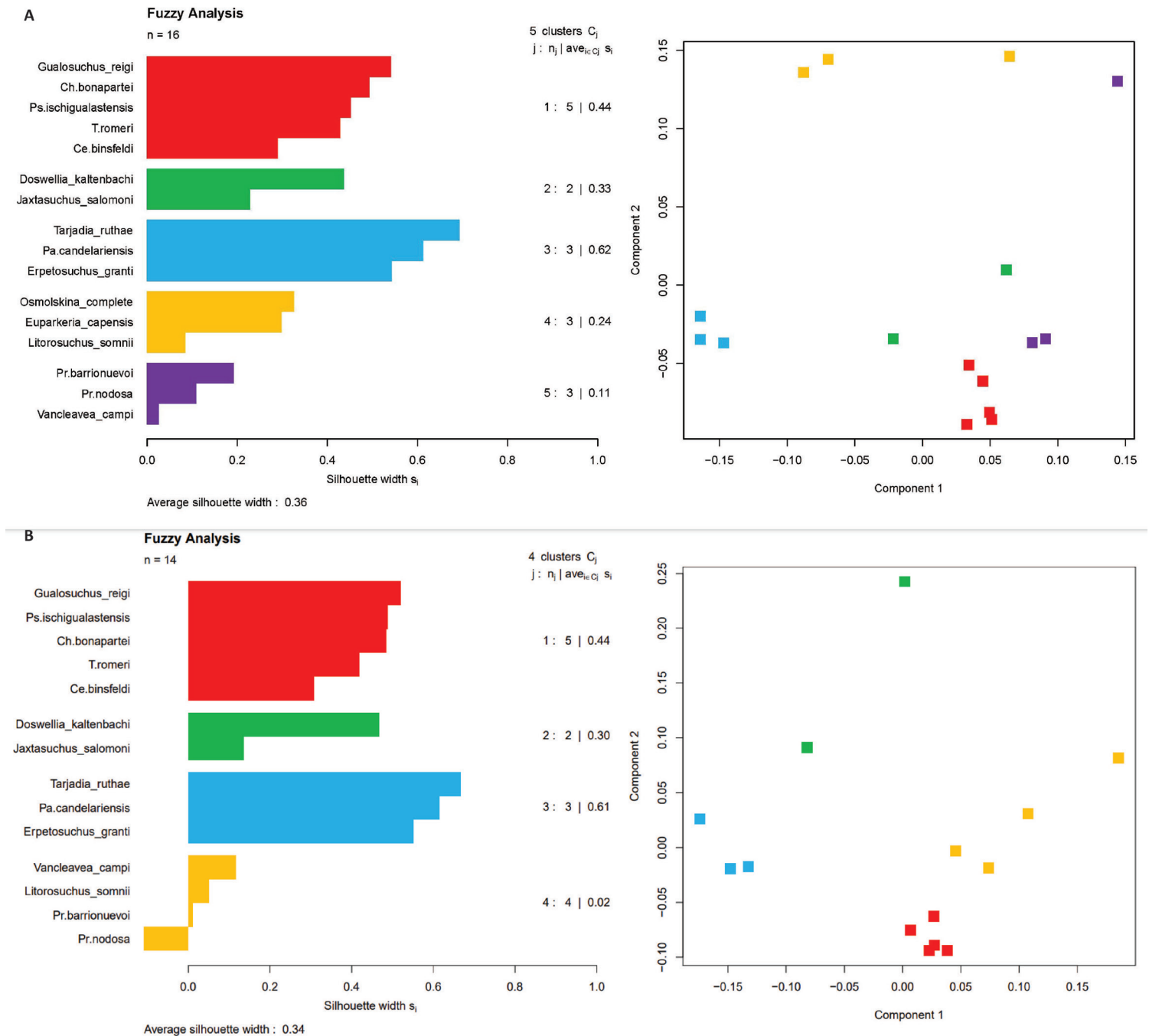
Figure 22. Proterochampsia FANNY Silhouette Plot A) including outgroup at five groups B) no outgroup at four groups.

with a negative silhouette value), and a group with the rest of the pterosaurs; whereas the four-group model made a new group that contained *Rhamphorhynchus*, *Dimorphodon*, *Eudimorphodon*, and *Scleromochlus*, all with negative silhouette values.

N. "Basal" Avemetatarsalia

The Spearman and Pearson BDC plots for the "basal" avemetatarsalian subset analyses were almost identical, each containing three blocks of positive correlation: 1) Silesauridae + *Lagosuchus*, 2) Aphanosauria, and 3) Lagerpetidae (Figure 47). The likely lagerpetid *Scleromochlus* does not correlate positively or negatively with any other taxon in the analysis. The MDS results (Figure 48) agree with the BDC plots in showing three clusters of taxa. Both *Scleromochlus* and *Dromomeron* are far removed from the other lagerpetids.

The PAM results (Figure 49) had the highest average silhouette values at three groups (0.43) or four groups (0.4). The three-group model recognized Silesauridae + *Lagosuchus*, Lagerpetidae + *Dromomeron*, and Aphanosauria + *Scleromochlus*; whereas the four-group model separated out *Dromomeron* into its own group.

The FANNY results (Figure 50) had essentially the same average silhouette values and taxic composition of groups at three groups (0.43) and four groups (0.4), but it had its largest average silhouette value of 0.46 at two groups. This two-group model places the silesaurids, aphanosaurs, and *Lagosuchus* in one group and the lagerpetids, *Dromomeron*, and *Scleromochlus* in the other group.

DISCUSSION

A. "Protorosauria"

There is strong evidence for continuity within and between Tanystropheidae and Dinocephalosauridae, and those groups are, in turn, surrounded by discontinuity as indicated in BDC, MDS, PAM, and FANNY. We do not find convincing evidence for continuity between *Protorosaurus* and these animals. As such, we suggest that Tanystropheidae + Dinocephalosauridae is a holobaramin, and "Protorosauria" is either apobaraminic or polybaraminic. Interestingly, *Jesairosaurus* showed positive correlation with the dinocephalosaurids in BDC and was united with them in the four-group PAM analysis. This matches a recent phylogenetic analysis that recovered it as the sister taxon to *Dinocephalosaurus* (De Oliveira et al. 2020).

Unfortunately, our analyses did not contain any sharovipterygids, which are recognized as close relatives in phylogenetic studies of "protorosaurs" (Spiekman et al. 2021). Future analyses focusing on "protorosaurs" as well as creatures that may or may not be archosauromorphs like drepanosauromorphs and weigeltisaurids would be of great help to understanding the baraminic relationships of these enigmatic creatures.

B. Allokotosauria

The BDC, MDS, PAM, and FANNY results all show strong evidence for discontinuity surrounding Allokotosauria, making it an apobaramin. However, the internal continuity of Allokotosauria is not so clear. The Spearman BDC shows evidence for continuity among the allokotosaurs, but the Pearson BDC splits the group up into its two families: Trilophosauridae and Azendohsauridae. The MDS results show little evidence of discontinuity between the two. FANNY is slightly better when viewing them as separate groups, but PAM has higher silhouette width values when they are united. Some of these issues may reflect the choice of outgroup, since some of the outgroup

taxa are drastically different from one another (e.g., *Vancleavea* vs. *Sarmatosuchus*). Given these results, we tentatively conclude that Allokotosauria may be a holobaramin made of two monobaramins: Azendohsauridae and Trilophosauridae. Future analyses more focused on this group and including more taxa may recognize each as its own holobaramin, however.

C. Rhynchosauria

With the inclusion of taxa with low taxic relevance scores, such as *Noteosuchus, Eohyosaurus,* and *Langeronyx*, the BDC and MDS results can be difficult to understand. When those three species are removed, three main groupings of continuity and discontinuity can be seen within the order Rhynchosauria. There is a possibility that, even though there is little known about these species, they provide a link between the rhynchosaurids and "basal" forms. However, we think the best interpretation is that the "basal" rhynchosaurs may be in a separate holobaramin than the rhynchosaurids, sometimes clustering and correlating more closely with the outgroup than the other rhynchosaurs. The subgroups Hyperodapedontinae and the non-hyperodapedontine rhynchosaurids may both be monobaramins within the holobaramin of Rhynchosauridae. Alternatively, it may be that Rhynchosauridae is an apobaramin made up of two holobaramins.
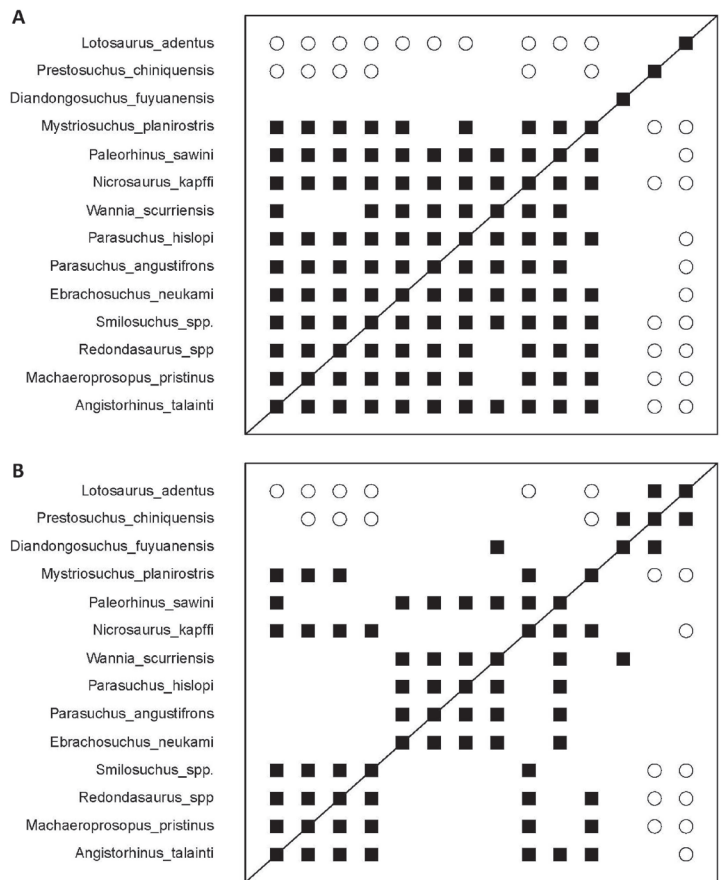
Figure 23. Baraminic distance correlation (BDC) results for the Phytosauria subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.

A

B **C**
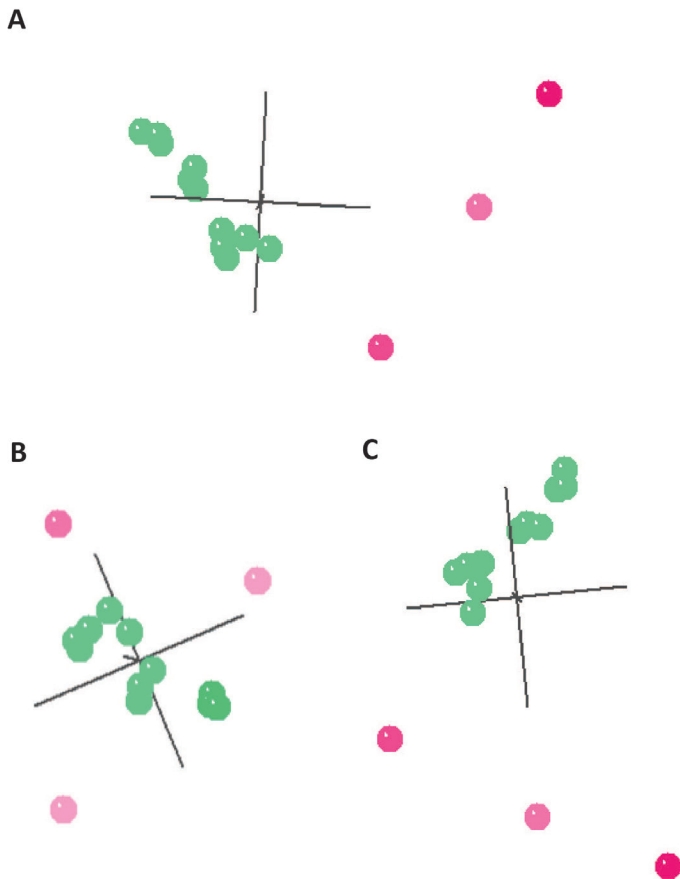
Figure 24: 3D multidimensional scaling (MDS) results for the Phytosauria subset dataset in three views: A, B, and C. Phytosaurs are represented by green and outgroup taxa (including *Diandongosuchus*) by red.

Because there is continuity between the groups in the Pearson BDC results, it would make sense that the two groups are part of a single holobaramin, but not all of the methods agree. PAM and FANNY also separate the two from each other and from the "basal" rhynchosaurs. Where *Noteosuchus, Eohyosaurus,* and *Langeronyx* fall into these baramins can be researched in greater detail once more fossils are discovered that provide us with greater detail of their morphology.

D. Proterosuchidae, Erythrosuchidae, and Euparkeriidae

Based on the BDC, MDS, PAM, and FANNY results, we believe that two groups best represent the taxa: Proterosuchidae and Erythrosuchidae. Each group shows strong evidence for internal continuity, and they are discontinuous from each other and from *Euparkeria*. *Sarmatosuchus* was a problematic taxon, showing correlation with neither group in Pearson and Spearman BDC results, although it clustered with the proterosuchids in MDS (yet at a distance). FANNY results placed *Sarmatosuchus* in with the erythrosuchids, whereas it grouped with proterosuchids in PAM. However, in both cases *Sarmatosuchus* had low silhouette values.

We conclude from these results that there are likely two holobaramins: Erythrosuchidae and Proterosuchidae. Alternatively, it is also possible that these are two monobaramins in one holobaramin with *Sarmatosuchus* linking the two, although the inclusion of *Euparkeria* and *Osmolskina* to the analysis (Supplemental Figures 4

and 5) did not remove the evidence of discontinuity between Proterosuchidae and Erythrosuchidae. Surprisingly, *Osmolskina* did not cluster with *Euparkeria* and instead grouped with the erythrosuchids. *Euparkeria* may be in its own holobaramin (since it shows strong evidence of discontinuity separating it from Proterosuchidae and Erythrosuchidae), although further research is needed since Euparkeriidae including *Osmolskina* appears to be polybaraminic according to this analysis.

E. Proterochampsia

Removing the outgroup from the proterochampsian dataset did not significantly alter the results. The position of Doswelliidae within the clade Proterochampsia is not universally acknowledged, so there is little surprise that there was essentially no evidence of positive correlation or close clustering in MDS between the families Proterochampsidae and Doswelliidae. The continuity within Proterochampsidae is not surprising and was expected. However, the evidence for incredible discontinuity between the species in Doswelliidae is something to note. From these data, it would appear that the families Proterochampsidae and Erpetosuchidae are each holobaramins. *Vancleavea + Litorosuchus* may also be a separate holobaramin. These, in turn, are separate from the "true" doswelliids (*Doswellia* and *Jaxtasuchus*) that show some evidence for continuity, although not in all analyses. Because of the uncertainty of where the "true" doswellids (*Doswelliia + Jaxtasuchus*) go, we cannot state with confidence the baraminic status of the Doswelliidae.

F. Phytosauria

As expected, the BDC, MDS, and PAM results all strongly indicate that Parasuchidae (traditional Phytosauria) has internal continuity and is surrounded by discontinuity. FANNY was an outlier among the methods, and we suspect that the results are not particularly informative. As such, we recognize Parasuchidae as a holobaramin. The position of *Diandongosuchus* is not so clear, as the Pearson BDC and MDS results show clear evidence of discontinuity, whereas the Spearman BDC and PAM results show weak evidence of continuity. Given that even the best evidence for continuity between *Diandongosuchus* and other phytosaurs is very weak, we propose that it is not part of the phytosaur (parasuchid) holobaramin.

G. Pseudosuchia

It is important to note—before diving into the particulars of this analysis—that pseudosuchian diversity and disparity are very poorly represented by this analysis. Only three of the twenty or so aetosaur genera were included, and the "stem aetosaur" *Revueltosaurus* was not included. The study lacks any shuvosaurids or poposaurids, resulting in a depleted Poposauroidea. A few "basal" loricatans are included, but not a single member of Crocodylomorpha. As such, these results should be interpreted with great caution.

A few things are very clear. Firstly, *Lotosaurus* is a very unique animal. This has already been recognized in the conventional literature, as evidenced by it being the only member of the family Lotosauridae (Zhang 1975). It is tempting to suggest at this stage that *Lotosaurus* (and therefore Lotosauridae) is a holobaramin, but no shuvosaurids or poposaurids were included. There is good evidence for continuity between the other poposauroids, and this may be evidence for continuity between Ctenosauriscidae and *Qilosuchus*, but once again, without more poposauroid taxa, these results are very tentative.

There is evidence for discontinuity separating the Poposauroidea from Loricata in the Pearson BDC, MDS, PAM, and FANNY results. As such, we propose that, currently, Poposauroidea and Loricata should both be recognized as apobaramins and strongly encourage further study into these groups.

