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## SUPPLEMENTARY ONLINE MATERIAL FOR

### **New specimens of the multituberculate mammal *Sphenopsalis* from China: Implications for phylogeny and biology of taeniolabidoids**

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Published in *Acta Palaeontologica Polonica* 2016 61 (2): 429-454.  
<http://dx.doi.org/10.4202/app.00117.2014>

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## SOM 2. Character list

We adopted the character list from Yuan et al. (2013), the most recent study that has incorporated morphological characters from various sources concerning multituberculates and their relatives (see Phylogeny in the main text). We have kept the original character list of Yuan et al. (2013) as much as possible, including where “order” and “ordered” were placed in different places in the list.

Abbreviations (mainly from Yuan et al., 2013): KJ-H ## - characters from Kielan-Jaworowska and Hurum (2001). In Yuan et al.’s character list, instead of KJ-H##, “ZJK-H##” was used, which does not correctly represent Zofia Kielan-Jaworowska and Hurum. Thus, we have changed all “ZJK-H##” to KJ-H## in the list. Luo## - characters from Luo et al.(2002)’s mammaliaform character list (this list did not have a reference). R## - characters from Rougier et al. (1997). W## - characters from Weil (1998). C## - characters on M2 from Cifelli et al. (2013). Y## - characters introduced by Yuan et al. (2013). For any character that did not have a reference in Yuan et al. (2013), we regard it as from Yuan et al. (2013).

The coding for *Sphenopsalis* is primarily based on the material reported in this study. The coding for *Prionessus* is based on Matthew et al. (1928), Meng et al. (1998) and our observations of the specimens housed in the AMNH and IVPP. These two taxa were not included in the phylogenetic analyses from which we adopted the characters. The coding for *Catopsalis* is primarily based on Rougier et al. (1997). This genus, however, was not included in Yuan et al. (2013). Because the characters used by Rougier et al. (1997) and Yuan et al. (2013) are slightly different so that we have to decide how to code characters for *Catopsalis* that were used in Yuan et al. (2013) but not used, or used differently, in Rougier et al. (1997). This choice is difficult because the genus was considered to be non-monophyletic (Simmons and Miao, 1986; Fox, 1989; Lucas et al., 1997). For the characters of *Catopsalis* that were not coded by Rougier et al. (1997), we base our coding on several taxa that are represented by relatively better preserved material, including *Catopsalis foliatus*, *C. fissidens*, *Catopsalis joyneri* and *C. alexanderi* (Granger and Simpson, 1929; Sloan and Van Valen, 1965; Kielan-Jaworowska and Sloan, 1979; Middleton, 1982; Carlson and Krause, 1985; Simmons and Miao, 1986; Lucas et al., 1997). Modifications in coding *Taeniolabis* are based on *Taeniolabis taoensis* (Granger and Simpson, 1929) and our own observation of the specimens of this species housed in the American Museum of Natural History. Modifications in coding *Lambdopsalis bulla* is based on Miao (1986; 1988) and our observations

of new specimens of the species we collected during the last two decades. Modifications in coding *Microcosmodon* is based *M. conus* (Fox, 2005) (Several craniodental characters are available for the genus but were not coded in Yuan et al. [2013]). Coding for other taxa was directly from Yuan et al. (2013). For any change we made, we provide a short comment in each character to explain the reason and source of data. For convenience of reading, we highlight the coding for *Sphenopsalis*, *Prionessus*, and *Catopsalis* and present brief comments on changes we made in smaller font.

There are 19 characters that were listed as ordered in the character list of Yuan et al. (2013), among which characters 43, 51 and 55 were marked as “order” and the others (17, 25, 26, 29, 31, 32, 46, 47, 48, 49, 52, 58, 59, 61, 72, 85) were marked as “ordered”. In the character-status summary associated with the cladogram (Yuan et al., 2013: Supple. Info.), it stated: “Of 102 total characters, 18 characters are of type 'ord' (Wagner), 84 characters are of type 'unord’”. We are unable to tell which one of the 19 characters was not ordered in the analysis of Yuan et al. (2013) so that in our additional PAUP searches we ordered all the 19 characters as listed to be ordered by Yuan et al. (2013).

### **Mandibular Features**

1. (Luo1) Postdentary trough: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

2. (Luo2) Meckel’s sulcus presence: (0) Present; (1) Vestigial or absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

3. (Luo et al. 2002: 20) Anterior-ventral extension of masseteric fossa to mandibular body below m1: (0) Absent; (1) Present and extending to below m1; (2) Present and extending more anteriorly than the p4-m1 junction.

***Sphenopsalis* =?; *Prionessus* =2; *Catopsalis* =2**

4. Coronoid or coronoid scar on mandible: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* = 1; *Catopsalis* =1**

5. (Luo33, KJ-H57 states are switched, distribution same) Angle of the coronoid anterior margin to the molar alveolar line on the mandibular body: (0) > 45 degrees (Luo33 states 1-2; Note: more steep in plesiomorphic taxa than in cimolodontans); (1) Low < 45 degrees (Luo33 states 2-3).

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =0**

6. (KJ-H 58) Coronoid process orientation in parasagittal plane: (0) Parallel to the rest of the outer wall of the dentary; (1) Flared laterally.

***Sphenopsalis* =?; *Prionessus* = ?; *Catopsalis* =0**

7. (R67; KJ-H 35) Angle between the lower margin of the dentary and alveolar line of the lower p4 and molars: (0) 11-17 degrees; (1) 18 degrees or above.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =0**

8. (Luo 31) Gracile and elongate dentary peduncle: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

9. (KJ-H60) Mandibular condyle height to the m1-m2 alveolar line: (0) Opposite or below the level of the molar alveoli; (1) Above the level of the molars.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =0&1**

10. Mandibular angle: presence vs. absence: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

### **Incisor and Canine Features**

11. (Luo142) Number of lower incisors: (0) Four or More; (1) One.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

12. (Luo166) Procumbency and enlargement of the lower anterior-most incisors: (0) Absent; (1) Present (at least 50% longer than the adjacent incisor).

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

13. (R2) Lower incisor 1 root posterior extension: (0) Not extending below p3; (1) Extending posteriorly beyond p3-p4 junction.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

14. (Luo167) Enlarged diastema in lower incisor-canine region (More developed in older individuals): (0) Present and behind the canine; (1) Present and behind the posterior incisor.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

15. (KJ-H21) Lower incisor robustness: (0) Robust; (1) Gracile.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

16. (R3; KJ-H 20) Enamel covering of lower incisor of uniform thickness (0); thicker on labial surface than on lingual surface (1); or completely restricted to labial surface of tooth (2).

Yuan et al. (2013) converted the three character states into two: Enamel covering of lower incisor (0) Of uniform thickness; (1) Thicker or restricted to the ventro-labial surface. We resumed the three state coding used in Rougier et al. (1997) and Kielan-Jaworowska and Hurum (2001) because the original coding contains more differential information. The enamel coverage of the lower incisor differs at various stage of development in *Taeniolabis* (Granger and Simpson, 1929) and *Catopsalis* (Middleton, 1982). In our understanding the coding (2) for *Taeniolabis* is based on the adult condition of the incisor in Rougier et al. (1997) and Kielan-Jaworowska and Hurum (2001), which we follow here.

*Catopsalis* was coded following Middleton's (1982: 1201) observation: "The lower incisor is gliriform, with enamel largely restricted to an anteroventral band and extending for a short distance inside the alveolus." A similar statement was also made by Lucas et al. (1997: 487): "The lower incisor is gliriform, with an anteroventral enamel band as is typical of other species of *Catopsalis*."

*Henkelodon* was coded as "?" in Yuan et al. (2013) and Kielan-Jaworowska and Hurum (2001), but "0" in Rougier et al. (1997). We use "?" for this taxon.

***Sphenopsalis* =2; *Prionessus* =2; *Catopsalis* =2**

17. (R18; Luo143) Number of upper incisors (Ordered): (0) Four or more; (1) Three; (2) Two.

***Sphenopsalis* =2; *Prionessus* =2; *Catopsalis* =2**

18. (Y18) Diastema between Upper Incisor 2 and Incisor 3: (0) No large diastema between the

second incisor and third upper incisors; (1) I2-I3 diastema.

There is no large diastema between I2 and I3 in *Sphenopsalis*. Although state “1” was scored for *Lambdopsalis* (Yuan et al., 2013), we think it should be “0” according to Miao (1988) and our observation on several new specimens. However, whether a diastema is small or large is subjective. For instance, *Taeniolabis* was coded as “1” by Yuan et al. (2013) but its diastema between I2 and I3 is by no means the same of, for instance, *Meniscoessus* and *Styginmys*, not to mention *Kryptobaatar* and *Nemegtbaatar*. Because *Taeniolabis* and *Catopsalis* do have a small diastema (Granger and Simpson, 1929; Middleton, 1982), compared to the condition in *Sphenopsalis* and *Lambdopsalis*, we code “0/1” for *Taeniolabis* and *Catopsalis*.

***Sphenopsalis* =0; *Prionessus* =?; *Catopsalis* =0/1**

19. (R19; KJ-H3: states and distribution revised) Upper Incisor 2 (or penultimate incisor) morphology: (0) Peg-like or single cusp; (1) Two-cusped, or more.

Yuan et al. (2013) coded *Taeniolabis* as “0”, but we think it should be coded as “1” because of the following observations made by Granger and Simpson (1929: 606): “The tip was bifid with two sharp points, one, slightly smaller, directly external to the larger one. On the posterior edge about one centimeter from the unworn apex is a distinct small accessory cusp.” The condition in *Catopsalis* is uncertain. However, based on his observation, Middleton (1982: 1200) wrote: “It is likely the tip was multi-cusped, but with use was quickly worn down to a single chisel-like blade.” Thus, we coded *Catopsalis* as “1”.

***Sphenopsalis* =0; *Prionessus* =?; *Catopsalis* =1**

20. (R21; Modified from KJ-H4) Upper Incisor 3 (or ultimate upper incisor) morphology: (0) Single cusped or peg-like; (1) 2-cusped; (2) 3-4-cusped.

Yuan et al. (2013) coded *Taeniolabis* as “1”. When reporting the morphology of I3 in *Taeniolabis*, Granger and Simpson (1929: 607) stated: “It is somewhat compressed anteroposteriorly and slightly recurved, with a simple tip.” Thus, we changed the coding to “0” for *Taeniolabis*. Middleton (1982: 1200) considered that the I3 morphology of *Catopsalis* is “almost identical to that of *Taeniolabis* as well”; thus we code “0” for *Catopsalis*. Yuan et al. (2013) also coded *Lambdopsalis* as “1”, which, according to Miao (1986) and our observation of several skull specimens, should be “0”.

***Sphenopsalis* =0; *Prionessus* =?; *Catopsalis* =0**

21. (R22; KJ-H 13) Placement of posterior upper incisor (I3): (0) On the margin of premaxilla; (1) Medial to the margin-crest of facio-palatal faces of premaxilla; (2) More internal on the palatal part (close to the first premolar).

In Rougier et al. (1997) and Kielan-Jaworowska and Hurum (2001), the position of I3 has two states: located on margin of palate (0), or in medial position near sagittal midline (1). In those two studies, *Taeniolabis*,



*Lambdopsalis*, and *Catopsalis* (only scored in Rougier et al., 1997) were coded as “0”. In Yuan et al. (2013), *Taeniolabis* and *Lambdopsalis* were coded as “1”, but we think they should be coded as “0”. As Middleton (1982: 1200) observed that I3 of *Catopsalis* is “on the margin of the palate as in *Taeniolabis*”; we coded it as “0”.

***Sphenopsalis* =0; *Prionessus* =?; *Catopsalis* =0**

22. (R23; KJ-H5-Luo148) Upper canine - presence vs. absence, and size: (0) Present and enlarged; (1) Present and small; (2) Absent.

***Sphenopsalis* =2; *Prionessus* =2; *Catopsalis* =2**

23. (R24) Upper canine – number of cusps: (0) Peg-like with single cusp; (1) Two or more cusps.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

24. (Luo150) Lower canine - presence vs. absence: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

### **Premolar Features**

25. (KJ-H15) Ratio [of the length] between I3 & first maxillary tooth vs. length of upper premolars and molars (Ordered): (0) Below 0.09; (1) Between 0.1-0.19; (2) 0.2 or above.

***Sphenopsalis* =2; *Prionessus* =?; *Catopsalis* =2**

26. (KJ-H6; Luo152) Number of upper premolars (only applicable to taxa with premolar vs. molar differentiation) (Ordered): (0) Five; (1) Four; (2) Three; (3) Two or one.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =3**

27. (R31, R34; KJ-H14) Root(s) of posterior upper premolar(s): (0) Double-rooted; (1) Single-rooted.

This character is a bit confusing. In Kielan-Jaworowska and Hurum (2001), the character (14) is “Anterior upper premolars double-rooted (0) or single-rooted (1)”. In Rougier et al. (1997) character 31 is: “P2 double-rooted (0), or single-rooted (1)” and character 34 is: “P3 double-rooted (0), or single-rooted (1).” For both characters 31 and 34, Rougier et al. (1997) coded *Catopsalis*, *Lambdopsalis* and *Taeniolabis* as “?” because these taxa do not have P2-3. For their character 37 (P4 double-rooted [0], or single-rooted [1]), Rougier et al. (1997) coded the three taxa as “1”. Because Yuan et al. (2013) coded *Lambdopsalis* and *Taeniolabis* as “1”, which

implies that this character must include at least P4, or perhaps more precisely, only P4. We follow Rougier et al. (1997) to code *Catopsalis*, *Lambdopsalia* and *Taeniolabis* for the P4 root condition although this structure is not crystal clear in the original reports (e.g, Granger and Simpson, 1929; Sloan and Van Valen, 1965; Middleton, 1982).

***Sphenopsalis* =1; *Prionessus* =0/1; *Catopsalis* =1**

28. (KJ-H7) Labial cuspules on posterior upper premolars: (0) Absent; (1) Present.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

29. (KJ-H8) Upper premolars/upper molars length ratio (re-measured and revised) (Ordered): (0) 1.5 or more; (1) 1.5-0.8; (2) 0.8 or less.

***Sphenopsalis* =2; *Prionessus* =2; *Catopsalis* =2**

30. (KJ-H9) Last upper premolar: number and length of cusp rows: (0) Two main and equal rows of cusps; (1) Two equal rows of cusps and a continuous row of labial cingular cuspules or cingulum; (2) One main row and a shorter buccal row (anterior or posterior); (3) One main row only on P4.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =2**

31. P4 (or penultimate upper premolar) [cusp number] - the main labial cusp row (excluding the labial cingular cuspules) (KJ-H18, modified; herein the multituberculate labial row is considered the same row as the main row of upper premolar of *Morganucodon*) (ordered): (0) 1-4; (1) 5-8; (2) 9-10.

The coding of *Pentacosmodon* was changed from “?” to “0” based on *P. bowensis* (Fox, 2005). In describing the P4 of *Catopsalis alexanderi*, Middleton (1982: 1200) wrote “It is similar to the P4 of *C. joyneri* [see Sloan and Van Valen, 1965], with a cusp formula of 1-3:5:2.” Thus, we code “1” for *Catopsalis*.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =1**

32. (KJ-H19) Width ratio of ultimate upper premolar vs M1 (Ordered): (0) More than 0.9; (1) 0.9-.07; (2) 0.69-0.4; (3) 0.39-0.2.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =3**

33. (R5; KJ-H22, distribution revised) Lower p1: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

34. (R6; KJ-H23) Lower p2: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

35. (R7; KJ-H24, modified) Lower p3 (or penultimate premolar) presence vs. absence: (0) Present; (1) Absent.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

36. (Luo160) p3 (or penultimate lower premolar) laterally compressed to be bladelike: (0) No (including taxa with peg-like p3); (1) Yes.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

37. (R8; KJ-H24, modified) Lower p3 (or penultimate premolar) cusp/serration count: (0) Present, with 3-5 cusps; (1) Present, with 1-2 cusps.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

38. (KJ-H25) Shape of p3: (0) Single row of cusps; (1) Blade-like rectangular; (2) Blade-like triangular; (3) Peg-like.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

39. (KJ-H 26) Labial basal cuspules on p3 (applicable to bladed lower premolars): (0) Present; (1) Absent.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

40. Contact of penultimate and ultimate lower premolars: (0) Juxtaposition; (1) Staged: p4 overhanging p3.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

41. (Luo160) Lower p4 (or ultimate lower premolar) laterally compressed to be bladelike: (0)

No; (1) Yes.

This character was coded as 1 for *Taeniolabis* and *Lambdopsalis* in Yuan et al. (2013), but p4 in these taxa are not really “bladelike”. We changed the coding to “0” for the two taxa.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

42. (R11; KJ-H27) Lower p4 (or ultimate premolar) profile in lateral view: (0) Tricuspate; (1) Rectangular; (2) Arcuate; (3) Triangular.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =3**

43. (R9; KJ-H28) Order: Blade-like p4 serration count (character state modified): (0) 7 or less; (1) 8-10; (2) More than 10.

Yuan et al. (2013) coded *Taeniolabis* and *Lambdopsalis* as “0”, but this character is better be coded as inapplicable to multituberculates that don’t have a bladelike p4. We therefore code *Sphenopsalis*, *Prionessus*, *Catopsalis*, *Taeniolabis* and *Lambdopsalis* as “?”.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

44. (Y44) Lower p4 anterior root - Exoedaenodont at crown-root junction (Krause (1977), synonymous as the “triangular premolar lobe” of Kielan-Jaworowska et al. (2004)): (0) Absent; (1) Present.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

45. (KJ-H34) Dorsal margin of p4 to m1: (0) On the level of molars; (1) Protruding dorsally over molars.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

46. (KJ-H29) p3/p4 maximum length ratio (ordered): (0) Above 0.7; (1) 0.7 – 0.4; (2) 0.39-0.11; (3) 0.10 or less.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

47. (KJ-H30) Labial basal cuspules on p4 (ordered): (0) Absent; (1) Single cusp or a simple cingulid; (2) Several-single row; (3) Several-double rows.

In describing the morphology of the p4 in *Catopsalis*, Middleton (1982: 1202) wrote: “A basal cusp is situated on

the posteroexternal margin of the tooth.” Yuan et al. (2013) coded *Taeniolabis* as “0”, but Granger and Simpson (1929: 607) wrote that in the p4 of *Taeniolabis* “unless removed by wear, there is always also a still smaller posteroexternal basal cusplule”. Based on these descriptions, we code *Catopsalis* and *Taeniolabis* as “1”.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =1**

48. (W14; KJ-H31) Ratio of p4:m1 length (ordered): (0) Less than 0.99; (1) 1-1.49; (2) 1.5-1.99; (3) 2 or greater.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

### **Molar Features**

49. (Luo154) Number of lower molars or molariform postcanines (ordered): (0) Three or more; (1) Two molars.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

50. (Luo155) Number of upper molars or molariform postcanines: (0) Three or more; (1) Two.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

51. (Luo156) Total number of upper postcanine loci (order): (0) More than 8 (including the loci plus the alveoli of shed anterior postcanines); (1) Seven loci; (2) Six; (3) Five or fewer.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =3**

52. (Luo157) Number of lower postcanine loci (ordered): (0) Eight or more; (1) Six; (2) Five or less.

