**Supplemental Text S1:**

**Additional Information relating to Phylogenetic analyses**

New small-bodied ornithopods (Dinosauria, Neornithischia) from the Early Cretaceous Wonthaggi Formation (Strzelecki Group) of the Australian-Antarctic rift system with revision of *Qantassaurus intrepidus* Rich & Vickers-Rich, 1999

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# 1. Phylogenetic taxonomy

The majority of the following phylogenetic definitions follow those listed in Madzia et al. (2018: Supplemental Appendix 1), to which readers may refer for additional remarks on clade definitions. However, several of the definitions are further revised here.

**Ornithischia** Seeley (1887)—Stem-based: the most inclusive clade containing *Triceratops* *horridus* but not *Passer domesticus* or *Saltasaurus loricatus* (also see Norman et al., 2004; sensu Sereno, 2005; Baron et al., 2017 for similar, compatible definitions).

**Genasauria** Sereno (1986)—Node-based: the least inclusive clade containing *Ankylosaurus magniventris*, *Parasaurolophus* *walkeri* and *Triceratops* *horridus* (sensu Sereno, 1998).

**Thyreophora** Nopcsa (1915)—Stem-based: the most inclusive clade containing *Ankylosaurus magniventris* but not *Triceratops* *horridus* (sensu Sereno, 1998).

**Neornithischia** Cooper (1985)—Stem-based: the most inclusive clade containing *Triceratops* *horridus* and *Parasaurolophus* *walkeri* but not *Ankylosaurus magniventris* (sensu Butler et al., 2008).

**Jeholosauridae** Han et al. (2012)—Stem-based: the most inclusive clade containing *Jeholosaurus* *shangyuanensis* but not *Hypsilophodon* *foxii*, *Iguanodon* *bernissartensis*, *Protoceratops* *andrewsi*, *Pachycephalosaurus* *wyomingensis* or *Thescelosaurus* *neglectus* (original definition of Han et al., 2012)

**Thescelosauridae** Sternberg (1937)—Node-based: the least inclusive clade containing *Thescelosaurus neglectus* and *Orodromeus makelai*, but not *Iguanodon* *bernissartensis* (sensu Madzia et al., 2018: Supplemental Appendix 1).

Comment—In the scenario where this clade includes both *Parksosaurus* *warreni* and *Thescelosaurus* *neglectus*, the name Thescelosauridae Sternberg (1937) has priority over Parksosauridae (Buchholz, 2003) by 66 years, and is contrary to some recent works that have instead misused the junior synonym (e.g., Boyd, 2015; Rivera-Sylva et al., 2018).

**Elasmaria** Calvo et al. (2007)—Stem-based: the most inclusive clade containing *Macrogryphosaurus* *gondwanicus* and *Talenkauen* *santacrucensis*, but not *Iguanodon* *bernissartensis* or *Hypsilophodon* *foxii* (revised definition).

Comment—When originally established in Calvo et al. (2007), the proposed definition of Elasmaria contained only the species *Macrogryphosaurus* *gondwanicus* and *Talenkauen* *santacrucensis*, implying it was a node-based clade (although not specified). This definition was reiterated by Madzia et al. (2018: Supplemental Appendix 1). However, an issue with the original definition without external specifiers is that in situations where one of *M.* *gondwanicus* or *T.* *santacrucensis* is found to be closer to Iguanodontia than the other, Elasmaria would then include iguanodontians. In this scenario, depending on the position of the specifiers Elasmaria could become synonymous with Ornithopoda or Clypeodonta. Clearly, such an expansive application of the node Elasmaria was not originally intended. To avoid such a scenario, we augmented the definition in Madzia et al. (2018) with external specifiers. Thus, if *M.* *gondwanicus* and *T.* *santacrucensis* do ever form paraphyletic branches relative to more nested neornithischians, the revised ‘self-destructing’ aspect of the definition allows for its non-use.

Secondly, we have elected to **re-define Elasmaria as a stem- rather than node-based clade**. The exact arrangement within the taxic assemblage we consider to be ‘elasmarians’ is presently fluid and alters with minor adjustments in the underlying data (see main text Figs. 26; also see Rozadilla et al., 2016: fig.7). One plausible topology is where *M.* *gondwanicus* and *T.* *santacrucensis* are sister taxa nested inside a larger clade that includes other taxa such as *Anabisetia* or *Gasparinisaura*. In this scenario, retaining the node-based definition would render the name only applicable to the limited *M.* *gondwanicus* + *T.* *santacrucensis* node, while the larger clade would be without a name. Given that the larger plexus of taxa is under more consideration, both in this work and recently by others (e.g., Rozadilla et al., 2016; Madzia et al., 2018), the best practice would be to reallocate use of the name Elasmaria to this context, rather than create new names (particularly for poorly supported clades).