Among the non-paracrocodylomorphs, some groups are well-represented, like Ornithosuchidae and Gracilisuchidae, whereas Aetosauria is missing a great many taxa. Nevertheless, there is strong evidence for discontinuity separating Aetosauria, Gracilisuchidae, and Ornithosuchidae and continuity within each of these groups as evidenced by the clustering patterns (MDS, PAM, and FANNY) and correlations (BDC). Nevertheless, certain taxa are more difficult to sort out: *Parringtonia*, *Ticinosuchus*, and *Nundasuchus*. *Nundasu-*

chus is the least ambiguous of the three, consistently clustering with the Gracilisuchidae in all analyses. *Ticinosuchus* positively correlates with Gracilisuchidae + *Nundasuchus* in Pearson and Spearman BDC, but it also positively correlates with the Loricata in the Paracrocodylomorpha subset analysis. Thus, we ran some additional analyses that combined *Ticinosuchus*, Gracilisuchidae, and the Paracrocodylomorpha taxa that were somewhat inconclusive. *Ticinosuchus* does not correlate with any taxa in the Pearson BDC (Supplemental Figure 6a), but it does correlate positively with *Mandasuchus*, which correlates positively with the paracrocodylomorph *Deucriasuchus* in the Spearman BDC (Supplemental Figure 6b). In MDS (Supplemental Figure 7), *Ticinosuchus* is closest to the paracrocodylomorph taxa, and not the gracilisuchids. Given these analyses, we propose that Ornitho-
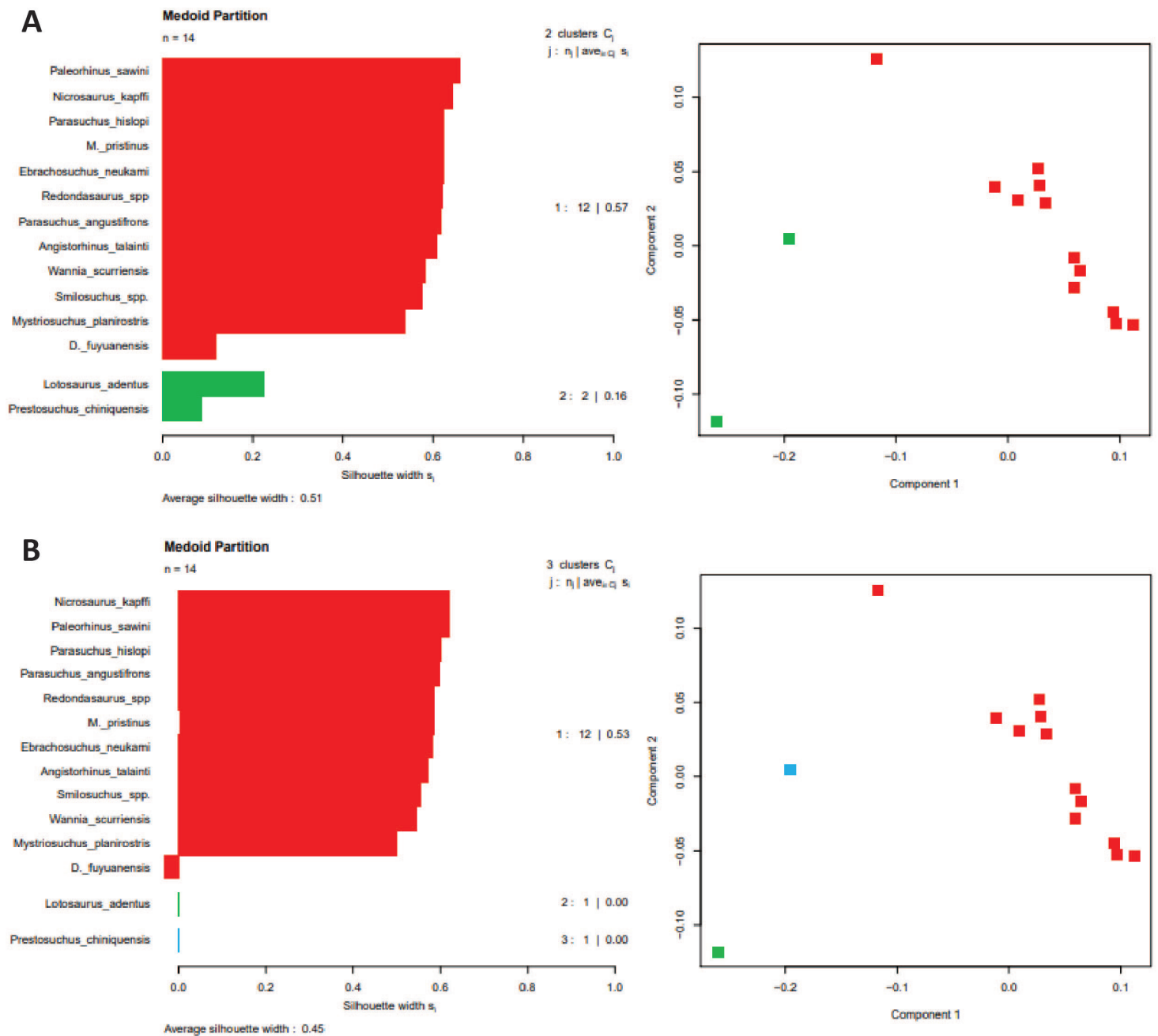
Figure 25. Partitions around medoids (PAM) analysis of the Phytosauria subset dataset in A) two groups and B) three groups.
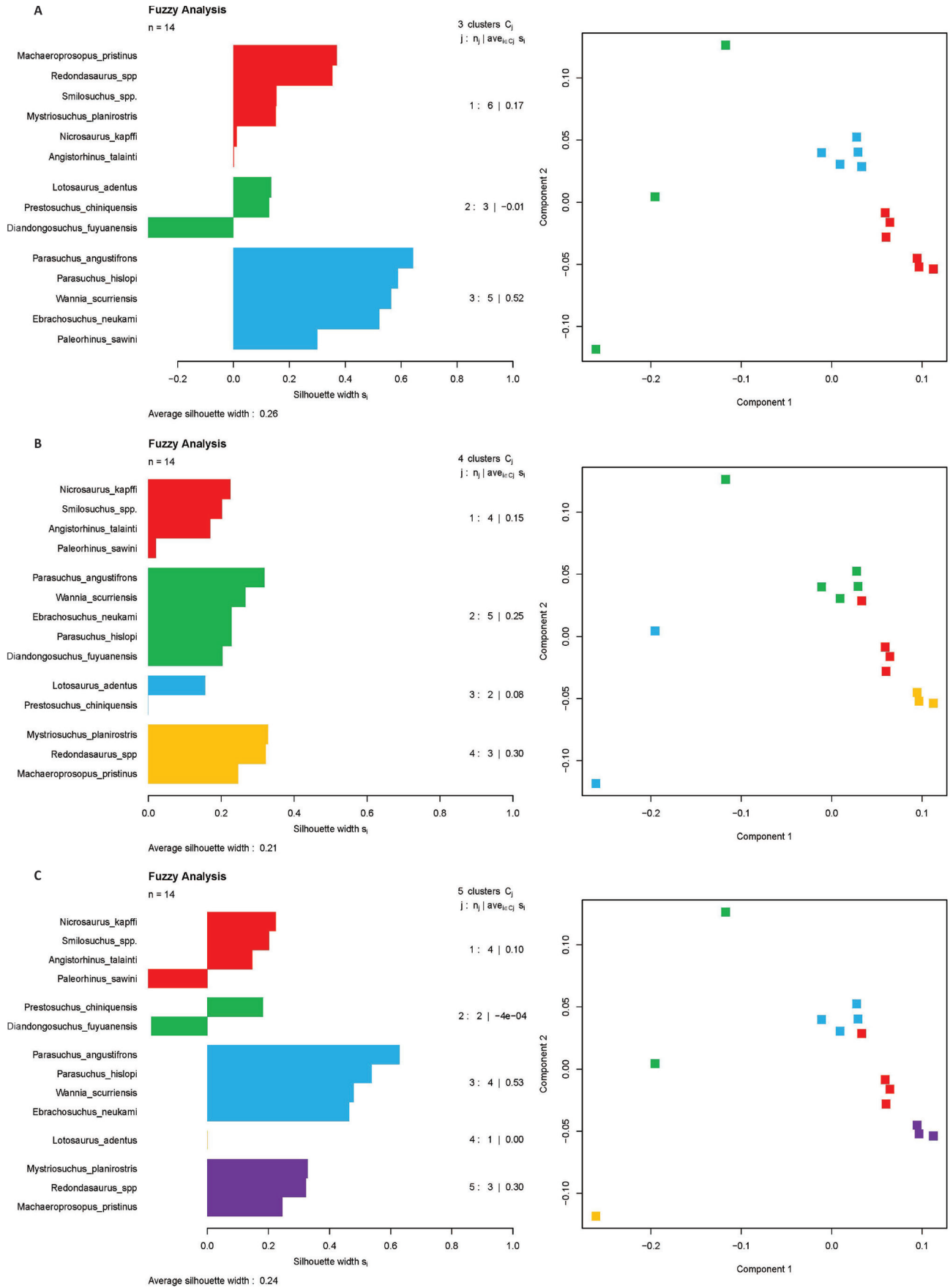
Figure 26. Fuzzy analysis (FANNY) of the Phytosauria subset dataset in: A) three groups, B) four groups, and C) five groups.

suchidae is a holobaramin, Gracilisuchidae + *Nundasuchus* is a likely holobaramin, and Aetosauria is likely either a holobaramin or apobaramin (although the group is in desperate need of baraminological analysis with datasets that include *Revueltosaurus*). *Parringtonia* is considered an erpetosuchid (Nesbitt and Butler, 2012). The other erpetosuchids were analyzed alongside Proterochampsia. As a result, we also reanalyzed the non-paracrocodylomorph Pseudosuchia subset but including the three erpetosuchid taxa (*Erpetosuchus*, *Pagosvenator*, and *Tarjadia*) with BDC, MDS, PAM, and FANNY (Supplemental Figures 8-11). These results support *Parringtonia* as a member of the Erpetosuchidae holobaramin.

H. Avemetatarsalia

There is weak evidence for discontinuity between Dinosauromorpha + Aphanosauria and Pterosauromorpha, but there is strong evidence for multiple holobaramins within Avemetatarsalia. Aphanosaurs share continuity and show no evidence of continuity with other avemetatarsalians, although *Scleromochlus* groups with them in the PAM and FANNY results. However, this dataset was constructed before *Scleromochlus* was redescribed following the CT scanning of all six specimens, which showed strong evidence for its placement near or within Lagerpetidae (Foffa et al. 2022). Thus, Aphanosauria

is likely a holobaramin to the exclusion of *Scleromochlus*. Within Dinosauromorpha, the silesaurids consistently showed close clustering and shared positive correlation, indicating evidence for continuity. They also appear to be discontinuous from all other avemetatarsalian taxa except for *Lagosuchus*. Future analyses with more silesaurids will help to refine this picture, but at this stage it seems reasonable to suggest that Silesauridae + *Lagosuchus* is a holobaramin.

Dinosaurs have been studied in much greater detail in other studies (e.g., Doran et al. 2018), and there are very few dinosaur taxa represented in the dataset, but it is interesting to note that there was clear evidence of discontinuity between Ornithischia and Saurischia in the BDC and MDS results and in the four-group PAM and FANNY results. More surprising is the lack of obvious discontinuity within Saurischia, except in the four-group PAM and FANNY results. This is likely due to the low number of taxa and few characters present useful for defining saurischian relationships.

Lagerpetidae shows strong evidence for internal continuity in all methods, and there is decent evidence for discontinuity surrounding the group in both the "basal" Avemetatarsalia and 0.29 Pterosauromorpha subset analyses. As discussed above, the Kellner et al. (2022) dataset was compiled without the newest information available on
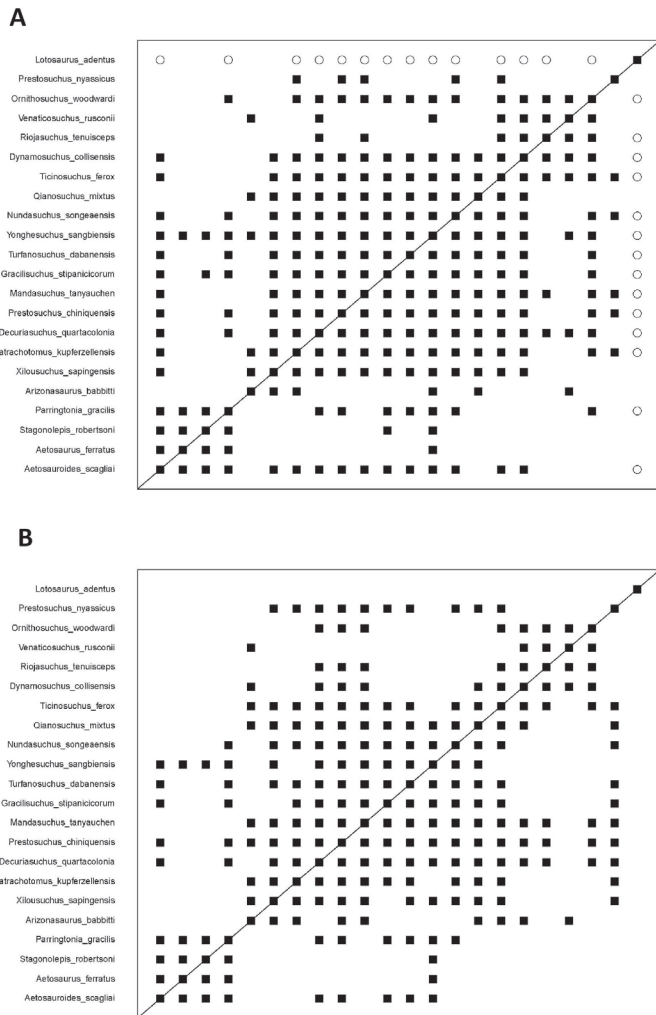
Figure 27. Baraminic distance correlation (BDC) results for the Pseudosuchia subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
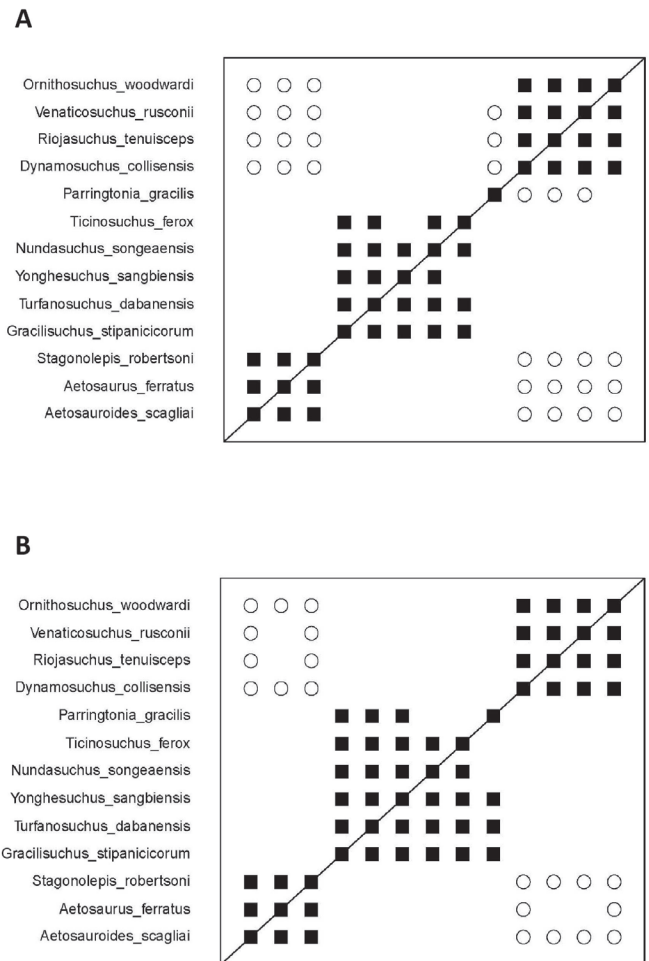

Figure 28. Baraminic distance correlation (BDC) results for the non-paracrocodylomorph Pseudosuchia subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.

Scleromochlus (Foffa et al. 2022). As such, we predict that it will fall within the lagerpetid holobaramin in future studies that incorporate newer data.