***Sphenopsalis* =2; *Prionessus* =2; *Catopsalis* =2**

53. (Luo168 originally from Butler, 2000) U-shaped transverse ridge(s) between b1-11, or b2-12 cusps in lower molars: (0) Absent; (1) Present; (2) Sharp crest closes the narrow central valley.

This character is confusing. We assume that the U-shaped transverse ridge(s) is equivalent to the “U-ridge” used in Butler (2000), which is a ridge connecting cusp rows a and b and closes the central valley at the distal end of the lower molar. The ridge should be between cusp b and cusp a at the distal end of the cusp rows. We are

unaware of what “b1 and l2” actually are. In addition, cusp b1 or b2 is at the mesial end of the lower teeth in the terminology of Butler (2000), but the mesial end of the lower molar in haramiyids is open, without a ridge. By examining the scoring in the data matrix, we assume this character is the U-ridge used by Butler (2000). In *Lambdopsalis* and *Sphenopsalis* the distal cusp on the lingual row has an elongate crest that connects to the distal cusp of the buccal row to close a narrow central valley distally. We add a new state “2” to the character.

***Sphenopsalis* =2; *Prionessus* =0; *Catopsalis* =0**

54. (Luo169 originally from Butler, 2000) Lower molar 1 longitudinal cusp row(s) (the buccal row in case of multi-rows) – relative cusp height: (0) Second mesial cusp (b2 of Butler 2000) highest; (1) All cusps are of equal height.

As pointed out by Zheng et al. (2013), the orientation of some haramiyid teeth is incorrect; what has been denoted as b2 on the lower molar is actually a1, which is further supported by additional evidence (Bi et al., 2014). We change this character as: Lower molar cusp height (0) Uneven; (1) Even.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

55. Order: M1 lingual row cusp count (applicable only to teeth with multi-row of multicusps): (0) 4 or fewer; (1) 5; (2) 7-9 or more.

We did not use this character for two reasons: First, of the three states, only “0” and “1” were coded in Yuan et al. (2013) from the data matrix we obtained. Second, this character is related to the cusp formula used in other studies cited. Usually, the lingual row cusps vary in number even within the same species, so that state (1) here may not reflect the variations commonly presented in multituberculates. Thus, we use the character of Rougier et al. (1997) and Kielan-Jarworowska and Hurum (2001), which encompasses character 55 of Yuan et al. (2013), although the descriptions of the character in the two studies are slightly different.

(R38; KJ-H10) M1 cusp formula 2-3:2-4:0 (0), 4-5:4-5:0-1 (1), 5-7:5-8:2-5 (2), or 5-11:7-10:6-11 (3). For this character, we code “?” for *Sinoconodon*, *Morganucodon*, and haramiyids; “0&1” for *Rugosodon*. For those that are coded differently as either “2” or “3” in Rougier et al. (1997) and Kielan-Jarworowska and Hurum (2001), we code them as “2&3”.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =3**

56. (Luo170 originally from Butler, 2000) Penultimate upper molar 1 (M1) of multirowed upper molar (or postcanines) - cusp height ratio in the lingual row: (0) Distal cusp or second distal cusp highest, with a gradient of anteriorly decreasing height; (1) Cusps in same row of equal height.

As pointed out by Zheng et al. (2013), the orientation of some haramiyid teeth is incorrect; what has been denoted as

lingual cusp on the upper molar is actually buccal, which is further supported by additional evidence (Bi et al., 2014). We change this character to: M1 cusp height (0) Uneven; (1) Even.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

57. (KJ-H 12) M1 posterolingual wing (applicable to molars with multi-rows of multiple cusps):  
(0) Absent; (1) Present.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

58. (W18, KJ-H11) M1 posterolingual wing length to M1 length (applicable to M1 with multi-rows) (ordered): (0) Present and below 0.2; (1) Present and between 0.2 and 0.5; (2) Present and more than 0.5.

***Sphenopsalis* =2; *Prionessus* =2; *Catopsalis* =2**

59. (KJ-H12) M1 posterolingual wing morphology (applicable only to M1s with posterolingual wing) (ordered): (0) Wing smooth; (1) Wing is crested; (2) Wing cusps with 3-4 cusps; (3) Wing cusps with 5 or more cusps.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =3**

60. (Luo171) Off-set alignment of main cusp-row(s) of the first and second upper molars: (0) Absent; (1) Present.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

61. (C2) Upper M2 (or ultimate upper molar) middle row cusp count (ordered): (0) Two cusps; (1) Three cusps; (2) Four cusps or more (modified for the reason that some specimens of *Taeniolabis* have more than 4 cusps in the middle row).

*Lambdopsalis* was coded as “1” in Yuan et al. (2013), but the fact is that the middle cusp row of *Lambdopsalis* has two cusps (Miao, 1986; Simmons and Miao, 1986; personal observations); we accordingly changed the coding to “0”. The same condition “0” is present in *Sphenopsalis* and *Prionessus*. *Buginbaatar* was coded as “3” in Yuan et al. (2013), which is incorrect; it should be “2”. For *Taeniolabis* the middle row cusp of M2 varies so that Granger and Simpson (1929: 610) wrote that “the only possible general formula is 1:3-5:4-6”. Therefore, we code “1&2” for *Taeniolabis*. *Catopsalis* has three cusps in the middle row, which appears to be stable (Simmons and Miao, 1986; personal observations).

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =1**

62. (C9-modified) Anterior end of middle valley of Upper M2 (or ultimate upper molar): (0) Middle valley absent; (1) Present as a uniform groove along most length but anterior end closed by a crescentic rim; (2) Uniform valley posteriorly (anteriorly) open.

We found that character states 1 and 2 are confusing and that “posteriorly” is most likely a typo of “anteriorly”, given the character description and its original discussion (Cifelli et al., 2013). As we show in this study, the central valley of M2 is anteriorly closed by a ridge in *Sphenopsalis* (see Fig. 4) and the same condition is present in *Lambdopsalis* based on our observations of numerous specimens. This condition is sharply different from that of *Taeniolabis* and *Catopsalis*.

***Sphenopsalis* =1; *Prionessus* =2; *Catopsalis* =2.**

63. (Y63) Middle valley of Upper M1 (or penultimate molar): (0) Middle valley absent; (1) Valley present along the tooth length but its posterior end closed by a rim or rim with tiny cusps; (2) Valley present along most of the tooth length but posterior end closed by a single enlarged cusp in mid position; (3) Uniform valley posteriorly open; (4) Valley indistinctive owing to inflation of tooth cusps.

We added a state (4) to this character, because unlike other multituberculates, the M1 of *Catopsalis* and *Taeniolabis* does not have a “valley” between cusp rows because of the inflation of the cusps.

***Sphenopsalis* =3; *Prionessus* =3; *Catopsalis* =4**

64. (C12-modified) Curvature of lingual cusp row of M2 (applicable to multi-rowed M2): (0) Straight; (1) Curved posterolabially.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

65. (Y65) M2 middle valley posterior end (applicable to multi-rowed M2): (0) Valley posteriorly open; (1) Valley closed by a posterior cusp; (2) Valley absent due to inflation of tooth cusps.

We add the state 2 to reflect the condition in *Taeniolabis*, in which the valley of M2 gives its way to the inflated cusps. In *Catopsalis*, the condition seems to be between states 1 and 2 so that we code it as “1&2”.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =1&2**

66. M2 anterobuccal ridge (sensu Butler and Hooker, 2005 = crista anterobuccalis of Hahn and



Hahn, 1998a) (This was not listed in Yuan et al. [2013], but we think it should be Hahn and Hahn [1998a, b].) (State 2 adopted from Cifelli et al., 2013 character 8): (0) Absent; (1) Present; (2) Present and expanded to mesial margin of main labial cusp row.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

67. (KJ-H36) m1 main lingual row cusp count (distribution revised): (0) 4 or fewer; (1) 5; (2) 6 or higher.

In Yuan et al. (2013), *Lambdopsalis* was scored as “1” in this character. However, the m1 lingual row of *Lambdopsalis* actually has four cusps (Miao, 1986; Simmons and Miao, 1986; Kielan-Jaworowska and Hurum, 2001; personal observations) so that it should be scored as “0”. The same is true for *Sphenopsalis* and *Prionessus*. In *Catopsalis* the lingual row usually has four cusps, but the five cusp condition is also present (Simmons and Miao, 1986), and as such we score “0&1” for that genus.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0&1**

68. Lower m1 middle valley: (0) Middle valley absent; (1) Present and posteriorly open and completely separating distal cusps of lingual vs. labial rows; (2) Middle valley present, but rimmed posteriorly and projected distally.

In Yuan et al. (2013), *Lambdopsalis* was scored as “1”. However, in describing the teeth of *Lambdopsalis*, Miao (1986: 71) wrote: “The last cusps of both external and internal rows converge with each other posteriorly, and thus give rise to a sharp posterior end of m1.” The same is true for *Sphenopsalis*, as we described in this study. Thus, we code “2” for these two genera.

***Sphenopsalis* =2; *Prionessus* =1; *Catopsalis* =1**

69. (KJ-H33, modified) m2 middle longitudinal valley: (0) Middle valley absent; (1) Present and completely separating two rows of cusps; (2) Middle valley present, incomplete and rimmed anteriorly and/or posteriorly (we would reword this as “middle valley present and closed distally by a ridge).

In Yuan et al. (2013), *Lambdopsalis* was scored as “1”. However, in describing the teeth of *Lambdopsalis*, Miao (1986: 71) wrote: “The second internal cusp has a long posteromedially extended wear facet ridge that converges with the last external cusp at the posterior margin of the crown, producing a narrow posterior end.” Here we think that the “posteromedially” should be “posterolaterally” or “posterobuccally”. As with m2 of *Sphenopsalis*, the distal end of the central valley on m2 is closed by a ridge in *Lambdopsalis*. Thus, we code “2” for these two genera.

***Sphenopsalis* =2; *Prionessus* =1; *Catopsalis* =1**

70. Coalescence of m2 labial row cusps (applicable only to teeth with multi-rows of multiple cusps): (0) Absent; (1) Present.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

71. (R17) Complete rim of m2 basin (applicable only to teeth with multi-rows of multiple cusps): (0) Absent; (1) Present.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

72. (KJ-H 37, modified to restrict to lingual row, switched states 1 vs. 2) m2 lingual row cusp count (ordered): (0) One trenchant anterior cusp; (1) 2-3; (2) 4-5.

In Yuan et al. (2013) this character in *Lambdopsalis* was coded as “2”, but it should be “1” (Miao, 1986; Simmons and Miao, 1986; personal observations).

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

73. (Luo 171) Ultimate lower molar (or m2) with multi-rows – ratio of row length: (0) Labial cusp row about equal as lingual cusp row; (1) Labial row is longer (by at least half-cusp length) than lingual row.

In Yuan et al. (2013) *Taeniolabis* was coded as “1”, which is incorrect. The two main cusp rows in *Taeniolabis* are subequal (Simpson, 1929; personal observations).

***Sphenopsalis* =1; *Prionessus* =0; *Catopsalis* =0**

74. (KJ-H38) Cusp shape on lower molars: (0) Conical; (1) Crescentic; (2) inflated.

We added the state (2) to reflect the inflated cusp shape in *Taeniolabis* and *Catopsalis*.

***Sphenopsalis* =1; *Prionessus* =0; *Catopsalis* =2**

75. (Hahn and Hahn, 1998) (This was not listed in Yuan et al. [2013], but we think it should be Hahn and Hahn, [1998a, b].) Enlarged trenchant second cusp of lingual row enclosed into the basin on lower m1 (applicable only to molars with multi-rows of multiple cusps) (0) Absent; (1) b2 cusp enlarged; (2) b2 cusp enlarged and encircled into the basin.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

76. (KJ-H 39; C1) Molar enamel surface: (0) Not ornamented; (1) Covered with grooves, pits and ridges.

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =0**

77. (KJ-H1) Enamel microstructure: (0) prismless (preprismatic of Simmons 1993): (1) Gigantoprismatic; (2) Small prismatic.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

78. Differentiation of premolars vs. molars: (0) Absent; (1) Present.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =1**

79. Diphyodont dental replacement: (0) Absent; (1) Present.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

#### **Cranial Features (from R 1997 and KJ-H 2001)**

80. (R43; KJ-H16) Infraorbital foramen: (0) Double; (1) Single.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “1” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

81. (KJ-H17) Palatal vacuities: (0) Absent; (1) Present and single; (2) Present and double.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “0” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis* =0; *Prionessus* =0; *Catopsalis* =?**

82. (KJ-H40) Sharp ridge between the palate and lateral walls of premaxilla (0) Absent; (1) Present.

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =?**

83. Curvature of anterior zygomatic root (best viewed in dorsal view) (R48; Modified from KJ-

H41): (0) Zygomatic root aligned with (or lightly incurved into) facial part of rostrum; (1) Zygomatic root is more transverse and deeply incurved with facial part of rostrum.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “1” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

84. (KJ-H42) Number of pairs of vascular foramina on nasal: (0) Absent; (1) One; (2) Two; (3) Three or more.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

85. (R44; KJ-H43) Posterior-most infraorbital foramen positions (ordered): (0) Dorsal to P3 or P4, or more posterior; (1) Dorsal to P2; (2) Dorsal to P1.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “0” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

86. (R49; KJ-H44) Base of zygomatic arch as marked by posterior edge: (0) Dorsal to P4 or more anterior; (1) Dorsal or posterior to P5/M1 or P4/M1 embrasure, or further posterior.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “0” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis* =1; *Prionessus* =1; *Catopsalis* =?**

87. (R47) Bony roof over anterior orbital space: (0) Absent; (1) Present.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

88. (R50, KJ-H45) Postorbital process: (0) Absent; (1) Present and short; (2) Present and long.

***Sphenopsalis* =1; *Prionessus* =?; *Catopsalis* =?**

89. (R52, KJ-H46) Snout length: (0) < 49 percent of total skull length; (1) > 50 percent of skull length.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

90. (KJ-H47, modified) Frontal/nasal suture pattern: (0) With subtransverse anterior margins or zigzag line; (1) Pointed anteriorly and not deeply inserted between the nasals; (2) Frontal deeply inserted between the nasals.

***Sphenopsalis =2; Prionessus =?; Catopsalis =?***

91. (R53, KJ-H48) Frontal-parietal suture: (0) Roughly V-shaped parietal lappet into frontal; (1) U-shaped.

***Sphenopsalis =0; Prionessus =?; Catopsalis =?***

92. (R54; KJ-H 49) Contacts between nasals and parietals: (0) Absent; (1) Present.

***Sphenopsalis =?; Prionessus =?; Catopsalis =?***

93. (KJ-H50) Facial exposure of lacrimal: (0) Very small and arcuate; (1) Large, roughly rectangular.

***Sphenopsalis =?; Prionessus =?; Catopsalis =?***

94. (R56; KJ-H51) Thickening in palatal process of premaxilla: (0) Absent; (1) Present.

***Sphenopsalis =?; Prionessus =?; Catopsalis =?***

95. (KJ-H52) Incisive foramen positioned: (0) Within premaxilla; (1) Limited posteriorly by maxilla.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “1” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis =1; Prionessus =?; Catopsalis =?***

96. (R61; KJ-H53) Foramen ovale inferium placement: (0) Medial to foramen masticatorium: (1) Posterior to foramen masticatorium:

***Sphenopsalis =?; Prionessus =?; Catopsalis =?***

97. (R62; KJ-H54) Jugular fossa: (0) Small and shallow: (1) Large and deep.

***Sphenopsalis =?; Prionessus =?; Catopsalis =?***

98. (KJ-H55) Anterior part of promontorium (sensu Hurum et al. 1996): (0) Oval; (1) Irregular within curvatures on both sides.

***Sphenopsalis* =1; *Prionessus* =?; *Catopsalis* =?**

99. (KJ-H56) Glenoid fossa length-width ratio (length as measured as maximum dimension from anterolateral to posteromedial end of glenoid for multituberculates) (re-measured and distribution modified): (0) 1.5 or more; (1) Below 1.49.

The coding of *Microcosmodon* is changed from “?” (Yuan et al., 2013) to “1” based on the observation of *M. conus* (Fox, 2005).

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

100. (KJ-H59) Post-temporal fossa: (0) Large; (1) Reduced to a small foramen.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

101. (KJ-H61) Width of the snout: skull length ratio (change of character state partition: (0) Above 0.4; (1) Below 0.39.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

102. (KJ-H62) Skull width/length ratio: (0) 0.79 and below; (1) Above 0.8.

***Sphenopsalis* =?; *Prionessus* =?; *Catopsalis* =?**

### SOM 3. Phylogenetic Analyses with all characters unordered

Source of trees from which consensus(es) calculated...

