Supplementary Methods, Results and Discussion

1. *Character Matrix*.

We created the most taxon-rich morphological character matrix of Eutheria (plus the metatherians *Deltatheridium*, *Mayulestes* and *Pucadelphys* and the stem-therians *Nanolestes*, *Peramus* and *Vincelestes* as outgroup taxa) currently available by combining matrices from five recent studies [1-5] which represent differently modified versions of an earlier eutherian matrix [6]. All revised scorings and additional characters added to the original matrix in these subsequent studies were incorporated into our matrix. All characters were specified as unordered, as in their source studies. Two studies [4, 5] scored *Arctocyon* independently, and so we created a composite *Arctocyon* terminal by merging these scores; where *Arctocyon* was scored differently for a particular character, our composite *Arctocyon* terminal was treated as variable (MrBayes 3.2 treats all variable character scores as unknown, so this was effectively equivalent to treating each character with conflicting scores as '?'). The following four taxa were deleted, as previous studies found them to be particularly unstable: *Alymlestes*, *Kharmerungulatum*, *Lainodon* and *Montanalestes* (see also [2]). The first three are each known from a single tooth, while the precise affinities of *Montanalestes* (either a eutherian or stem-therian; [7, 8]) remain controversial.

The final matrix comprises 102 taxa and 421 characters. In terms of number of morphological characters, this is larger than most mammal datasets. Although an order of magnitude smaller than the recent phenomic study of O'Leary et al. [9], which used 4541 characters, our matrix exhibits much denser sampling of Mesozoic eutherians (>30 versus 3), inclusion of which is likely to be critical for determining

divergence dates and evolutionary rates for eutherians before and after the K-Pg boundary.

Despite the wide taxon sampling, we note that our matrix does not include representatives of many 'archaic' early Palaeogene eutherian groups, such as dinoceratans, taeniodonts, tillodonts or pantodonts, inclusion of which may give additional insight into phylogeny and evolutionary rates during the initial radiation of Placentalia

We combined sequence data from six nuclear protein-coding genes (ADRA2B, BRCA1, GHR, IRBP, RAG1 and VWF) for the 14 extant placentals present in our morphological matrix. Alignments for these genes were taken from Meredith et al. [10], with some additional sequences downloaded from GenBank and added manually. To minimise missing data, we combined sequence data from closely related genera for four of our terminals, which therefore corresponded to the families Dasypodidae, Myrmecophagidae, Soricidae and the subfamily Potamogalinae (versus *Chaetophractus*, *Tamandua*, *Blarina* and *Potamogale* respectively in the morphology-only matrix).

2. *Taxon Ages.*

All extant taxa in our matrix were assigned an age of 0 million years (Ma). Fossil taxa were assigned ages using the primary literature and the 2012 geological time scale [11]. Where possible, we used absolute radiometric dates, or midpoints of these dates if given as a range, but these were not available for most taxa; in such cases, we used a point estimate (usually the midpoint) for each taxon, based on its proposed stratigraphic range. MrBayes 3.2 allows terminal taxa to be assigned ages as ranges rather than point estimates, but preliminary analyses revealed a significant slowdown

in analytic speed, and difficulty with achieving convergence (stationarity), if each taxon was assigned an age range. For most fossil taxa, their proposed stratigraphic ranges spanned less than 5% either side of the point estimate; thus, the use of point estimates is unlikely to have a major impact on our results.

The assumed ages of our taxa (and full justifications for these) are as follows:

Taxon: *Nanolestes*

Age: 154.7 Ma old

Justification: The most complete material of *Nanolestes* (*N. drescherae*) is from the Guimarota coal mine in Portugal, which is currently interpreted as Kimmeridgian in age (a second species, *N. krusati*, is known from two teeth from Porto Pinheiro in Portugal, which is somewhat younger, namely Tithonian-Berriasian) [12]. The Kimmeridgian is 152.1-157.3 Ma [11]; the midpoint of this range is used here.

Taxon: *Peramus*

Age: 142.4 Ma old

Justification: All specimens of *Peramus tenuirostris* (the species used for scoring purposes by Wible et al. [6]; note that the taxonomy of peramurans was recently revised by Davis [13]) are from the Purbeck Group in southwestern England, which is currently interpreted as Berriasian in age [13]. The Berriasian is 139.8-145.0 Ma [11]; the midpoint of this range is used here.

Taxon: *Vincelestes*

Age: 129.4 Ma old

Justification: All known specimens of the only known species, *Vincelestes neuquenianus*, are from the basal unit of the La Amarga Formation, namely the Pichi Picun Lefu Member [14]. The age of the La Amarga Formation remains somewhat unclear, with some authors suggesting a Late Hauterivian-Barremian age [14, 15] and others an entirely Barremian age [16]. Given that *Vincelestes* comes from the basal unit of the La Amarga Formation, it has been dated here as corresponding to the Hauterivian-Barremian boundary, which is 129.4 Ma [11].

Taxon: *Kielantherium*

Age: 113.0 Ma old

Justification: All known specimens of the only known species, *Kielantherium gobiense,* are from the Höövör locality, northern Gobi Desert, Mongolia [17]. Höövör is currently estimated to be Aptian–Albian [17], and so the age of Aptian-Albian boundary (113.0 Ma [11]) has been used here.

Taxon: *Deltatheridium*

Age: 77.85 Ma old

Justification: The best-preserved material of *Deltatheridium pretrituberculare* (the species used for scoring purposes by Wible et al. [6]) is from the Ukhaa Tolgod locality in the Gobi Desert of Mongolia [18]. Ukhaa Tolgod is within the Djadokhta Formation, which is Campanian in age [19]. The Campanian is 72.1-83.6 Ma [11]; the midpoint of this range is used here.

Taxon: *Mayulestes*

Age: 61.6 Ma old

Justification: All known material of the single known species of *Mayulestes* (*M. ferox*) is from the Tiupampa locality in Bolivia [20]. The age of Tiupampa remains somewhat controversial, with some authors suggesting an early Palaeocene age [21] and others a middle-late Palaeocene age [22, 23]. The age of the early Palaeocene (Danian)-middle Palaeocene (Selandian) boundary (61.6 Ma [11]) has been used here.

Taxon: *Pucadelphys*

Age: 61.6 Ma old

Justification: Like *Mayulestes*, the single described species of *Pucadelphys* (*P. andinus*) is known only from Tiupampa, Bolivia [24, 25]. See *Mayulestes* for a discussion of the age of Tiupampa.