The pterosaurs, as seems to consistently be the case in baraminological analyses (see, for example, Clausen and McLain 2021), were difficult to read. We can see evidence for discontinuity surrounding the group in the 0.29 Pterosauromorpha subset analysis, but not as much as we might expect. This is likely due to the low numbers of characters included in the dataset to set apart pterosaurs from other taxa. The included pterosaurs are all non-pterodactyloid and mainly Triassic forms (with the exception of *Rhamphorhynchus*, *Dimorphodon*, and *Cacibupteryx*). It is not surprising that *Rhamphorhynchus* does not quite fall close to the other pterosaurs given the lack of other rhamphorhynchids (e.g., *Dorygnathus*, *Scaphognathus*) in the 0.29 Pterosauromorpha subset analysis" between "pterosaurs" and "giv-

en".. It is interesting that the 0.29 Pterosauromorpha BDC and MDS results recovered two different groups of Triassic pterosaurs sharing positive correlation: Eudimorphodontoidea and Preondactylia + Dimorphodontidae. The PAM and FANNY results had relatively similar numbers for three- and four-group models (and two and five groups for PAM), and these three and four group models did differentiate these same pterosaur bins. McLain (2022) found evidence for discontinuity between Rhamphorhynchidae and Triassic pterosaurs, which agrees with these results, but he did not find evidence for two Triassic monobaramins. However, the dataset McLain (2022) used (Yang et al. 2022) only included five Triassic pterosaur taxa (*Eudimorphodon*, *Carniadactylus*, *Raeticodactylus*, *Austriadactylus*, and *Preondactylus*). Indeed, McLain (2021) used a dataset (Wei et al. 2021) where six Triassic pterosaurs were retained in the analysis (*Raeticodactylus*, *Eudimorphodon*, *Seazzadactylus*, *Carniadactylus*,
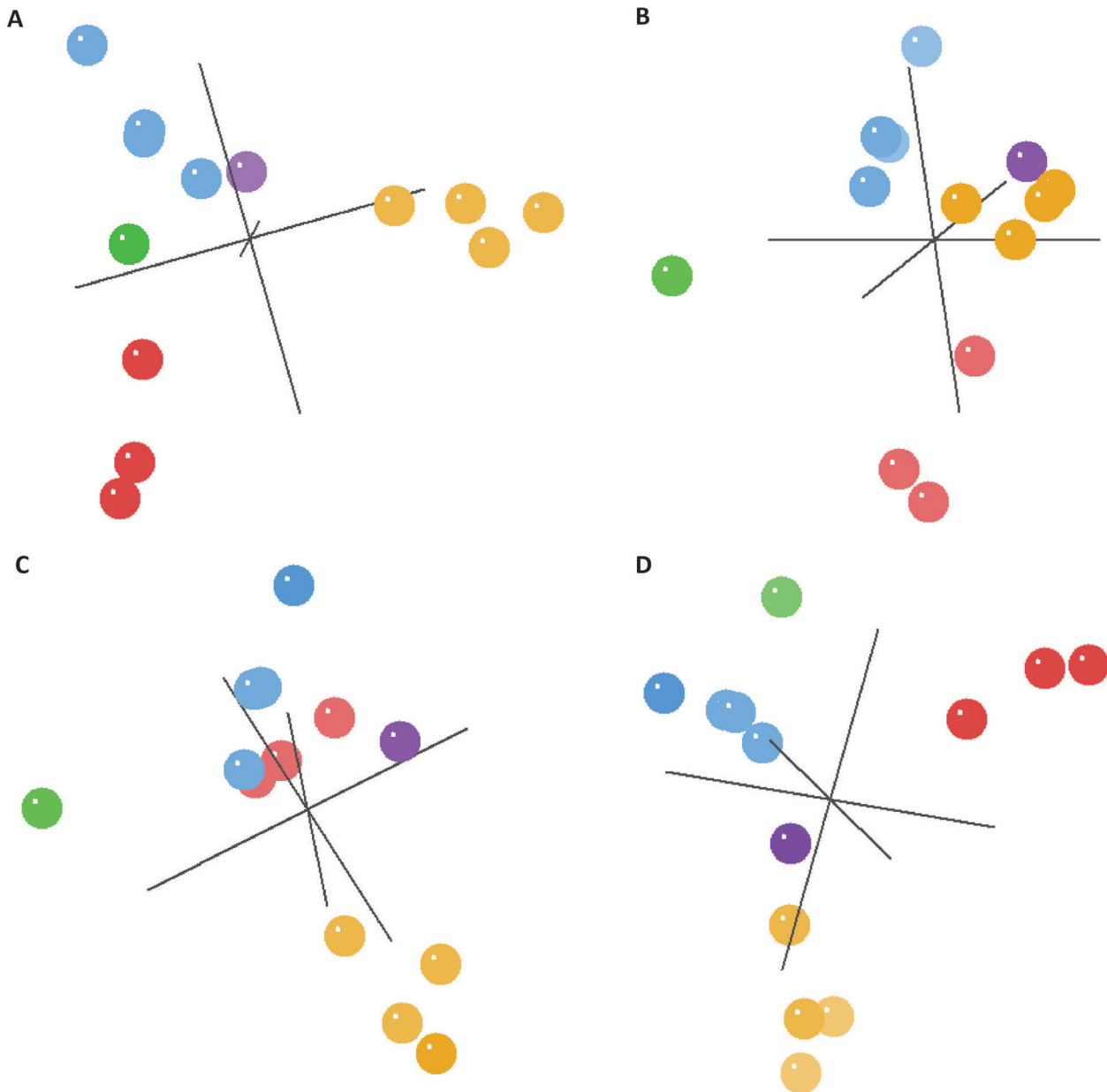
Figure 29. 3D multidimensional scaling (MDS) results for the non-paracrocodylomorph Pseudosuchia subset dataset in four views: A, B, C, and D. Colors: Yellow - Ornithosuchidae; Red - Aetosauria; Blue - Gracilisuchidae; Green - *Parringtonia*; Purple - *Ticinosuchus*.

Preondactylus, and *Austriadactylus*), and he did find evidence for two different monobaramins of Triassic pterosaurs: Preondactylia and Eudimorphodontinae, which matches nicely with the results of this study. Future baraminological analyses using datasets more focused on pterosaur relationships will hopefully bring greater clarity to this group, as the best we can say from this study is that Pterosauria is likely apobaraminic and that Triassic pterosaurs may form a holobaramin made up of two monobaramins: Eudimorphodontoidea and Preondactylia + Dimorphodontidae.

CONCLUSION

Our attempt to take a large morphological dataset of a group that we suspected contained many created kinds and tease those out with baraminological methods was successful. We identified 16 likely holobaramins, two pterosaur monobaramins, and evidence for discontinuity surrounding Pterosauria, Ornithischia, Saurischia, Poposauroidea, and Loricata. Certainly this is not the final baraminological word for any of these groups, as they all need more in-depth study. Nevertheless, the discovery of abundant discontinuity throughout this group is encouraging for the creationist perspective on the pattern of life. Rather than a tree of life with each twig leading back to a single common origin in the trunk, we see an orchard of life with over 16 different trees finding their independent biological origins in a single week by a single Creator.
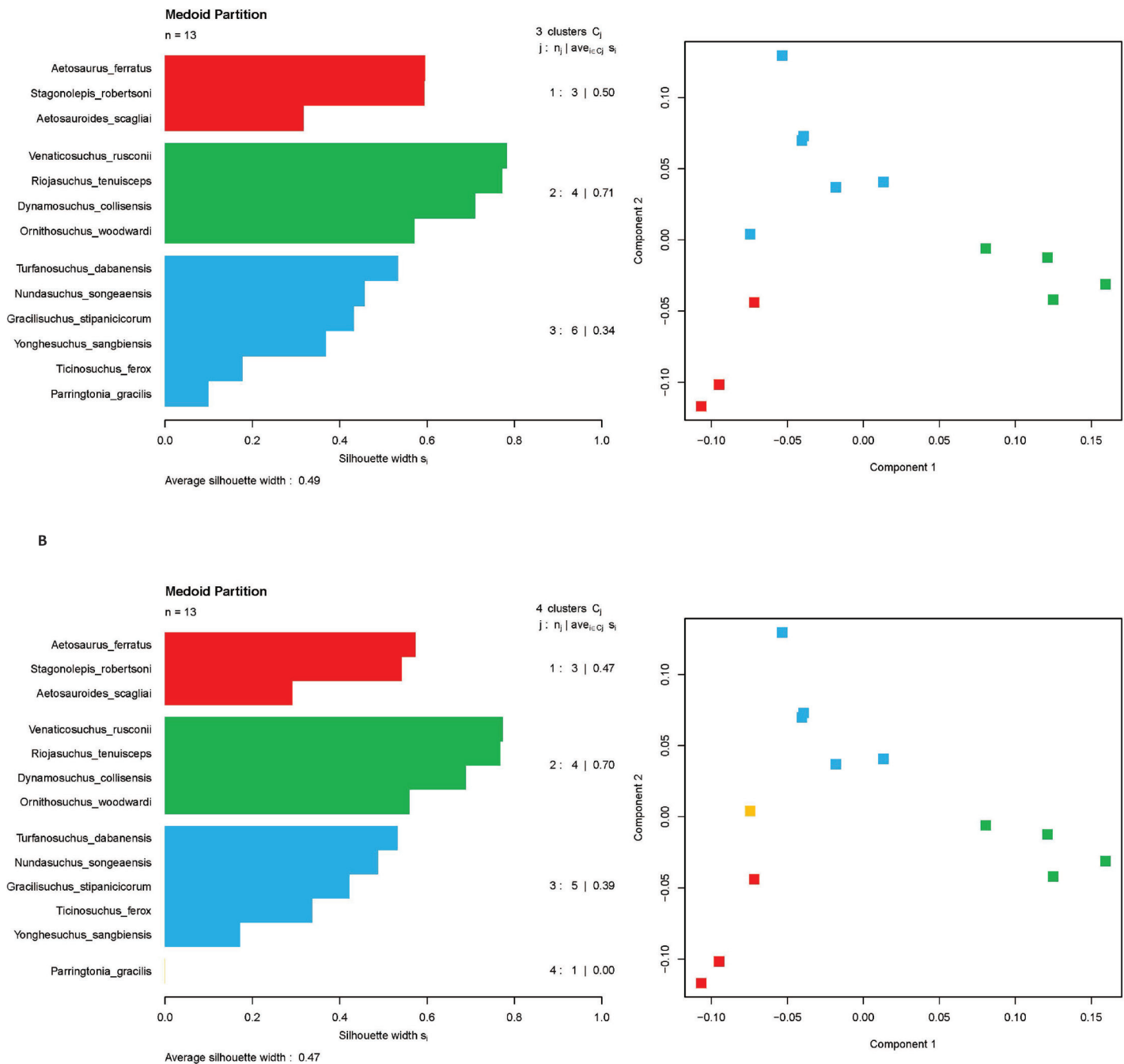
Figure 30. Partitions around medoids (PAM) analysis of the non-paracrocodylomorph Pseudosuchia subset dataset in: A) three groups and B) four groups.
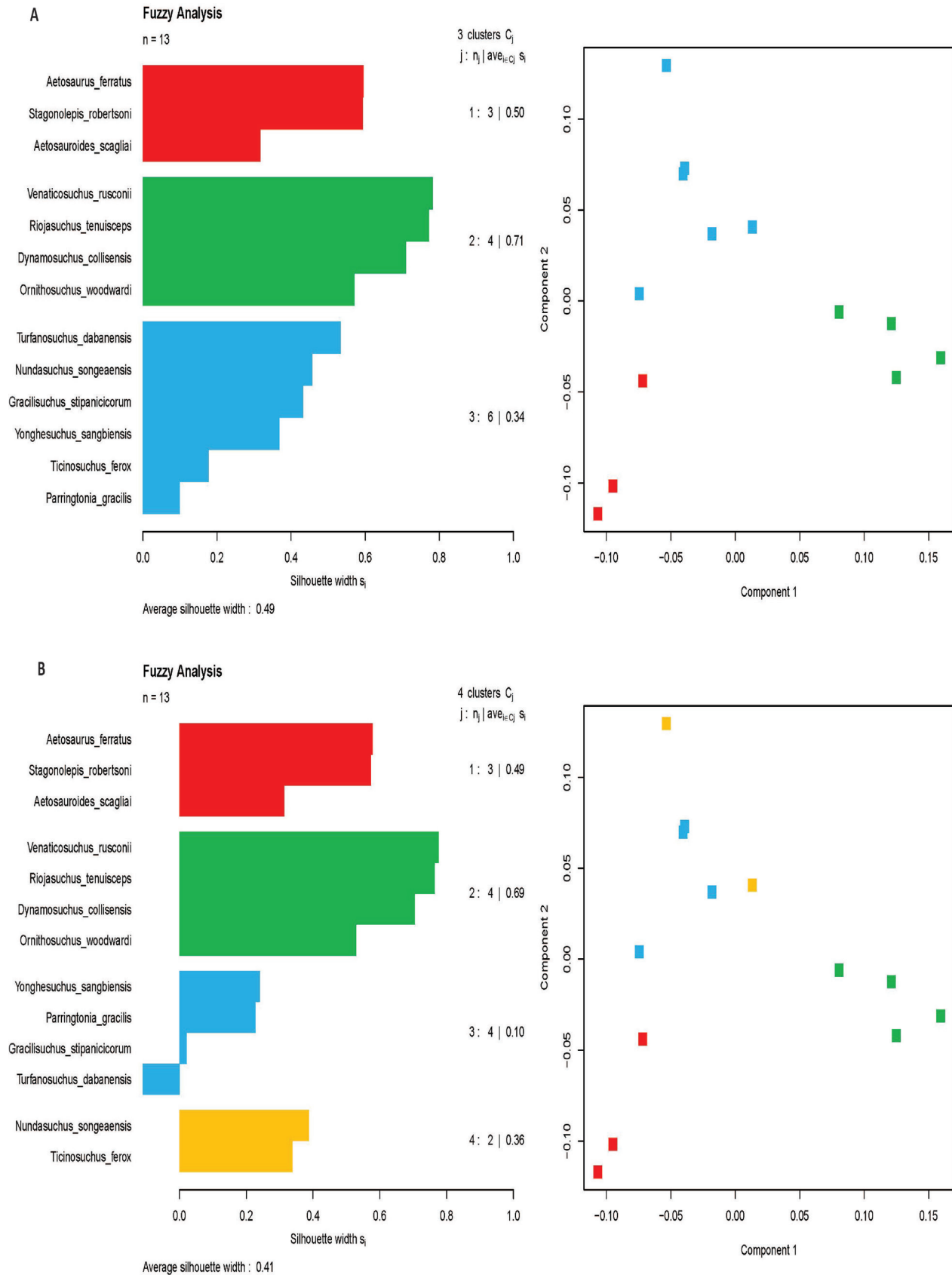
Figure 31. Fuzzy analysis (FANNY) of the non-paracrocodylomorph Pseudosuchia subset dataset in: A) three groups, B) four groups.

ACKNOWLEDGMENTS

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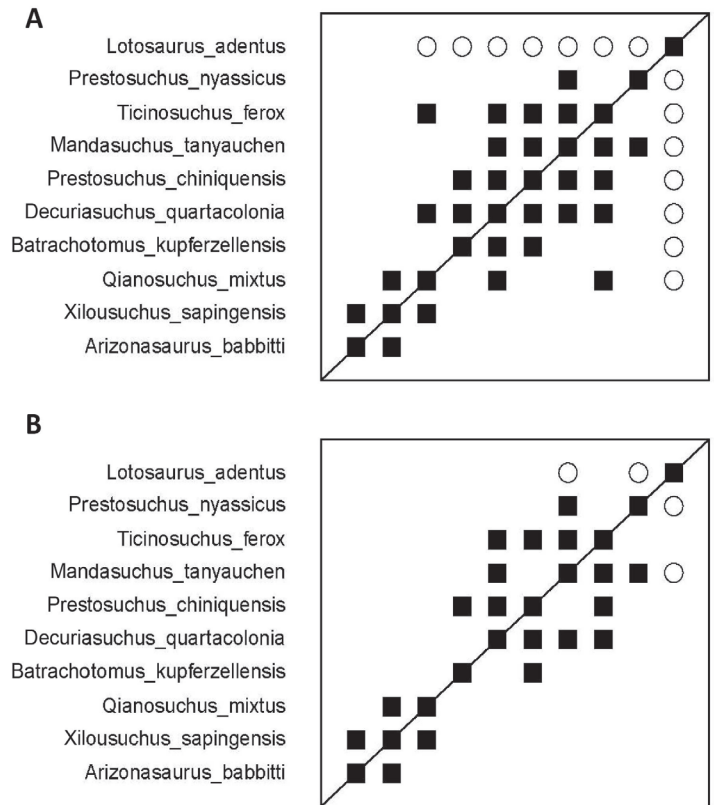
Figure 32. Baraminic distance correlation (BDC) results for the Paracrocodylomorpha subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
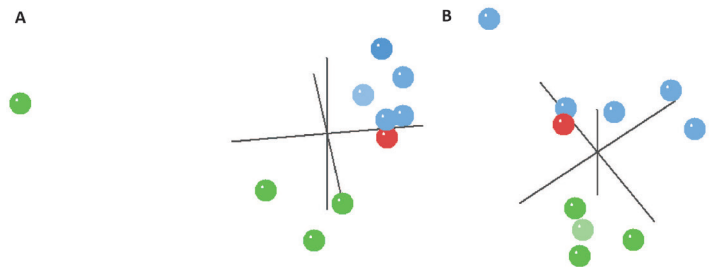