Heuristic search settings:

Optimality criterion = parsimony

Character-status summary:

Of 102 total characters:

All characters are of type 'unord'

All characters have equal weight

2 characters are parsimony-uninformative

Number of parsimony-informative characters = 100

Gaps are treated as "missing"

Multistate taxa interpreted as polymorphism

Starting tree(s) obtained via stepwise addition

Addition sequence: random

Number of replicates = 1000

Starting seed = 306405717

Number of trees held at each step during stepwise addition = 10

Branch-swapping algorithm: tree-bisection-reconnection (TBR)

Steepest descent option not in effect

Initial 'MaxTrees' setting = 10000 (will be auto-increased by 100)

Branches collapsed (creating polytomies) if maximum branch length is zero

'MulTrees' option not in effect; only 1 tree will be saved per replicate

Topological constraints not enforced

Trees are unrooted

Heuristic search completed

Total number of rearrangements tried = 46808140

Score of best tree(s) found = 344

Number of trees retained = 194

Time used = 00:01:01.0

Tree description:

Unrooted tree(s) rooted using outgroup method

Optimality criterion = parsimony

Character-status summary:

Of 102 total characters:

All characters are of type 'unord'

All characters have equal weight

2 characters are parsimony-uninformative

Number of parsimony-informative characters = 100

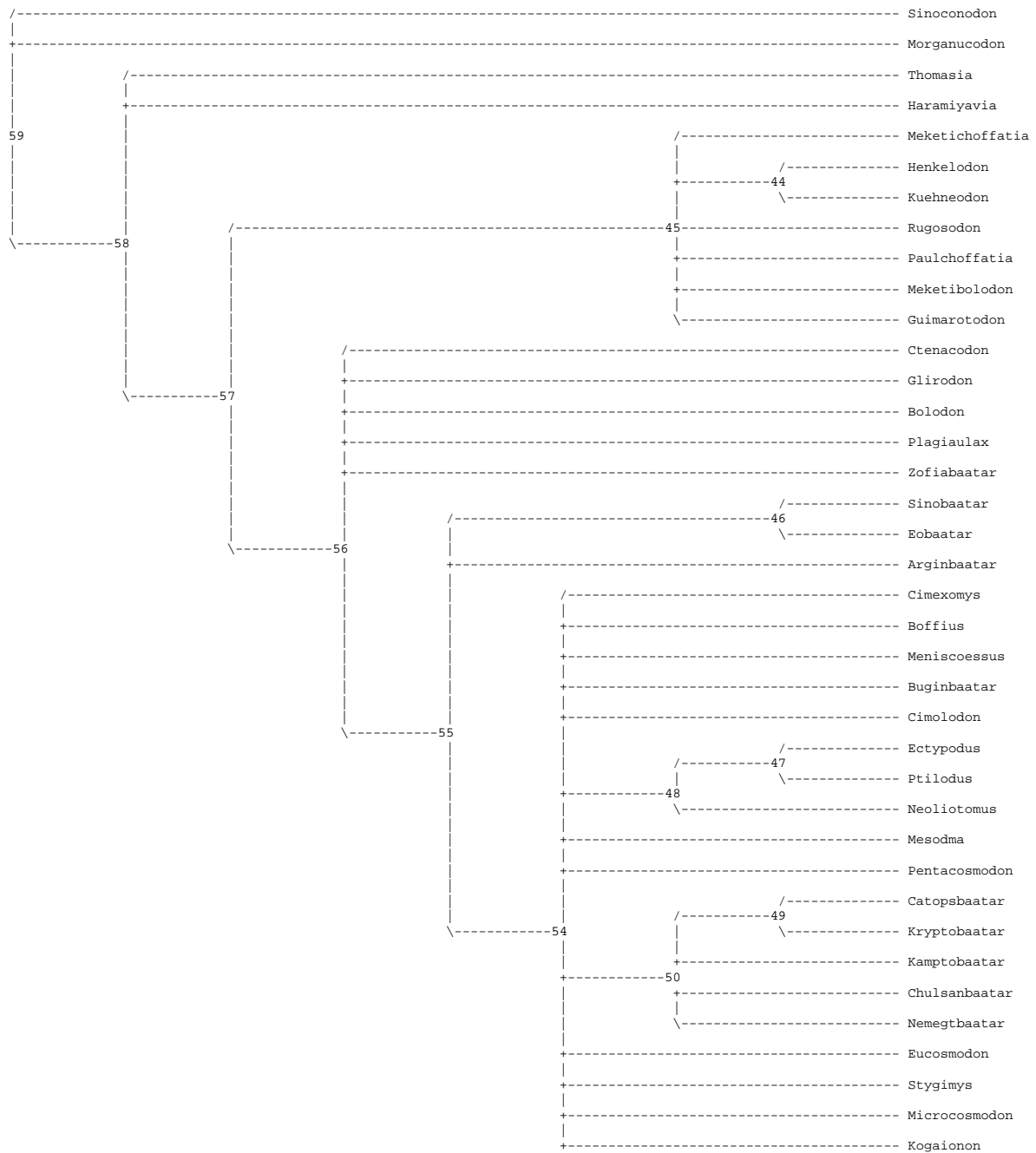
Gaps are treated as "missing"

Multistate taxa interpreted as polymorphism ("min" values for CI, RI, and RC are minimum-possible character lengths)

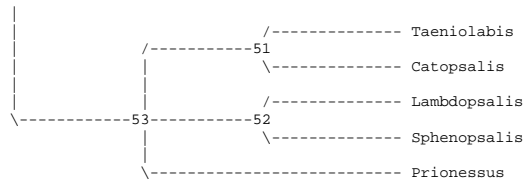
Character-state optimization: Accelerated transformation (ACCTRAN)

**Figure 1 - Strict Consensus Tree (of 194 EMTs) with all character unordered (see main text Fig. 16A)**

Tree length = 403  
 Consistency index (CI) = 0.4342  
 Homoplasy index (HI) = 0.6079  
 CI excluding uninformative characters = 0.4314  
 HI excluding uninformative characters = 0.5686  
 Retention index (RI) = 0.6976  
 Rescaled consistency index (RC) = 0.3029







**Apomorphy lists:**

Branch	Character	Steps	CI	Change
node_59 --> Sinoconodon	78	1	1.000	1 ==> 0
	79	1	1.000	1 ==> 0
node_59 --> Morganucodon	84	1	0.500	1 ==> 0
node_59 --> node_58	4	1	0.500	0 --> 1
	5	1	0.100	0 --> 1
	12	1	1.000	0 ==> 1
	22	1	0.667	0 ==> 1
	42	1	0.600	0 --> 1
	53	1	0.667	0 ==> 1
	62	1	0.500	0 ==> 1
	63	1	1.000	0 ==> 3
	66	1	0.667	0 --> 1
	68	1	0.667	0 ==> 1
	69	1	0.667	0 ==> 2
	77	1	0.333	0 --> 1
	89	1	0.500	1 --> 0
	93	1	0.333	0 --> 1
	95	1	0.500	0 --> 1
	101	1	0.500	0 --> 1
node_58 --> Thomasia	26	1	0.500	0 ==> 3
	32	1	0.375	0 ==> 1
	66	1	0.667	1 --> 0
node_58 --> Haramiyavia	18	1	0.600	0 ==> 1
	42	1	0.600	1 --> 0
node_58 --> node_57	1	1	1.000	0 ==> 1
	2	1	1.000	0 ==> 1
	3	1	0.400	0 ==> 1
	8	1	1.000	0 ==> 1
	10	1	1.000	0 ==> 1
	11	1	1.000	0 ==> 1
	14	1	1.000	0 ==> 1
	17	1	1.000	0 ==> 1
	19	1	0.167	0 ==> 1
	20	1	0.667	0 ==> 1
	24	1	1.000	0 ==> 1
	28	1	0.500	0 ==> 1
	29	1	0.286	2 ==> 0
	36	1	0.333	0 ==> 1
	38	1	0.500	0 ==> 1
	41	1	0.500	0 ==> 1
	45	1	0.200	0 ==> 1
	47	1	0.333	0 ==> 2
	48	1	0.231	0 ==> 1
	49	1	1.000	0 ==> 1

	50	1	1.000	0	==>	1
	51	1	0.600	0	==>	1
	52	1	1.000	0	==>	1
	56	1	0.500	0	==>	1
	60	1	1.000	0	==>	1
	61	1	0.231	1	==>	0
	72	1	0.250	2	-->	0
node_57 --> node_45	23	1	1.000	0	==>	1
	46	1	0.750	1	==>	0
	63	1	1.000	3	==>	1
	64	1	0.500	0	==>	1
	65	1	1.000	0	==>	1
	66	1	0.667	1	-->	2
	68	1	0.667	1	==>	2
	70	1	0.500	0	==>	1
	71	1	1.000	0	==>	1
	75	1	1.000	0	==>	2
	76	1	0.125	0	==>	1
	94	1	0.333	0	-->	1
node_45 --> Meketichoffatia	56	1	0.500	1	==>	0
node_45 --> node_44	4	1	0.500	1	-->	0
	13	1	0.333	0	-->	1
	20	1	0.667	1	==>	2
	63	1	1.000	1	==>	2
	72	1	0.250	0	-->	1
node_44 --> Henkelodon	22	1	0.667	1	==>	2
node_44 --> Kuehneodon	26	1	0.500	0	==>	1
	51	1	0.600	1	==>	2
node_45 --> Rugosodon	13	1	0.333	0	==>	1
	75	1	1.000	2	==>	1
node_45 --> Meketibolodon	47	1	0.333	2	==>	3
node_45 --> Guimarotodon	47	1	0.333	2	==>	3
node_57 --> node_56	5	1	0.100	1	-->	0
	7	1	0.143	0	==>	1
	9	1	0.222	0	==>	1
	13	1	0.333	0	==>	1
	30	1	0.500	0	==>	1
	39	1	1.000	0	-->	1
	53	1	0.667	1	==>	0
	54	1	1.000	0	==>	1
	57	1	0.500	0	==>	1
	62	1	0.500	1	==>	2
	69	1	0.667	2	==>	1
	72	1	0.250	0	-->	1
	73	1	0.500	0	==>	1
	77	1	0.333	1	-->	0
	82	1	0.667	0	==>	1
	85	1	0.286	0	-->	1
	97	1	0.500	0	-->	1
	99	1	0.500	0	-->	1
node_56 --> Ctenacodon	55	1	0.600	0	==>	1
node_56 --> Glirodon	16	1	0.182	0	==>	1
	57	1	0.500	1	==>	0
node_56 --> Bolodon	5	1	0.100	0	==>	1

	38	1	0.500	1	==>	2
	76	1	0.125	0	==>	1
node_56 --> Plagiaulax	33	1	0.500	0	==>	1
	38	1	0.500	1	==>	2
	43	1	0.200	0	==>	1
node_56 --> Zofiabaatar	48	1	0.231	1	==>	3
node_56 --> node_55	3	1	0.400	1	-->	2
	9	1	0.222	1	-->	0
	17	1	1.000	1	==>	2
	18	1	0.600	0	==>	1
	21	1	0.667	0	-->	1
	22	1	0.667	1	==>	2
	28	1	0.500	1	==>	0
	30	1	0.500	1	==>	0
	32	1	0.375	0	==>	1
	33	1	0.500	0	==>	1
	36	1	0.333	1	-->	0
	37	1	0.500	0	==>	1
	38	1	0.500	1	==>	2
	40	1	0.500	0	-->	1
	42	1	0.600	1	==>	2
	43	1	0.200	0	==>	2
	44	1	0.250	0	==>	1
	46	1	0.750	1	==>	2
	47	1	0.333	2	==>	0
	52	1	1.000	1	==>	2
	61	1	0.231	0	-->	1
	77	1	0.333	0	==>	1
	80	1	0.333	0	-->	1
	85	1	0.286	1	-->	0
node_55 --> node_46	3	1	0.400	2	-->	1
	19	1	0.167	1	-->	0
	36	1	0.333	0	-->	1
	40	1	0.500	1	-->	0
	43	1	0.200	2	==>	1
	47	1	0.333	0	==>	1
	48	1	0.231	1	-->	2
	58	1	0.182	0	==>	1
	70	1	0.500	0	==>	1
	76	1	0.125	0	==>	1
	86	1	0.167	0	-->	1
node_46 --> Sinobaatar	30	1	0.500	0	-->	2
	55	1	0.600	0	==>	1
	77	1	0.333	1	==>	0
node_46 --> Eobaatar	16	1	0.182	0	==>	2
	37	1	0.500	1	==>	0
node_55 --> Arginbaatar	48	1	0.231	1	==>	3
	61	1	0.231	1	-->	0
	80	1	0.333	1	-->	0
node_55 --> node_54	5	1	0.100	0	==>	1
	7	1	0.143	1	==>	0
	26	1	0.500	0	==>	1
	29	1	0.286	0	==>	1
	30	1	0.500	0	-->	2

	31	1	0.250	0	==>	1
	34	1	0.500	0	==>	1
	38	1	0.500	2	==>	3
	45	1	0.200	1	==>	0
	46	1	0.750	2	==>	3
	51	1	0.600	1	==>	2
	55	1	0.600	0	==>	2
	58	1	0.182	0	==>	2
	59	1	0.444	0	==>	3
	67	1	0.333	0	==>	2
	84	1	0.500	1	==>	3
	93	1	0.333	1	-->	0
node_54 --> Cimexomys	32	1	0.375	1	==>	2
	34	1	0.500	1	==>	0
	43	1	0.200	2	==>	1
	48	1	0.231	1	==>	2
	59	1	0.444	3	==>	2
	67	1	0.333	2	==>	1
	76	1	0.125	0	==>	1
	84	1	0.500	3	==>	1
	86	1	0.167	0	==>	1
node_54 --> Boffius	16	1	0.182	0	==>	1
node_54 --> Meniscoessus	25	1	0.400	0	==>	2
	29	1	0.286	1	==>	2
	31	1	0.250	1	==>	0
	32	1	0.375	1	==>	2
	43	1	0.200	2	==>	1
	48	1	0.231	1	==>	0
	61	1	0.231	1	==>	2
	67	1	0.333	2	==>	1
	72	1	0.250	1	==>	2
	74	1	0.500	0	==>	1
	76	1	0.125	0	==>	1
	80	1	0.333	1	==>	0
	81	1	0.500	0	==>	2
	86	1	0.167	0	==>	1
node_54 --> Buginbaatar	3	1	0.400	2	==>	1
	32	1	0.375	1	==>	3
	35	1	0.200	0	==>	1
	43	1	0.200	2	==>	0
	44	1	0.250	1	==>	0
	48	1	0.231	1	==>	0
	55	1	0.600	2	==>	3
	58	1	0.182	2	==>	1
	61	1	0.231	1	==>	2
node_54 --> Cimolodon	5	1	0.100	1	==>	0
	45	1	0.200	0	==>	1
	46	1	0.750	3	==>	2
	59	1	0.444	3	==>	2
	61	1	0.231	1	==>	2
	72	1	0.250	1	==>	2
	76	1	0.125	0	==>	1
node_54 --> node_48	19	1	0.167	1	==>	0
	31	1	0.250	1	==>	2

	45	1	0.200	0	==>	1
	48	1	0.231	1	==>	3
	55	1	0.600	2	-->	3
	72	1	0.250	1	==>	2
	76	1	0.125	0	==>	1
	77	1	0.333	1	==>	2
	81	1	0.500	0	-->	1
	84	1	0.500	3	-->	2
	97	1	0.500	1	-->	0
node_48 --> node_47	5	1	0.100	1	==>	0
	15	1	0.500	0	==>	1
	58	1	0.182	2	==>	1
node_47 --> Ectypodus	64	1	0.500	0	==>	1
	9	1	0.222	0	-->	1
	83	1	0.400	0	==>	2
node_47 --> Ptilodus	86	1	0.167	0	==>	1
	29	1	0.286	1	==>	0
	48	1	0.231	3	==>	2
	96	1	0.333	1	==>	0
node_48 --> Neoliotomus	16	1	0.182	0	==>	2
	74	1	0.500	0	==>	1
node_54 --> Mesodma	15	1	0.500	0	==>	1
	45	1	0.200	0	==>	1
	58	1	0.182	2	==>	1
	76	1	0.125	0	==>	1
	77	1	0.333	1	==>	2
node_54 --> Pentacosmodon	5	1	0.100	1	==>	0
	7	1	0.143	0	==>	1
	9	1	0.222	0	-->	1
	16	1	0.182	0	==>	1
	31	1	0.250	1	==>	0
	35	1	0.200	0	==>	1
	43	1	0.200	2	==>	0
	47	1	0.333	0	==>	1
	48	1	0.231	1	==>	0
	58	1	0.182	2	==>	1
	67	1	0.333	2	==>	0
	82	1	0.667	1	==>	2
	83	1	0.400	0	==>	1
node_54 --> node_50	16	1	0.182	0	==>	2
	19	1	0.167	1	==>	0
	21	1	0.667	1	==>	2
	32	1	0.375	1	==>	2
	43	1	0.200	2	==>	1
	55	1	0.600	2	==>	1
	58	1	0.182	2	-->	0
	59	1	0.444	3	-->	1
	67	1	0.333	2	==>	0
	82	1	0.667	1	==>	2
	85	1	0.286	0	-->	1
	87	1	1.000	0	==>	1
	90	1	1.000	0	==>	1
	91	1	1.000	0	==>	1
	93	1	0.333	0	-->	1

	94	1	0.333	0	==>	1
	99	1	0.500	1	==>	0
node_50 --> node_49	59	1	0.444	1	-->	2
	61	1	0.231	1	-->	0
	83	1	0.400	0	==>	2
	84	1	0.500	3	==>	2
	88	1	0.500	0	==>	1
	89	1	0.500	0	==>	1
	98	1	0.500	0	==>	1
	101	1	0.500	1	==>	0
	102	1	0.500	0	==>	1
node_49 --> Catopsbaatar	5	1	0.100	1	==>	0
	7	1	0.143	0	==>	1
	9	1	0.222	0	-->	1
	26	1	0.500	1	==>	2
	29	1	0.286	1	==>	2
	42	1	0.600	2	==>	1
	43	1	0.200	1	==>	0
	44	1	0.250	1	==>	0
	48	1	0.231	1	==>	2
	51	1	0.600	2	==>	3
	55	1	0.600	1	==>	2
	58	1	0.182	0	-->	2
	59	1	0.444	2	-->	3
	85	1	0.286	1	-->	0
	86	1	0.167	0	==>	1
	95	1	0.500	1	==>	0
node_49 --> Kryptobaatar	61	1	0.231	0	-->	2
node_50 --> Kamptobaatar	6	1	0.500	0	==>	1
	9	1	0.222	0	-->	1
	16	1	0.182	2	==>	1
	85	1	0.286	1	-->	2
	96	1	0.333	1	==>	0
node_50 --> Chulsanbaatar	7	1	0.143	0	==>	1
	84	1	0.500	3	==>	2
	85	1	0.286	1	-->	2
node_50 --> Nemegtbaatar	25	1	0.400	0	==>	1
	58	1	0.182	0	-->	2
	59	1	0.444	1	-->	2
	61	1	0.231	1	==>	2
	81	1	0.500	0	==>	2
	96	1	0.333	1	==>	0
node_54 --> Eucosmodon	7	1	0.143	0	==>	1
	16	1	0.182	0	==>	2
	26	1	0.500	1	==>	2
	35	1	0.200	0	==>	1
	67	1	0.333	2	==>	1
	72	1	0.250	1	==>	2
node_54 --> Stygimys	3	1	0.400	2	==>	1
	16	1	0.182	0	==>	2
	25	1	0.400	0	==>	1
	31	1	0.250	1	==>	2
	35	1	0.200	0	==>	1
	47	1	0.333	0	==>	1