Taxon: *Acristatherium*

Age: 123.2 Ma old

Justification: The single known specimen of *Acristatherium yanensis* is from the Lujiatun bed of the Yixian Formation [26], which has been radiometrically dated as 123.2 +/- 1.0 Ma [27].

Taxon: *Eomaia*

Age: 125.0 Ma old

Justification: The single known specimen of *Eomaia scansoria* is from the Dawangzhangzi locality in the Yixian Formation, which is estimated as ~125 Ma old [28].

Taxon: *Juramaia*

Age: 160.75 Ma old

Justification: The single known specimen of *Juramaia sinensis* is from the Daxigou site in the Tiaojishan Formation [3], of previously controversial age [29]. However, the horizon that produced *Juramaia* has now been dated using SHRIMP U–Pb zircon dating to between 160.5 and 161.0 Ma [29]; the midpoint of this range has been used here.

Taxon: *Prokennalestes*

Age: 113.0 Ma old

Justification: Both *Prokennalestes trofimovi* and *P. minor* are from the Höövör locality, northern Gobi Desert, Mongolia [30]. See *Kielantherium* for a discussion of the age of Höövör.

Taxon: *Murtoilestes*

Age: 125.0 Ma old

Justification: All known material of the only known species, *Murtoilestes abramovi*, is from the Mogoito Member of the Murtoi Formation, which is currently recognised as spanning the upper Barremian-middle Aptian [31]. In the absence of a more precise age determination, the age of the Barremian-Aptian boundary (125.0 Ma [11]) has been used here.

Taxon: *Bobolestes*

Age: 96 Ma old

Justification: The single known species, *Bobolestes zenge*, is from the Sheikhdzheili Local Fauna in the Khodzhakul Formation, western Uzbekistan [32]. The Khodzhakul Formation is estimated to be ~93-99 Ma old [33], and the midpoint of this range has been used here.

Taxon: *Sheikhdzheilia*

Age: 96 Ma old

Justification: The single known species, *Sheikhdzheilia rezvyii*, is from the Sheikhdzheili Local Fauna in the Khodzhakul Formation, western Uzbekistan [32]. See *Bobolestes* for a discussion of the age of the Khodzhakul Formation.

Taxon: *Alostera*

Age: 67.25 Ma old

Justification: The single known species, *Alostera saskatchewanensis*, is from the Lancian of North America [34, 35]. Radiometric dates suggest that the Lancian is ~65.5-69.0 Ma old [36], and the midpoint of this range has been used here.

Taxon: *Avitotherium*

Age: 77.5 Ma old

Justification: The single known species, *Avitotherium utahensis*, is from the Judithian of North America [37]. Radiometric dates for the Wahweap Formation, which appears to be coeval with the Judithian, are ~76-81 Ma old [38], whereas geochronometric data suggest an age range of ~74-79 Ma for the Judithian [36]. Based on this evidence, we assume that the Judithian is 74-81 Ma old, and use the midpoint of this range here.

Taxon: *Gallolestes*

Age: 77.5 Ma old

Justification: The two species of *Gallolestes* used by Wible et al. [6] for scoring purposes, namely *G. pachymandibularis* and *G. agujaensis*, are known from the Judithian of North America [39-42]. See *Avitotherium* for a discussion of the age of the Judithian.

Taxon: *Parazhelestes*

Age: 90.0 Ma old

Justification: The two species of *Parazhelestes* used by Wible et al. [6] for scoring purposes, namely *P. robustus* and *P. mynbulakensis*, are known from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Aspanlestes*

Age: 90.0 Ma old

Justification: The species of *Aspanlestes* used by Wible et al. [6] for scoring purposes, namely *A. aptap*, is known from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Zhelestes*

Age: 90.0 Ma old

Justification: The single known species of *Zhelestes*, *Z. temirkaysk*, is from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Paranyctoides*

Age: 90.0 Ma old

Justification: Wible et al. [6] scored *Paranyctoides* based on both North American (*P. sternbergi*, *P. maleficus*, *P. megakeros*) and Asian (*P. aralensis*) species. The taxonomy of this genus remains controversial: for example, it has recently been proposed that '*P. megakeros*' is in fact a junior synonym of *Alostera saskatchewanensis* [43], and there is currently debate as to whether the Asian species, *P. aralensis*, belongs to this genus [5, 43-45]. We have used Archibald and Averianov's [5] revised scorings for *Paranyctoides* in our matrix, most of which are based on *P. aralensis*. This species is known from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Eozhelestes*

Age: 96.0 Ma

Justification: The single known species, *Eozhelestes mangit*, is from the Sheikhdzheili Local Fauna in the Khodzhakul Formation, western Uzbekistan [32]. See *Bobolestes* for a discussion of the age of the Khodzhakul Formation.

Taxon: *Cimolestes*

Age: 67.25 Ma

Justification: The oldest well-preserved material of *Cimolestes* is Lancian in age [46-48]. See *Alostera* for a discussion of the age of the Lancian.

Taxon: *Maelestes*

Age: 77.85 Ma

Justification: The only known species, *M. gobiensis*, is represented by a single specimen from the Ukhaa Tolgod locality in the Gobi Desert of Mongolia [1, 6]. See *Deltatheridium* for a discussion of the age of Ukhaa Tolgod.

Taxon: *Batodon*

Age: 67.25 Ma

Justification: The oldest well-preserved material of *Batodon* is Lancian in age [46, 47]. See *Alostera* for a discussion of the age of the Lancian.

Taxon: *Bulaklestes*

Age: 90.0 Ma

Justification: The single known species of *Bulaklestes*, *B. kezbe*, is from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Daulestes*

Age: 90.0 Ma

Justification: The two known species of *Daulestes*, namely *D. kulbeckensis* and *D. inobservabilis*, are both from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Uchkudukodon*

Age: 90.0 Ma

Justification: The single known species of *Uchkudukodon*, *U. nessovi*, is from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33].

Taxon: *Kennalestes*

Age: 77.85 Ma

Justification: The best preserved material of the species used by Wible et al. [6] for scoring purposes, namely *K. gobiensis*, is from the Djadokhta Formation of Mongolia [49-51]. See *Deltatheridium* for a discussion of the age of the Djadokhta Formation.