Figure 33: 3D multidimensional scaling (MDS) results for the Paracrocodylomorpha subset dataset in two views: A and B. Colors: Green - Poposauroidea; blue - Loricata; red - *Ticinosuchus*.
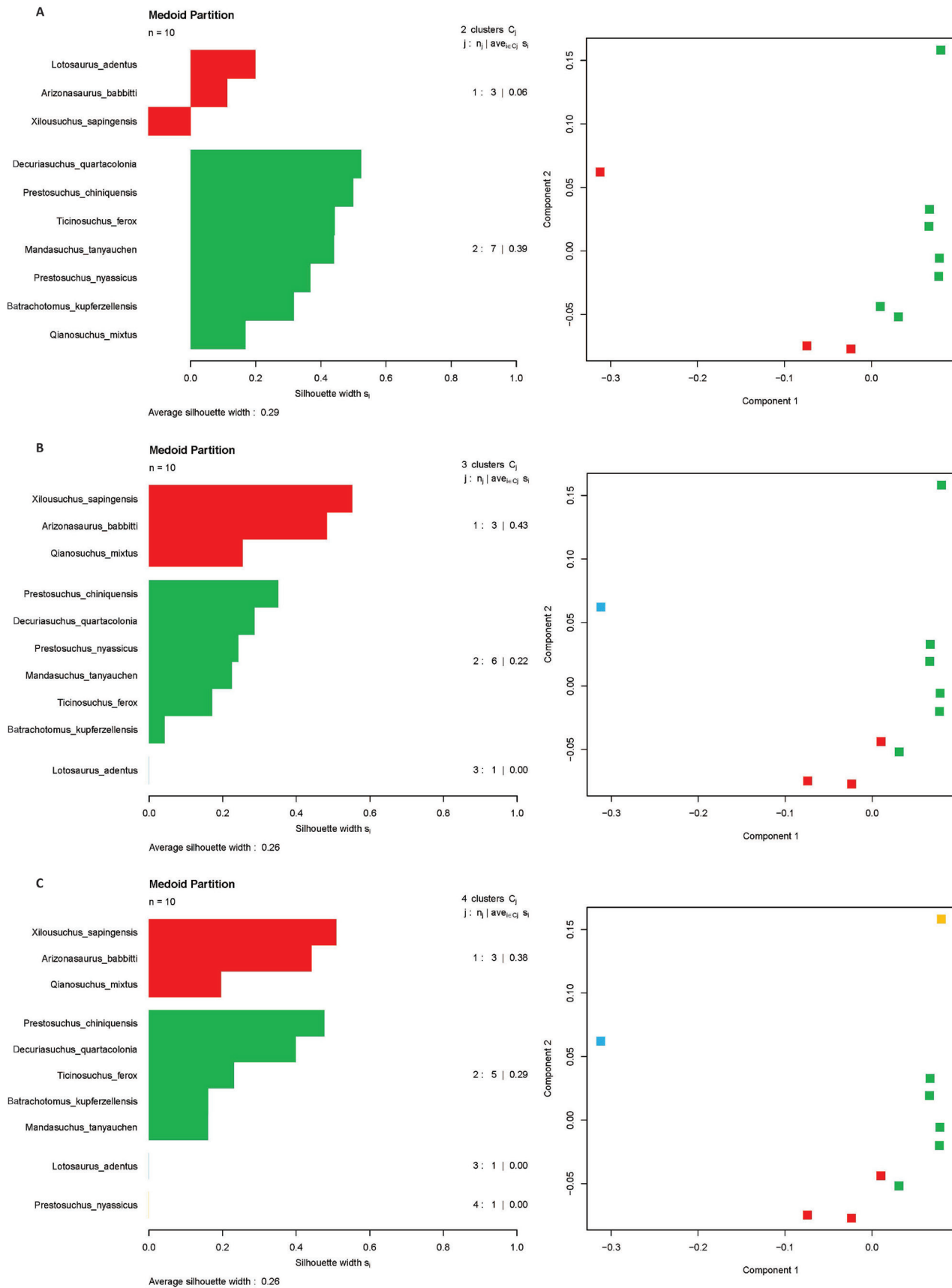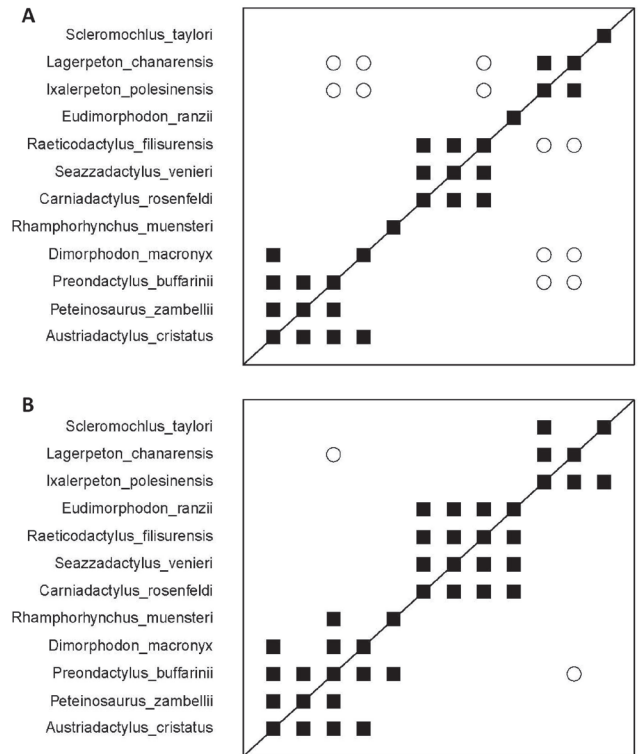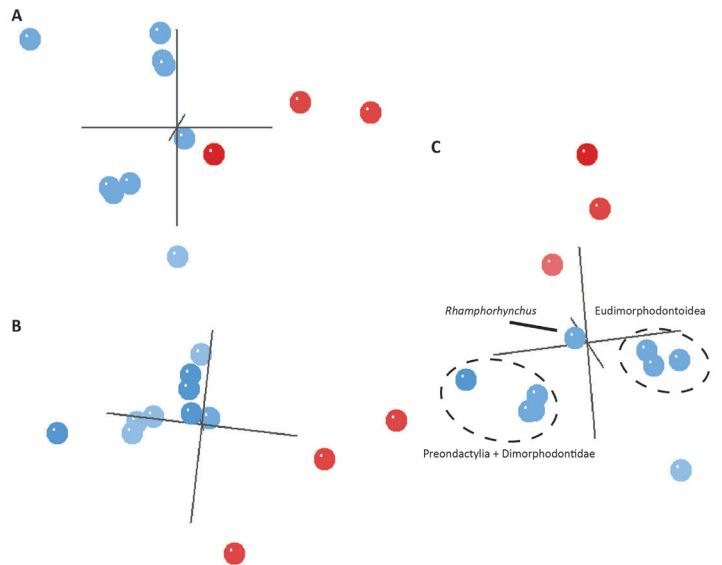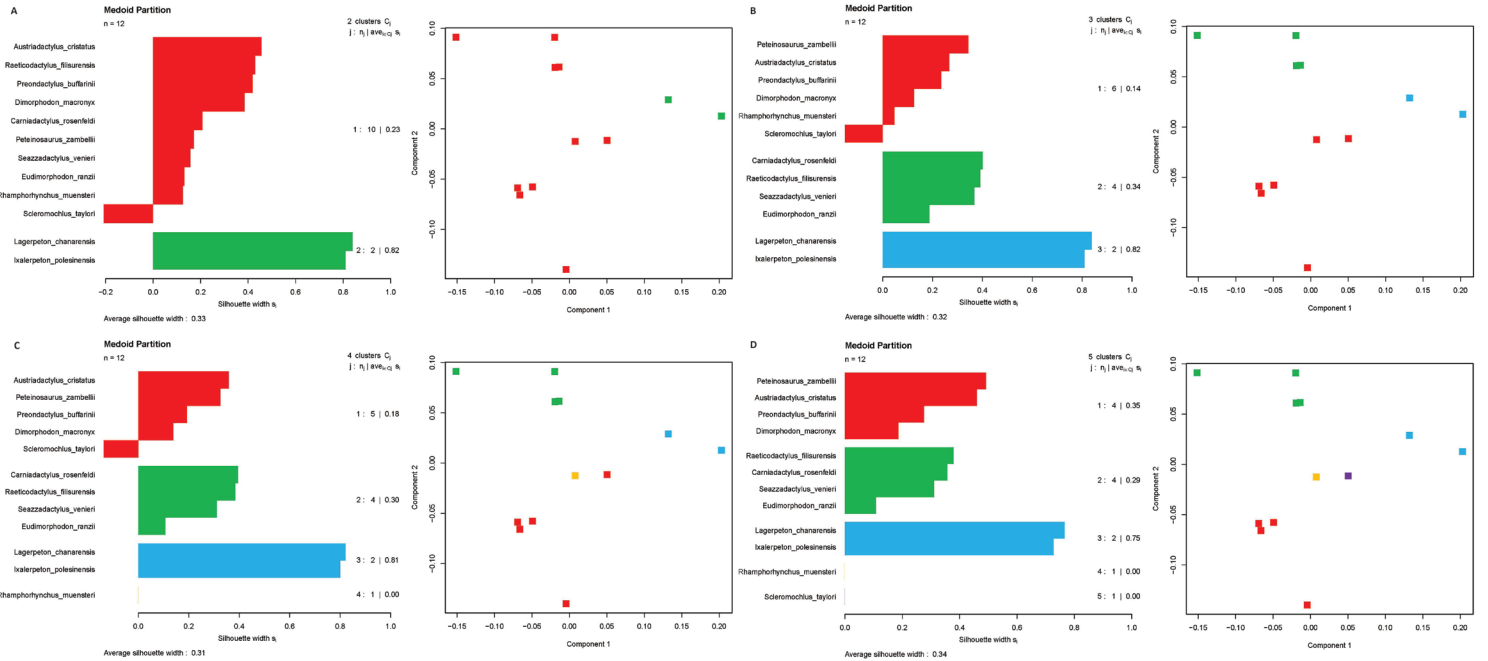
Figure 34. Partitions around medoids (PAM) analysis of the Paracrocodylomorpha subset dataset in: A) two groups, B) three groups, and C) four groups.
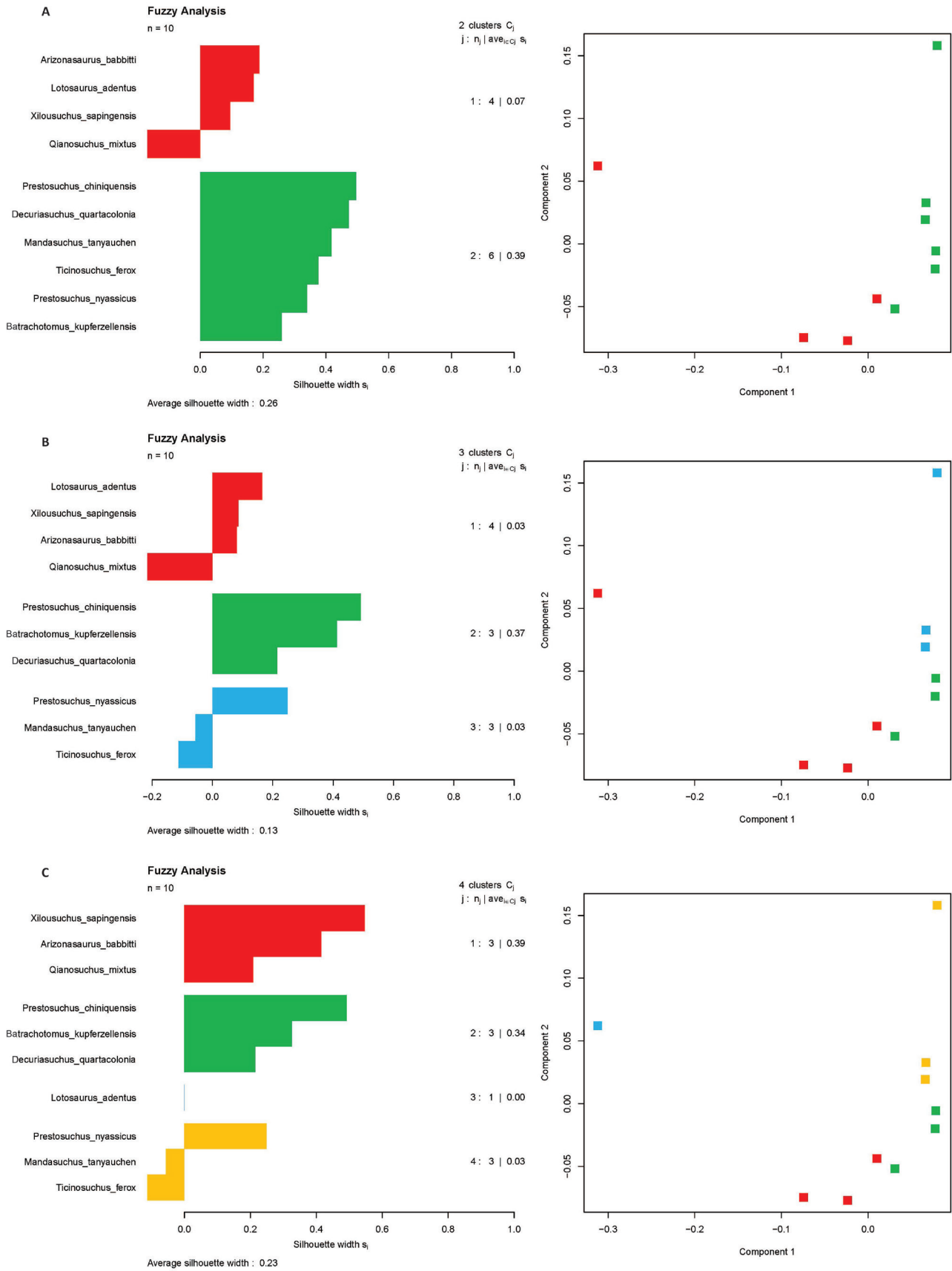
Figure 35. Fuzzy analysis (FANNY) of the Paracrocodylomorpha subset dataset in: A) two groups, B) three groups, and C) four groups.
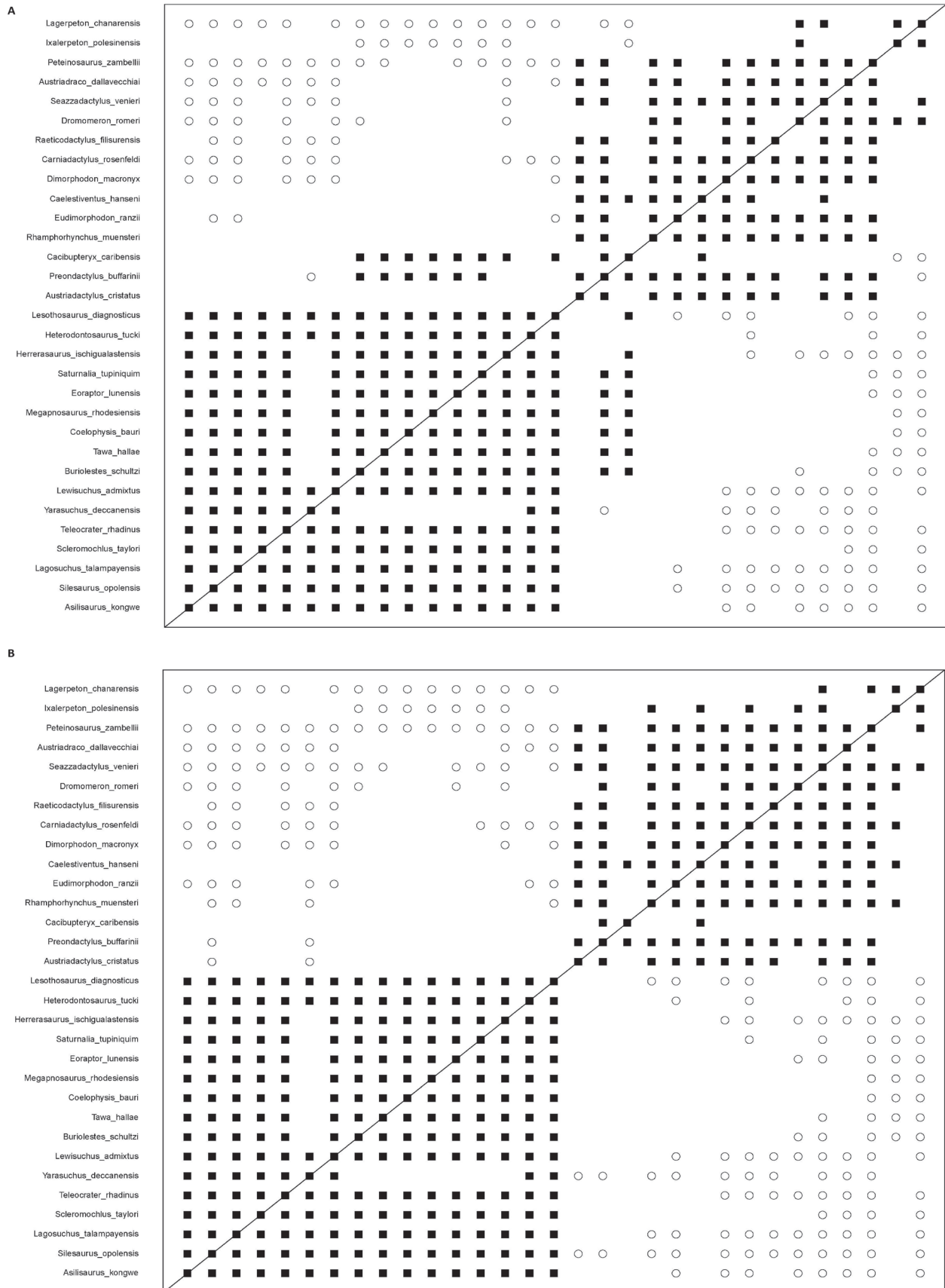
Figure 36. Baraminic distance correlation (BDC) results for the Avemetatarsalia subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
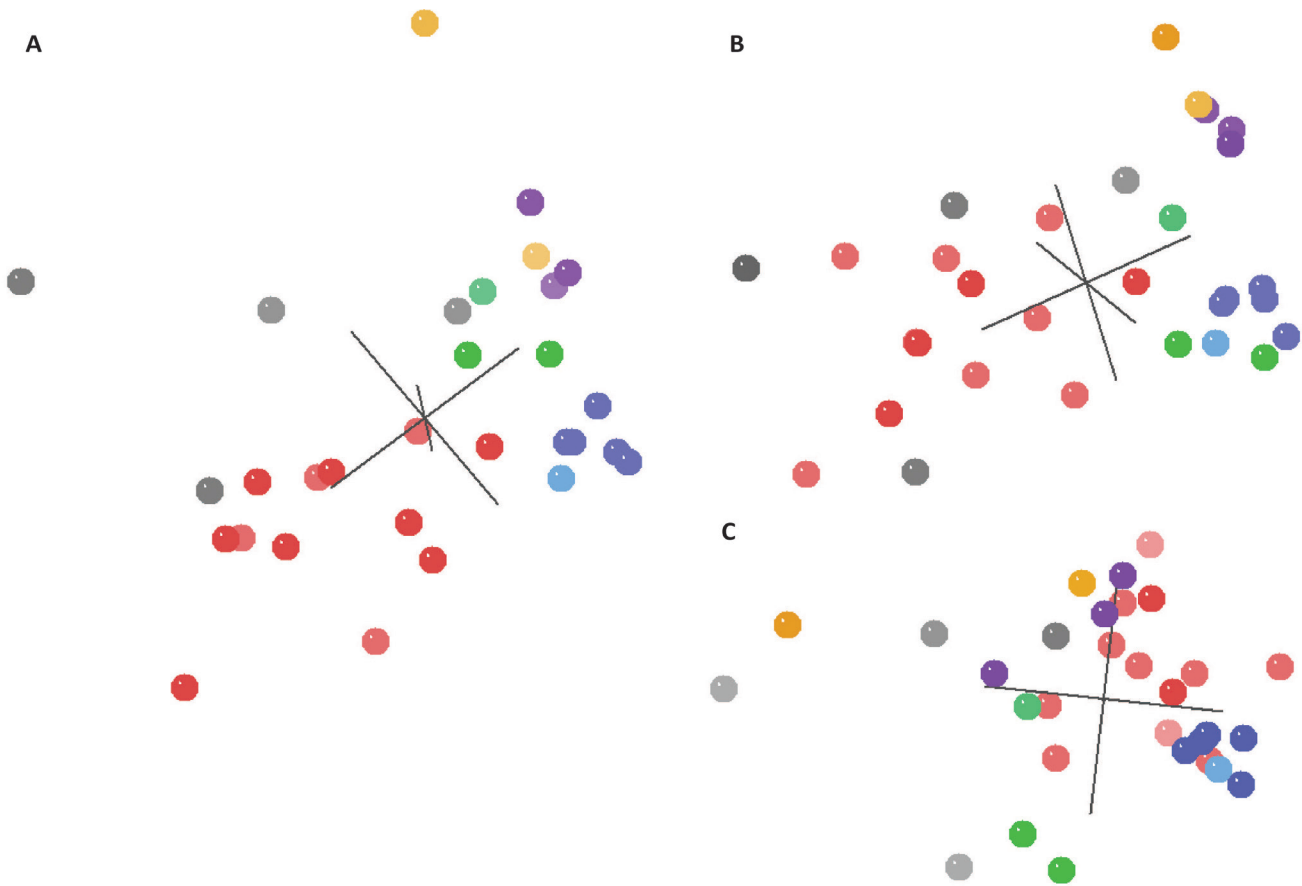
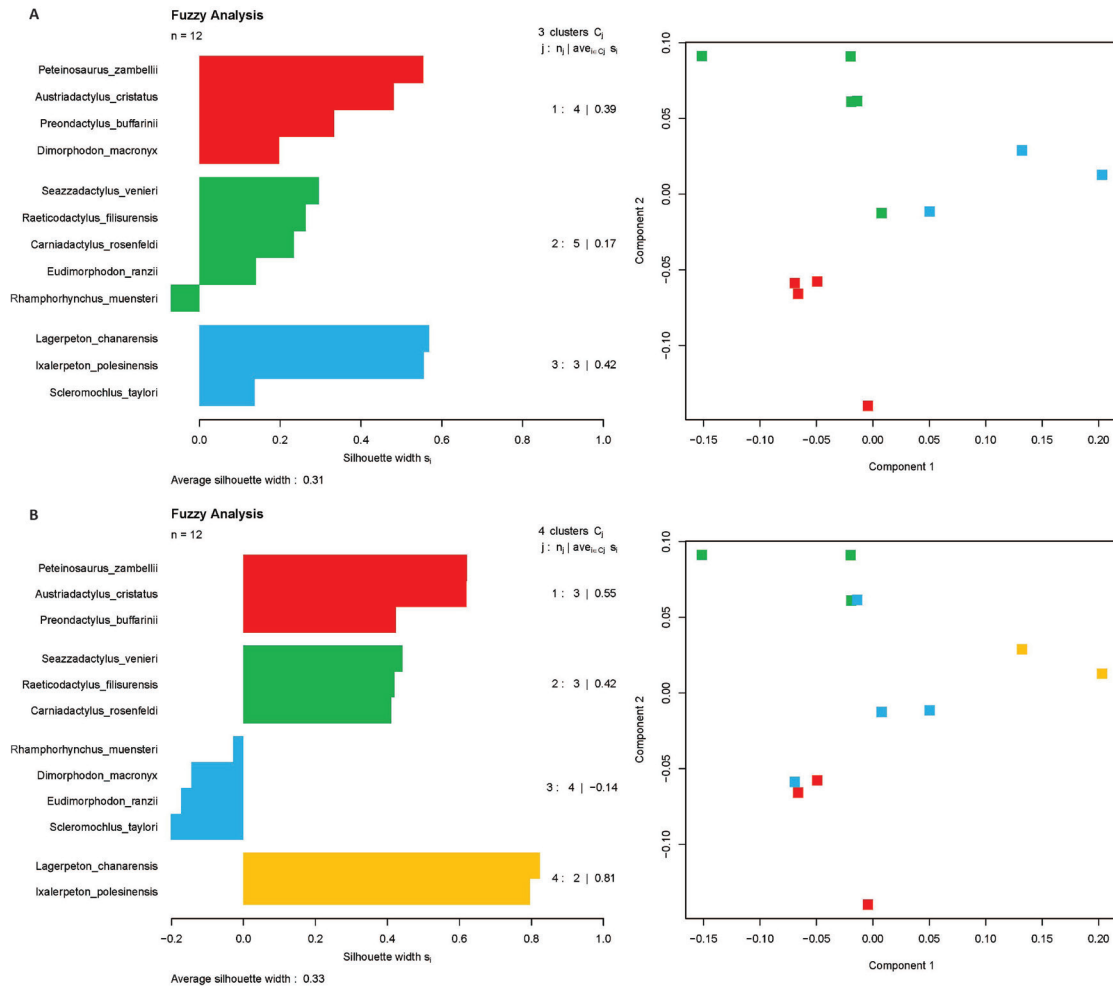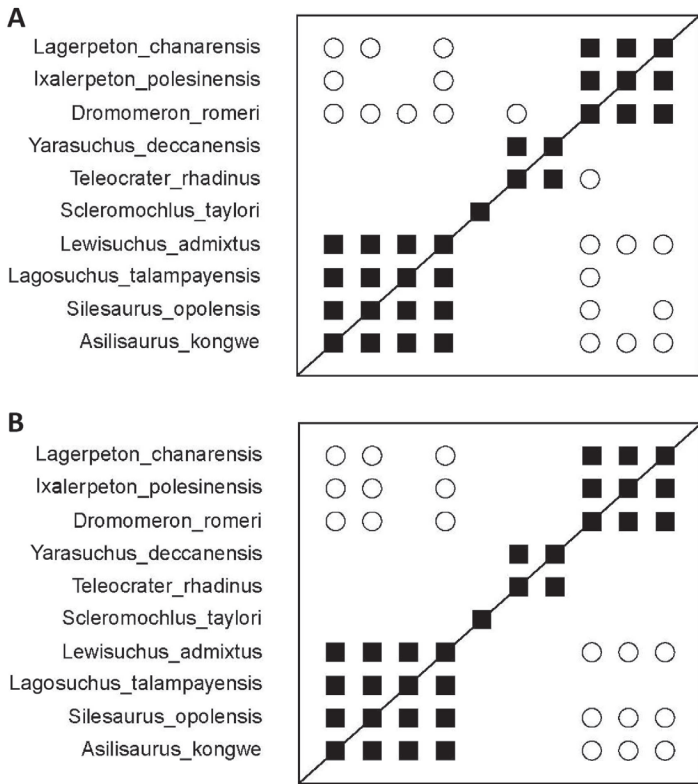**Figure 37.