	58	1	0.182	2	==>	1
	81	1	0.500	0	==>	2
	85	1	0.286	0	==>	2
	94	1	0.333	0	==>	1
node_54 --> Microcosmodon	5	1	0.100	1	==>	0
	9	1	0.222	0	-->	1
	16	1	0.182	0	==>	1
	32	1	0.375	1	==>	2
	38	1	0.500	3	==>	2
	43	1	0.200	2	==>	0
	47	1	0.333	0	==>	1
	48	1	0.231	1	==>	2
node_54 --> Kogaionon	58	1	0.182	2	==>	1
	19	1	0.167	1	==>	0
	25	1	0.400	0	==>	1
	29	1	0.286	1	==>	0
	30	1	0.500	2	==>	3
	31	1	0.250	1	==>	0
	55	1	0.600	2	==>	3
	59	1	0.444	3	==>	2
	61	1	0.231	1	==>	0
	83	1	0.400	0	==>	1
node_54 --> node_53	5	1	0.100	1	==>	0
	9	1	0.222	0	-->	1
	16	1	0.182	0	==>	2
	18	1	0.600	1	-->	0
	20	1	0.667	1	==>	0
	21	1	0.667	1	==>	0
	25	1	0.400	0	==>	2
	26	1	0.500	1	==>	3
	27	1	1.000	0	==>	1
	29	1	0.286	1	==>	2
	30	1	0.500	2	-->	3
	31	1	0.250	1	==>	0
	32	1	0.375	1	==>	3
	35	1	0.200	0	==>	1
	41	1	0.500	1	==>	0
	42	1	0.600	2	==>	3
	44	1	0.250	1	==>	0
	48	1	0.231	1	==>	0
	51	1	0.600	2	==>	3
	55	1	0.600	2	==>	3
	61	1	0.231	1	-->	0
	62	1	0.500	2	-->	1
	67	1	0.333	2	==>	0
	73	1	0.500	1	-->	0
	83	1	0.400	0	==>	1
	86	1	0.167	0	==>	1
	88	1	0.500	0	-->	1
	90	1	1.000	0	==>	2
	92	1	1.000	0	==>	1
	98	1	0.500	0	-->	1
	100	1	1.000	0	==>	1
	102	1	0.500	0	==>	1

node_53 --> node_51	30	1	0.500	3	-->	2
	47	1	0.333	0	==>	1
	61	1	0.231	0	-->	1
	62	1	0.500	1	-->	2
	63	1	1.000	3	==>	4
	65	1	1.000	0	==>	2
	74	1	0.500	0	==>	2
node_51 --> Taeniolabis	67	1	0.333	0	==>	2
	72	1	0.250	1	==>	2
node_51 --> Catopsalis	31	1	0.250	0	==>	1
node_53 --> node_52	6	1	0.500	0	-->	1
	7	1	0.143	0	-->	1
	19	1	0.167	1	==>	0
	53	1	0.667	0	==>	2
	68	1	0.667	1	==>	2
	69	1	0.667	1	==>	2
	73	1	0.500	0	-->	1
	74	1	0.500	0	==>	1

**Character diagnostics:**

Character	Range	Min steps	Tree steps	Max steps	CI	RI	RC	HI	G-fit
1	1	1	1	3	1.000	1.000	1.000	0.000	1.000
2	1	1	1	3	1.000	1.000	1.000	0.000	1.000
3	2	2	5	16	0.400	0.786	0.314	0.600	0.500
4	1	1	2	3	0.500	0.500	0.250	0.500	0.750
5	1	1	10	17	0.100	0.438	0.044	0.900	0.250
6	1	1	2	2	0.500	0.000	0.000	0.500	0.750
7	1	1	7	11	0.143	0.400	0.057	0.857	0.333
8	1	1	1	3	1.000	1.000	1.000	0.000	1.000
9	1	2	9	12	0.222	0.300	0.067	0.889	0.273
10	1	1	1	3	1.000	1.000	1.000	0.000	1.000
11	1	1	1	4	1.000	1.000	1.000	0.000	1.000
12	1	1	1	2	1.000	1.000	1.000	0.000	1.000
13	1	1	3	6	0.333	0.600	0.200	0.667	0.600
14	1	1	1	3	1.000	1.000	1.000	0.000	1.000
15	1	1	2	3	0.500	0.500	0.250	0.500	0.750
16	2	2	11	18	0.182	0.438	0.080	0.818	0.250
17	2	2	2	9	1.000	1.000	1.000	0.000	1.000
18	1	3	5	11	0.600	0.750	0.450	0.800	0.429
19	1	1	6	12	0.167	0.545	0.091	0.833	0.375
20	2	2	3	10	0.667	0.875	0.583	0.333	0.750
21	2	2	3	12	0.667	0.900	0.600	0.333	0.750
22	2	2	3	9	0.667	0.857	0.571	0.333	0.750
23	1	1	1	3	1.000	1.000	1.000	0.000	1.000
24	1	1	1	3	1.000	1.000	1.000	0.000	1.000
25	2	2	5	8	0.400	0.500	0.200	0.600	0.500
26	3	3	6	19	0.500	0.813	0.406	0.500	0.500
27	1	2	2	5	1.000	1.000	1.000	0.500	0.750
28	1	1	2	6	0.500	0.800	0.400	0.500	0.750
29	2	2	7	20	0.286	0.722	0.206	0.714	0.375
30	3	4	8	15	0.500	0.636	0.318	0.625	0.375

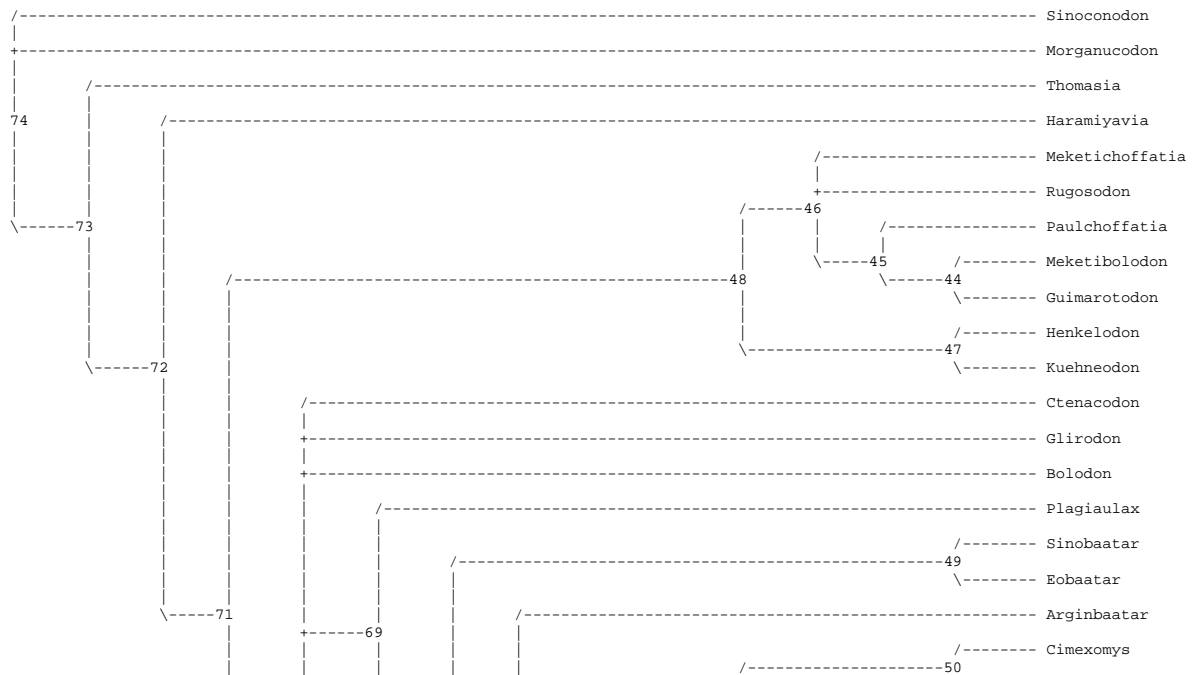


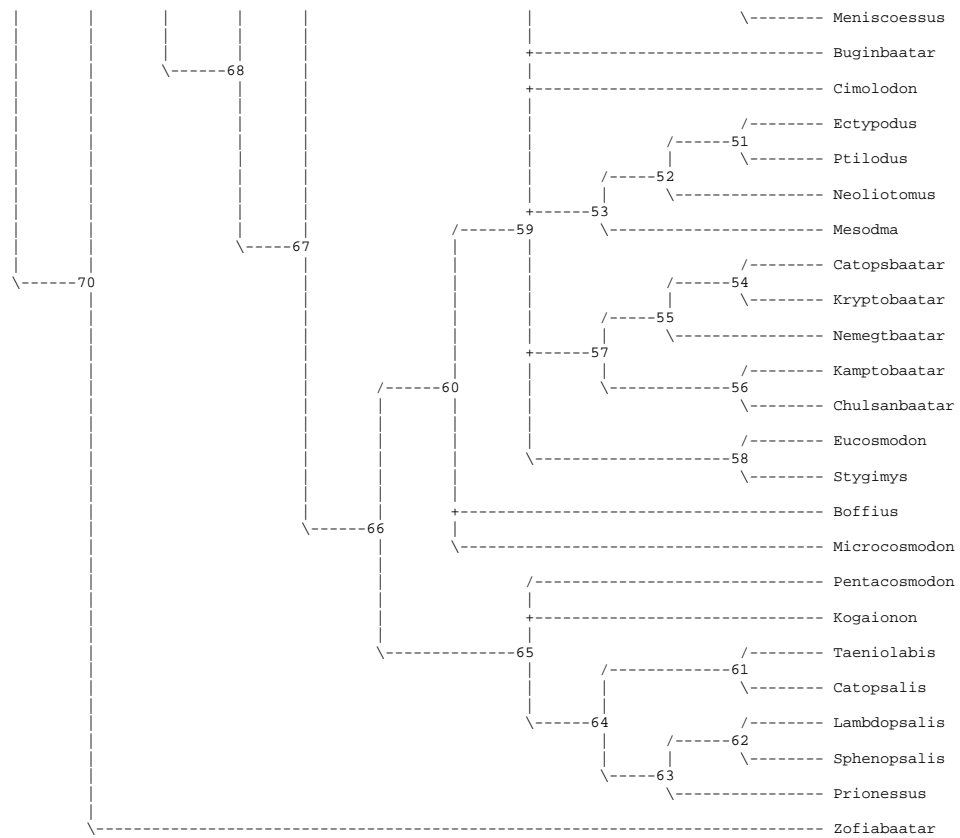
31	2	2	8	16	0.250	0.571	0.143	0.750	0.333
32	3	3	8	22	0.375	0.737	0.276	0.625	0.375
33	1	1	2	12	0.500	0.909	0.455	0.500	0.750
34	1	1	2	17	0.500	0.938	0.469	0.500	0.750
35	1	1	5	9	0.200	0.500	0.100	0.800	0.429
36	1	1	3	11	0.333	0.800	0.267	0.667	0.600
37	1	1	2	14	0.500	0.923	0.462	0.500	0.750
38	3	3	6	18	0.500	0.800	0.400	0.500	0.500
39	1	1	1	4	1.000	1.000	1.000	0.000	1.000
40	1	1	2	15	0.500	0.929	0.464	0.500	0.750
41	1	1	2	9	0.500	0.875	0.438	0.500	0.750
42	3	3	5	20	0.600	0.882	0.529	0.400	0.600
43	2	2	10	17	0.200	0.467	0.093	0.800	0.273
44	1	1	4	18	0.250	0.824	0.206	0.750	0.500
45	1	1	5	16	0.200	0.733	0.147	0.800	0.429
46	3	3	4	16	0.750	0.923	0.692	0.250	0.750
47	3	3	9	16	0.333	0.538	0.179	0.667	0.333
48	3	3	13	21	0.231	0.444	0.103	0.769	0.231
49	1	1	1	3	1.000	1.000	1.000	0.000	1.000
50	1	1	1	3	1.000	1.000	1.000	0.000	1.000
51	3	3	5	18	0.600	0.867	0.520	0.400	0.600
52	2	2	2	12	1.000	1.000	1.000	0.000	1.000
53	2	2	3	8	0.667	0.833	0.556	0.333	0.750
54	1	1	1	8	1.000	1.000	1.000	0.000	1.000
55	3	9	15	29	0.600	0.700	0.420	0.800	0.200
56	1	1	2	5	0.500	0.750	0.375	0.500	0.750
57	1	1	2	7	0.500	0.833	0.417	0.500	0.750
58	2	2	11	15	0.182	0.308	0.056	0.818	0.250
59	3	4	9	13	0.444	0.444	0.198	0.667	0.333
60	1	1	1	4	1.000	1.000	1.000	0.000	1.000
61	2	3	13	17	0.231	0.286	0.066	0.846	0.214
62	2	2	4	11	0.500	0.778	0.389	0.500	0.600
63	4	4	4	8	1.000	1.000	1.000	0.000	1.000
64	1	1	2	4	0.500	0.667	0.333	0.500	0.750
65	2	3	3	5	1.000	1.000	1.000	0.333	0.750
66	2	2	3	5	0.667	0.667	0.444	0.333	0.750
67	2	3	9	13	0.333	0.400	0.133	0.778	0.300
68	2	2	3	9	0.667	0.857	0.571	0.333	0.750
69	2	2	3	10	0.667	0.875	0.583	0.333	0.750
70	1	1	2	6	0.500	0.800	0.400	0.500	0.750
71	1	1	1	4	1.000	1.000	1.000	0.000	1.000
72	2	2	8	13	0.250	0.455	0.114	0.750	0.333
73	1	2	4	9	0.500	0.714	0.357	0.750	0.500
74	2	2	4	6	0.500	0.500	0.250	0.500	0.600
75	2	3	3	6	1.000	1.000	1.000	0.333	0.750
76	1	1	8	17	0.125	0.563	0.070	0.875	0.300
77	2	2	6	12	0.333	0.600	0.200	0.667	0.429
78	1	1	1	1	1.000	0/0	0/0	0.000	1.000
79	1	1	1	1	1.000	0/0	0/0	0.000	1.000
80	1	1	3	11	0.333	0.800	0.267	0.667	0.600
81	2	2	4	5	0.500	0.333	0.167	0.500	0.600
82	2	2	3	9	0.667	0.857	0.571	0.333	0.750
83	2	2	5	7	0.400	0.400	0.160	0.600	0.500
84	3	3	6	9	0.500	0.500	0.250	0.500	0.500

85	2	2	7	7	0.286	0.000	0.000	0.714	0.375
86	1	1	6	8	0.167	0.286	0.048	0.833	0.375
87	1	1	1	5	1.000	1.000	1.000	0.000	1.000
88	1	1	2	4	0.500	0.667	0.333	0.500	0.750
89	1	1	2	4	0.500	0.667	0.333	0.500	0.750
90	2	2	2	8	1.000	1.000	1.000	0.000	1.000
91	1	1	1	5	1.000	1.000	1.000	0.000	1.000
92	1	1	1	2	1.000	1.000	1.000	0.000	1.000
93	1	1	3	5	0.333	0.500	0.167	0.667	0.600
94	1	1	3	6	0.333	0.600	0.200	0.667	0.600
95	1	1	2	3	0.500	0.500	0.250	0.500	0.750
96	1	1	3	3	0.333	0.000	0.000	0.667	0.600
97	1	1	2	5	0.500	0.750	0.375	0.500	0.750
98	1	1	2	4	0.500	0.667	0.333	0.500	0.750
99	1	1	2	5	0.500	0.750	0.375	0.500	0.750
100	1	1	1	2	1.000	1.000	1.000	0.000	1.000
101	1	1	2	4	0.500	0.667	0.333	0.500	0.750
102	1	1	2	4	0.500	0.667	0.333	0.500	0.750

**Figure 2 - 50% Majority Rule Consensus Tree with all character unordered (see main text Fig. 16B)**

Tree length = 355  
 Consistency index (CI) = 0.4930  
 Homoplasy index (HI) = 0.5549  
 CI excluding uninformative characters = 0.4901  
 HI excluding uninformative characters = 0.5099  
 Retention index (RI) = 0.7613  
 Rescaled consistency index (RC) = 0.3753





**Apomorphy lists:**

Branch	Character	Steps	CI	Change
node_74 --> Sinoconodon	78	1	1.000	1 ==> 0
	79	1	1.000	1 ==> 0
node_74 --> Morganucodon	84	1	0.500	1 ==> 0
node_74 --> node_73	4	1	0.500	0 --> 1
	5	1	0.143	0 --> 1
	12	1	1.000	0 ==> 1
	22	1	0.667	0 --> 1
	42	1	0.600	0 --> 1
	53	1	0.667	0 ==> 1
	62	1	0.667	0 ==> 1
	63	1	1.000	0 ==> 3
	68	1	0.667	0 --> 1
	69	1	0.667	0 ==> 2
	77	1	0.400	0 --> 1
	89	1	0.500	1 --> 0
	93	1	0.333	0 --> 1
	95	1	0.500	0 --> 1
101	1	0.500	0 --> 1	
node_73 --> Thomasia	26	1	0.500	0 ==> 3
node_73 --> node_72	32	1	0.429	0 ==> 1
	28	1	0.500	0 --> 1
	29	1	0.333	2 --> 0

	66	1	1.000	0	==>	1
node_72 --> Haramiyavia	18	1	0.600	0	==>	1
	42	1	0.600	1	-->	0
node_72 --> node_71	1	1	1.000	0	==>	1
	2	1	1.000	0	==>	1
	3	1	0.500	0	==>	1
	8	1	1.000	0	==>	1
	10	1	1.000	0	==>	1
	11	1	1.000	0	==>	1
	13	1	0.500	0	==>	1
	14	1	1.000	0	==>	1
	17	1	1.000	0	==>	1
	19	1	0.167	0	==>	1
	20	1	0.667	0	==>	1
	24	1	1.000	0	==>	1
	36	1	0.500	0	==>	1
	38	1	0.750	0	==>	1
	41	1	0.500	0	==>	1
	45	1	0.250	0	==>	1
	47	1	0.429	0	==>	2
	48	1	0.250	0	==>	1
	49	1	1.000	0	==>	1
	50	1	1.000	0	==>	1
	51	1	0.600	0	==>	1
	52	1	1.000	0	==>	1
	56	1	0.500	0	==>	1
	60	1	1.000	0	==>	1
	61	1	0.300	1	==>	0
	72	1	0.286	2	==>	1
node_71 --> node_48	23	1	1.000	0	==>	1
	46	1	0.750	1	==>	0
	63	1	1.000	3	-->	1
	64	1	0.500	0	==>	1
	65	1	1.000	0	==>	1
	66	1	1.000	1	==>	2
	68	1	0.667	1	==>	2
	70	1	0.500	0	==>	1
	71	1	1.000	0	==>	1
	75	1	1.000	0	==>	1
	76	1	0.167	0	==>	1
	94	1	0.333	0	-->	1
node_48 --> node_46	72	1	0.286	1	==>	0
node_46 --> Meketichoffatia	56	1	0.500	1	==>	0
node_46 --> node_45	13	1	0.500	1	==>	0
	75	1	1.000	1	-->	2
node_45 --> node_44	47	1	0.429	2	==>	3
node_48 --> node_47	4	1	0.500	1	-->	0
	20	1	0.667	1	==>	2
	63	1	1.000	1	-->	2
node_47 --> Henkelodon	22	1	0.667	1	==>	2
node_47 --> Kuehneodon	26	1	0.500	0	==>	1
	51	1	0.600	1	==>	2
node_71 --> node_70	5	1	0.143	1	-->	0
	7	1	0.167	0	==>	1