Taxon: *Asioryctes*

Age: 77.85 Ma

Justification: The only known species, *A. nemegtensis*, is known from fossil localities in the Barun Goyot/Baruungoyot Formation of the Gobi Desert, Mongolia [50-52]. The age of the Barun Goyot/Baruungoyot Formation, particularly relative to Ukhaa Tolgod and other localities in the Djadokhta Formation, remains controversial; both formations appear to be Campanian in age, although the Djadokhta Formation is

usually interpreted to be younger [19, 53, 54]. However, in the absence of more exact dates, we assume a Campanian age (83.6-72.1 Ma [11]) for this taxon, and assume the midpoint of the Campanian here.

Taxon: *Ukhaatherium*

Age: 77.85 Ma old

Justification: The only known species, *U. nessovi*, is from the Ukhaa Tolgod locality in the Gobi Desert of Mongolia [55]. See *Deltatheridium* for a discussion of the age of Ukhaa Tolgod.

Taxon: *Deccanolestes hislopi*

Age: 69.05 Ma old

Justification: All known material of *D. hislopi* is from the Intertrappean Beds of India, which are Maastrichtian (66.0-72.1 Ma [11]) in age [2, 56-60]; we assume the midpoint of the Maastrichtian here.

Taxon: *Deccanolestes* cf. *hislopi*

Age: 69.05 Ma old

Justification: All known material of *D.* cf. *hislopi* is from the Intertrappean Beds of India, which are Maastrichtian (66.0-72.1 Ma [11]) in age [2, 56, 60]; we assume the midpoint of the Maastrichtian here.

Taxon: *Deccanolestes robustus*

Age: 69.05 Ma old

Justification: All known material of *D. robustus* is from the Intertrappean Beds of India, which are Maastrichtian (66.0-72.1 Ma [11]) in age [2, 58, 60]; we assume the midpoint of the Maastrichtian here.

Taxon: *Deccanolestes narmadensis*

Age: 69.05 Ma old

Justification: All known material of *D. narmadensis* is from the Intertrappean Beds of India, which are Maastrichtian (66.0-72.1 Ma [11]) in age [2, 61]; we assume the midpoint of the Maastrichtian here.

Taxon: *Afrodon germanicus*

Age: 59.2 Ma old

Justification: The oldest known record of *A. germanicus* is from the Walbeck fissure fills in Germany, which are considered as probably representing Mammal Paleogene zone MP5 (it is also known from slightly younger deposits at Cernay in France) [62, 63]. MP5 has been suggested to be late Selandian in age [63], but may in fact be early Thanetian [11]. We have used the age of the Selandian-Thanetian boundary (59.2 Ma [11]) here.

Taxon: *Afrodon chleuhi*

Age: 58.8 Ma old

Justification: *A. chleuhi* is known from the Ouarzazate Basin in Morocco, which is late Palaeocene in age [64, 65]. We have used the midpoint of the entire range of the Selandian-Thanetian (56.0-61.6 Ma [11]).

Taxon: *Kulbeckia*

Age: 90 Ma

Justification: The majority of specimens of the *Kulbeckia* species used by Wible et al. [6] for coding purposes, namely *K. kulbecke*, is from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [33, 66, 67].

Taxon: *Zhangolestes*

Age: 109.45 Ma old

Justification: The single known species, *Z. jilinensis*, is known from the Quantou Formation, near Gongzhuling City in Jilin Province, China [68]. The age of the Quantou Formation is poorly constrained, but is probably Aptian-Cenomanian [68] (93.9-125.0 Ma [11]), and we use the midpoint of this range here.

Taxon: *Zalambdalestes*

Age: 77.85 Ma old

Justification: The best preserved material of the only known species, *Z. lechei*, is from the Djadokhta Formation [69]. See *Deltatheridium* for a discussion of the age of the Djadokhta Formation.

Taxon: *Barunlestes*

Age: 77.85 Ma

Justification: The single known species, *Barunlestes butleri*, is known from fossil localities in the Barun Goyot/Baruungoyot Formation of the Gobi Desert, Mongolia [52, 70, 71]. See *Asioryctes* for a discussion of the age of the Barun Goyot/Baruungoyot Formation.

Taxon: *Gypsonictops*

Age: 77.5 Ma old

Justification: The oldest species of *Gypsonictops* used by Wible et al. [6] for scoring purposes, *G. lewisi*, is from the Judithian of North America [72, 73]. See *Avitotherium* for a discussion of the age of the Judithian.

Taxon: *Leptictis*

Age: 33.6 Ma old

Justification: The best preserved material of *Leptictis* is from the Brule Formation of North America [74, 75], which is Orellan in age [76]. The Orellan is ~33.3-33.9 Ma [11], and the midpoint of this range is used here.

Taxon: *Purgatorius*

Age: 64.43 Ma old

Justification: The two *Purgatorius* species used by Wible et al. [6] for scoring purposes**,** namely *P. unio* and *P. janisae*, are from middle or late Puercan (Pu 2–3 Interval Zones) faunas in the Western Interior of North America [77-79]. These faunas are estimated as spanning 64.11-64.75 Ma [79], and the midpoint of this range has been used here.

Taxon: *Protungulatum*

Age: 64.955 Ma old

Justification: The oldest material of *Protungulatum* used by Wible et al. [6] for scoring purposes is from the early Puercan (Pu 1 Interval Zone) Bug Creek

assemblage localities in northeastern Montana [79, 80]. These faunas are estimated as

spanning 64.75-65.16 Ma [79], and the midpoint of this range has been used here.

Taxon: *Oxyprimus*

Age: 64.955 Ma old

Justification: The *Oxyprimus* species used by Wible et al. [6] for scoring purposes, *O. erikseni*, is from the early Puercan (Pu 1 Interval Zone) Bug Creek assemblage localities in northeastern Montana. See *Protungulatum* for a discussion of the age of these localities.

Taxon: *Vulpavus*

Age: 54.2 Ma old

Justification: The oldest specimens of *Vulpavus* used by Wible et al. [6] for scoring purposes are postcranials from the Willwood Formation [81]. The Willwood Formation spans ~52.6-55.8 Ma [82], and the midpoint of this range has been used here.

Taxon: *Miacis*

Age: 47.85 Ma

Justification: The holotype (AMNH FM 5019) of one of the *Miacis* species used by Wible et al. [6] for scoring purposes, *M. parvivorus*, is from the Black's Fork Member of the Bridger Formation [83], which is ~46.7-49.0 Ma [84]; the midpoint of this range has been used here.