**Clypeodonta** Norman (2014)—Node-based: the least inclusive clade containing *Hypsilophodon foxii* and *Edmontosaurus regalis* (sensu Norman, 2015; for additional remarks pertinent to the prevailing use of Clypeodonta in this work, see Madzia et al., 2018: Supplemental Appendix 1).

**Cerapoda** Sereno (1986)—Node-based: the least inclusive clade containing *Triceratops* *horridus* and *Parasaurolophus* *walkeri* (sensu Butler et al., 2008).

**Marginocephalia** Sereno (1986)—Stem-based: the most inclusive clade containing *Triceratops* *horridus* and *Pachycephalosaurus* *wyomingensis* but not *Parasaurolophus* *walkeri* (new revised definition).

Comment—Concurrent definitions of Marginocephalia are node-based, employing ceratopsian and pachycephalosaurian taxa as internal specifiers (e.g., Madzia et al., 2018: Supplemental Appendix 1). However, such definitions are not complementary with present definitions of Cerapoda and Ornithopoda within a node-stem triplet arrangement of clades (Sereno, 1998; Sereno, 1999). Here, re-definition of Marginocephalia as a stem now mirrors its sister stem clade, Ornithopoda, within a node-based Cerapoda. As a result, this stabilization of definition allows for the definitive assignment of all cerapodan OTUs either as ornithopods or marginocephalians.

The re-definition does not have a bearing on the referral of existing ‘basal’ marginocephalian OTUs to either the ceratopsian and pachycephalosaurian stem lineages. This is because so far no taxa have been consistently referred with robust support to the base of the “marginocephalian stem” (*sensu* *lato*) but outside the *now* unnamed node “Ceratopsia+Pachycephalosauria.” If such a potential situation arises, the arrangement and definitions of clades within Marginocephalia will require additional revision.

**Ornithopoda** (Marsh, 1881)—Stem-based: the most inclusive clade containing *Parasaurolophus* *walkeri* but not *Triceratops* *horridus* or *Pachycephalosaurus* *wyomingensis* (modified from the definition of Madzia et al., 2018: Supplemental Appendix 1).

**Iguanodontia** (Baur, 1891)—Node-based: the least inclusive clade containing *Iguanodon* *bernissartensis*, *Dryosaurus* *altus*, *Rhabdodon* *priscus*, and *Tenontosaurus* *tilletti*, but not *Triceratops* *horridus* (modified from the definition of Madzia et al., 2018: Supplemental Appendix 1).

Comment—(1) It is worth stressing that the current definition of Iguanodontia that we follow is much more inclusive than other concepts of Iguanodontia (e.g., Norman, 2015), by virtue of *active* inclusion of rhabdodontids and *Tenontosaurus*. Nonetheless, the possibility, albeit highly remote, that the internal specifiers *Rhabdodon* *priscus*, and *Tenontosaurus* *tilletti* might be found in a position outside of Cerapoda by some analyses, rendering the clades Iguanodontia and Cerapoda synonyms if the clade definitions of Madzia et al. (2018) are strictly followed. Our addition of an external specifier, *Triceratops* *horridus*, attempts to prevent such a potential predicament. Notably, the recent topological results of Norman (2015: fig. 52) may suggest such a potential relationship, however the lack of inclusion of marginocephalians, and therefore the definite pinpointing of “Cerapoda,” in Norman’s results in ambiguity.