** 3D multidimensional scaling (MDS) results for the Avemetatarsalia subset dataset in three views: A, B, and C. Colors: Red - Pterosauria; gray - Lagerpetidae; yellow - Aphanosauria; purple - Silesauridae; sea green - *Lagosuchus*; green - Ornithischia; blue - Saurischia.
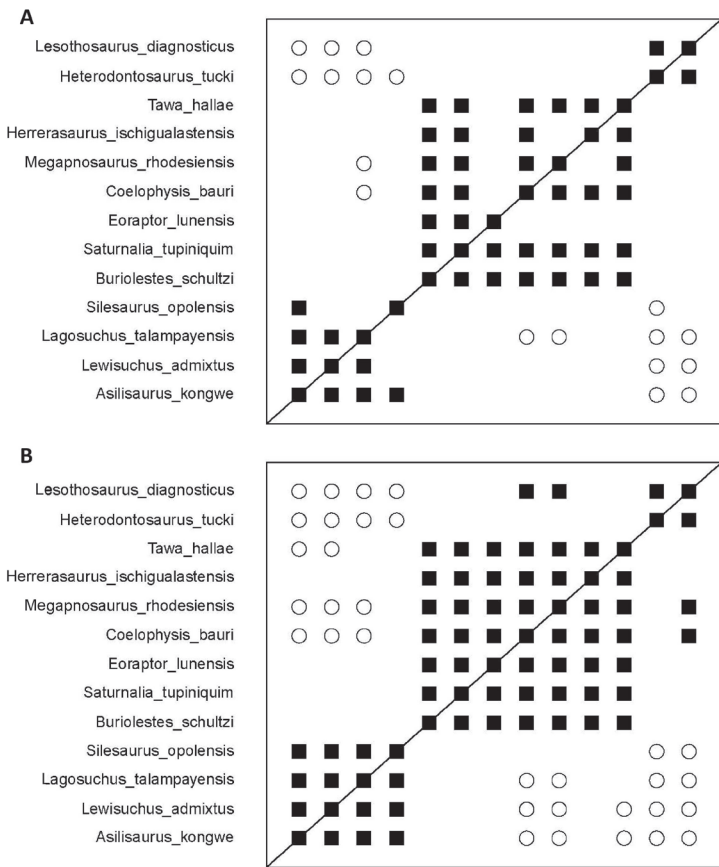
Figure 38. Baraminic distance correlation (BDC) results for the Dinosauromorpha subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
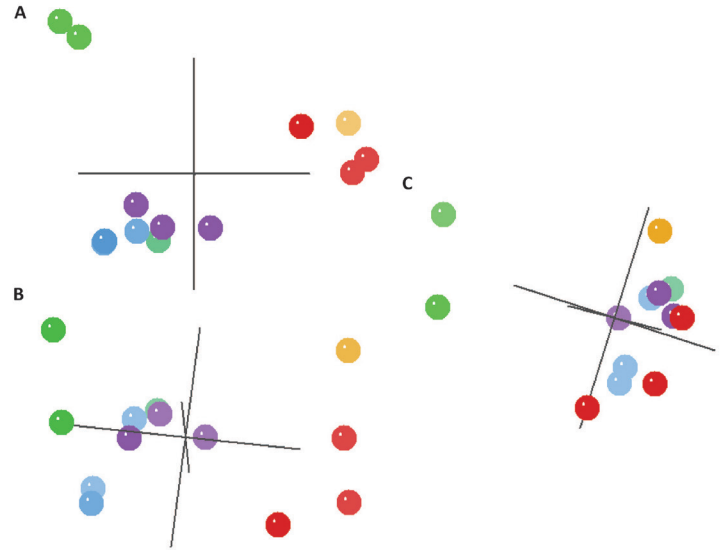
Figure 39. 3D multidimensional scaling (MDS) results for the Dinosauromorpha subset dataset in three views: A, B, and C. Colors: Green - Ornithischia; red - Silesauridae; yellow - *Lagosuchus*; purple - Sauropodomorpha; blue - Theropoda; sea green - Herrerasauridae.
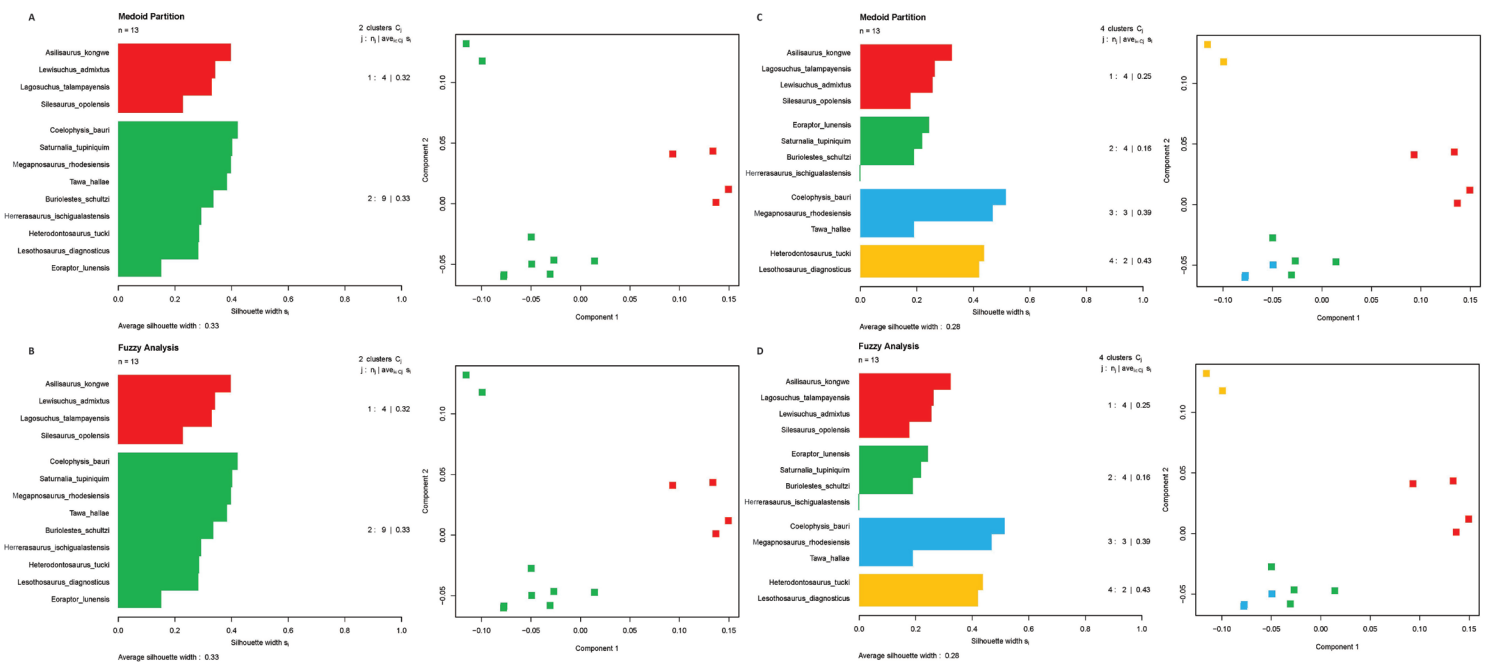
Figure 40. Partitions around medoids (PAM) analysis and Fuzzy analysis (FANNY) of the Dinosauromorpha subset dataset: A) PAM in two groups, B) PAM in four groups, C) FANNY in two groups, and D) FANNY in four groups.
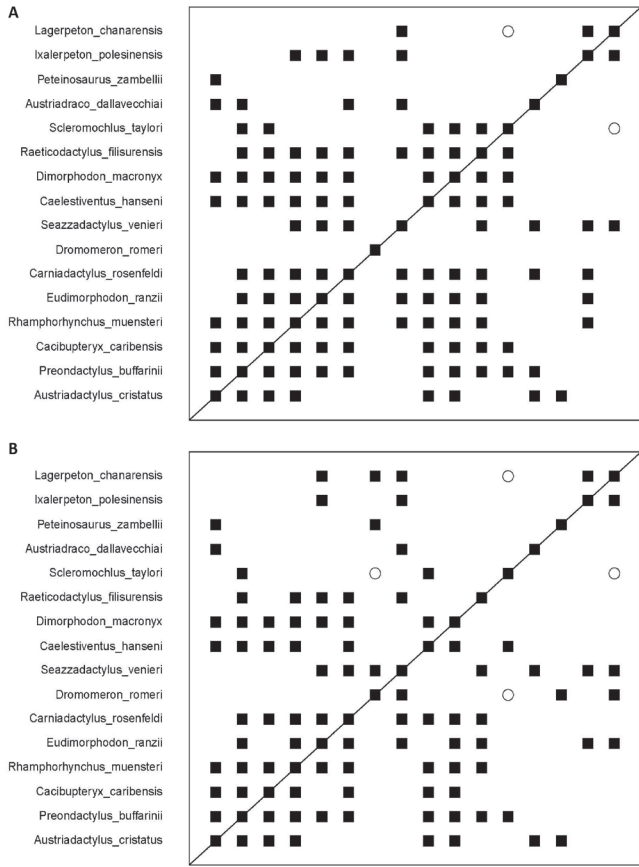
Figure 41. Baraminic distance correlation (BDC) results for the Pterosauromorpha subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.