Taxon: *Gujaratia*

Age: 47.8 Ma

Justification: The *Gujaratia* species used by Wible et al. [6] for scoring purposes, *G. pakistanensis*, is known from the Barbora Banda Local Fauna [85, 86], which is in the Kuldana Formation [87]. The Kuldana Formation itself is either late early Eocene or early middle Eocene [87], and so we use the age of the early Eocene (Ypresian)-middle Eocene (Lutetian) boundary here.

Taxon: *Hyopsodus*

Age: 48.6 Ma

Justification: the best-preserved material of *Hyopsodus* is *H. paulus* [88], which first appears in the fossil record during the Bridgerian Biochronological Zone Br2 [89]. Br2 is ~47.0-50.2 Ma [11], and the midpoint of this range has been used here.

Taxon: *Meniscotherium*

Age: 53.0 Ma old

Justification: The most abundant and best-preserved material of *Meniscotherium* is from the San Jose Formation, San Juan Basin, New Mexico [90, 91]. Most of the San Jose Formation faunas appear to represent Wasatchian Biochronological Zone Wa6 [92], which is ~52.8-53.2 Ma [11]; the midpoint of this range has been used here.

Taxon: *Phenacodus*

Age: 54.2 Ma old

Justification: The most detailed description of the anatomy of *Phenacodus* is that of Thewissen [93], who based his cranial description mainly on YPM(PU) 14864 (*P. intermedius*) and YPM 20524 (*P. vortmani*); both of these specimens are from the

Willwood Formation. See *Vulpavus* for a discussion of the age of the Willwood Formation.

Taxon: *Ptilocercus*

Age: 0 Ma old

Justification: Extant

Taxon: *Plesiadapis*

Age: 59.2 Ma old

Justification: The older of the two *Plesiadapis* species used by Wible et al. [6] for scoring purposes is *P. gidleyi* (assigned to the genus *Nannodectes* by Gingerich [94, 95]), the best-preserved material of which is from the Mason Pocket Local Fauna in the northern San Juan Basin of southwestern Colorado [95]. The Mason Pocket Local Fauna appears to correspond to Tiffanian Biochronological Zone Ti4, which is ~58.9-59.5 Ma [96]; the midpoint of this range has been used here.

Taxon: *Notharctus*

Age: 48.6 Ma old

Justification: The best preserved material of *Notharctus* is from the Bridgerian Biochronological Zone Br2 [97]. Br2 is ~47.0-50.2 Ma [11], and the midpoint of this range has been used here.

Taxon: *Adapis*

Age: 37.0 Ma old

Justification: Assigning an age to *Adapis* is difficult, because the best preserved specimens of both species used by Wible et al. [6] for scoring purposes, namely *A. parisiensis* and *A. magnus* (the latter species sometimes placed in the genus *Leptadapis* [98]), are the result of early collections from Quercy, which lack accurate stratigraphic and biochronological information [98]. Subsequently collected material has better stratigraphic information but is less well-preserved [98]. However, *Adapis* (=*Leptadapis*) *magnus* is the older of the two species [99], and its first appearance is Mammal Paleogene zone MP17a [100], which is ~36.8-37.2 Ma [11]; the midpoint of this range has been used here.

Taxon: *Tribosphenomys*

Age: 57.6 Ma old

Justification: Both known species of *Tribosphenomys*, namely *T. minutus* and *T. secundus*, are from the Gashatan Asian Land Mammal Age of Mongolia and China [101-103]. The Gashatan appears to be approximately equivalent to the Thanetian [103, 104], which is 56.0-59.2 Ma old [11]; the midpoint of this range has been used here.

Taxon: *Paramys*

Age: 54.2 Ma old

Justification: The species of *Paramys* used by Wible et al. [6] for scoring purposes span a wide age range [105-108]; however, amongst the oldest material are the postcranial specimens described by Rose and Chinnery [108], which are from the Willwood Formation. See *Vulpavus* for a discussion of the age of the Willwood Formation.

Taxon: *Rhombomylus*

Age: 51.9 Ma old

Justification: The species of *Rhombomylus* used by Wible et al. [6] for scoring purposes, *R. turpanensis*, is from the Bumbanian Asian Land Mammal Age of China and Mongolia [103, 109]. The Bumbanian appears to be approximately equivalent to the Ypresian [103, 104], which is 47.8-56.0 Ma old [11]; the midpoint of this range has been used here.

Taxon: *Gomphos*

Age: 51.9 Ma old

Justification: The species of *Gomphos* used by Wible et al. [6] for scoring purposes, *R. elkema*, is from the Bumbanian Asian Land Mammal Age of China and Mongolia [103, 110, 111]. See *Rhombomylus* for a dicussion of the age of the Bumbanian.

Taxon: *Mimotona*

Age: 60.4 Ma old

Justification: The species of *Mimotona* used by Wible et al. [6] for scoring purposes, *M. wana*, is from the Nongshanian Asian Land Mammal Age of China [103, 112]. The Nongshanian appears to be approximately equivalent to the Selandian [103, 104], which is 59.2-61.6 Ma old [11]; the midpoint of this range has been used here.

Taxon: *Blarina*

Age: 0 Ma old

Justification: Extant

Taxon: *Erinaceus*

Age: 0 Ma old

Justification: Extant

Taxon: *Solenodon*

Age: 0 Ma old

Justification: Extant

Taxon: *Eoryctes*

Age: 55.3 Ma old

Justification: The oldest known specimens of the single known species, *E. melanus*, are from Wasatchian Biochronological Zone Wa1 [113], which is ~55.2-55.4 Ma old [11]; the midpoint of this range has been used here.

Taxon: *Potamogale*

Age: 0 Ma old

Justification: Extant

Taxon: *Orycteropus*

Age: 0 Ma old

Justification: Extant

Taxon: *Rhynchocyon*

Age: 0 Ma old

Justification: Extant

Taxon: *Procavia*

Age: 0 Ma old

Justification: Extant

Taxon: *Moeritherium*

Age: 31 Ma old

Justification: The species of *Moeritherium* used by Wible et al. [6] for scoring

purposes, *M. trigodon*, is from the early Oligocene of North Africa [114]. We assume

that the early Oligocene corresponds to the Rupelian, which is 28.1-33.9 Ma old [11];

the midpoint of this range has been used here.