(2) The authorship of Iguanodontia is regularly misattributed, often being confused with the family-group name Iguanodontidae (earliest use by Cope, 1869, p. 91). Because Iguanodontidae is a family-group name its authorship is governed by the “Principle of Coordination” (ICZN, Article 36.1), which importantly does not apply to Iguanodontia. The first proposal of Iguanodontia was made by Baur (1891), who suggested the name as one of three major groups of dinosaurs (in Baur’s view, Dinosauria was an unnatural group and thus required separation). The establishment of Iguanodontia was made without reference to Iguanodontidae, and in the context of Baur’s arguments, cannot possibly be construed as a coordinated family-group name (Baur, 1891: however, he was aware of Iguanodontidae as a separately pre-established name, by mentioning it several times early in his paper). The earliest phylogenetic employment of Iguanodontia was by Sereno (1986), who attributed the name to Dollo (1888). Dollo’s paper, however, made no mention of Iguanodontia, only to the family Iguanodontidae (which, irrespective, should have been attributed to Cope, 1869, among multiple authors who preceded Dollo [1888] in using that name). Unfortunately, subsequent works have followed Sereno (1986), in misattributing Iguanodontia to Dollo, 1888 (e.g., Sereno, 1998; Sereno, 2005; Carpenter and Ishida, 2010; Norman, 2011; Norman, 2012; Madzia et al., 2018) or even to Sereno, 1986 (e.g., Norman, 2015). In summary, non-coordination (via ICZN article 36.1) between Iguanodontia (Baur, 1891) and Iguanodontidae (Cope, 1869) renders Baur, 1891 the correct nominal author of the former name.

**Rhabdodontidae** Weishampel et al. (2003)—Node-based: the least inclusive clade containing *Rhabdodon* *priscus* and *Zalmoxes robustus* (sensu Weishampel et al., 2003).

**Dryomorpha** Sereno (1986)—Node-based: the least inclusive clade containing *Dryosaurus altus* and *Parasaurolophus* *walkeri* (sensu Madzia et al., 2018: Supplemental Appendix 1).

**Dryosauridae** Milner and Norman (1984)—Stem-based: the most inclusive clade containing *Dryosaurus altus* but not *Parasaurolophus* *walkeri* (sensu Sereno, 1998).

**Ankylopollexia** Sereno (1986)—Node-based: the least inclusive clade containing *Camptosaurus* *dispar* and *Parasaurolophus* *walkeri* (sensu Sereno, 1998).

Comment—Ankylopollexia and its branching stems (Styracosterna and Camptosauridae/*Camptosaurus* spp.) form a node-stem-triplet.

**Camptosauridae** Marsh (1889: in replacement of Camptonotidae [Marsh, 1881])—Stem-based: the most inclusive clade containing *Camptosaurus* *dispar* but not *Parasaurolophus* *walkeri* (sensu Sereno, 1998).

**Styracosterna** Sereno (1986)—Stem-based: the most inclusive clade containing *Parasaurolophus* *walkeri* but not *Camptosaurus* *dispar* (sensu Sereno, 1998).

**Remark on clade names in phylogenetic figures**

Selected clade labels in Figure 25 follow a strict application of the pre-agreed phylogenetic taxonomy (see section 1, above) in combination with only fully unambiguously resolved clades — i.e., “approximately-resolved clades” in polytomies are not labelled because they breach aspects of the phylogenetic definitions. In short, a polytomy prevents the strict reporting of conventional stem and node clades at that position, within the scope of the specific topology being shown.

# 2. Further remarks on operational taxonomic units and dataset completeness

*Pisanosaurus* *mertii* is now understood to be a probable silesaurid, and not an ornithischian (let alone a dinosaur) (Agnolín and Rozadilla, 2018). It was removed as a problematic OTU from the dataset of Dieudonné et al. (2016), due its high missing data coupled with potentially ambiguous character scores made under the prevailing view the taxon was an ornithischian.

Five marginocephalian taxa were added to the dataset of Dieudonné et al. (2016): *Homalocephale* *calathocercos*, *Stegoceras* *validum*, *Goyocephale* *lattimorei*, *Liaoceratops* *yanzigouensis* and *Protoceratops* *andrewsi* (Gilmore, 1924; Brown and Schlaikjer, 1940; Maryanska and Osmolska, 1974; Perle et al., 1982; Galton and Sues, 1983; Xu et al., 2002; Tanoue et al., 2009; He et al., 2018) . The decision to include additional marginocephalians arose out of a problem observed in a previous analysis (Herne et al., 2018), where the position of the major node Cerapoda was highly volatile with minor changes to the dataset of Dieudonné et al. (2016), rendering the assignment of many OTUs within and external to the clade uncertain. Cerapoda is composed of two branches—Ornithopoda and Marginocephalia, however, the purported ornithopodan affinities of certain taxa of key interest cannot be appropriately confirmed if marginocephalians are not appropriately represented. Specifically: (1), pachycephalosaurs, comprising a major sub-branch of Marginocephalia, were not represented as OTUs in the dataset of Dieudonné et al. (2016), and (2), the marginocephalians that were included therein were found be frequently mis-scored or not scored at all in instances when character data was available. Regarding the latter, approximately 43% of the scores have been altered for the OTU Psittacosauridae; however, the substantial filling of the previously missing data in *Yinlong* *downsi* is understandable due to the postcranial information being only recently available (Han et al., 2018).