Figure 43. Baraminic distance correlation (BDC) results for the Pterosauromorpha subset dataset at a 0.29 taxic relevance cutoff using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
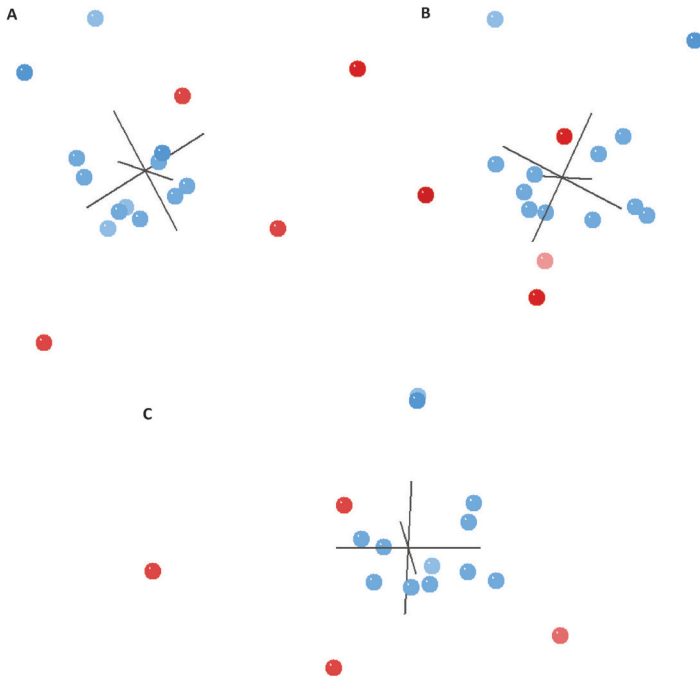
Figure 42. 3D multidimensional scaling (MDS) results for the Pterosauromorpha subset dataset in three views: A, B, and C. Colors: Blue - Pterosauria; red - Lagerpetidae.