Taxon: *Chaetophractus*

Age: 0 Ma old

Justification: Extant

Taxon: *Bradypus*

Age: 0 Ma old

Justification: Extant

Taxon: *Tamandua*

Age: 0 Ma old

Justification: Extant

Taxon: *Dilambdogale*

Age: 37 Ma old

Justification: The single known species, *D. gheerbranti* from Birket

Qarun Locality 2 (BQ-2) in the Umm Rigl Member of the Birket Qarun Formation,

northern Egypt, is ~37 Ma old [115].

Taxon: *Widanelfarasia*

Age: 34 Ma old

Justification: The two known species of *Widanelfarasia*, namely *W. bowni* and *W.*

rasmusseni, both from the Quarry L-41 in the lower sequence of the Jebel Qatrani

Formation, northern Egypt, are ~34 Ma old [115-118].

Taxon: *Todralestes*

Age: 58.8 Ma old

Justification: Of the two species of *Todralestes* currently known, namely *T. variabilis*

and *T. butleri*, *T. variabilis* from the Ouarzazate Basin in Morocco is the older and

better-preserved [119-121]. See *Afrodon chleuhi* for a discussion of the age of the

Ouarzazate Basin.

Taxon: *Microgale*

Age: 0 Ma old

Justification: Extant

Taxon: *Borisodon*

Age: 92.875 Ma old

Justification: Material of the only known species, *B. kara*, is from a drilling core taken near Ashchikol' Lake in Kyzylorda Province, Kazakhstan, reported to be lower Turonian in age [5]. The Turonian is 89.8-93.9 Ma old [11], and we have assumed the midpoint of the first half of the Turonian (91.85-93.9 Ma old) here.

Taxon: *Eoungulatum*

Age: 90.0 Ma old

Justification: The best preserved material of *Eoungulatum* is represented by *E. kudukensis* from the Bissekty Local Fauna at Dzharakuduk in central Uzbekistan, which is ~90 Ma old [5, 33].

Taxon: *Arctocyon*

Age: 62.5 Ma old

Justification: The oldest material of *Arctocyon* used by Giallombardo [4] for scoring purposes are specimens of *A. ferox* from multiple localities in Nacimiento Formation of the San Juan Basin, New Mexico, which are within Torrejonian Biochronological Zone To2 [122, 123]. To2 is ~62.0-63.0 Ma old [11], and the midpoint of this range has been used here.

Taxon: unnamed zalambdalestid

Age: 83.6 Ma old

Justification: This taxon is from the Shine Us Khudag redbeds of the Javkhlant formation, in the Gobi Desert of Mongolia [4], which are tentatively interpreted as

being Santonian-Campanian in age [124]; the Santonian-Campanian boundary (83.6 Ma old; [11]) has been assumed here.

Taxon: unnamed cimolestid

Age: 83.6 Ma old

Justification: This taxon is from the Shine Us Khudag redbeds of the Javkhlant formation, in the Gobi Desert of Mongolia [4]. See 'unnamed zalambdalestid' for discussion of the age of the Shine Us Khudag redbeds.

Taxon: *Protictis*

Age: 63.65 Ma old

Justification: The oldest species of *Protictis* used by Giallombardo [4] for scoring purposes is *P. haydenianus*, with a number of specimens (AMNH FM 948, 17059 and 16540) scored reported to be from the 'San Juan basin, probably lower Torrejon' [125]. The Torrejonian is ~61.7-64.3 Ma old [11], and we have assumed the midpoint of the first half (63.0-64.3 Ma) here.

Taxon: *Diacodexis*

Age: 54.2 Ma old

Justification: The oldest specimens of *Diacodexis* used by Giallombardo [4] for scoring purposes are from the Willwood Formation. See *Vulpavus* for a discussion of the age of the Willwood Formation.

Taxon: *Mioclaenus*

Age: 63.0 Ma old

Justification: The single known species, *M. turgidus*, is from the Torrejonian of New Mexico [123]. The Torrejonian is ~61.7-64.3 Ma old [11], and the midpoint of this range has been used here.

Taxon: *Periptychus*

Age: 63.0 Ma old

Justification: The species of *Periptychus* used by Giallombardo [4] for scoring purposes, *P. carinidens*, is from the Torrejonian of New Mexico [123]. The Torrejonian is ~61.7-64.3 Ma old [11], and the midpoint of this range has been used here.

Taxon: *Paulacoutoia*

Age: 56.0 Ma old

Justification: The single known species, *P. protocenica*, is known only from fissure fills in the Itaboraí Basin, southeastern Brazil [126]. The age of the Itaboraí fossils remains controversial, with estimates ranging from the middle Palaeocene to the early Eocene [21]; the Palaeocene-Eocene boundary (56.0 Ma [11]) has been assumed here.

Taxon: *Didolodus*

Age: 36.47 Ma old

Justification: The species used by Giallombardo [4] for scoring purposes, *D. multicuspis*, is from the Gran Barrancan member of the Sarmiento Formation, Chubut Province, Argentina [127], which has been radiometrically dated to between 35.34 and 37.60 Ma old [128]; the midpoint of this range has been used here.

Taxon: *Chriacus*

Age: 63.0 Ma old

Justification: The oldest species of *Chriacus* used by Giallombardo [4] for scoring purposes, *C. pelvidens*, is from the Torrejonian of New Mexico [123]. The Torrejonian is ~61.7-64.3 Ma old [11], and the midpoint of this range has been used here.

Taxon: *Oxyclaenus*

Age: 64.9 Ma old

Justification: The majority of specimens of *Oxyclaenus* used by Giallombardo [4] for scoring purposes represent *O. cuspidatus*, which is known from the Puercan of New Mexico and Wyoming [123]. The Puercan is ~64.3-65.5 Ma old [11], and the midpoint of this range has been used here.

Taxon: *Icaronycteris*

Age: 50.3825 Ma old

Justification: The species of *Icaronycteris* used by Giallombardo [4] for scoring purposes, *I. index*, is from the Green River Formation [129]. Two ashbeds in the Green River Formation have been radiometrically dated [130]: the Firehole ashbed is 51.53 Ma old (mean of U-Pb and Ar/Ar dates), and the Analcite ashbed as 49.235 Ma (mean of U-Pb and Ar/Ar dates). The mean of these two dates has been used here.