Following revision of character codings and a rescoring of the dataset, a survey of missing data (by OTU) was made. Several taxa, especially the Victorian taxa focal to this work, remain among the most poorly scored of the OTUs (in bold):

|  |  |
| --- | --- |
| Taxon | Proportion of missing data |
| *Lycorhinus angustidens* | 91.8% |
| ***Galleonosaurus dorisae*** | 91.7% |
| *Owenodon hoggii* | 90.4% |
| *Echinodon becklesii* | 89.8% |
| ***Qantassaurus intrepidus*** | 89.7% |
| ***Diluvicursor pickeringi*** | 89.4% |
| *Mochlodon suessi* | 89.4% |
| *Yueosaurus tiantaiensis* | 87.4% |
| *Macrogryphosaurus gondwanicus* | 87.4% |
| *Koreanosaurus boseongensis* | 84.4% |
| Vegagete ornithopod | 82.4% |
| ***Leaellynasaura amicagraphica*** | 81.7% |
| *Mochlodon vorosi* | 79.1% |

# 3. Implied weighted K-factor selection

**Homoplasy and character weighting**

The best fit a binomial character can achieve during a heuristic tree search in a cladistic analysis is one step (Farris, 1969). Thus, a binary character is 100% consistent to the cladogram if it undergoes only one change (step) at a single node. A character that transforms its state in steps beyond one is less than 100% consistent and is homoplastic. Homoplasy naturally occurs during evolution, which is evident as convergence (e.g., Witmer, 1997, on the highly homoplastic character of the antorbital sinuses in dinosaurs). Naturally occurring reversals (convergence) may be detected in a cladistic analysis. Problematically, however, homoplastic character-state reversals can also result from coding (poorly construed characters) and scoring errors.

In cladistic analyses, highly homoplastic characters that undergo multiple reversals are less reliable, or less consistent (Farris 1969). During analyses, some characters are unstable, being more homoplastic in some trees and less in others, while some characters perform poorly in all trees (Farris, 1969). Still other characters have better fit in all trees, and in this aspect are more reliable, or congruent (Farris, 1969).

In a hypothetical character set in which all the characters are highly reliable, hierarchic correlations will emerge (following Farris, 1969). In practice, correlation of hierarchical pattern will be evident in well-resolved groups following the strict consensus of the most parsimonious trees. Unreliable characters will vary from the expected phylogeny in random ways during different analyses. Thus, according to Farris (1969), hierarchical patterns (groups/clades) are more likely to emerge from character data containing highly reliable characters than data sets containing highly unreliable characters.

Under equal weighting methodology, the weight or value of each character is allocated an equal value (a character weight of 1), which seemingly allows the analysis of parsimony to determine relationships without any *a priori* assumptions of the importance of some characters over others. Conceptually, equal weighting of characters during a heuristic search implies no bias towards particular characters. However, equal weighting is a misnomer as the reliability/quality of characters inherently differ. Under equal weighting, less reliable characters are in effect, arbitrarily up-weighted to equal the weight of more reliable characters (Goloboff, 1993; Goloboff et al., 2008). Thus, equal weighting ignores potential differences in character congruence as a factor during parsimony analysis. According to Goloboff et al. (2008), the weight of characters must be considered integral to the outcome of any analysis. However, while the potential importance of some characters over others is understood, reweighting of characters *a priori*, based on arguments of importance, is often problematic (Kitching et al., 1998).

**Character weighting *a posteriori***

In simulation tests conducted by Farris (1969), iterative *a posteriori* adjustment of character weighting was applied to the characters. Increasingly more homoplastic characters were increasingly down-weighted. Farris (1969) found that a logarithmic (concave) function applied to characters gave the closest estimate of the true tree. Farris (1969) also explored linear and convexly decreasing functions; however, these functions were inappropriate to the expected tree. According to Farris (1969), a “concave weight function … achieves a perfect estimate of the true tree even when unreliable characters outnumber reliable characters five to one.” On a concave function, the character weight rapidly decreases within a few extra steps from best fit (i.e., a character with no additional steps beyond one step). On a concave function, the level of down weighting also increases in characters that are increasingly more homoplastic.