Figure 44. 3D multidimensional scaling (MDS) results for the Pterosauromorpha subset dataset at a 0.29 taxic relevance cutoff in three views: A, B, and C. Colors: Blue - Pterosauria; red - Lagerpetidae.

Figure 45. Partitions around medoids (PAM) analysis of the Pterosauromorpha subset dataset at a 0.29 taxic relevance cutoff in: A) two groups, B) three groups, C) four groups, and D) five groups.

Figure 46. Fuzzy analysis (FANNY) of the Pterosauromorpha subset dataset at a 0.29 taxic relevance cutoff in: A) three groups and B) four groups.

Figure 47. Baraminic distance correlation (BDC) results for the "basal" Avemetatarsalia subset dataset using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
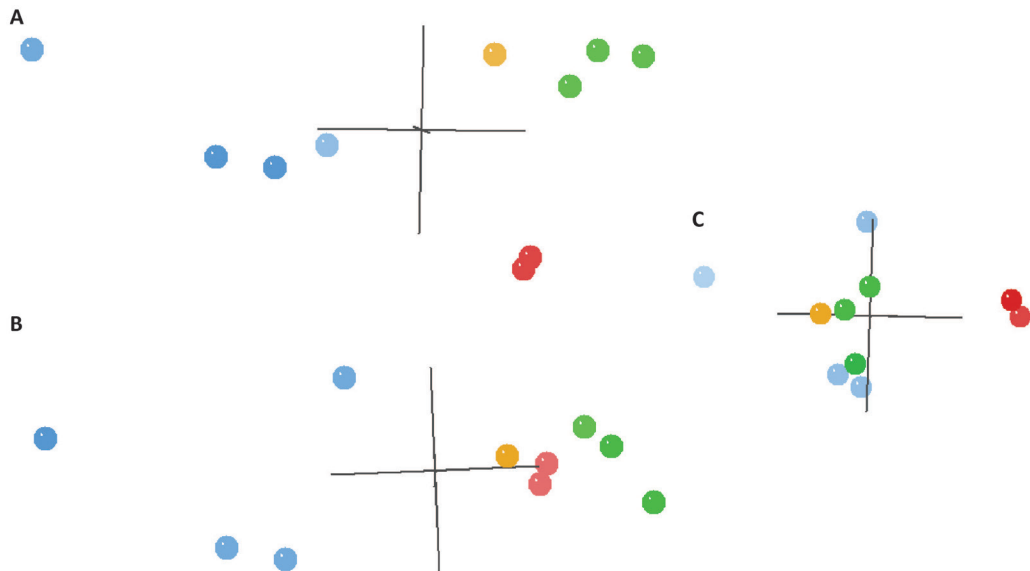
Figure 48. 3D multidimensional scaling (MDS) results for the "basal" Avemetatarsalia subset dataset in three views: A, B, and C. Colors: Blue - Lagerpetidae; red - Aphanosauria; green - Silesauridae; yellow - *Lagosuchus*.
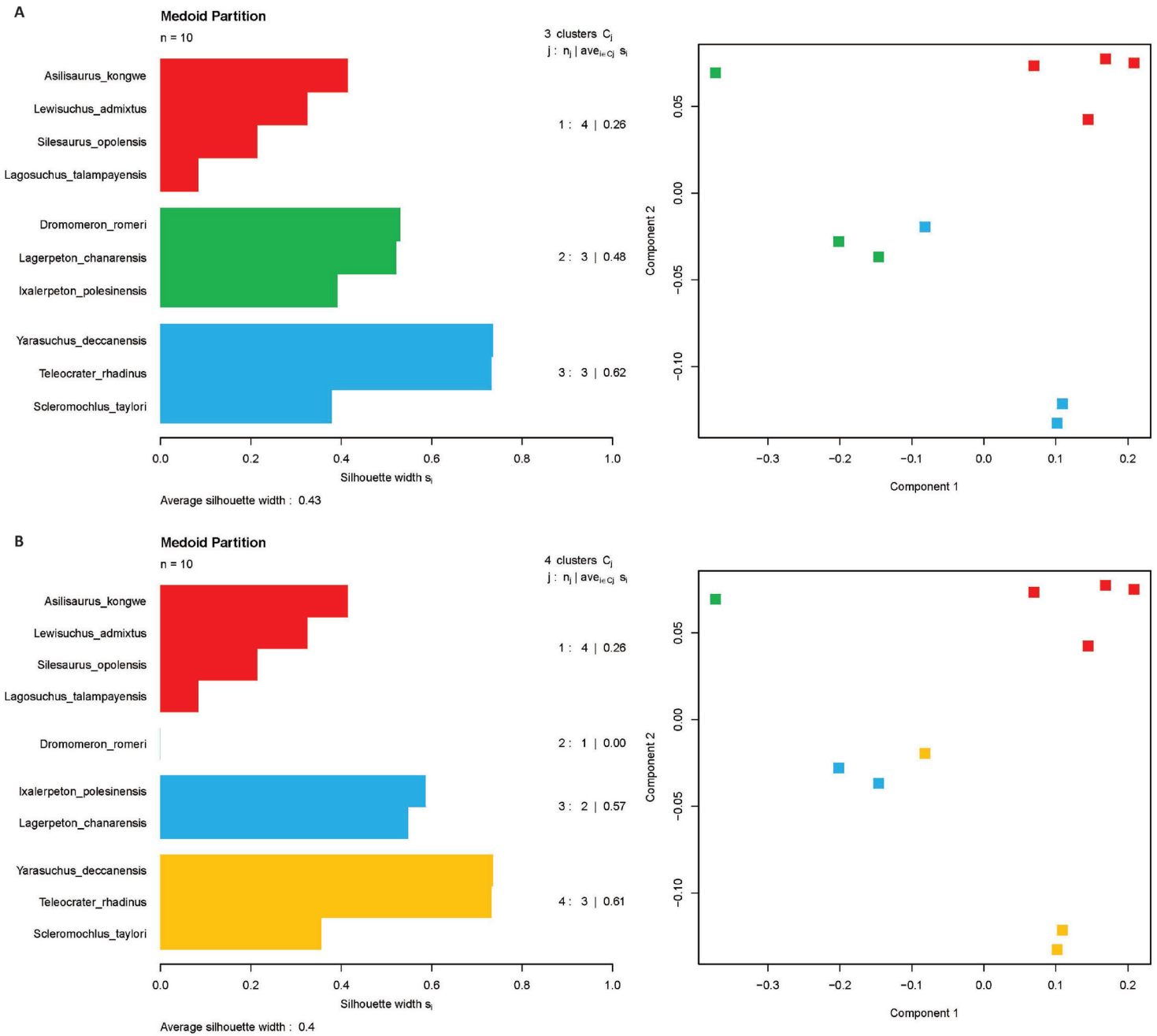
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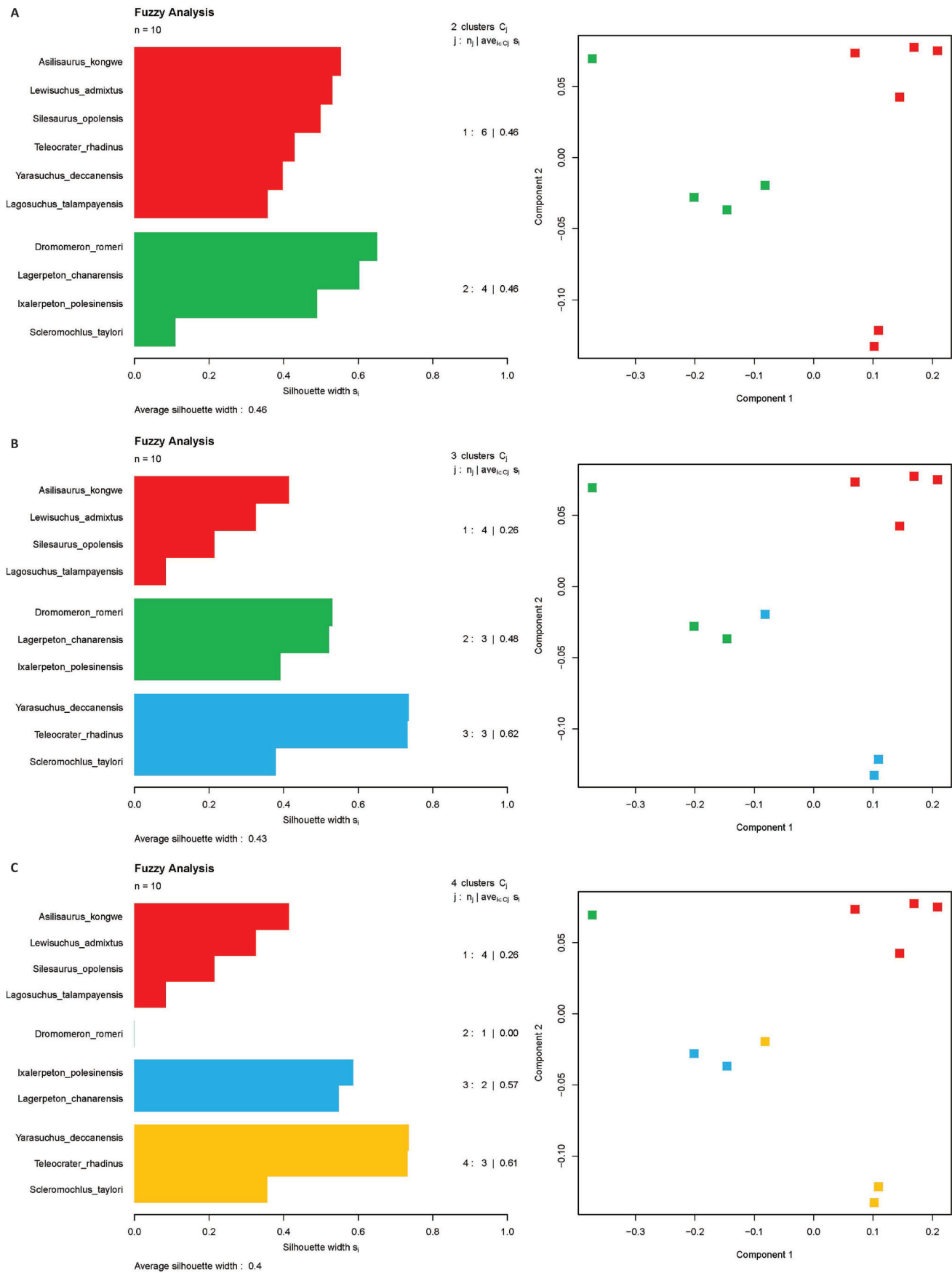
Figure 50. Fuzzy analysis (FANNY) of the "basal" Avemetatarsalia subset dataset in: A) two groups, B) three groups, and C) four groups.
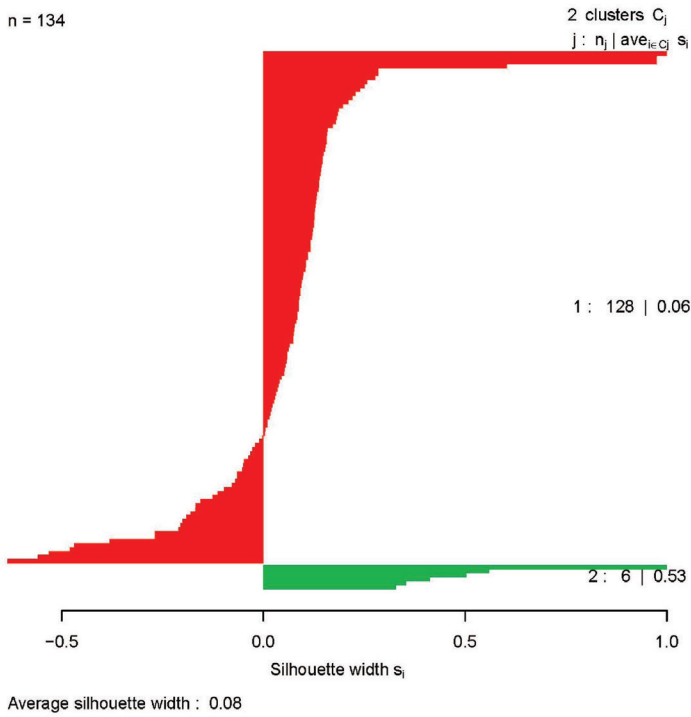
SUPPLEMENTAL FIGURES AND TABLE
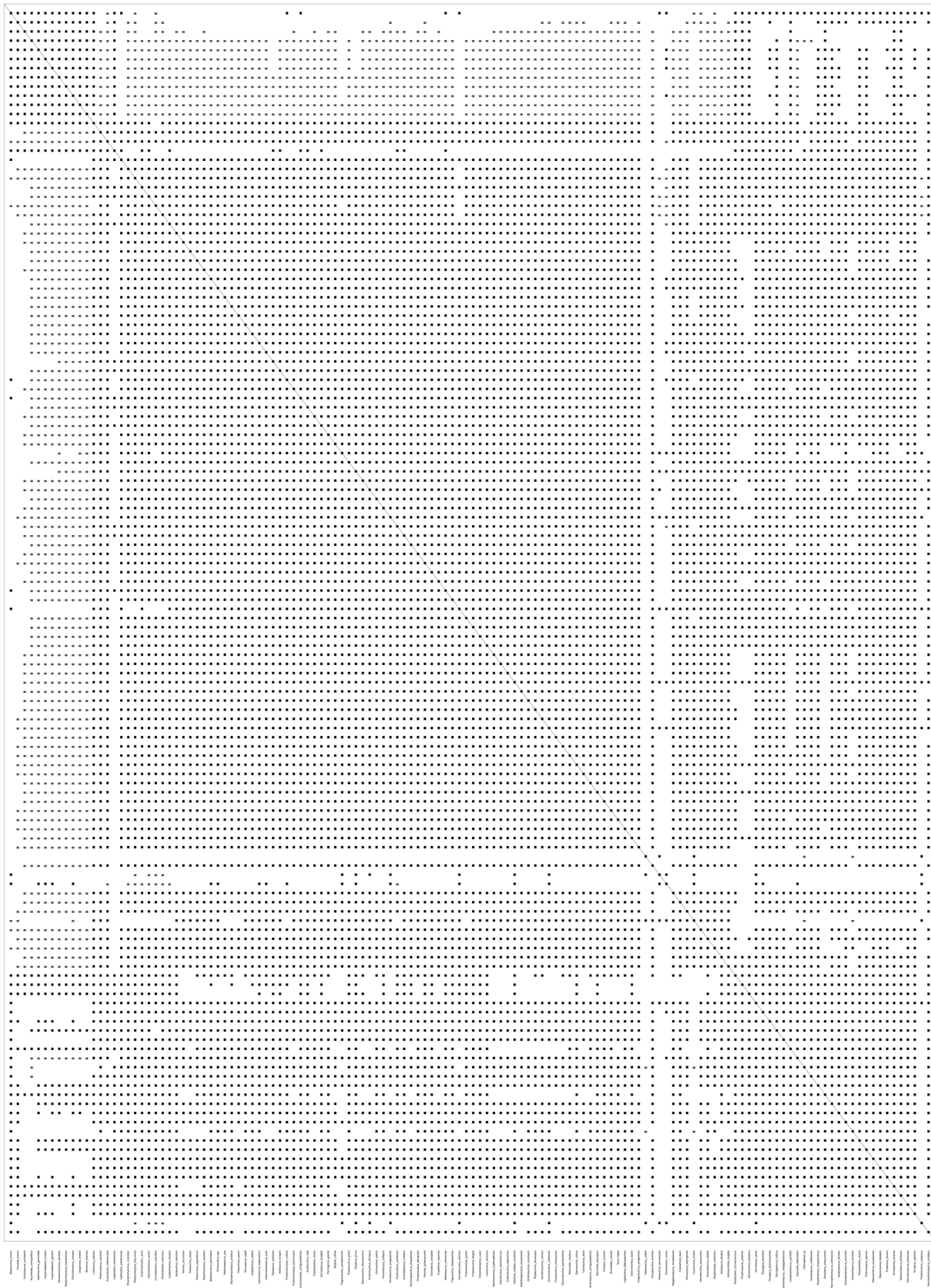
Supplemental Figure 1. Pearson baraminic distance correlation (BDC) results for all of the taxa in the dataset. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
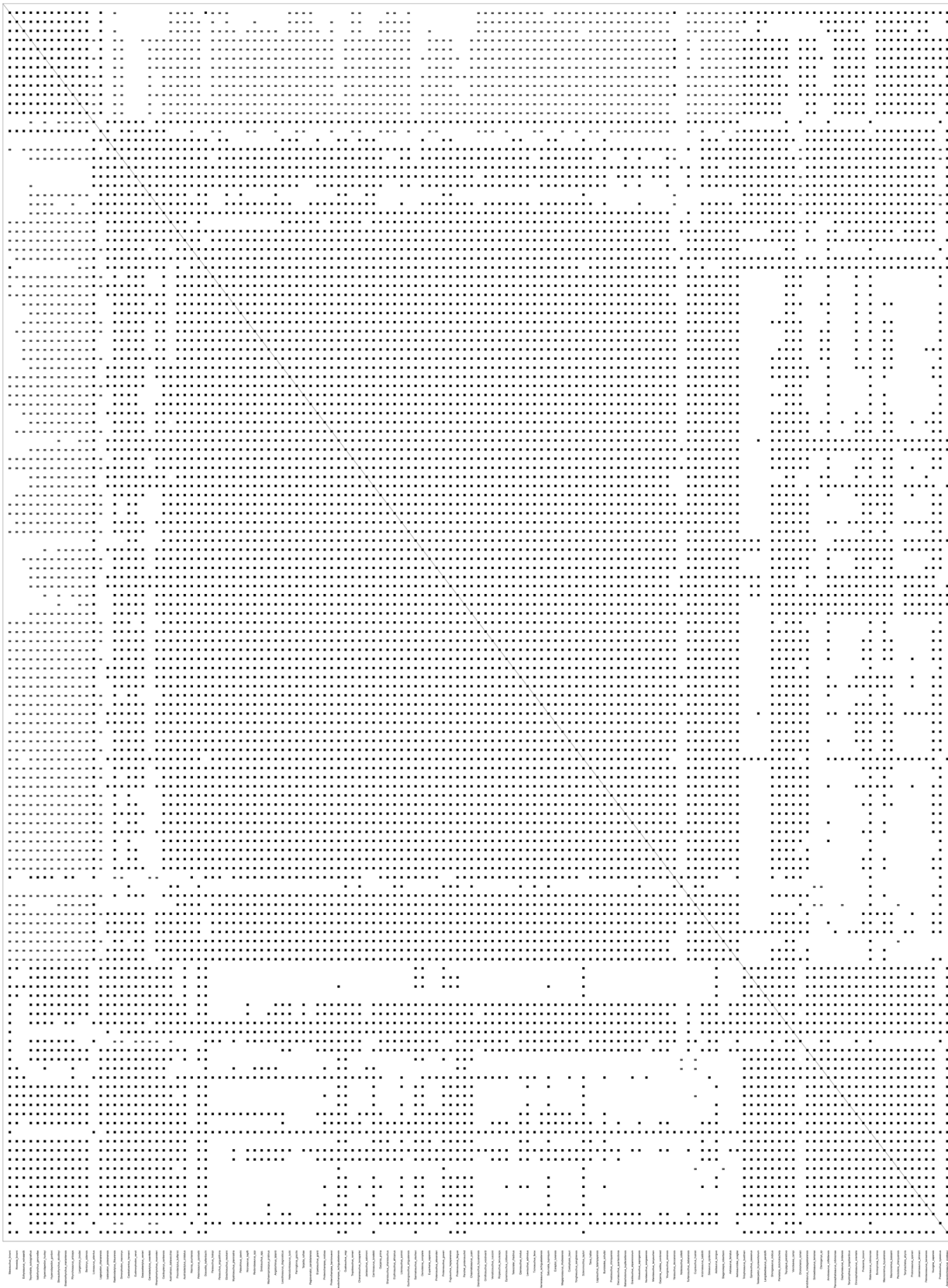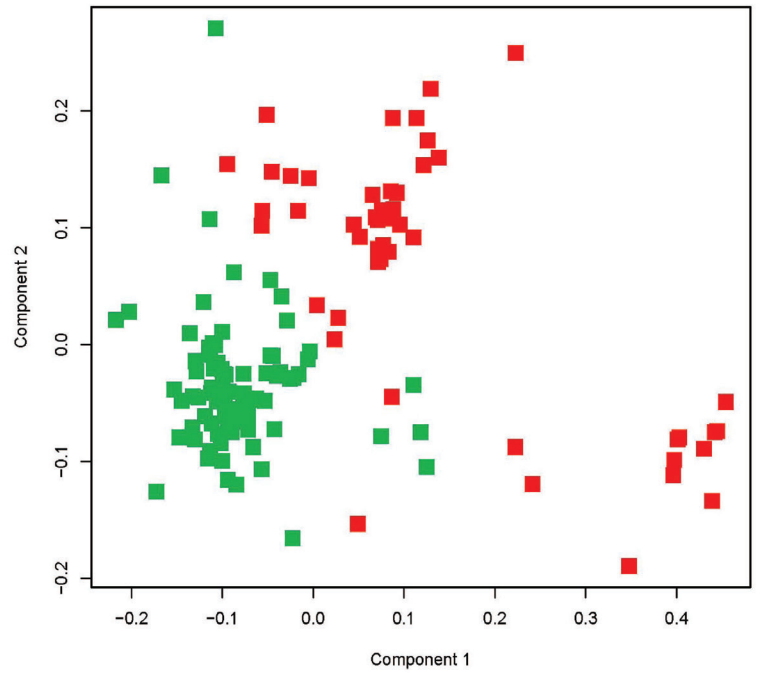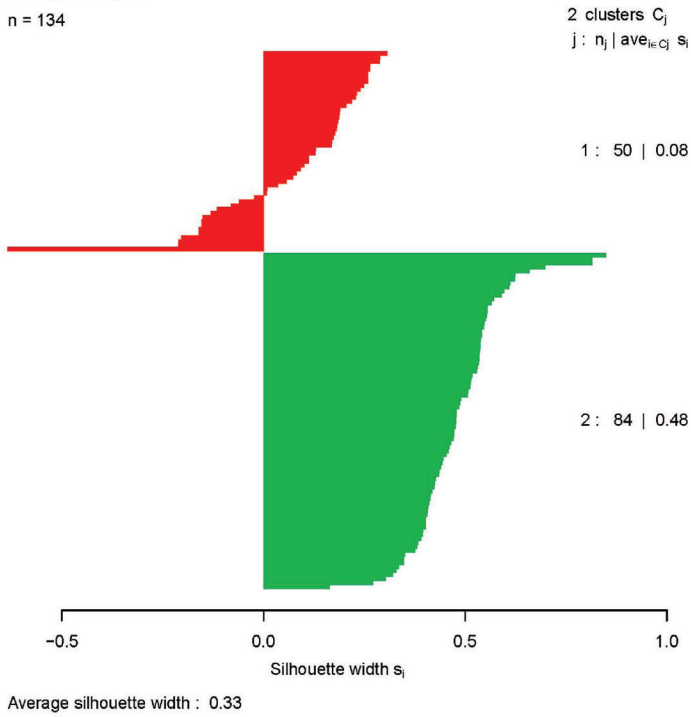
Supplemental Figure 2. Spearman baraminic distance correlation (BDC) results for all of the taxa in the dataset. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
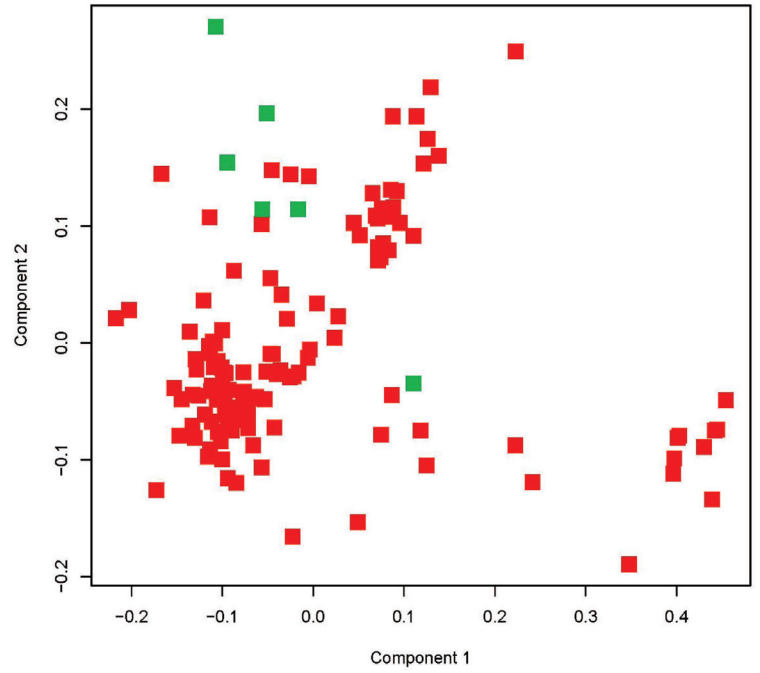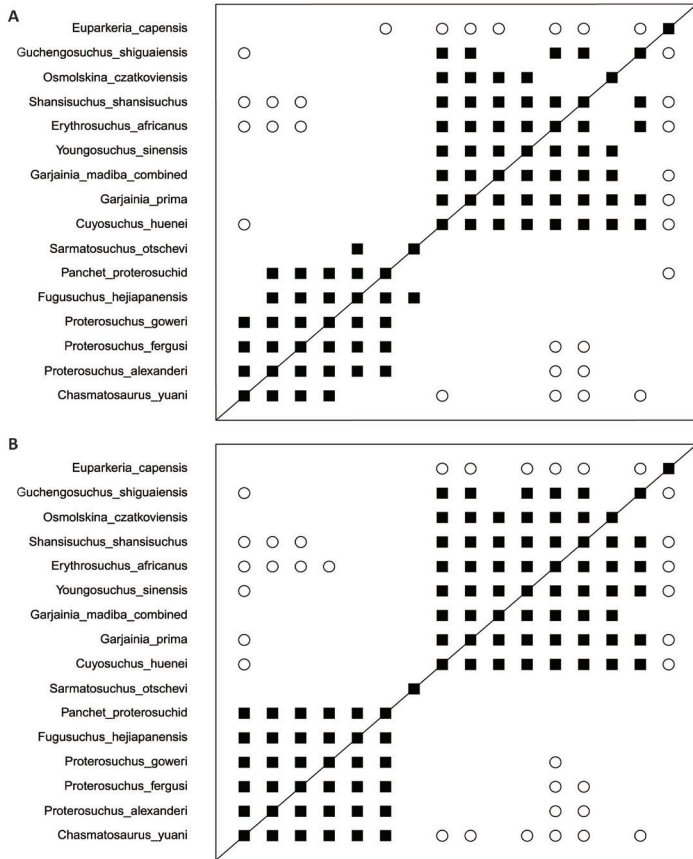
Supplemental Figure 3. Partitions around medoids (PAM) and fuzzy analysis (FANNY) for all of the taxa in the dataset: A) PAM and B) FANNY.
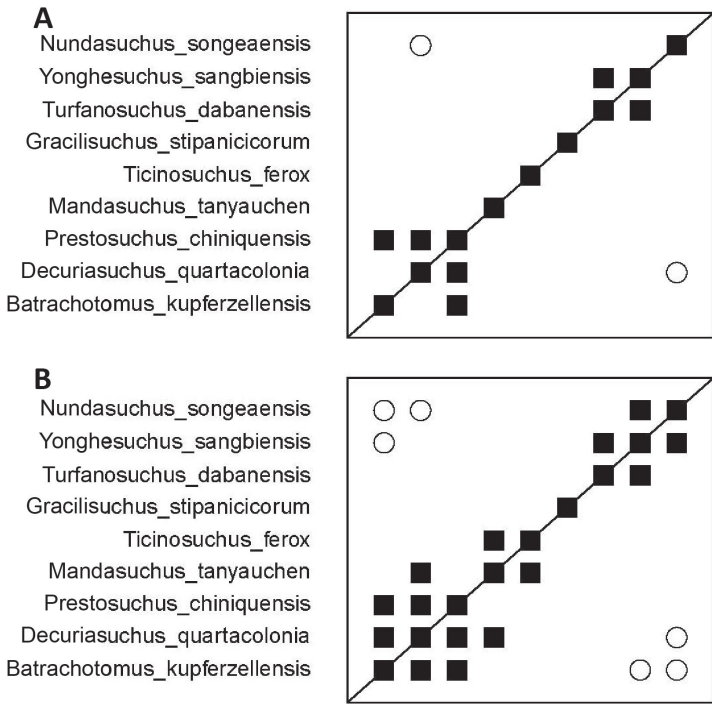
Supplemental Figure 4. Baraminic distance correlation (BDC) results for the Proterosuchidae + Erythrosuchidae subset dataset including *Euparkeria* and *Osmolskina* using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
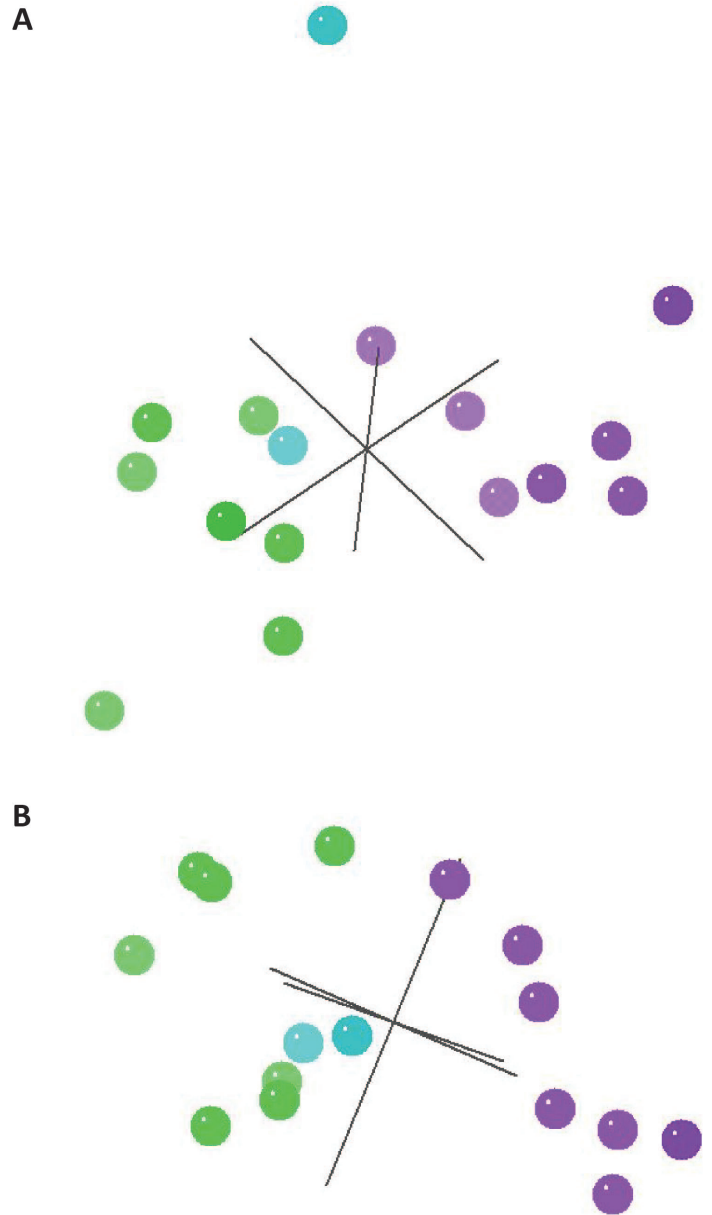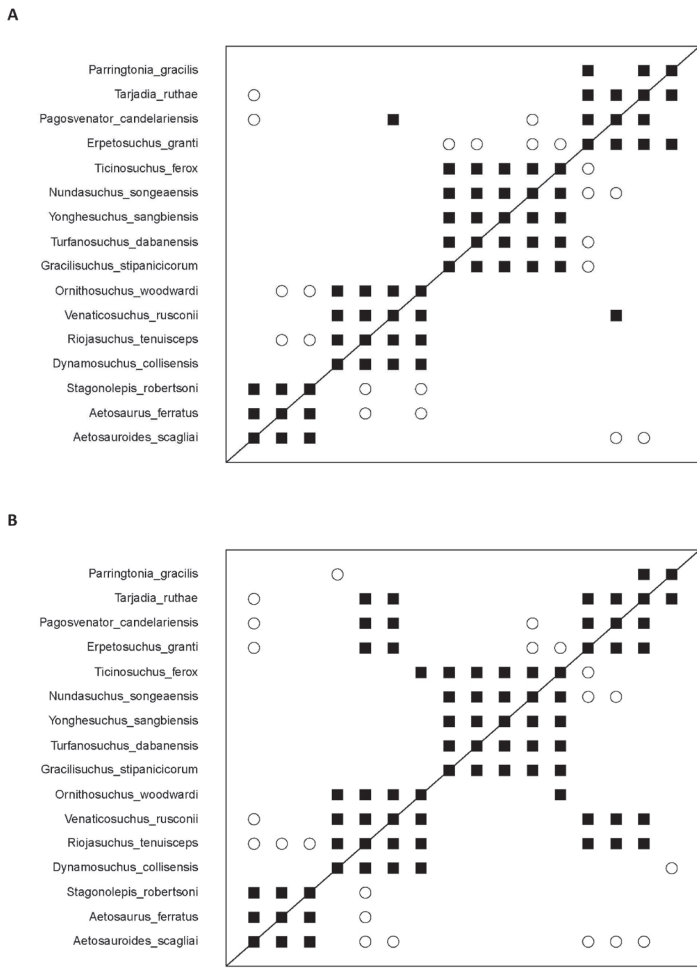

Supplemental Figure 5. 3D multidimensional scaling (MDS) results for the Proterosuchidae + Erythrosuchidae subset dataset including *Euparkeria* and *Osmolskina* in three views: A, B, and C. Colors: Green – Erythrosuchidae; purple – Proterosuchidae; light blue – Euparkeriidae (*Euparkeria* and *Osmolskina*).