	9	1	0.286	0	==>	1
	30	1	0.571	0	==>	1
	39	1	1.000	0	-->	1
	53	1	0.667	1	==>	0
	54	1	1.000	0	==>	1
	57	1	0.500	0	==>	1
	62	1	0.667	1	==>	2
	69	1	0.667	2	==>	1
	73	1	0.500	0	==>	1
	77	1	0.400	1	-->	0
	82	1	0.667	0	==>	1
	85	1	0.333	0	-->	1
	97	1	0.500	0	-->	1
	99	1	0.500	0	-->	1
node_70 --> Ctenacodon	55	1	0.643	0	==>	1
node_70 --> Glirodon	16	1	0.222	0	==>	1
	57	1	0.500	1	==>	0
node_70 --> Bolodon	5	1	0.143	0	==>	1
	38	1	0.750	1	==>	2
	76	1	0.167	0	==>	1
node_70 --> node_69	17	1	1.000	1	-->	2
	18	1	0.600	0	-->	1
	19	1	0.167	1	-->	0
	21	1	0.667	0	-->	1
	22	1	0.667	1	-->	2
	28	1	0.500	1	-->	0
	30	1	0.571	1	-->	0
	32	1	0.429	0	-->	1
	33	1	1.000	0	==>	1
	38	1	0.750	1	==>	2
	43	1	0.250	0	-->	1
	48	1	0.250	1	-->	2
	80	1	0.333	0	-->	1
	85	1	0.333	1	-->	0
node_69 --> node_68	37	1	0.500	0	-->	1
	42	1	0.600	1	==>	2
	44	1	0.250	0	==>	1
	46	1	0.750	1	==>	2
	47	1	0.429	2	==>	1
	52	1	1.000	1	==>	2
	77	1	0.400	0	-->	1
node_68 --> node_49	9	1	0.286	1	-->	0
	58	1	0.200	0	==>	1
	61	1	0.300	0	==>	1
	70	1	0.500	0	==>	1
	76	1	0.167	0	==>	1
	86	1	0.200	0	-->	1
node_49 --> Sinobaatar	30	1	0.571	0	-->	2
	55	1	0.643	0	==>	1
	77	1	0.400	1	-->	0
node_49 --> Eobaatar	16	1	0.222	0	==>	2
	37	1	0.500	1	-->	0
node_68 --> node_67	3	1	0.500	1	==>	2
	36	1	0.500	1	==>	0

	40	1	1.000	0	==>	1
	43	1	0.250	1	-->	0
	84	1	0.500	1	-->	2
	93	1	0.333	1	-->	0
node_67 --> Arginbaatar	43	1	0.250	0	-->	2
	47	1	0.429	1	==>	0
	48	1	0.250	2	==>	3
	80	1	0.333	1	-->	0
node_67 --> node_66	16	1	0.222	0	==>	1
	26	1	0.500	0	==>	1
	30	1	0.571	0	-->	2
	34	1	0.500	0	==>	1
	45	1	0.250	1	==>	0
	46	1	0.750	2	-->	3
	51	1	0.600	1	==>	2
	55	1	0.643	0	-->	2
	58	1	0.200	0	==>	2
	59	1	0.500	0	==>	3
node_66 --> node_60	7	1	0.167	1	==>	0
	19	1	0.167	0	-->	1
	29	1	0.333	0	==>	1
	31	1	0.400	0	==>	1
	61	1	0.300	0	==>	1
	67	1	0.500	0	==>	2
	81	1	0.500	0	-->	2
node_60 --> node_59	5	1	0.143	0	==>	1
	9	1	0.286	1	==>	0
	16	1	0.222	1	==>	0
	38	1	0.750	2	==>	3
	43	1	0.250	0	-->	2
	47	1	0.429	1	==>	0
	48	1	0.250	2	-->	1
node_59 --> node_50	25	1	0.400	0	-->	2
	32	1	0.429	1	==>	2
	43	1	0.250	2	==>	1
	48	1	0.250	1	-->	0
	67	1	0.500	2	==>	1
	76	1	0.167	0	==>	1
	84	1	0.500	2	-->	1
	86	1	0.200	0	==>	1
node_50 --> Cimexomys	34	1	0.500	1	==>	0
	48	1	0.250	0	-->	2
	59	1	0.500	3	==>	2
node_50 --> Meniscoessus	29	1	0.333	1	==>	2
	31	1	0.400	1	==>	0
	61	1	0.300	1	==>	2
	72	1	0.286	1	==>	2
	74	1	0.500	0	==>	1
	80	1	0.333	1	==>	0
node_59 --> Buginbaatar	3	1	0.500	2	==>	1
	32	1	0.429	1	==>	3
	35	1	0.333	0	==>	1
	43	1	0.250	2	==>	0
	44	1	0.250	1	==>	0

	48	1	0.250	1	==>	0
	55	1	0.643	2	==>	3
	58	1	0.200	2	==>	1
	61	1	0.300	1	==>	2
node_59 --> Cimolodon	5	1	0.143	1	==>	0
	45	1	0.250	0	==>	1
	46	1	0.750	3	==>	2
	59	1	0.500	3	==>	2
	61	1	0.300	1	==>	2
	72	1	0.286	1	==>	2
	76	1	0.167	0	==>	1
node_59 --> node_53	15	1	0.500	0	-->	1
	45	1	0.250	0	==>	1
	58	1	0.200	2	-->	1
	76	1	0.167	0	==>	1
	77	1	0.400	1	==>	2
	81	1	0.500	2	-->	1
	97	1	0.500	1	-->	0
node_53 --> node_52	19	1	0.167	1	==>	0
	31	1	0.400	1	==>	2
	48	1	0.250	1	==>	3
	55	1	0.643	2	-->	3
	72	1	0.286	1	==>	2
node_52 --> node_51	5	1	0.143	1	==>	0
	64	1	0.500	0	==>	1
node_51 --> Ectypodus	9	1	0.286	0	==>	1
	83	1	0.667	0	==>	2
	86	1	0.200	0	==>	1
node_51 --> Ptilodus	29	1	0.333	1	==>	0
	48	1	0.250	3	==>	2
	96	1	0.333	1	==>	0
node_52 --> Neoliotomus	15	1	0.500	1	-->	0
	16	1	0.222	0	==>	2
	58	1	0.200	1	-->	2
	74	1	0.500	0	==>	1
node_59 --> node_57	16	1	0.222	0	==>	2
	19	1	0.167	1	==>	0
	21	1	0.667	1	==>	2
	32	1	0.429	1	==>	2
	43	1	0.250	2	==>	1
	55	1	0.643	2	-->	1
	59	1	0.500	3	-->	1
	67	1	0.500	2	==>	0
	81	1	0.500	2	-->	0
	82	1	0.667	1	==>	2
	85	1	0.333	0	-->	1
	87	1	1.000	0	==>	1
	90	1	1.000	0	==>	1
	91	1	1.000	0	==>	1
	93	1	0.333	0	-->	1
	94	1	0.333	0	==>	1
	99	1	0.500	1	-->	0
node_57 --> node_55	59	1	0.500	1	-->	2
	61	1	0.300	1	==>	2

node_55 --> node_54	83	1	0.667	0	==>	2
	88	1	0.500	0	==>	1
	89	1	0.500	0	==>	1
	98	1	0.500	0	==>	1
	101	1	0.500	1	==>	0
	102	1	0.500	0	==>	1
node_54 --> Catopsbaatar	5	1	0.143	1	==>	0
	7	1	0.167	0	==>	1
	9	1	0.286	0	==>	1
	26	1	0.500	1	==>	2
	29	1	0.333	1	==>	2
	42	1	0.600	2	==>	1
	43	1	0.250	1	==>	0
	44	1	0.250	1	==>	0
	48	1	0.250	1	==>	2
	51	1	0.600	2	==>	3
	55	1	0.643	1	-->	2
	59	1	0.500	2	-->	3
	61	1	0.300	2	==>	0
	85	1	0.333	1	-->	0
	86	1	0.200	0	==>	1
	95	1	0.500	1	==>	0
node_54 --> Kryptobaatar	58	1	0.200	2	==>	0
node_55 --> Nemegtbaatar	25	1	0.400	0	==>	1
	81	1	0.500	0	-->	2
	84	1	0.500	2	-->	3
	96	1	0.333	1	==>	0
node_57 --> node_56	58	1	0.200	2	==>	0
	85	1	0.333	1	-->	2
node_56 --> Kamptobaatar	6	1	0.500	0	==>	1
	9	1	0.286	0	==>	1
	16	1	0.222	2	==>	1
	84	1	0.500	2	-->	3
	96	1	0.333	1	==>	0
node_56 --> Chulsanbaatar	7	1	0.167	0	==>	1
node_59 --> node_58	16	1	0.222	0	==>	2
	25	1	0.400	0	-->	1
	31	1	0.400	1	-->	2
	35	1	0.333	0	==>	1
	58	1	0.200	2	-->	1
	85	1	0.333	0	-->	2
	94	1	0.333	0	-->	1
node_58 --> Eucosmodon	7	1	0.167	0	==>	1
	26	1	0.500	1	==>	2
	67	1	0.500	2	==>	1
	72	1	0.286	1	==>	2
node_58 --> Stygimys	3	1	0.500	2	==>	1
	47	1	0.429	0	==>	1
node_60 --> Microcosmodon	32	1	0.429	1	==>	2
	58	1	0.200	2	==>	1
node_66 --> node_65	25	1	0.400	0	-->	1
	30	1	0.571	2	-->	3
	35	1	0.333	0	==>	1
	48	1	0.250	2	==>	0



	55	1	0.643	2	-->	3
	83	1	0.667	0	==>	1
	84	1	0.500	2	-->	3
	98	1	0.500	0	-->	1
	100	1	1.000	0	-->	1
node_65 --> Pentacosmodon	58	1	0.200	2	==>	1
	82	1	0.667	1	==>	2
node_65 --> Kogaionon	59	1	0.500	3	==>	2
node_65 --> node_64	16	1	0.222	1	==>	2
	18	1	0.600	1	-->	0
	20	1	0.667	1	==>	0
	21	1	0.667	1	-->	0
	25	1	0.400	1	-->	2
	26	1	0.500	1	==>	3
	27	1	1.000	0	==>	1
	29	1	0.333	0	==>	2
	32	1	0.429	1	==>	3
	41	1	0.500	1	==>	0
	42	1	0.600	2	==>	3
	44	1	0.250	1	==>	0
	51	1	0.600	2	==>	3
	73	1	0.500	1	-->	0
	86	1	0.200	0	-->	1
	88	1	0.500	0	-->	1
	90	1	1.000	0	==>	2
	92	1	1.000	0	==>	1
	102	1	0.500	0	==>	1
node_64 --> node_61	7	1	0.167	1	==>	0
	19	1	0.167	0	-->	1
	30	1	0.571	3	-->	2
	61	1	0.300	0	==>	1
	63	1	1.000	3	==>	4
	65	1	1.000	0	==>	2
	74	1	0.500	0	==>	2
node_61 --> Taeniolabis	67	1	0.500	0	==>	2
	72	1	0.286	1	==>	2
node_61 --> Catopsalis	31	1	0.400	0	==>	1
node_64 --> node_63	6	1	0.500	0	-->	1
	47	1	0.429	1	==>	0
	62	1	0.667	2	==>	1
node_63 --> node_62	53	1	0.667	0	==>	2
	68	1	0.667	1	==>	2
	69	1	0.667	1	==>	2
	73	1	0.500	0	-->	1
	74	1	0.500	0	==>	1
node_70 --> Zofiabaatar	48	1	0.250	1	==>	3

**Character diagnostics:**

Character	Range	Min steps	Tree steps	Max steps	CI	RI	RC	HI	G-fit
1	1	1	1	3	1.000	1.000	1.000	0.000	1.000

2	1	1	1	3	1.000	1.000	1.000	0.000	1.000
3	2	2	4	16	0.500	0.857	0.429	0.500	0.600
4	1	1	2	3	0.500	0.500	0.250	0.500	0.750
5	1	1	7	17	0.143	0.625	0.089	0.857	0.333
6	1	1	2	2	0.500	0.000	0.000	0.500	0.750
7	1	1	6	11	0.167	0.500	0.083	0.833	0.375
8	1	1	1	3	1.000	1.000	1.000	0.000	1.000
9	1	2	7	12	0.286	0.500	0.143	0.857	0.333
10	1	1	1	3	1.000	1.000	1.000	0.000	1.000
11	1	1	1	4	1.000	1.000	1.000	0.000	1.000
12	1	1	1	2	1.000	1.000	1.000	0.000	1.000
13	1	1	2	6	0.500	0.800	0.400	0.500	0.750
14	1	1	1	3	1.000	1.000	1.000	0.000	1.000
15	1	1	2	3	0.500	0.500	0.250	0.500	0.750
16	2	2	9	18	0.222	0.563	0.125	0.778	0.300
17	2	2	2	9	1.000	1.000	1.000	0.000	1.000
18	1	3	5	11	0.600	0.750	0.450	0.800	0.429
19	1	1	6	12	0.167	0.545	0.091	0.833	0.375
20	2	2	3	10	0.667	0.875	0.583	0.333	0.750
21	2	2	3	12	0.667	0.900	0.600	0.333	0.750
22	2	2	3	9	0.667	0.857	0.571	0.333	0.750
23	1	1	1	3	1.000	1.000	1.000	0.000	1.000
24	1	1	1	3	1.000	1.000	1.000	0.000	1.000
25	2	2	5	8	0.400	0.500	0.200	0.600	0.500
26	3	3	6	19	0.500	0.813	0.406	0.500	0.500
27	1	2	2	5	1.000	1.000	1.000	0.500	0.750
28	1	1	2	6	0.500	0.800	0.400	0.500	0.750
29	2	2	6	20	0.333	0.778	0.259	0.667	0.429
30	3	4	7	15	0.571	0.727	0.416	0.571	0.429
31	2	2	5	16	0.400	0.786	0.314	0.600	0.500
32	3	3	7	22	0.429	0.789	0.338	0.571	0.429
33	1	1	1	12	1.000	1.000	1.000	0.000	1.000
34	1	1	2	17	0.500	0.938	0.469	0.500	0.750
35	1	1	3	9	0.333	0.750	0.250	0.667	0.600
36	1	1	2	11	0.500	0.900	0.450	0.500	0.750
37	1	1	2	14	0.500	0.923	0.462	0.500	0.750
38	3	3	4	18	0.750	0.933	0.700	0.250	0.750
39	1	1	1	4	1.000	1.000	1.000	0.000	1.000
40	1	1	1	15	1.000	1.000	1.000	0.000	1.000
41	1	1	2	9	0.500	0.875	0.438	0.500	0.750
42	3	3	5	20	0.600	0.882	0.529	0.400	0.600
43	2	2	8	17	0.250	0.600	0.150	0.750	0.333
44	1	1	4	18	0.250	0.824	0.206	0.750	0.500
45	1	1	4	16	0.250	0.800	0.200	0.750	0.500
46	3	3	4	16	0.750	0.923	0.692	0.250	0.750
47	3	3	7	16	0.429	0.692	0.297	0.571	0.429
48	3	3	12	21	0.250	0.500	0.125	0.750	0.250
49	1	1	1	3	1.000	1.000	1.000	0.000	1.000
50	1	1	1	3	1.000	1.000	1.000	0.000	1.000
51	3	3	5	18	0.600	0.867	0.520	0.400	0.600
52	2	2	2	12	1.000	1.000	1.000	0.000	1.000
53	2	2	3	8	0.667	0.833	0.556	0.333	0.750
54	1	1	1	8	1.000	1.000	1.000	0.000	1.000
55	3	9	14	29	0.643	0.750	0.482	0.786	0.214

56	1	1	2	5	0.500	0.750	0.375	0.500	0.750
57	1	1	2	7	0.500	0.833	0.417	0.500	0.750
58	2	2	10	15	0.200	0.385	0.077	0.800	0.273
59	3	4	8	13	0.500	0.556	0.278	0.625	0.375
60	1	1	1	4	1.000	1.000	1.000	0.000	1.000
61	2	3	10	17	0.300	0.500	0.150	0.800	0.273
62	2	2	3	11	0.667	0.889	0.593	0.333	0.750
63	4	4	4	8	1.000	1.000	1.000	0.000	1.000
64	1	1	2	4	0.500	0.667	0.333	0.500	0.750
65	2	3	3	5	1.000	1.000	1.000	0.333	0.750
66	2	2	2	5	1.000	1.000	1.000	0.000	1.000
67	2	3	6	13	0.500	0.700	0.350	0.667	0.429
68	2	2	3	9	0.667	0.857	0.571	0.333	0.750
69	2	2	3	10	0.667	0.875	0.583	0.333	0.750
70	1	1	2	6	0.500	0.800	0.400	0.500	0.750
71	1	1	1	4	1.000	1.000	1.000	0.000	1.000
72	2	2	7	13	0.286	0.545	0.156	0.714	0.375
73	1	2	4	9	0.500	0.714	0.357	0.750	0.500
74	2	2	4	6	0.500	0.500	0.250	0.500	0.600
75	2	3	3	6	1.000	1.000	1.000	0.333	0.750
76	1	1	6	17	0.167	0.688	0.115	0.833	0.375
77	2	2	5	12	0.400	0.700	0.280	0.600	0.500
78	1	1	1	1	1.000	0/0	0/0	0.000	1.000
79	1	1	1	1	1.000	0/0	0/0	0.000	1.000
80	1	1	3	11	0.333	0.800	0.267	0.667	0.600
81	2	2	4	5	0.500	0.333	0.167	0.500	0.600
82	2	2	3	9	0.667	0.857	0.571	0.333	0.750
83	2	2	3	7	0.667	0.800	0.533	0.333	0.750
84	3	3	6	9	0.500	0.500	0.250	0.500	0.500
85	2	2	6	7	0.333	0.200	0.067	0.667	0.429
86	1	1	5	8	0.200	0.429	0.086	0.800	0.429
87	1	1	1	5	1.000	1.000	1.000	0.000	1.000
88	1	1	2	4	0.500	0.667	0.333	0.500	0.750
89	1	1	2	4	0.500	0.667	0.333	0.500	0.750
90	2	2	2	8	1.000	1.000	1.000	0.000	1.000
91	1	1	1	5	1.000	1.000	1.000	0.000	1.000
92	1	1	1	2	1.000	1.000	1.000	0.000	1.000
93	1	1	3	5	0.333	0.500	0.167	0.667	0.600
94	1	1	3	6	0.333	0.600	0.200	0.667	0.600
95	1	1	2	3	0.500	0.500	0.250	0.500	0.750
96	1	1	3	3	0.333	0.000	0.000	0.667	0.600
97	1	1	2	5	0.500	0.750	0.375	0.500	0.750
98	1	1	2	4	0.500	0.667	0.333	0.500	0.750
99	1	1	2	5	0.500	0.750	0.375	0.500	0.750
100	1	1	1	2	1.000	1.000	1.000	0.000	1.000
101	1	1	2	4	0.500	0.667	0.333	0.500	0.750
102	1	1	2	4	0.500	0.667	0.333	0.500	0.750

## SOM 4. Phylogenetic Analyses with 19 characters ordered.

Source of trees from which consensus(es) calculated...