Under an iterative *a posteriori* weighting method called successive weighting, developed by Farris (1969), characters are re-weighted based upon consistency to the expected true phyletic tree from the data set. Successive trees are constructed from characters that have been weighted based upon their reliability in the preceding tree. Thus, under *a posteriori* weighting methodology, characters are down-weighted during the analysis according to their degree of homoplasy, which is measured by the consistency, or fit of the character during the analysis. These analyses are therefore self-consistent (Goloboff, 1993).

The degree of homoplasy of each character is determined by the number of extra steps beyond that of best fit (i.e., additional steps beyond 1) on a logarithmic curve, controlled by the concavity constant (*k*). The weight (W) of a character is calculated by W= *k*/(*k*+1), where W equals the weight and k is the concavity constant Farris (1969). A low concavity constant (e.g., *k*=1) results in a highly concave curve (Fig. C2.1). Thus, in a highly concave weighting function, such as *k*=1, a low number of additional steps (reversals) applies an aggressive reduction in weight to characters with one additional step, while weight reduction is increasingly less for increasingly homoplastic characters. Thus, the optimal *k* value is not too low and not too high (Farris, 1969). A low value, such as ‘1’ will result in a clique (an unnatural grouping), while a high value approaches that of equal weighting (Fig. C2.1).

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**Above:** Example plots of concavity constants upon which a posteriori weighting methods are based. Increasing values of k approaches equal character weighting (=1). Abbreviations: IW(k#) = Implied weighting concavity constant; and W = character weight.

**Basis for implied weighting method (in TNT)**

Under implied weighting, the weight of a homoplastic character is determined during the succession of heuristic tree searches. Homoplastic characters are down-weighted to values below the optimum (i.e., fractions <1), as determined by the concavity constant (*k*). As the best fit all characters can have one step, the trees with the highest congruence will have the greatest length. In other words, the most parsimonious trees selected have the least amount of homoplasy. This conceptually differs from parsimony analysis through equal weighting where trees are selected by the shortest number of steps.

According to Goloboff (1993), there is no optimal value of *k* that can be readily assigned as the best weighting function for all data sets. Different character data behave differently, and the most suitable value of *k* will be matrix dependent (also see Mirande, 2009, p. 576). Furthermore, different groups (clades) within the data are also likely to behave differently (Goloboff, 1993). For this reason, a number of values for *k* are typically applied, and the preferred strict consensus tree is chosen from the range of hypothesised trees from the IW analyses that consistently resolve similar group relationships (following Goloboff, 1993). Although implied weighting is not a perfect method, it provides better resolution of potential relationships than is possible under equal weighting methods (Goloboff, 1993; Goloboff et al., 2008). Following this approach, a *k* value of 7.0 (k7) was decided for the IW analyses herein.



**Above:** Plot of k7 concavity constant weighting for characters used in the cladistic analysis.

# 4. Support measures for the strict consensus trees

**Equal weighted (EW) search:**

To avoid cluttering, bootstrap and Bremer support values were omitted from Fig. 25.1. In the EW strict consensus tree below, top row numbers are bootstrap support values reported as frequency distributions (see main text; only values >20 are reported). Bottom row numbers are Bremer values (only values >1 are reported).



**Implied weighted (IW) search**

To avoid cluttering, symmetric resampling and Bremer support values were omitted from Fig. 25.2. In the IW strict consensus tree below, top row numbers are symmetric resampling support values reported as frequency distributions (see main text; only values >20 are reported). Bottom row numbers are Bremer values (only values >fit scores of 0.08 are reported.

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# 5. Iterative PCR

**Iterative PCR of the IW set of most parsimonious trees**

Application of iterative PCR of the implied weighted (IW) set of 26 MPTs sequentially pruned:

1. *Qantassaurus* (iteration 1)

2. *Diluvicursor* (iteration 2)

The first iteration achieved the node Elasmaria, previously unresolved among basal ornithopods in the full IW strict consensus (see Figure 25.2). The second iteration produced additional resolution within Elasmaria, ultimately grouping *Galleonosaurus* and *Leaellynasaura* as sister taxa:



**Iterative PCR of the EW set of most parsimonious trees**

As we reported in the main text, iterative PCR of the equally weighted (EW) set of 814 MPTs pruned the majority of neornithischian OTUs (41), including all taxa of particular interest to this work. The resulting strict consensus (based on 4 MPTs) of retained OTUs shows only 15 taxa: *Herrerasaurus*, heterodontosaurids, thyreophorans, *Lesothosaurus*, *Agilisaurus*, *Yandusaurus* and *Hexinlusaurus*. Accordingly, we have elected not to report these results in any further detail.