Taxon: *Cynocephalus*

Age: 0 Ma old

Justification: Extant

Taxon: *Hyracotherium*

Age: 52.5 Ma old

Justification: Of the two species of *Hyracotherium* used by Giallombardo [4] for scoring purposes, namely *H. vasacciense* and *H. tapirinum*, *H. vasacciense* is the older, first appearing in Wasatchian Biochronological Zone Wa7 [89]. Wa7 is ~52.2-52.8 Ma old [11], and the midpoint of this range has been used here.

Taxon: *Pezosiren*

Age: 50.0 Ma old

Justification: The single known species, *P. portelli*, is from the Guys Hill Member of the Chapelton Formation in Jamaica, which is ~50 Ma old [131].

Taxon: *Trichechus*

Age: 0 Ma old

Justification: Extant

Taxon: *Patriomanis*

Age: 35.55 Ma old

Justification: The single known species, *P. americanus*, is from the White River Formation in central Wyoming, and is Chadronian in age [132, 133]. The Chadronian is 33.9-37.2 Ma old [11], and the midpoint of this range has been used here.

Taxon: *Henricosbornia*

Age: 52 Ma old

Justification: Two of the specimens (AMNH 28837 and 28751) of *Henricosbornia lophodonta* (the species used by Giallombardo [4] for scoring purposes) are from Cañadón Vaca [134], which is part of the Vacan subage of the Casamayoran and may therefore be middle Eocene in age [21]. However, a third specimen (AMNH 28968) appears to be older, coming from the Río Chico horizon in the Bajo de la Palangana [134], which is part of the Koluel-Kaike Formation and Riochican in age [135]. The Koluel-Kaike Formation is estimated as spanning ~51-53 Ma [21], and the midpoint of this range has been used here.

Taxon: *Thomashuxleya*

Age: 44 Ma old

Justification: Specimens of *Thomashuxleya* used by Giallombardo [4] for scoring purposes are from fossil sites at Colhue-Huapi, Cañadón Hondo and Cañadón Vaca, most of which appear to be Vacan in age [134, 135]. The Vacan has been estimated to be ~42-46 Ma old [21], and the midpoint of this range has been used here

Taxon: *Simpsonotus*

Age: 52 Ma old

Justification: *Simpsonotus* is known only from the Mealla Formation [136], which is currently assumed to be Riochican in age [137]. The Riochican is estimated as spanning ~51-53 Ma [21], and the midpoint of this range has been used here.

Taxon: *Diadiaphorus*

Age: 16.37 Ma old

Justification: Specimens of *D. majusculus* (the species of *Diadiaphorus* used by Giallombardo [4] for scoring purposes) are from the Santa Cruz Formation in southern Argentina [138]. Radiometric dates from the Santa Cruz Formation presented by Vizcaíno et al. [139] span 16.18-16.56 Ma, and the midpoint of this range has been used here.

Taxon: *Pyrotherium*

Age: 27.6 Ma old

Justification: Material of *Pyrotherium macfaddeni* used by Giallombardo [4] for scoring purposes is from Salla, Bolivia, which is Deseadan in age [140]. According to Kay et al. [141], *Pyrotherium* remains at Salla span 25.8-29.4 Ma, and the midpoint of this range has been used here.

Taxon: *Trigonostylops*

Age: 36.47 Ma old

Justification: Most of Giallombardo's [4] character scorings for *Trigonostylops* are based on AMNH 28700, a skull of *T. wortmani* that was collected 'Casamayor Beds south of Lago Colhue-Huapi, Chubut' [142]; this appears to correspond to the Gran Barrancan member of the Sarmiento Formation. See *Didolodus* for a discussion of the age of the Gran Barrancan member.

3. Topological Constraints

One set of analyses of the matrix were performed without any topological constraints besides specifying the position of the root between *Nanolestes* and the remaining taxa. However, these resulted in topologies with a number of conflicts with our current

understanding of placental phylogeny (a pattern common for morphological matrices; [143-145]). We therefore ran additional analyses which enforced nine *a priori* topological constraints within Placentalia, resulting in topologies that are in much better agreement with the current phylogenetic consensus [10, 146]: six of these were 'full' constraints, with the monophyly of specific clades enforced; the remaining three were 'partial', with relationships among only a subset of taxa enforced so that they acted as a 'scaffold' or 'backbone' for the remaining, unconstrained taxa. These additional topological constraints are as follows (note that the node names used here and in Section 4 below are informal and might not correspond to particular formal phylogenetic definitions in the literature):

Clade: 'Paenungulata'

Type of constraint: full/monophyly

Included taxa: *Procavia*, *Moeritherium*, *Trichechus*, *Pezosiren*

Clade: 'Tenrecidae'

Type of constraint: full/monophyly

Included taxa: *Microgale*, *Potamogale*

Clade: 'Euarchonta'

Type of constraint: full/monophyly

Included taxa: *Ptilocercus*, *Cynocephalus*, *Notharctus*, *Adapis*, *Plesiadapis*, *Purgatorius*

Clade: 'Primates'

Type of constraint: full/monophyly

Included taxa: *Notharctus, Adapis, Plesiadapis, Purgatorius*

Clade: 'Notoungulata'

Type of constraint: full/monophyly

Included taxa: *Henricosbornia, Simpsonotus, Thomashuxleya, Pyrotherium*

Clade: 'Ferae'

Type of constraint: full/monophyly

Included taxa: *Vulpavus, Miacis, Protictis, Patriomanis*

Clade: 'Afrotheria'

Type of constraint: partial/scaffold

Included taxa: *Procavia, Moeritherium, Trichechus, Pezosiren, Todralestes,*

Widanelfarasia, Dilambdogale, Microgale, Potamogale, Orycteropus, Rhynchocyon

Excluded taxa: *Chaetophractus, Tamandua, Bradypus, Gomphos, Mimotona,*

Rhombomylus, Tribosphenomys, Paramys, Vulpavus, Miacis, Protictis, Patriomanis,

Notharctus, Adapis, Plesiadapis, Purgatorius, Diacodexis, Gujaratia, Deltatheridium,

Erinaceus, Mayulestes, Ptilocercus, Pucadelphys, Solenodon, Blarina, Icaronycteris,

Cynocephalus, Hyracotherium, Nanolestes, Vincelestes, Peramus

Clade: 'Laurasiatheria'

Type of constraint: partial/scaffold

Included taxa: *Vulpavus, Miacis, Protictis, Patriomanis, Diacodexis, Gujaratia,*