Heuristic search settings:

Optimality criterion = parsimony

Character-status summary:

Of 102 total characters:

19 characters are of type 'ord' (Wagner)

83 characters are of type 'unord'

All characters have equal weight

2 characters are parsimony-uninformative

Number of parsimony-informative characters = 100

Gaps are treated as "missing"

Multistate taxa interpreted as polymorphism

Starting tree(s) obtained via stepwise addition

Addition sequence: random

Number of replicates = 1000

Starting seed = 965527416

Number of trees held at each step during stepwise addition = 10

Branch-swapping algorithm: tree-bisection-reconnection (TBR)

Steepest descent option not in effect

Initial 'MaxTrees' setting = 10000 (will be auto-increased by 100)

Branches collapsed (creating polytomies) if maximum branch length is zero

'MulTrees' option not in effect; only 1 tree will be saved per replicate

Topological constraints not enforced

Trees are unrooted

Heuristic search completed

Total number of rearrangements tried = 45574771

Score of best tree(s) found = 358

Number of trees retained = 10

Time used = 00:01:03.4

Tree description:

Unrooted tree(s) rooted using outgroup method

Optimality criterion = parsimony

Character-status summary:

Of 102 total characters:

19 characters are of type 'ord' (Wagner)

83 characters are of type 'unord'

All characters have equal weight

2 characters are parsimony-uninformative

Number of parsimony-informative characters = 100

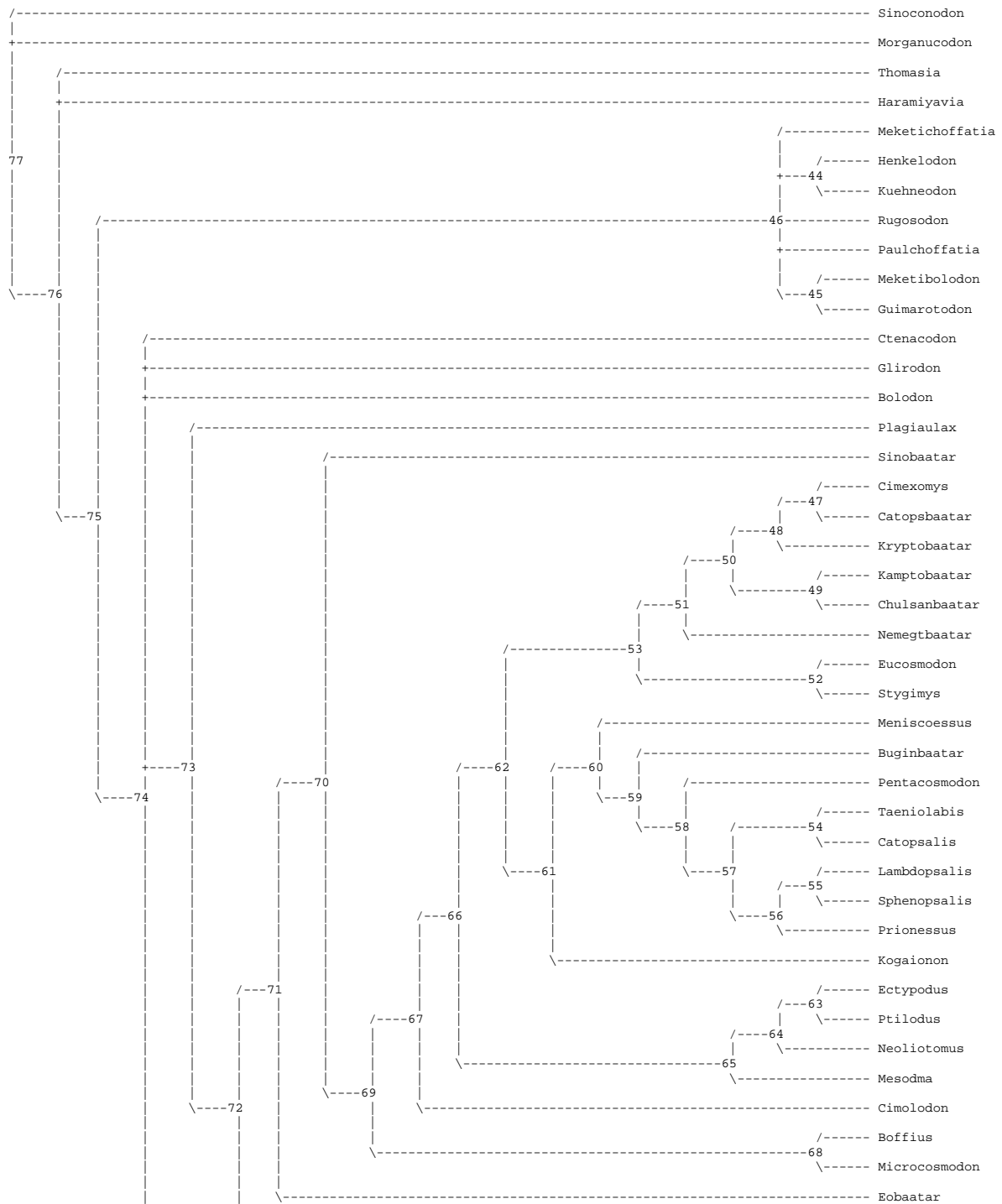
Gaps are treated as "missing"

Multistate taxa interpreted as uncertainty

Character-state optimization: Accelerated transformation (ACCTRAN)

### Figure 3 - Strict Consensus Tree (of 10 EMTs) with 19 characters ordered

Tree length = 347  
 Consistency index (CI) = 0.4553  
 Homoplasy index (HI) = 0.5447  
 CI excluding uninformative characters = 0.4522  
 HI excluding uninformative characters = 0.5478  
 Retention index (RI) = 0.7763  
 Rescaled consistency index (RC) = 0.3535





**Apomorphy lists:**

Branch	Character	Steps	CI	Change
node_77 --> Sinoconodon	78	1	1.000	1 ==> 0
	79	1	1.000	1 ==> 0
node_77 --> Morganucodon	84	1	0.500	1 ==> 0
node_77 --> node_76	4	1	0.500	0 --> 1
	5	1	0.143	0 --> 1
	12	1	1.000	0 ==> 1
	22	1	0.667	0 ==> 1
	42	1	0.600	0 --> 1
	53	1	0.667	0 ==> 1
	62	1	0.667	0 ==> 1
	63	1	1.000	0 ==> 3
	66	1	0.667	0 --> 1
	68	1	0.667	0 ==> 1
	69	1	0.667	0 ==> 2
	77	1	0.400	0 --> 1
	89	1	0.500	1 --> 0
	93	1	0.333	0 --> 1
	95	1	0.500	0 --> 1
	101	1	0.500	0 --> 1
	node_76 --> Thomasia	26	3	0.333
32		1	0.500	0 ==> 1
66		1	0.667	1 --> 0
node_76 --> Haramiyavia	18	1	0.333	0 ==> 1
	42	1	0.600	1 --> 0
node_76 --> node_75	1	1	1.000	0 ==> 1
	2	1	1.000	0 ==> 1
	3	1	0.400	0 ==> 1
	8	1	1.000	0 ==> 1
	10	1	1.000	0 ==> 1
	11	1	1.000	0 ==> 1
	13	1	0.333	0 --> 1
	14	1	1.000	0 ==> 1
	17	1	1.000	0 ==> 1
	19	1	0.167	0 ==> 1
	20	1	0.667	0 ==> 1
	24	1	1.000	0 ==> 1
	28	1	0.500	0 ==> 1
	29	2	0.286	2 ==> 0
	36	1	0.333	0 ==> 1
38	1	0.750	0 ==> 1	
41	1	0.500	0 ==> 1	
45	1	0.333	0 ==> 1	
47	2	0.333	0 ==> 2	
48	1	0.273	0 ==> 1	
49	1	1.000	0 ==> 1	
50	1	1.000	0 ==> 1	
51	1	0.600	0 ==> 1	

	52	1	1.000	0	==>	1
	56	1	0.500	0	==>	1
	60	1	1.000	0	==>	1
	61	1	0.200	1	==>	0
	72	1	0.250	2	==>	1
node_75 --> node_46	23	1	1.000	0	==>	1
	46	1	1.000	1	==>	0
	63	1	1.000	3	==>	1
	64	1	0.500	0	==>	1
	65	1	1.000	0	==>	1
	66	1	0.667	1	-->	2
	68	1	0.667	1	==>	2
	70	1	0.333	0	==>	1
	71	1	1.000	0	==>	1
	72	1	0.250	1	==>	0
	75	1	1.000	0	==>	2
	76	1	0.143	0	==>	1
	94	1	0.500	0	-->	1
node_46 --> Meketichoffatia	56	1	0.500	1	==>	0
node_46 --> node_44	4	1	0.500	1	-->	0
	20	1	0.667	1	==>	2
	63	1	1.000	1	==>	2
	72	1	0.250	0	-->	1
node_44 --> Henkelodon	22	1	0.667	1	==>	2
node_44 --> Kuehneodon	26	1	0.333	0	==>	1
	51	1	0.600	1	==>	2
node_46 --> Rugosodon	75	1	1.000	2	==>	1
node_46 --> Paulchoffatia	13	1	0.333	1	-->	0
node_46 --> node_45	13	1	0.333	1	-->	0
	47	1	0.333	2	==>	3
node_75 --> node_74	5	1	0.143	1	-->	0
	7	1	0.143	0	==>	1
	9	1	0.167	0	==>	1
	30	1	0.600	0	==>	1
	39	1	1.000	0	-->	1
	53	1	0.667	1	==>	0
	54	1	1.000	0	==>	1
	57	1	0.500	0	==>	1
	62	1	0.667	1	==>	2
	69	1	0.667	2	==>	1
	73	1	0.333	0	==>	1
	77	1	0.400	1	-->	0
	82	1	0.667	0	==>	1
	85	1	0.333	0	-->	1
	99	1	0.500	0	-->	1
node_74 --> Ctenacodon	55	1	0.429	0	==>	1
node_74 --> Glirodon	16	1	0.222	0	==>	1
	57	1	0.500	1	==>	0
node_74 --> Bolodon	5	1	0.143	0	==>	1
	38	1	0.750	1	==>	2
	76	1	0.143	0	==>	1
node_74 --> node_73	17	1	1.000	1	-->	2
	18	1	0.333	0	-->	1
	21	1	0.667	0	-->	1

	22	1	0.667	1	-->	2
	28	1	0.500	1	-->	0
	30	1	0.600	1	-->	0
	32	1	0.500	0	-->	1
	33	1	1.000	0	==>	1
	38	1	0.750	1	==>	2
	43	1	0.250	0	==>	1
	48	1	0.273	1	-->	2
	85	1	0.333	1	-->	0
node_73 --> node_72	3	1	0.400	1	-->	2
	37	1	0.500	0	-->	1
	42	1	0.600	1	==>	2
	44	1	0.250	0	==>	1
	46	1	1.000	1	==>	2
	47	1	0.333	2	==>	1
	52	1	1.000	1	==>	2
	77	1	0.400	0	==>	1
node_72 --> node_71	58	1	0.182	0	==>	1
	61	1	0.200	0	==>	1
	70	1	0.333	0	-->	1
	76	1	0.143	0	==>	1
	80	1	0.500	0	-->	1
node_71 --> node_70	30	1	0.600	0	==>	2
	55	1	0.429	0	==>	1
node_70 --> Sinobaatar	3	1	0.400	2	-->	1
	9	1	0.167	1	==>	0
	19	1	0.167	1	==>	0
	77	1	0.400	1	==>	0
	86	1	0.200	0	==>	1
node_70 --> node_69	7	1	0.143	1	==>	0
	26	1	0.333	0	==>	1
	29	1	0.286	0	==>	1
	31	1	0.333	0	==>	1
	34	1	0.500	0	==>	1
	36	1	0.333	1	==>	0
	40	1	0.500	0	==>	1
	51	1	0.600	1	==>	2
	55	1	0.429	1	==>	2
	59	2	0.429	0	==>	2
	67	1	0.286	0	==>	2
	70	1	0.333	1	-->	0
	84	1	0.500	1	-->	2
	93	1	0.333	1	-->	0
node_69 --> node_67	38	1	0.750	2	==>	3
	43	1	0.250	1	-->	2
	47	1	0.333	1	==>	0
	48	1	0.273	2	==>	1
node_67 --> node_66	5	1	0.143	0	==>	1
	46	1	1.000	2	==>	3
node_66 --> node_62	25	1	0.667	0	==>	1
	43	1	0.250	2	-->	1
	45	1	0.333	1	==>	0
	76	1	0.143	1	==>	0
	84	1	0.500	2	-->	3



	97	1	1.000	0	==>	1
node_62 --> node_53	9	1	0.167	1	==>	0
	16	1	0.222	0	==>	2
	81	1	0.500	0	-->	2
	85	1	0.333	0	==>	1
	87	1	1.000	0	-->	1
	90	1	1.000	0	-->	1
	91	1	1.000	0	-->	1
	93	1	0.333	0	-->	1
	94	1	0.500	0	==>	1
	99	1	0.500	1	-->	0
node_53 --> node_51	19	1	0.167	1	==>	0
	21	1	0.667	1	==>	2
	32	1	0.500	1	==>	2
	55	1	0.429	2	-->	1
	67	1	0.286	2	==>	0
	82	1	0.667	1	==>	2
node_51 --> node_50	25	1	0.667	1	==>	0
	58	1	0.182	1	-->	0
	81	1	0.500	2	-->	0
	84	1	0.500	3	-->	2
node_50 --> node_48	83	1	0.500	0	==>	2
	88	1	0.500	0	==>	1
	89	1	0.500	0	==>	1
	98	1	0.500	0	==>	1
	101	1	0.500	1	==>	0
	102	1	0.500	0	==>	1
node_48 --> node_47	5	1	0.143	1	-->	0
	7	1	0.143	0	-->	1
	9	1	0.167	0	-->	1
	48	1	0.273	1	==>	2
	55	1	0.429	1	-->	2
	58	2	0.182	0	==>	2
	85	1	0.333	1	==>	0
	86	1	0.200	0	==>	1
	95	1	0.500	1	-->	0
node_47 --> Cimexomys	16	1	0.222	2	==>	0
	34	1	0.500	1	==>	0
	67	1	0.286	0	==>	1
	76	1	0.143	0	==>	1
	84	1	0.500	2	==>	1
node_47 --> Catopsbaatar	26	1	0.333	1	==>	2
	29	1	0.286	1	==>	2
	42	1	0.600	2	==>	1
	43	1	0.250	1	==>	0
	44	1	0.250	1	==>	0
	51	1	0.600	2	==>	3
	59	1	0.429	2	==>	3
	61	1	0.200	1	==>	0
node_48 --> Kryptobaatar	61	1	0.200	1	==>	2
node_50 --> node_49	59	1	0.429	2	==>	1
	85	1	0.333	1	==>	2
node_49 --> Kamptobaatar	6	1	0.500	0	==>	1
	9	1	0.167	0	==>	1

	16	1	0.222	2	==>	1
	84	1	0.500	2	-->	3
	96	1	0.333	1	==>	0
node_49 --> Chulsanbaatar	7	1	0.143	0	==>	1
node_51 --> Nemegtbaatar	58	1	0.182	1	==>	2
	61	1	0.200	1	==>	2
	96	1	0.333	1	==>	0
node_53 --> node_52	31	1	0.333	1	-->	2
	35	1	0.500	0	==>	1
	43	1	0.250	1	-->	2
	85	1	0.333	1	-->	2
node_52 --> Eucosmodon	7	1	0.143	0	==>	1
	26	1	0.333	1	==>	2
	67	1	0.286	2	==>	1
	72	1	0.250	1	==>	2
node_52 --> Stygimys	3	1	0.400	2	==>	1
	47	1	0.333	0	==>	1
node_62 --> node_61	31	1	0.333	1	==>	0
	48	1	0.273	1	-->	0
	55	1	0.429	2	==>	3
	58	1	0.182	1	-->	2
	83	1	0.500	0	-->	1
	98	1	0.500	0	-->	1
	100	1	1.000	0	-->	1
node_61 --> node_60	25	1	0.667	1	==>	2
	29	1	0.286	1	==>	2
	32	1	0.500	1	==>	2
	59	1	0.429	2	==>	3
	61	1	0.200	1	-->	2
	86	1	0.200	0	-->	1
	88	1	0.500	0	-->	1
	90	1	1.000	0	-->	2
	92	1	1.000	0	-->	1
	102	1	0.500	0	-->	1
node_60 --> Meniscoessus	67	1	0.286	2	==>	1
	72	1	0.250	1	==>	2
	74	1	0.500	0	==>	1
	76	1	0.143	0	==>	1
	80	1	0.500	1	==>	0
	81	1	0.500	0	==>	2
	83	1	0.500	1	-->	0
node_60 --> node_59	18	1	0.333	1	-->	0
	20	1	0.667	1	-->	0
	21	1	0.667	1	-->	0
	26	2	0.333	1	-->	3
	27	1	1.000	0	-->	1
	32	1	0.500	2	==>	3
	35	1	0.500	0	==>	1
	43	1	0.250	1	==>	0
	44	1	0.250	1	-->	0
	51	1	0.600	2	-->	3
	58	1	0.182	2	-->	1
node_59 --> Buginbaatar	3	1	0.400	2	==>	1
	31	1	0.333	0	==>	1

node_59 --> node_58	5	1	0.143	1	==>	0
	7	1	0.143	0	-->	1
	16	1	0.222	0	-->	1
	47	1	0.333	0	-->	1
	61	1	0.200	2	-->	1
	67	1	0.286	2	==>	0
node_58 --> Pentacosmodon	44	1	0.250	0	-->	1
	82	1	0.667	1	==>	2
	86	1	0.200	1	-->	0
node_58 --> node_57	16	1	0.222	1	-->	2
	41	1	0.500	1	==>	0
	42	1	0.600	2	==>	3
	58	1	0.182	1	-->	2
	73	1	0.333	1	-->	0
node_57 --> node_54	7	1	0.143	1	-->	0
	63	1	1.000	3	==>	4
	65	1	1.000	0	==>	2
	74	1	0.500	0	==>	2
node_54 --> Taeniolabis	67	1	0.286	0	==>	2
	72	1	0.250	1	==>	2
node_54 --> Catopsalis	31	1	0.333	0	==>	1
node_57 --> node_56	6	1	0.500	0	-->	1
	19	1	0.167	1	-->	0
	30	1	0.600	2	==>	3
	47	1	0.333	1	-->	0
	61	1	0.200	1	==>	0
	62	1	0.667	2	==>	1
node_56 --> node_55	53	1	0.667	0	==>	2
	68	1	0.667	1	==>	2
	69	1	0.667	1	==>	2
	73	1	0.333	0	-->	1
	74	1	0.500	0	==>	1
node_61 --> Kogaionon	19	1	0.167	1	==>	0
	29	1	0.286	1	==>	0
	30	1	0.600	2	==>	3
	61	1	0.200	1	==>	0
node_66 --> node_65	15	1	0.500	0	-->	1
	59	1	0.429	2	==>	3
	77	1	0.400	1	==>	2
	81	1	0.500	0	-->	1
node_65 --> node_64	19	1	0.167	1	==>	0
	31	1	0.333	1	==>	2
	48	2	0.273	1	==>	3
	55	1	0.429	2	-->	3
	72	1	0.250	1	==>	2
node_64 --> node_63	5	1	0.143	1	==>	0
	64	1	0.500	0	==>	1
node_63 --> Ectypodus	83	1	0.500	0	==>	2
	86	1	0.200	0	==>	1
node_63 --> Ptilodus	9	1	0.167	1	==>	0
	29	1	0.286	1	==>	0
	48	1	0.273	3	-->	2
	96	1	0.333	1	==>	0
node_64 --> Neoliotomus	15	1	0.500	1	-->	0