# 6. List of character state changes (optimized synapomorphies)

The following is a list of supporting characters for selected nodes of the strict consensus following the *a priori* exclusion of *Qantassaurus intrepidus*, after its identification as a wildcard taxon by the iterative PCR protocol (See main text; Fig. 26). The IW search produced 3 MPTs, with the resulting strict consensus tree (depicted below) being 933 steps long (CI = 0.37; RI = 0.61). The annotations on the tree below identify the selected nodes of interest, and their lists of supporting characters that follow. Abbreviation: MNT = More nested taxa.



**Node 1: *Lesothosaurus* + MNT (Neornithischia)**

Character 137: 0 → 1

Character 163: 0 → 1

Character 244: 0 → 1

**Node 2: Jeholosauridae**

Character 48: 1 → 0

Character 59: 0 → 1

Character 117: 1 → 2

Character 192: 1 → 0

Character 201: 0 → 1

**Node 3: Thescelosauridae**

Character 29: 0 → 1

Character 80: 0 → 1

Character 118: 0 → 1

Character 170: 2 → 3

**Node 4: *Nanosaurus* + Jeholosauridae + Thescelosauridae**

Character 110: 0 → 1

Character 181: 0 → 1

**Node 5: Cerapoda + Node 4**

Character 115: 0 → 1

Character 126: 3 → 2

Character 170: 1 → 2

Character 226: 0 → 1

Character 228: 0 → 1

Character 249: 0 → 1

**Node 6: Cerapoda**

Character 38: 1 → 0

Character 73: 1 → 0

Character 146: 0 → 1

Character 162: 0 → 1

Character 185: 0 → 1

Character 241: 0 → 1

**Node 7: Marginocephalia**

Character 2: 0 → 1

Character 17: 1 → 0

Character 20: 0 → 1

Character 22: 0 → 1

Character 54: 0 → 1

Character 61: 0 → 1

Character 75: 0 → 1

Character 80: 0 → 1

Character 104: 0 → 1

Character 105: 0 → 1

Character 117: 1 → 0

Character 134: 0 → 1

Character 235: 1 → 0

Character 240: 0 → 1

Character 243: 2 → 0

Character 269: 0 → 2

**Node 8: Pachycephalosauria**

Character 3: 0 → 1

Character 5: 0 → 1

Character 27: 0 → 1

Character 45: 0 → 1

Character 47: 0 → 1

Character 51: 0 → 1

Character 56: 0 → 1

Character 100: 0 → 1

Character 124: 1 → 0

Character 130: 0 → 1

Character 154: 1 → 0

Character 184: 0 → 1

Character 196: 0 → 1

Character 200: 0 → 1

Character 202: 0 → 1

Character 219: 0 → 1

Character 224: 1 → 2

Character 293: 0 → 1

Character 298: 0 → 1

Character 303: 0 → 1

Character 330: 0 → 1

**Node 10: Ceratopsia**

Character 4: 0 → 1

Character 6: 0 → 1

Character 106: 1 → 0

Character 118: 0 → 2

Character 244: 1 → 0

Character 245: 0 → 1

Character 300: 0 → 1

Character 306: 0 → 2

**Node 10: *Parksosaurus* + MNT (Ornithopoda)**

Character 59: 0 → 1

Character 96: 0 → 1

Character 142: 0 → 1

Character 158: 0 → 1

Character 160: 0 → 1

Character 166: 0 → 1

Character 310: 0 → 1

Character 315: 0 → 1

**Node 11: Elasmaria + Clypeodonta**

Character 125: 0 → 1

Character 306: 0 → 2

**Node 12: Elasmaria**

Character 233 Pubis, prepubic process shape: 1 → 0

Character 308 Maxillary crowns, labial primary or prominent ridge position: 0 → 1

Character 311 Maxillary crowns, alignment of fully extending apicobasal ridges: 1 → 0

Character 334 Metatarsal I, distal end with T-shaped profile: 0 → 1

**Node 13:**

Character 328 Scapula, presence of supraglenoid fossa: 0 → 1

Character 335 Metatarsal II, form in proximal view: 0 → 1

**Node 14: *Galleonosaurus* + *Diluvicursor* + *Leaellynasaura* + *Anabisetia***

Character 180 Caudal ribs, location: 1 → 2

Character 322 Caudal vertebral neural spine angle relative to dorsal plane: 0 → 1