Supplemental Figure 6. Baraminic distance correlation (BDC) results for the extra *Ticinosuchus* subset analysis using: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
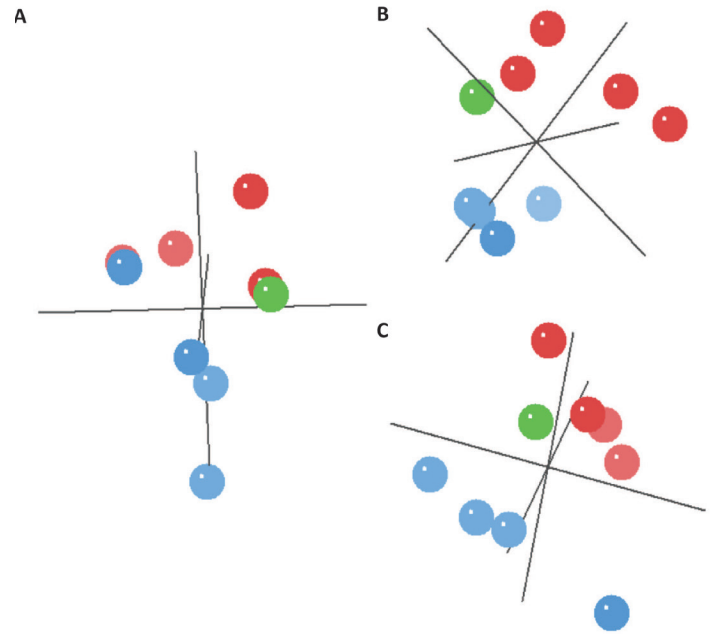

Supplemental Figure 7. 3D multidimensional scaling (MDS) results for the extra *Ticinosuchus* subset dataset in three views: A, B, and C. Colors: Blue – Gracilisuchidae + *Nundasuchus*; red – Loricata; green – *Ticinosuchus*.

Supplemental Figure 8. Baraminic distance correlation (BDC) results for the Erpetosuchidae + non-paracrocodylomorph Pseudosuchia subset dataset: A) Pearson correlation coefficient and B) Spearman correlation coefficient. Black squares indicate significant positive correlation, whereas open circles indicate significant negative correlation.
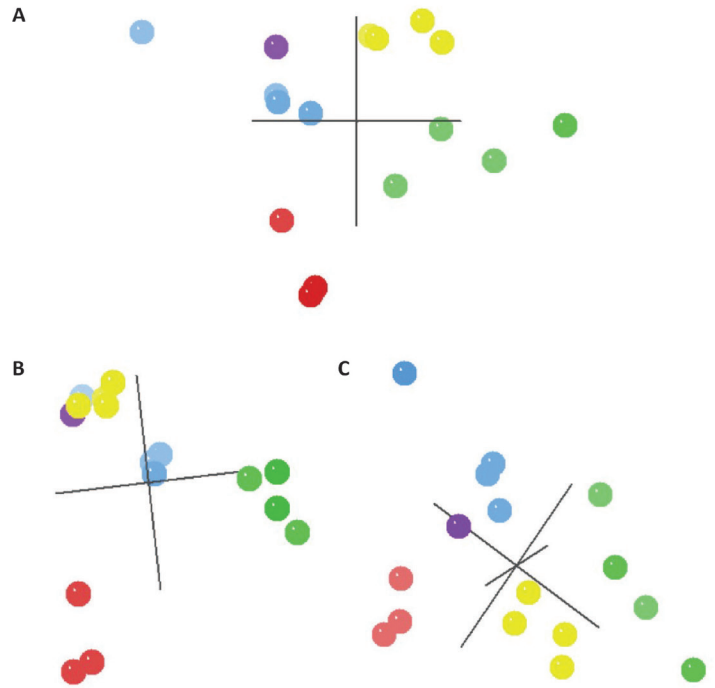

Supplemental Figure 9. 3D multidimensional scaling (MDS) results for the Erpetosuchidae + non-paracrocodylomorph Pseudosuchia subset dataset in three views: A, B, and C. Colors: Yellow - Ornithosuchidae; Red - Aetosauria; Blue - Gracilisuchidae; Green – Erpetosuchidae (including *Parringtonia*); Purple - *Ticinosuchus*.
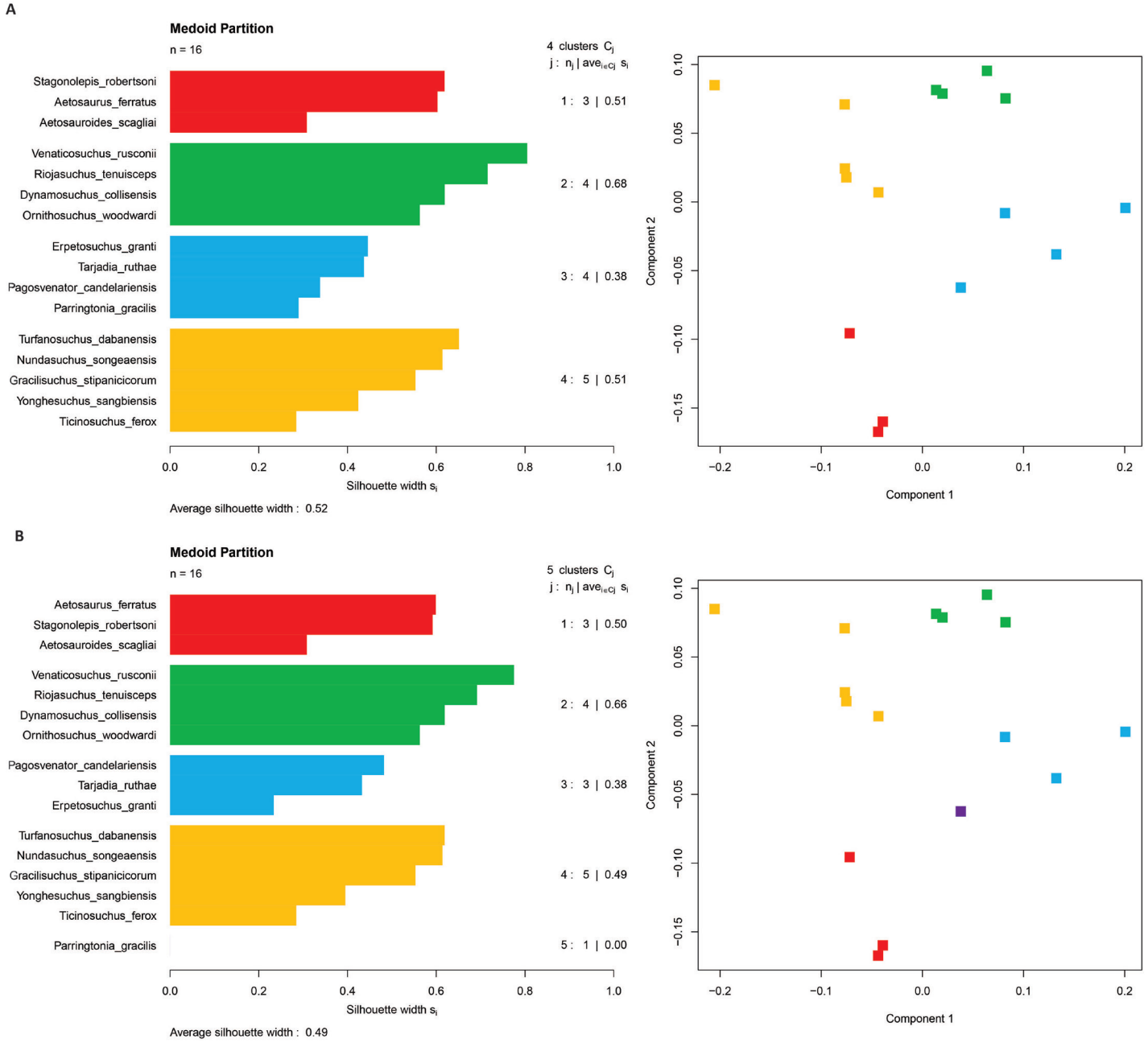
Supplemental Figure 10. Partitions around medoids (PAM) analysis of the Erpetosuchidae + non-paracrocodylomorph Pseudosuchia subset dataset in: A) four groups and B) five groups.
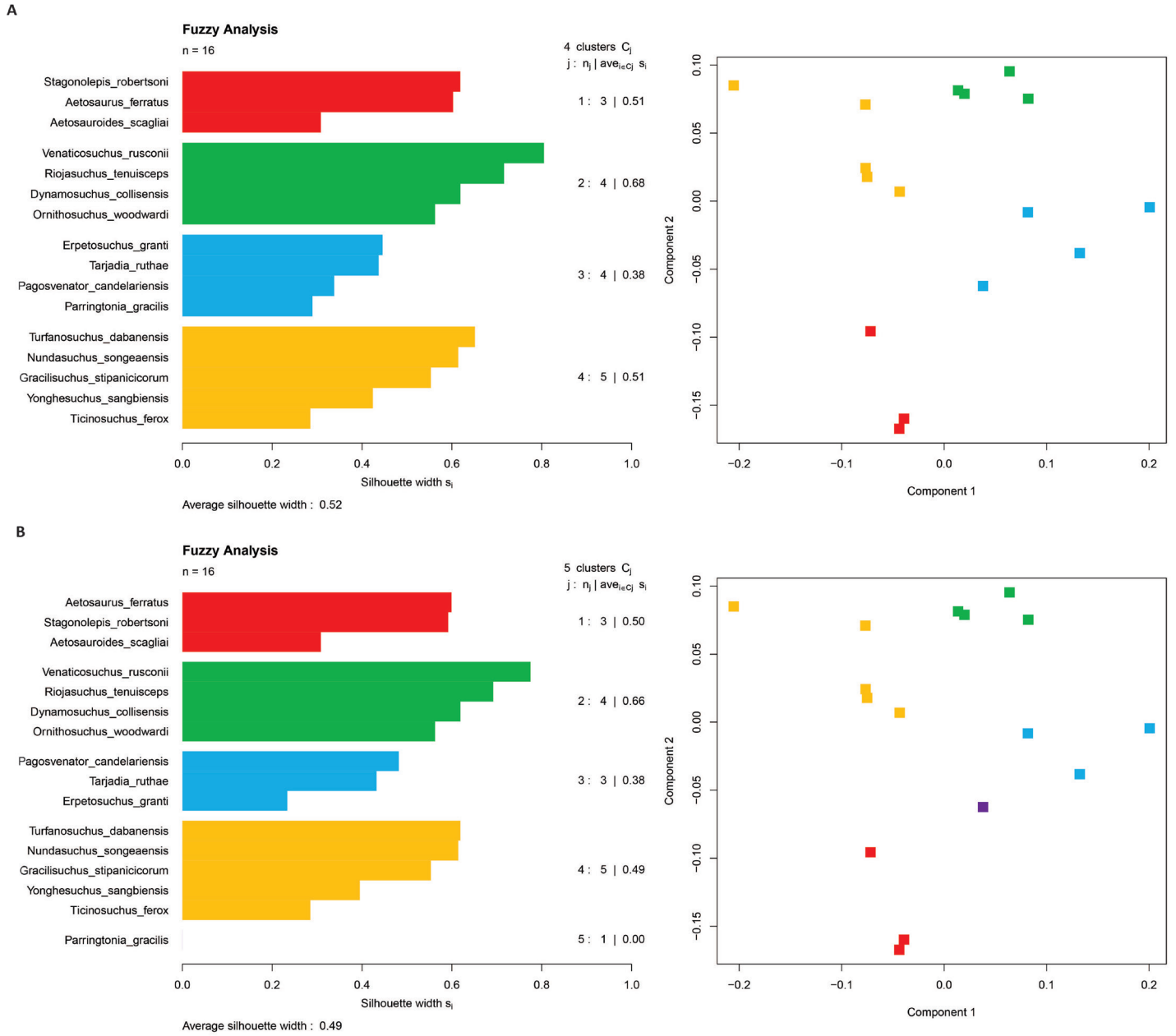
Supplemental Figure 11. Fuzzy analysis (FANNY) of the Erpetosuchidae + non-paracrocodylomorph Pseudosuchia subset dataset in: A) four groups and B) five groups.

SUPPLEMENTAL TABLE

Supplemental Table 1. List of poorly known taxa in the Kellner, et al. (2022) dataset that were excluded by a 0.2 character relevance cutoff.

Taxon	Taxonomic Group	Completeness
Aenigmastropheus_parringtoni	"Protorosauria"	0.055
Allkaruen_koi	Pterosauria	0.162
Ammorhynchus_navajoi	Rhynchosauria	0.086
Antarctanax_shackletoni	Archosauriformes i.s.	0.087
Archeopelta_arborensis	Erpetosuchidae	0.142
Archosaurus_complete	Proterosuchidae	0.123
Archosaurus_rossicus_holotype	Proterosuchidae	0.027
Arctosaurus_osborni	Allokotosauria?	0.017
Asperoris_mnyama	Archosauriformes i.s.	0.152
Augustaburiania_vatagini	Tanystropheidae	0.104
Azendohsaurus_laaroussi	Azendohsauridae	0.095
Bromsgroveia_walkeri	Ctenosauriscidae	0.05
Bystrowisuchus_flerovi	Ctenosauriscidae	0.022
C_magnus_combined	Proterosuchidae	0.036
C_rossicus_combined	Proterosuchidae	0.058
Chalishevia_cothurnata	Erythrosuchidae	0.141
Chanares_rhynchosaur	Rhynchosauria	0.069
Chasmatosuchus_vjushkovi	Proterosuchidae	0.033
Ctenosauriscus_koeneni	Ctenosauriscidae	0.061
Dagasuchus_santacruzensis	Loricata	0.038
Dongusuchus_efremovi	Aphanosauria	0.051
Dorosuchus_neoetus	Euparkeriidae?	0.152
Dromomeron_gigas	Lagerpetidae	0.044
Dromomeron_gregorii	Lagerpetidae	0.169
Dyoplax_arenaceus	Erpetosuchidae?	0.073
Eorasaurus_olsoni	Archosauromorpha i.s.	0.035
Erpetosuchus_sp	Erpetosuchidae	0.128
Faxinalipterus_minimus	Lagerpetidae?	0.046
Fodonyx_spenceri	Rhynchosauria	0.196
Fuyuansaurus_acutirostris	Tanystropheidae?	0.194
Halazhaisuchus_qiaoensis	Euparkeriidae?	0.126
Hypselorhachis_mirabilis	Ctenosauriscidae?	0.033
K_australiensis_combined	Prolacertidae	0.16
Kalisuchus_rewanensis_holotype	Archosauriformes i.s.	0.067
Koilamasuchus_gonzalezdiazi	Archosauriformes i.s.	0.04
Kongonaphon_kely	Lagerpetidae	0.1
Luperosuchus_fractus	Loricata	0.151
Lutungutali_sitwensis	Silesauridae	0.045
Macrocnemus_obristi	Tanystropheidae	0.114
Maehary_bonapartei	Lagerpetidae?	0.13
Mesodapedon_kuttyi	Rhynchosauria	0.058
Moenkopi_poposauroid	Poposauroidea	0.056

Taxon	Taxonomic Group	Completeness
NMQR_3570	Archosauriformes i.s.	0.056
Nyasasaurus_parringtoni	Dinosauria?	0.062
Osmolskina_czatkoviensis	Euparkeriidae?	0.038
Otter_Sandstone_archosaur	Archosauria i.s.	0.062
Paliguana_whitei	Lepidosauromorpha	0.159
Prolacertoides_jimusarensis	Archosauromorpha i.s.	0.126
Protanystropheus_antiquus	Dinocephalosauridae	0.026
PVSJ_883	Lagerpetidae	0.012
Rhadinosuchus_gracilis	Proterochampsidae	0.163
Shansisuchus_kuyeheensis	Erythrosuchidae	0.122
Spondylosoma_absconditum	Aphanosauria	0.104
Tanystropheus_haasi	Tanystropheidae	0.013
Tasmaniosaurus_triassicus	Proterosuchidae?	0.162
Trachelosaurus_fischeri	"Protorosauria"	0.115
Triopticus_primus	Protopyknosia	0.128
Uralosaurus_combined	Erythrosuchidae	0.049
Vonhuenia_fredericki	Archosauriformes i.s.	0.029
Vytshegdosuchus_zbeshartensis	Paracrocodylomorpha	0.012
Waldhaus_poposauroid	Poposauroidea	0.41