Hyracotherium, Solenodon, Erinaceus, Blarina, Icaronycteris

Excluded taxa: *Notharctus*,*Adapis*, *Plesiadapis*, *Purgatorius*, *Bradypus*, *Chaetophractus*, *Deltatheridium*, *Dilambdogale*, *Gomphos*, *Kielantherium*, *Mayulestes*, *Microgale*, *Mimotona*, *Moeritherium*, *Tamandua*, *Orycteropus*, *Paramys*, *Potamogale*, *Procavia*, *Ptilocercus*, *Pucadelphys*, *Rhombomylus*, *Rhynchocyon*, *Todralestes*, *Tribosphenomys*, *Widanelfarasia*, *Cynocephalus*, *Pezosiren*, *Trichechus*, *Nanolestes*, *Vincelestes*, *Peramus*

Clade: 'Boreoeutheria'

Type of constraint: partial/scaffold

Included taxa: *Ptilocercus*, *Cynocephalus*, *Notharctus*, *Adapis*, *Plesiadapis*, *Purgatorius*, *Gomphos*, *Mimotona*, *Rhombomylus*, *Tribosphenomys*, *Paramys*, *Vulpavus*, *Miacis*, *Protictis*, *Patriomanis*, *Diacodexis*, *Gujaratia*, *Hyracotherium*, *Solenodon*, *Erinaceus*, *Blarina*, *Icaronycteris*

Excluded taxa: *Trichechus*, *Pezosiren*, *Bradypus*, *Chaetophractus*, *Deltatheridium*, *Dilambdogale*, *Kielantherium*, *Mayulestes*, *Microgale*, *Moeritherium*, *Tamandua*, *Orycteropus*, *Potamogale*, *Procavia*, *Pucadelphys*, *Rhynchocyon*, *Todralestes*, *Widanelfarasia*, *Nanolestes*, *Vincelestes*, *Peramus*

4. *Node Age Constraints.*

We investigated the effect on divergence times and rates of evolution of three different schemes of node age constraints.

(a) Root only. In these analyses, only the age of the root node was constrained, using a uniform prior of 161.001-199.6 Ma. The minimum bound is based on the oldest possible age (161 Ma) of the oldest fossil in our matrix, *Juramaia* [3, 29], with a tiny increment added to allow MrBayes to run. The maximum bound is based on

the absence of unequivocal (crown-group) mammals in the preceding ~40 million years, despite a relatively good record of other mammaliaforms; specifically, we use the maximum age of the well-preserved stem (i.e. non-mammalian) mammaliaform *Hadrocodium*, which is from the Sinemurian of China [147].

(b) Root + Internal. In additional to the above root constraint, the ages of a number of internal nodes were also constrained using conservative uniform priors. MrBayes requires enforcing full monophyly constraints on all nodes with temporal constraints: the taxonomic contents of each temporally-constrained node was therefore specified *a priori* (see 'included taxa' for each node below). MrBayes 3.2 failed to run when nested clades had the same minimum and maximum bounds on their ages; it should therefore be noted that, for some (more-inclusive) nodes, we had to increase these bounds by 0.001 Ma over our preferred values to run the analyses. Such a tiny extension is highly unlikely to have any effect on our results, particularly as we report estimated posterior ages to one decimal place only.

(c) Root + Internal + Placentalia <66Ma. In addition to the above root and internal node constraints, we further constrained the maximum age of Placentalia to be 66Ma, coincident with the KPg boundary. The minimum bound for Placentalia is 64.433 Ma, marginally older than the age of the oldest placental in our matrix, *Purgatorius* (64.43 Ma old); the tiny increment added is required for MrBayes to run. As noted above, MrBayes requires enforcing full monophyly constraints on all nodes with temporal constraints: the taxonomic contents of Placentalia was therefore specified *a priori* based on the topology recovered in non-clock Bayesian analyses.

The additional internal age constraints (and full justifications for these) used in analyses (b) and (c) are as follows:

Clade: 'Metatheria'

Included taxa: *Deltatheridium*, *Mayulestes*, *Pucadelphys*

Hard minimum bound: 77.8501 Ma

Hard maximum bound: 161.0 Ma

Justification: The minimum bound is very slightly older than the oldest member of the clade we refer to here as 'Metatheria', namely *Deltatheridium* (see above). The maximum bound is based on the maximum age of *Juramaia*, which (if it is a eutherian [3]) puts a minimum bound on the Eutheria-Metatheria split, but is far older than the oldest known metatherian, the ~125 Ma old *Sinodelphys*, which is outside the clade comprising *Deltatheridium*, *Mayulestes* and *Pucadelphys* [3, 148]. If *Juramaia* is not, in fact, a eutherian but rather a stem-therian [149], then this maximum bound is probably highly conservative (i.e. wide or loose). A less conservative soft maximum bound might be 125.0 Ma, based on the age of *Sinodelphys*.

Clade: 'Notometatheria'

Included taxa: *Mayulestes*, *Pucadelphys*

Hard minimum bound: 61.601 Ma

Hard maximum bound: 98.39 Ma

Justification: *Mayulestes* and *Pucadelphys* from the Tiupampa locality in Bolivia are among the oldest metatherians known from South America [20, 21, 24, 25]. The minimum bound is very slightly older than the age of Tiupampa assumed here (see above). Given that: 1) the most likely dispersal route of metatherians into South America was from North America [150]; 2) metatherians appear to have been absent from South America during the Campanian-Maastrichtian [149, 151]; and 3) there is

no clear evidence of close relatives of either *Mayulestes* and *Pucadelphys* in the North American fossil record (suggesting that the *Mayulestes-Pucadelphys* split occurred in South America), we use the age of the oldest definitive North American metatherians as a conservative maximum bound. These are from the Mussentuchit Local Fauna in the upper Cedar Mountain Formation of Utah [152-154], which has been radiometrically dated as 98.39 Ma old [154]. A less conservative soft maximum bound might be 83.6 Ma (the maximum age of the Campanian [11]), based on the assumption that the *Mayulestes-Pucadelphys* split occurred in South America, and that metatherians were absent from South America during the Campanian [149, 151].

Clade: 'Strepsirhini'

Included taxa: *Notharctus*, *Adapis*

Hard minimum bound: 48.601 Ma

Hard maximum bound: 66.0 Ma

Justification: *Notharctus* and *Adapis* are both stem-members of the euprimate (i.e. crown-primate) clade Strepsirhini [155, 156]. The minimum bound is very slightly older than the age of *Notharctus* (the older of the two included terminal taxa) assumed here (see above). Besides the enigmatic *Altiatlasius* from the late Paleocene of Morocco, the oldest definitive euprimates are earliest Eocene in age [157]. The K-Pg boundary therefore represents a conservative maximum bound on splits within Strepsirhini.