*Some trees:*

Character 309 Maxillary crowns, position of basal vertex relative to central axis of root: 0 → 1

**Node 15: *Hypsilophodon* + MNT (Clypeodonta)**

Character 70: 1 → 0

Character 117: 1 → 2

Character 163: 1 → 0

Character 305: 0 → 1

Character 312: 0 → 1

**Node 16: Iguanodontia**

Character 42: 0 → 1

Character 49: 0 → 1

Character 57: 0 → 1

Character 72: 0 → 1

Character 79: 0 → 1

Character 80: 0 → 1

Character 109: 1 → 0

Character 120: 0 → 1

Character 171: 0 → 1

Character 176: 0 → 1

Character 223: 1 → 0

Character 260: 0 → 1

**Node 17: Rhabdodontidae**

Character 126: 2 → 0

Character 157: 0 → 1

Character 240: 0 → 1

Character 261: 0 → 1

Character 300: 0 → 1

Character 307: 2 → 0

Character 311: 1 → 0

**Node 18: *Muttaburrasaurus* + MNT**

Character 13 Premaxilla, posterolateral process length: 0 → 1

Character 89 Supraoccipital, contribution to dorsal margin of the foramen magnum: 0 → 1

Character 259 Femur, form of posterior (flexor) intercondylar groove: 0 → 1

**Node 19:**

Character 19: 0 → 1

Character 90: 0 → 1

Character 233: 1 → 0

Character 269: 0 → 2

**Node 20: Dryomorpha**

Character 49: 1 → 0

Character 70: 0 → 1

Character 156: 0 → 1

Character 205: 0 → 1

Character 245: 0 → 1

Character 246: 0 → 1

Character 276: 0 → 1

Character 283: 0 → 2

Character 316: 0 → 1

**Node 21: Ankylopollexia**

Character 11: 0 → 1

Character 39: 0 → 1

Character 57: 1 → 0

Character 62: 0 → 1

Character 102: 1 → 2

Character 117: 2 → 3

Character 171: 1 → 2

Character 184: 0 → 1

Character 193: 0 → 1

Character 208: 0 → 1

Character 239: 0 → 1

Character 258: 0 → 1

Character 275: 1 → 0

# 7. Sources for taxon age ranges depicted in Figure 28

* *Anabisetia* (Coria and Calvo, 2002): Cerro Lisandro Formation, Rio Limay Subgroup, Neuquén Group (Leanza et al., 2004): late Cenomanian–early Turonian, Late Cretaceous (Leanza et al., 2004).
* *Camptosaurus* (Marsh, 1879; Marsh, 1885): From ‘Dinosaur Zones 2–3’ (Turner and Peterson, 1999), Salt Wash and Brushy Basin Members, Morrison Formation: middle Kimmeridgian–earliest Tithonian, Late Jurassic (Turner and Peterson, 1999).
* *Diluvicursor* (Herne et al., 2018): Eumeralla Formation, Otway Group: early Albian (Herne et al., 2018).
* Dryosauridae (Milner and Norman, 1984): The oldest record of a dryosaurid is *Callovosaurus leedsi* (Ruiz-Omeñaca et al., 2006; but see Gilmore, 1909 for an earlier assignment to *Dryosaurus*), from the lower Oxford Clay of the Peterborough Member, Oxford Clay Formation, considered to be middle Callovian in age (Ruiz-Omeñaca et al., 2006). The youngest record of a dryosaurid is an ilium, CD529 from New Zealand (Wiffen and Molnar, 1989), found in the Maungataniwha Sandstone Member, Tahora Formation (Crampton and Moore, 1990), and presently considered to be of middle Campanian age (Vajda and Raine, 2010). Although *Kangnasaurus* *coetzeei* (Haughton, 1915; Rogers, 1915) is sometimes considered to be a dryosaurid (e.g., Cooper, 1985 [as a 'dryosaurine']; Barrett et al., 2011), the precise age of its type locality is unknown beyond being of Late Cretaceous age (de Wit et al., 1992).
* *Galleonosaurus* n. gen.: Wonthaggi Formation, upper Strzelecki Group: late Barremian (this work).
* *Gasparinisaura* (Coria and Salgado, 1996): Anacelto Formation, Rio Colorado Subgroup, Neuquén Group (Leanza et al., 2004): early Campanian, Late Cretaceous (Leanza et al., 2004).
* *Hypsilophodon* (Huxley, 1870): Wessex Formation, Wealden Group: late Barremian, Early Cretaceous (Galton, 2012).
* *Leaellynasaura* (Rich and Rich, 1989): Eumeralla Formation, Otway Group: early Albian (Korasidis et al., 2016; Herne et al., 2018).