	16	1	0.222	0	==>	2
	58	1	0.182	1	==>	2
	74	1	0.500	0	==>	1
node_67 --> Cimolodon	58	1	0.182	1	==>	2
	61	1	0.200	1	==>	2
	72	1	0.250	1	==>	2
node_69 --> node_68	16	1	0.222	0	==>	1
	43	1	0.250	1	-->	0
	45	1	0.333	1	-->	0
	59	1	0.429	2	==>	3
	76	1	0.143	1	==>	0
node_68 --> Boffius	58	1	0.182	1	==>	2
node_68 --> Microcosmodon	32	1	0.500	1	==>	2
node_71 --> Eobaatar	16	1	0.222	0	==>	2
	37	1	0.500	1	-->	0
node_72 --> Arginbaatar	36	1	0.333	1	==>	0
	40	1	0.500	0	==>	1
	43	1	0.250	1	==>	2
	47	1	0.333	1	==>	0
	48	1	0.273	2	==>	3
node_74 --> Zofiabaatar	48	2	0.273	1	==>	3

#### Character diagnostics:

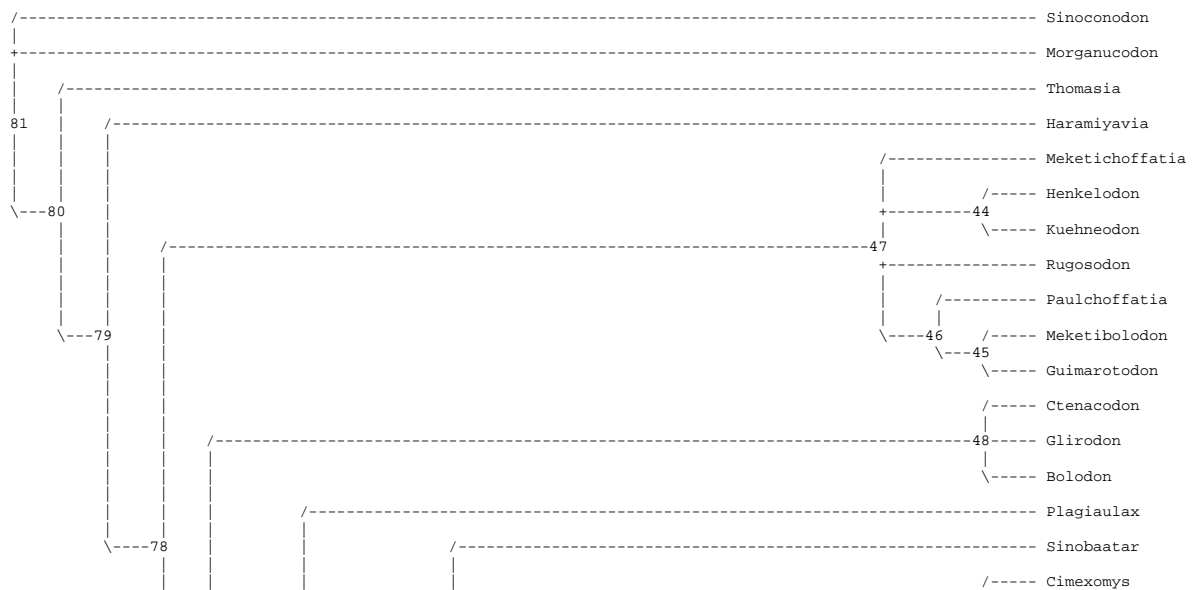
Character	Range	Min steps	Tree steps	Max steps	CI	RI	RC	HI	G-fit
1	1	1	1	3	1.000	1.000	1.000	0.000	1.000
2	1	1	1	3	1.000	1.000	1.000	0.000	1.000
3	2	2	5	16	0.400	0.786	0.314	0.600	0.500
4	1	1	2	3	0.500	0.500	0.250	0.500	0.750
5	1	1	7	17	0.143	0.625	0.089	0.857	0.333
6	1	1	2	2	0.500	0.000	0.000	0.500	0.750
7	1	1	7	11	0.143	0.400	0.057	0.857	0.333
8	1	1	1	3	1.000	1.000	1.000	0.000	1.000
9	1	1	6	11	0.167	0.500	0.083	0.833	0.375
10	1	1	1	3	1.000	1.000	1.000	0.000	1.000
11	1	1	1	4	1.000	1.000	1.000	0.000	1.000
12	1	1	1	2	1.000	1.000	1.000	0.000	1.000
13	1	1	3	6	0.333	0.600	0.200	0.667	0.600
14	1	1	1	3	1.000	1.000	1.000	0.000	1.000
15	1	1	2	3	0.500	0.500	0.250	0.500	0.750
16	2	2	9	18	0.222	0.563	0.125	0.778	0.300
17	2	2	2	13	1.000	1.000	1.000	0.000	1.000
18	1	1	3	9	0.333	0.750	0.250	0.667	0.600
19	1	1	6	12	0.167	0.545	0.091	0.833	0.375
20	2	2	3	10	0.667	0.875	0.583	0.333	0.750
21	2	2	3	12	0.667	0.900	0.600	0.333	0.750
22	2	2	3	9	0.667	0.857	0.571	0.333	0.750
23	1	1	1	3	1.000	1.000	1.000	0.000	1.000
24	1	1	1	3	1.000	1.000	1.000	0.000	1.000
25	2	2	3	13	0.667	0.909	0.606	0.333	0.750
26	3	3	9	25	0.333	0.727	0.242	0.667	0.333

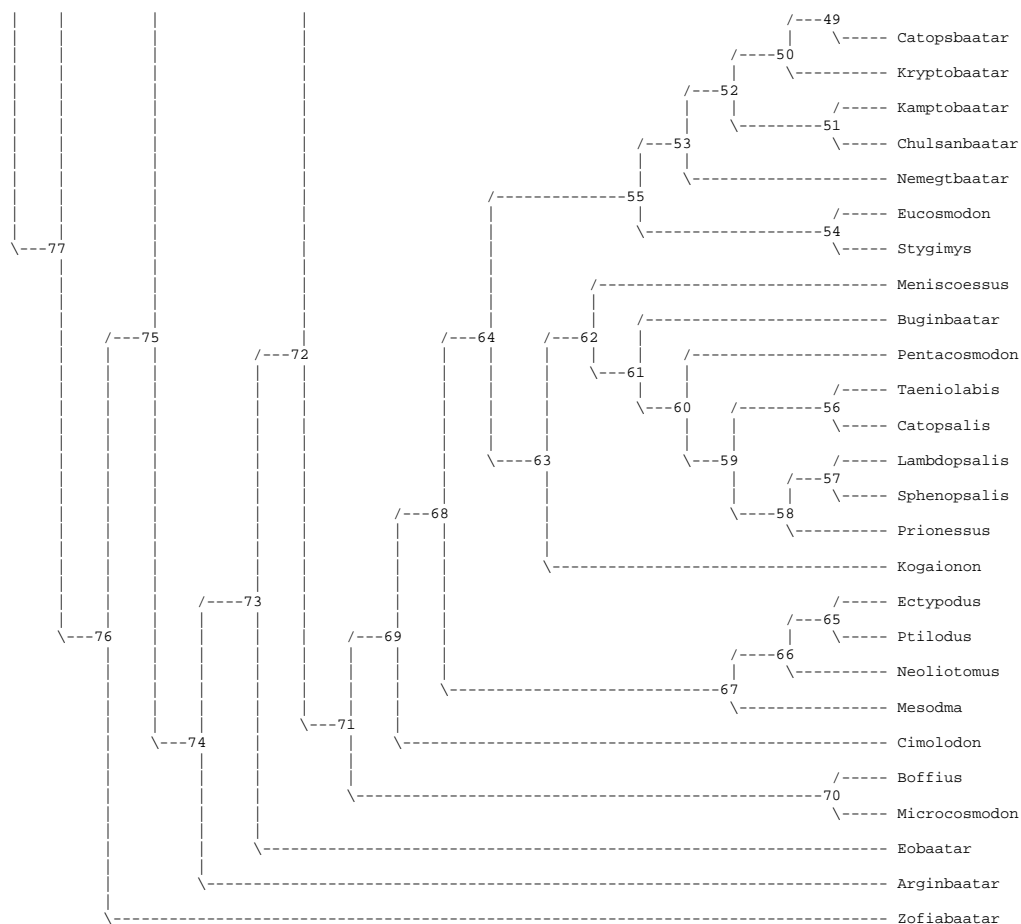
27	1	1	1	4	1.000	1.000	1.000	0.000	1.000
28	1	1	2	6	0.500	0.800	0.400	0.500	0.750
29	2	2	7	22	0.286	0.750	0.214	0.714	0.375
30	3	3	5	14	0.600	0.818	0.491	0.400	0.600
31	2	2	6	20	0.333	0.778	0.259	0.667	0.429
32	3	3	6	28	0.500	0.880	0.440	0.500	0.500
33	1	1	1	12	1.000	1.000	1.000	0.000	1.000
34	1	1	2	17	0.500	0.938	0.469	0.500	0.750
35	1	1	2	9	0.500	0.875	0.438	0.500	0.750
36	1	1	3	11	0.333	0.800	0.267	0.667	0.600
37	1	1	2	14	0.500	0.923	0.462	0.500	0.750
38	3	3	4	18	0.750	0.933	0.700	0.250	0.750
39	1	1	1	4	1.000	1.000	1.000	0.000	1.000
40	1	1	2	15	0.500	0.929	0.464	0.500	0.750
41	1	1	2	9	0.500	0.875	0.438	0.500	0.750
42	3	3	5	20	0.600	0.882	0.529	0.400	0.600
43	2	2	8	21	0.250	0.684	0.171	0.750	0.333
44	1	1	4	18	0.250	0.824	0.206	0.750	0.500
45	1	1	3	16	0.333	0.867	0.289	0.667	0.600
46	3	3	3	27	1.000	1.000	1.000	0.000	1.000
47	3	3	9	27	0.333	0.750	0.250	0.667	0.333
48	3	3	11	25	0.273	0.636	0.174	0.727	0.273
49	1	1	1	3	1.000	1.000	1.000	0.000	1.000
50	1	1	1	3	1.000	1.000	1.000	0.000	1.000
51	3	3	5	21	0.600	0.889	0.533	0.400	0.600
52	2	2	2	15	1.000	1.000	1.000	0.000	1.000
53	2	2	3	8	0.667	0.833	0.556	0.333	0.750
54	1	1	1	8	1.000	1.000	1.000	0.000	1.000
55	3	3	7	32	0.429	0.862	0.369	0.571	0.429
56	1	1	2	5	0.500	0.750	0.375	0.500	0.750
57	1	1	2	7	0.500	0.833	0.417	0.500	0.750
58	2	2	11	19	0.182	0.471	0.086	0.818	0.250
59	3	3	7	24	0.429	0.810	0.347	0.571	0.429
60	1	1	1	4	1.000	1.000	1.000	0.000	1.000
61	2	2	10	16	0.200	0.429	0.086	0.800	0.273
62	2	2	3	11	0.667	0.889	0.593	0.333	0.750
63	4	4	4	8	1.000	1.000	1.000	0.000	1.000
64	1	1	2	4	0.500	0.667	0.333	0.500	0.750
65	2	2	2	4	1.000	1.000	1.000	0.000	1.000
66	2	2	3	5	0.667	0.667	0.444	0.333	0.750
67	2	2	7	12	0.286	0.500	0.143	0.714	0.375
68	2	2	3	9	0.667	0.857	0.571	0.333	0.750
69	2	2	3	10	0.667	0.875	0.583	0.333	0.750
70	1	1	3	6	0.333	0.600	0.200	0.667	0.600
71	1	1	1	4	1.000	1.000	1.000	0.000	1.000
72	2	2	8	13	0.250	0.455	0.114	0.750	0.333
73	1	1	3	8	0.333	0.714	0.238	0.667	0.600
74	2	2	4	6	0.500	0.500	0.250	0.500	0.600
75	2	2	2	5	1.000	1.000	1.000	0.000	1.000
76	1	1	7	17	0.143	0.625	0.089	0.857	0.333
77	2	2	5	12	0.400	0.700	0.280	0.600	0.500
78	1	1	1	1	1.000	0/0	0/0	0.000	1.000
79	1	1	1	1	1.000	0/0	0/0	0.000	1.000
80	1	1	2	11	0.500	0.900	0.450	0.500	0.750

81	2	2	4	5	0.500	0.333	0.167	0.500	0.600
82	2	2	3	9	0.667	0.857	0.571	0.333	0.750
83	2	2	4	7	0.500	0.600	0.300	0.500	0.600
84	3	3	6	9	0.500	0.500	0.250	0.500	0.500
85	2	2	6	10	0.333	0.500	0.167	0.667	0.429
86	1	1	5	8	0.200	0.429	0.086	0.800	0.429
87	1	1	1	5	1.000	1.000	1.000	0.000	1.000
88	1	1	2	4	0.500	0.667	0.333	0.500	0.750
89	1	1	2	4	0.500	0.667	0.333	0.500	0.750
90	2	2	2	8	1.000	1.000	1.000	0.000	1.000
91	1	1	1	5	1.000	1.000	1.000	0.000	1.000
92	1	1	1	2	1.000	1.000	1.000	0.000	1.000
93	1	1	3	5	0.333	0.500	0.167	0.667	0.600
94	1	1	2	6	0.500	0.800	0.400	0.500	0.750
95	1	1	2	3	0.500	0.500	0.250	0.500	0.750
96	1	1	3	3	0.333	0.000	0.000	0.667	0.600
97	1	1	1	5	1.000	1.000	1.000	0.000	1.000
98	1	1	2	4	0.500	0.667	0.333	0.500	0.750
99	1	1	2	5	0.500	0.750	0.375	0.500	0.750
100	1	1	1	2	1.000	1.000	1.000	0.000	1.000
101	1	1	2	4	0.500	0.667	0.333	0.500	0.750
102	1	1	2	4	0.500	0.667	0.333	0.500	0.750

**Figure 4 - 50% Majority Rule Consensus Tree with 19 characters ordered**

Tree length = 342  
 Consistency index (CI) = 0.4620  
 Homoplasy index (HI) = 0.5380  
 CI excluding uninformative characters = 0.4588  
 HI excluding uninformative characters = 0.5412  
 Retention index (RI) = 0.7822  
 Rescaled consistency index (RC) = 0.3614





**Apomorphy lists:**

Branch	Character	Steps	CI	Change
node_81 --> Sinoconodon	78	1	1.000	1 ==> 0
	79	1	1.000	1 ==> 0
node_81 --> Morganucodon	84	1	0.500	1 ==> 0
node_81 --> node_80	4	1	0.500	0 --> 1
	5	1	0.143	0 --> 1
	12	1	1.000	0 ==> 1
	22	1	0.667	0 --> 1
	42	1	0.600	0 --> 1
	53	1	0.667	0 ==> 1
	62	1	0.667	0 ==> 1
	63	1	1.000	0 ==> 3
	68	1	0.667	0 --> 1
	69	1	0.667	0 ==> 2
	77	1	0.400	0 --> 1
	89	1	0.500	1 --> 0
	93	1	0.333	0 --> 1
	95	1	0.500	0 --> 1
101	1	0.500	0 --> 1	

node_80 --> Thomasia	26	3	0.333	0	==>	3
	32	1	0.500	0	==>	1
node_80 --> node_79	28	1	0.500	0	-->	1
	29	2	0.286	2	-->	0
	66	1	1.000	0	==>	1
node_79 --> Haramiyavia	18	1	0.333	0	==>	1
	42	1	0.600	1	-->	0
node_79 --> node_78	1	1	1.000	0	==>	1
	2	1	1.000	0	==>	1
	3	1	0.400	0	==>	1
	8	1	1.000	0	==>	1
	10	1	1.000	0	==>	1
	11	1	1.000	0	==>	1
	13	1	0.500	0	==>	1
	14	1	1.000	0	==>	1
	17	1	1.000	0	==>	1
	19	1	0.167	0	==>	1
	20	1	0.667	0	==>	1
	24	1	1.000	0	==>	1
	36	1	0.333	0	==>	1
	38	1	0.750	0	==>	1
	41	1	0.500	0	==>	1
	45	1	0.333	0	==>	1
	47	2	0.333	0	==>	2
	48	1	0.300	0	==>	1
	49	1	1.000	0	==>	1
	50	1	1.000	0	==>	1
	51	1	0.600	0	==>	1
	52	1	1.000	0	==>	1
	56	1	0.500	0	==>	1
	60	1	1.000	0	==>	1
	61	1	0.200	1	==>	0
	72	1	0.250	2	==>	1
node_78 --> node_47	23	1	1.000	0	==>	1
	46	1	1.000	1	==>	0
	63	1	1.000	3	==>	1
	64	1	0.500	0	==>	1
	65	1	1.000	0	==>	1
	66	1	1.000	1	==>	2
	68	1	0.667	1	==>	2
	70	1	0.333	0	==>	1
	71	1	1.000	0	==>	1
	72	1	0.250	1	-->	0
	75	1	1.000	0	==>	1
	76	1	0.143	0	==>	1
	94	1	0.500	0	-->	1
node_47 --> Meketichoffatia	56	1	0.500	1	==>	0
node_47 --> node_44	4	1	0.500	1	-->	0
	20	1	0.667	1	==>	2
	63	1	1.000	1	==>	2
	72	1	0.250	0	-->	1
node_44 --> Henkelodon	22	1	0.667	1	==>	2
node_44 --> Kuehneodon	26	1	0.333	0	==>	1
	51	1	0.600	1	==>	2



node_47 --> node_46	13	1	0.500	1	==>	0
	75	1	1.000	1	-->	2
node_46 --> node_45	47	1	0.333	2	==>	3
node_78 --> node_77	5	1	0.143	1	-->	0
	7	1	0.143	0	==>	1
	9	1	0.167	0	==>	1
	39	1	1.000	0	-->	1
	53	1	0.667	1	==>	0
	54	1	1.000	0	==>	1
	57	1	0.500	0	==>	1
	62	1	0.667	1	==>	2
	69	1	0.667	2	==>	1
	73	1	0.333	0	==>	1
	77	1	0.400	1	-->	0
	82	1	0.667	0	==>	1
	99	1	0.500	0	-->	1
node_77 --> node_48	30	1	0.750	0	==>	1
	85	1	0.400	0	==>	1
node_48 --> Ctenacodon	55	1	0.429	0	==>	1
node_48 --> Glirodon	16	1	0.222	0	==>	1
	57	1	0.500	1	==>	0
node_48 --> Bolodon	5	1	0.143	0	==>	1
	38	1	0.750	1	==>	2
	76	1	0.143	0	==>	1
node_77 --> node_76	17	1	1.000	1	-->	2
	18	1	0.333	0	-->	1
	21	1	0.667	0	-->	1
	22	1	0.667	1	-->	2
	28	1	0.500	1	-->	0
	32	1	0.500	0	-->	1
	48	2	0.300	1	==>	3
node_76 --> node_75	33	1	1.000	0	==>	1
	38	1	0.750	1	==>	2
	43	1	0.250	0	==>	1
node_75 --> node_74	3	1	0.400	1	-->	2
	37	1	0.500	0	-->	1
	42	1	0.600	1	==>	2
	44	1	0.250	0	==>	1
	46	1	1.000	1	==>	2
	47	1	0.333	2	==>	1
	52	1	1.000	1	==>	2
	77	1	0.400	0	==>	1
node_74 --> node_73	48	1	0.300	3	-->	2
	58	1	0.182	0	==>	1
	61	1	0.200	0	==>	1
	70	1	0.333	0	-->	1
	76	1	0.143	0	==>	1
	80	1	0.500	0	-->	1
node_73 --> node_72	30	1	0.750	0	==>	2
	55	1	0.429	0	==>	1
node_72 --> Sinobaatar	3	1	0.400	2	-->	1
	9	1	0.167	1	==>	0
	19	1	0.167	1	==>	0
	77	1	0.400	1	==>	0