* *Macrogryphosaurus* (Calvo et al., 2007): Portezuelo Formation, Rio Neuquén Subgroup, Neuquén Group (Leanza et al., 2004): late Turonian–early Coniacian, Late Cretaceous (Leanza et al., 2004).
* *Muttaburrasaurus* (Bartholomai and Molnar, 1981): Mackunda Formation, Manuka Subgroup, Rolling Downs Group (QM F6140: Bartholomai and Molnar, 1981): and Allaru Mudstone, Wilgunyah Subgroup, Rolling Downs Group (QM F14921: Molnar, 1996): both formations are of late Albian age (Early Cretaceous).
* *Owenodon* (Galton, 2009): Durlston Formation, Purbeck Group (formerly the Purbeck Limestone Formation): middle Berriasian, Early Cretaceous (Galton, 2012; Norman, 2012).
* *Parksosaurus* (Parks, 1926; Sternberg, 1937): Tolman Member, Horseshoe Canyon Formation: early–middle Maastrichtian (Eberth and Braman, 2012; Eberth and Bell, 2014).
* Rhabdodontidae (Weishampel et al., 2003): Although the majority of rhabdodontids are Campanian–late Maastrichtian in age (Matheron, 1869; Weishampel et al., 2003; Van Itterbeeck et al., 2005; Chanthasit, 2010; Brusatte et al., 2017; Godefroit et al., 2017), the oldest occurrence is constrained by our phylogenetic results that posit the late Barremian–lower Aptian Vegagete specimen (Dieudonné et al., 2016) being deeply nested within the group.
* Styracosterna (Sereno, 1986): The youngest styracosternans are latest Maastrichtian hadrosaurs. Although the oldest styracosternans are the Valanginian *Hypselospinus* *fittoni* and *Barilium* *dawsoni* (and their numerous synonyms; Norman, 2011; Norman, 2012; Norman, 2013; Norman, 2015), the oldest inferable age for Styracosterna (as a branch-defined clade) is constrained by the age of its sister lineage, Camptosauridae/*Camptosaurus* spp., which is therefore middle Kimmeridgian (see *Camptosaurus* above).
* *Talenkauen* (Novas et al., 2004): Cerro Fortaleza Formation (including the "Pari Aike Formation", previously suggested to be of Maastrichtian age: Novas et al., 2004; Ezcurra et al., 2010): Campanian–Maastrichtian, Late Cretaceous (Egerton, 2011; Egerton et al., 2013; Lacovara et al., 2014).
* *Tenontosaurus* (Ostrom, 1970): Cloverly, Twin Mountains, Antlers, Glen Rose, and Paluxy Formations: spanning the middle Aptian–middle Albian, Early Cretaceous (Ostrom, 1970; Forster, 1990; Jacobs et al., 1991; Winkler et al., 1997; Jacobs and Winkler, 1998; Winkler, 2006; Werning, 2012; Thomas, 2015).

# 8. EW maximum agreement subtree

We elected not to depict the topology resulting from the maximum agreement subtree derived from the 814 traditional (EW) most parsimonious trees in the main text. This is because the high number of pruned OTUs (22) renders the subtree to be, in effect, irrelevant with especial respect to the focal taxa of this study. It is unsurprising that a high number of OTUs were excluded, primarily because fewer taxa would have been predicted to have identical positions across all 814 MPTs, than compared to a result that may have produced fewer MPTs.



Two equally likely subtrees were derived from the set of 814 EW MPTs – resulting in the ‘mutual cladogram’ depicted above. The two subtrees differ only in the substitution between the basal neornithischians *Hexinlusaurus* and *Yandusaurus*. With at least one of these taxa included, the EW maximum agreement subtree retains 34/56 OTUs, which results in recognizably more resolved ‘back bone’ topology of ornithischians compared to the original strict consensus (see Fig. 25.1 of the main text). However, none of the purported Elasmarian taxa, including *Galleonosaurus*, were retained as having stable topological positions in the agreement subtrees. Other important taxa omitted include *Thescelosaurus* and its kin, and *Hypsilophodon*, the latter of which establishes the node Clypeodonta.

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