	86	1	0.200	0	==>	1
node_72 --> node_71	7	1	0.143	1	==>	0
	26	1	0.333	0	==>	1
	29	1	0.286	0	==>	1
	31	1	0.333	0	==>	1
	34	1	0.500	0	==>	1
	36	1	0.333	1	==>	0
	40	1	0.500	0	==>	1
	51	1	0.600	1	==>	2
	55	1	0.429	1	==>	2
	59	2	0.429	0	==>	2
	67	1	0.286	0	==>	2
	70	1	0.333	1	-->	0
	84	1	0.500	1	-->	2
	93	1	0.333	1	-->	0
node_71 --> node_69	38	1	0.750	2	==>	3
	43	1	0.250	1	-->	2
	47	1	0.333	1	==>	0
	48	1	0.300	2	==>	1
node_69 --> node_68	5	1	0.143	0	==>	1
	46	1	1.000	2	==>	3
node_68 --> node_64	25	1	0.667	0	==>	1
	43	1	0.250	2	-->	1
	45	1	0.333	1	==>	0
	76	1	0.143	1	==>	0
	84	1	0.500	2	-->	3
	97	1	1.000	0	==>	1
node_64 --> node_55	9	1	0.167	1	==>	0
	16	1	0.222	0	==>	2
	81	1	0.500	0	-->	2
	85	1	0.400	0	==>	1
	87	1	1.000	0	-->	1
	90	1	1.000	0	-->	1
	91	1	1.000	0	-->	1
	93	1	0.333	0	-->	1
	94	1	0.500	0	==>	1
	99	1	0.500	1	-->	0
node_55 --> node_53	19	1	0.167	1	==>	0
	21	1	0.667	1	==>	2
	32	1	0.500	1	==>	2
	55	1	0.429	2	-->	1
	67	1	0.286	2	==>	0
	82	1	0.667	1	==>	2
node_53 --> node_52	25	1	0.667	1	==>	0
	58	1	0.182	1	-->	0
	81	1	0.500	2	-->	0
	84	1	0.500	3	-->	2
node_52 --> node_50	83	1	0.500	0	==>	2
	88	1	0.500	0	==>	1
	89	1	0.500	0	==>	1
	98	1	0.500	0	==>	1
	101	1	0.500	1	==>	0
	102	1	0.500	0	==>	1
node_50 --> node_49	5	1	0.143	1	-->	0

	7	1	0.143	0	-->	1
	9	1	0.167	0	-->	1
	48	1	0.300	1	==>	2
	55	1	0.429	1	-->	2
	58	2	0.182	0	==>	2
	85	1	0.400	1	==>	0
	86	1	0.200	0	==>	1
	95	1	0.500	1	-->	0
node_49 --> Cimexomys	16	1	0.222	2	==>	0
	34	1	0.500	1	==>	0
	67	1	0.286	0	==>	1
	76	1	0.143	0	==>	1
node_49 --> Catopsbaatar	84	1	0.500	2	==>	1
	26	1	0.333	1	==>	2
	29	1	0.286	1	==>	2
	42	1	0.600	2	==>	1
	43	1	0.250	1	==>	0
	44	1	0.250	1	==>	0
	51	1	0.600	2	==>	3
	59	1	0.429	2	==>	3
node_50 --> Kryptobaatar	61	1	0.200	1	==>	0
node_52 --> node_51	61	1	0.200	1	==>	2
	59	1	0.429	2	==>	1
	85	1	0.400	1	==>	2
node_51 --> Kamptobaatar	6	1	0.500	0	==>	1
	9	1	0.167	0	==>	1
	16	1	0.222	2	==>	1
	84	1	0.500	2	-->	3
	96	1	0.333	1	==>	0
node_51 --> Chulsanbaatar	7	1	0.143	0	==>	1
node_53 --> Nemegtbaatar	58	1	0.182	1	==>	2
	61	1	0.200	1	==>	2
	96	1	0.333	1	==>	0
node_55 --> node_54	31	1	0.333	1	-->	2
	35	1	0.500	0	==>	1
	43	1	0.250	1	-->	2
	85	1	0.400	1	-->	2
node_54 --> Eucosmodon	7	1	0.143	0	==>	1
	26	1	0.333	1	==>	2
	67	1	0.286	2	==>	1
	72	1	0.250	1	==>	2
node_54 --> Stygimys	3	1	0.400	2	==>	1
	47	1	0.333	0	==>	1
node_64 --> node_63	31	1	0.333	1	==>	0
	48	1	0.300	1	-->	0
	55	1	0.429	2	==>	3
	58	1	0.182	1	-->	2
	83	1	0.500	0	-->	1
	98	1	0.500	0	-->	1
	100	1	1.000	0	-->	1
node_63 --> node_62	25	1	0.667	1	==>	2
	29	1	0.286	1	==>	2
	32	1	0.500	1	==>	2
	59	1	0.429	2	==>	3

	61	1	0.200	1	-->	2
	86	1	0.200	0	-->	1
	88	1	0.500	0	-->	1
	90	1	1.000	0	-->	2
	92	1	1.000	0	-->	1
	102	1	0.500	0	-->	1
node_62 --> Meniscoessus	67	1	0.286	2	==>	1
	72	1	0.250	1	==>	2
	74	1	0.500	0	==>	1
	76	1	0.143	0	==>	1
	80	1	0.500	1	==>	0
	81	1	0.500	0	==>	2
	83	1	0.500	1	-->	0
node_62 --> node_61	18	1	0.333	1	-->	0
	20	1	0.667	1	-->	0
	21	1	0.667	1	-->	0
	26	2	0.333	1	-->	3
	27	1	1.000	0	-->	1
	32	1	0.500	2	==>	3
	35	1	0.500	0	==>	1
	43	1	0.250	1	==>	0
	44	1	0.250	1	-->	0
	51	1	0.600	2	-->	3
	58	1	0.182	2	-->	1
node_61 --> Buginbaatar	3	1	0.400	2	==>	1
	31	1	0.333	0	==>	1
node_61 --> node_60	5	1	0.143	1	==>	0
	7	1	0.143	0	-->	1
	16	1	0.222	0	-->	1
	47	1	0.333	0	-->	1
	61	1	0.200	2	-->	1
	67	1	0.286	2	==>	0
node_60 --> Pentacosmodon	44	1	0.250	0	-->	1
	82	1	0.667	1	==>	2
	86	1	0.200	1	-->	0
node_60 --> node_59	16	1	0.222	1	-->	2
	41	1	0.500	1	==>	0
	42	1	0.600	2	==>	3
	58	1	0.182	1	-->	2
	73	1	0.333	1	-->	0
node_59 --> node_56	7	1	0.143	1	-->	0
	63	1	1.000	3	==>	4
	65	1	1.000	0	==>	2
	74	1	0.500	0	==>	2
node_56 --> Taeniolabis	67	1	0.286	0	==>	2
	72	1	0.250	1	==>	2
node_56 --> Catopsalis	31	1	0.333	0	==>	1
node_59 --> node_58	6	1	0.500	0	-->	1
	19	1	0.167	1	-->	0
	30	1	0.750	2	==>	3
	47	1	0.333	1	-->	0
	61	1	0.200	1	==>	0
	62	1	0.667	2	==>	1
node_58 --> node_57	53	1	0.667	0	==>	2

	68	1	0.667	1 ==>	2
	69	1	0.667	1 ==>	2
	73	1	0.333	0 -->	1
	74	1	0.500	0 ==>	1
node_63 --> Kogaionon	19	1	0.167	1 ==>	0
	29	1	0.286	1 ==>	0
	30	1	0.750	2 ==>	3
	61	1	0.200	1 ==>	0
node_68 --> node_67	15	1	0.500	0 -->	1
	59	1	0.429	2 ==>	3
	77	1	0.400	1 ==>	2
	81	1	0.500	0 -->	1
node_67 --> node_66	19	1	0.167	1 ==>	0
	31	1	0.333	1 ==>	2
	48	2	0.300	1 ==>	3
	55	1	0.429	2 -->	3
	72	1	0.250	1 ==>	2
node_66 --> node_65	5	1	0.143	1 ==>	0
	64	1	0.500	0 ==>	1
node_65 --> Ectypodus	83	1	0.500	0 ==>	2
	86	1	0.200	0 ==>	1
node_65 --> Ptilodus	9	1	0.167	1 ==>	0
	29	1	0.286	1 ==>	0
	48	1	0.300	3 -->	2
	96	1	0.333	1 ==>	0
node_66 --> Neoliotomus	15	1	0.500	1 -->	0
	16	1	0.222	0 ==>	2
	58	1	0.182	1 ==>	2
	74	1	0.500	0 ==>	1
node_69 --> Cimolodon	58	1	0.182	1 ==>	2
	61	1	0.200	1 ==>	2
	72	1	0.250	1 ==>	2
node_71 --> node_70	16	1	0.222	0 ==>	1
	43	1	0.250	1 -->	0
	45	1	0.333	1 -->	0
	59	1	0.429	2 ==>	3
	76	1	0.143	1 ==>	0
node_70 --> Boffius	58	1	0.182	1 ==>	2
node_70 --> Microcosmodon	32	1	0.500	1 ==>	2
node_73 --> Eobaatar	16	1	0.222	0 ==>	2
	37	1	0.500	1 -->	0
node_74 --> Arginbaatar	36	1	0.333	1 ==>	0
	40	1	0.500	0 ==>	1
	43	1	0.250	1 ==>	2
	47	1	0.333	1 ==>	0

**Character diagnostics:**

Character	Range	Min steps	Tree steps	Max steps	CI	RI	RC	HI	G-fit
1	1	1	1	3	1.000	1.000	1.000	0.000	1.000
2	1	1	1	3	1.000	1.000	1.000	0.000	1.000
3	2	2	5	16	0.400	0.786	0.314	0.600	0.500

4	1	1	2	3	0.500	0.500	0.250	0.500	0.750
5	1	1	7	17	0.143	0.625	0.089	0.857	0.333
6	1	1	2	2	0.500	0.000	0.000	0.500	0.750
7	1	1	7	11	0.143	0.400	0.057	0.857	0.333
8	1	1	1	3	1.000	1.000	1.000	0.000	1.000
9	1	1	6	11	0.167	0.500	0.083	0.833	0.375
10	1	1	1	3	1.000	1.000	1.000	0.000	1.000
11	1	1	1	4	1.000	1.000	1.000	0.000	1.000
12	1	1	1	2	1.000	1.000	1.000	0.000	1.000
13	1	1	2	6	0.500	0.800	0.400	0.500	0.750
14	1	1	1	3	1.000	1.000	1.000	0.000	1.000
15	1	1	2	3	0.500	0.500	0.250	0.500	0.750
16	2	2	9	18	0.222	0.563	0.125	0.778	0.300
17	2	2	2	13	1.000	1.000	1.000	0.000	1.000
18	1	1	3	9	0.333	0.750	0.250	0.667	0.600
19	1	1	6	12	0.167	0.545	0.091	0.833	0.375
20	2	2	3	10	0.667	0.875	0.583	0.333	0.750
21	2	2	3	12	0.667	0.900	0.600	0.333	0.750
22	2	2	3	9	0.667	0.857	0.571	0.333	0.750
23	1	1	1	3	1.000	1.000	1.000	0.000	1.000
24	1	1	1	3	1.000	1.000	1.000	0.000	1.000
25	2	2	3	13	0.667	0.909	0.606	0.333	0.750
26	3	3	9	25	0.333	0.727	0.242	0.667	0.333
27	1	1	1	4	1.000	1.000	1.000	0.000	1.000
28	1	1	2	6	0.500	0.800	0.400	0.500	0.750
29	2	2	7	22	0.286	0.750	0.214	0.714	0.375
30	3	3	4	14	0.750	0.909	0.682	0.250	0.750
31	2	2	6	20	0.333	0.778	0.259	0.667	0.429
32	3	3	6	28	0.500	0.880	0.440	0.500	0.500
33	1	1	1	12	1.000	1.000	1.000	0.000	1.000
34	1	1	2	17	0.500	0.938	0.469	0.500	0.750
35	1	1	2	9	0.500	0.875	0.438	0.500	0.750
36	1	1	3	11	0.333	0.800	0.267	0.667	0.600
37	1	1	2	14	0.500	0.923	0.462	0.500	0.750
38	3	3	4	18	0.750	0.933	0.700	0.250	0.750
39	1	1	1	4	1.000	1.000	1.000	0.000	1.000
40	1	1	2	15	0.500	0.929	0.464	0.500	0.750
41	1	1	2	9	0.500	0.875	0.438	0.500	0.750
42	3	3	5	20	0.600	0.882	0.529	0.400	0.600
43	2	2	8	21	0.250	0.684	0.171	0.750	0.333
44	1	1	4	18	0.250	0.824	0.206	0.750	0.500
45	1	1	3	16	0.333	0.867	0.289	0.667	0.600
46	3	3	3	27	1.000	1.000	1.000	0.000	1.000
47	3	3	9	27	0.333	0.750	0.250	0.667	0.333
48	3	3	10	25	0.300	0.682	0.205	0.700	0.300
49	1	1	1	3	1.000	1.000	1.000	0.000	1.000
50	1	1	1	3	1.000	1.000	1.000	0.000	1.000
51	3	3	5	21	0.600	0.889	0.533	0.400	0.600
52	2	2	2	15	1.000	1.000	1.000	0.000	1.000
53	2	2	3	8	0.667	0.833	0.556	0.333	0.750
54	1	1	1	8	1.000	1.000	1.000	0.000	1.000
55	3	3	7	32	0.429	0.862	0.369	0.571	0.429
56	1	1	2	5	0.500	0.750	0.375	0.500	0.750
57	1	1	2	7	0.500	0.833	0.417	0.500	0.750

58	2	2	11	19	0.182	0.471	0.086	0.818	0.250
59	3	3	7	24	0.429	0.810	0.347	0.571	0.429
60	1	1	1	4	1.000	1.000	1.000	0.000	1.000
61	2	2	10	16	0.200	0.429	0.086	0.800	0.273
62	2	2	3	11	0.667	0.889	0.593	0.333	0.750
63	4	4	4	8	1.000	1.000	1.000	0.000	1.000
64	1	1	2	4	0.500	0.667	0.333	0.500	0.750
65	2	2	2	4	1.000	1.000	1.000	0.000	1.000
66	2	2	2	5	1.000	1.000	1.000	0.000	1.000
67	2	2	7	12	0.286	0.500	0.143	0.714	0.375
68	2	2	3	9	0.667	0.857	0.571	0.333	0.750
69	2	2	3	10	0.667	0.875	0.583	0.333	0.750
70	1	1	3	6	0.333	0.600	0.200	0.667	0.600
71	1	1	1	4	1.000	1.000	1.000	0.000	1.000
72	2	2	8	13	0.250	0.455	0.114	0.750	0.333
73	1	1	3	8	0.333	0.714	0.238	0.667	0.600
74	2	2	4	6	0.500	0.500	0.250	0.500	0.600
75	2	2	2	5	1.000	1.000	1.000	0.000	1.000
76	1	1	7	17	0.143	0.625	0.089	0.857	0.333
77	2	2	5	12	0.400	0.700	0.280	0.600	0.500
78	1	1	1	1	1.000	0/0	0/0	0.000	1.000
79	1	1	1	1	1.000	0/0	0/0	0.000	1.000
80	1	1	2	11	0.500	0.900	0.450	0.500	0.750
81	2	2	4	5	0.500	0.333	0.167	0.500	0.600
82	2	2	3	9	0.667	0.857	0.571	0.333	0.750
83	2	2	4	7	0.500	0.600	0.300	0.500	0.600
84	3	3	6	9	0.500	0.500	0.250	0.500	0.500
85	2	2	5	10	0.400	0.625	0.250	0.600	0.500
86	1	1	5	8	0.200	0.429	0.086	0.800	0.429
87	1	1	1	5	1.000	1.000	1.000	0.000	1.000
88	1	1	2	4	0.500	0.667	0.333	0.500	0.750
89	1	1	2	4	0.500	0.667	0.333	0.500	0.750
90	2	2	2	8	1.000	1.000	1.000	0.000	1.000
91	1	1	1	5	1.000	1.000	1.000	0.000	1.000
92	1	1	1	2	1.000	1.000	1.000	0.000	1.000
93	1	1	3	5	0.333	0.500	0.167	0.667	0.600
94	1	1	2	6	0.500	0.800	0.400	0.500	0.750
95	1	1	2	3	0.500	0.500	0.250	0.500	0.750
96	1	1	3	3	0.333	0.000	0.000	0.667	0.600
97	1	1	1	5	1.000	1.000	1.000	0.000	1.000
98	1	1	2	4	0.500	0.667	0.333	0.500	0.750
99	1	1	2	5	0.500	0.750	0.375	0.500	0.750
100	1	1	1	2	1.000	1.000	1.000	0.000	1.000
101	1	1	2	4	0.500	0.667	0.333	0.500	0.750
102	1	1	2	4	0.500	0.667	0.333	0.500	0.750

## **SOM 5. Measurements of teeth (length/width in mm).**

V19025

Right I2: 4.3/3.5; I3: 4.5/3.4; left P4 (root cross-section): 2.9/3.0; left M1: 16.7/8.8; left M2 12.7/10.9

Right i1: 5.6/4.8 (measured at the base)

V19026

Right M2: 14.2/10.1\* (buccal side damaged)

V19027

Erupting right m2?: 8.2/7.9

V19028

Right m2: 13.9/9.3

V19029

Left M1: 15.7/7.6; left M2: 13.3/10; right M1: \*/7.5; right M2: 13.4/9.8;

Left m2: 13.8/9.0\*

V19030

Left m2: 12.7/9.9

V19032

Left M1: 16.8/9.3; M2: 13.8/10.2

Left p4: 4.6/3.0; left m1: 13.6/7.3; left m2: 14.1/11.6

V19033

Left m2: 15.1/10.5

V19034

Right lower incisor: 6.0/4.8 (at the alveolus)

V19035

Left? lower incisor: 6.3/4.9

V19036

Right m2: 13.0/9.1

V19037

Right m2: 13.7/9.5