Clade: 'Glires'

Included taxa: *Gomphos*, *Mimotona*, *Rhombomylus*, *Tribosphenomys*, *Paramys*

Hard minimum bound: 60.651 Ma

Hard maximum bound: 83.6 Ma

Justification: The minimum bound is slightly older than the age of *Mimotona* (the oldest of the five included terminal taxa) assumed here (see above). Although the Maastrichtian record of fossil mammals is good in North America, and lacks putative fossil relatives of Glires [158], the oldest record of Glires and probable close relatives (e.g. anagalids) is from the Palaeocene of Asia [103, 111, 159], and the Maastrichtian mammal record in Asia is very poor [158]. We therefore specify the maximum age of the Campanian [11] as a conservative maximum bound, to allow for the possibility that Glires may have begun to diversify in Asia prior to the K-Pg boundary.

Clade: 'Pilosa'

Included taxa: *Tamandua*, *Bradypus*

Hard minimum bound: 25.951 Ma

Hard maximum bound: 72.1 Ma

Justification: Meredith et al. [10] used a minimum bound of 31.5 Ma for this divergence based on the age of the pseudoglyptodont *Pseudoglyptodon chilensis*. McKenna et al. [160] tentatively suggested that pseudoglyptodonts are closer to sloths than to anteaters (listing some potential tardigrade apomorphies present in *Pseudoglyptodon*, based on the character list of Gaudin [161]); if so, *Pseudoglyptodon* can indeed be used to place a minimum bound on the age of the *Tamandua-Bradypus* split. However, McKenna et al. [160] had some doubts about the relationship between *Pseudoglyptodon* and sloths – raising the possibility that *Pseudoglyptodon* may in fact be closer to glyptodonts, which appear to be members of Cingulata, i.e. more closely related to dasypodids -, and they did not provide a formal phylogenetic analysis. Of particular importance is the fact that McKenna et al. [160] did not discuss the

possibility that sloth-like features may be plesiomorphic for Pilosa as a whole, which seems plausible given that myrmecophagids are highly autapomorphic. Indeed, Pujos and de Iulis [162] suggested that *Pseudoglyptodon* may be a stem-pilosan ('pre-pilosan' in their terminology), and hence it is inappropriate to use *Pseudoglyptodon* as a minimum for the *Tamandua-Bradypus* split. Instead, a better justified, more conservative minimum would be based on the oldest known myrmecophagid or oldest definitive sloth.

The oldest definitive myrmecophagid is *Protamandua*, from the Santa Cruz Formation (~16.3-17.5 Ma [163, 164]); however, it should be noted that Gaudin and Branham's [165] phylogeny places *Protamandua* closer to *Myrmecophaga* and *Tamandua* than to *Cyclopes*, and hence it probably significantly post-dates the *Tamandua-Bradypus* split. Turning now to sloths, MacPhee and Iturralde-Vinent [166] identified a proximal femur from the early Oligocene Juan Diaz Formation of Puerto Rico as a possible ?megalonychid sloth, but this referral was based on overall resemblance, with no obvious attempt to identify unequivocal sloth apomorphies. Its tentative referral to Megalonychidae rests purely on biogeographical grounds, specifically that Megalonychidae is 'the only sloth family that provably managed to colonize West Indian islands' [166]. Hence, this record does not represent a robust calibration. According to Gaudin [161], 'the oldest sloth known from reasonably complete skeletal remains' is *Octodontotherium*, which is Deseadan. Pujos and Iulis [162] described additional *Octodontotherium*-like material (as well as specimens of *Pseudoglyptodon*) from Unit 5 (= *Branisella* level) of the Deseadan Salla Beds, which has been dated as 25.95-25.99 Ma [141]. *Octodontotherium* was included in Gaudin's [161] phylogenetic analysis and is supported as a mylodontid sloth; thus, it postdates the *Bradypus-Choloepus* split and hence probably significantly postdates the

Tamandua-Bradypus split; nevertheless, it represents a conservative minimum on this node. Therefore, we use 25.951 Ma as a minimum bound here (a very slight extension was required for MrBayes to run).

The soft maximum of 65.5 Ma used by Meredith et al. [10] for this node is potentially somewhat too young. If the xenarthran fossils from Itaboraí in southeastern Brazil represent dasypodids [167, 168] (and this is admittedly questionable – see below), then crown-Xenarthra had begun to radiate by the early Eocene at the latest, assuming the youngest date for Itaboraí suggested by Gelfo et al. [21]. We consider the latest Cretaceous-early Palaeocene fossil record of mammals in South America to be too poor to rule out a somewhat earlier xenarthran radiation. There are good late Cretaceous (Maastrichtian) records of mammals from both southern South America and North America [158] – regions where crown-xenarthrans would seem likely to have been present if they existed at this time – but no crown- or stem-xenarthrans have been found (gondwanatherians were originally proposed to be xenarthrans, but now appear to be non-therian mammals, probably closely related to multituberculates [169]). A more conservative maximum, which we use here, is therefore the maximum age for the Maastrichtian, i.e. 72.1 Ma.

Clade: 'Xenarthra'

Included taxa: *Tamandua*, *Bradypus*, *Chaetophractus*

Hard minimum bound: 39.001 Ma

Hard maximum bound: 72.101 Ma

Justification: Notes: The minimum age used for this divergence by Meredith et al. [10], namely 58.5 Ma, is based on the assumption that *Riostegotherium* from the Itaboraí in Brazil is a dasypodid [167, 168]. However, this calibration is problematic

for a number of reasons. Firstly, the age of Itaboraí fauna is poorly constrained: a recent study by Gelfo et al. [21] proposed that the Itaboraí fauna may be early Eocene rather than late Palaeocene, and hence possibly as young as 48.4 Ma (assuming 'early Eocene' = Ypresian [11]). Secondly, it is possible that *Riostegotherium* may in fact be a stem- rather than crown-xenarthran; although this interpretation has not (to our knowledge) been proposed in the literature, the presence of osteoderms in mylodontid sloths raises the possibility that osteoderms may be plesiomorphic for Xenarthra as a whole [170]. Of particular note is Bergqvist et al.'s [167] suggestion that 'primitive cingulates possessed fewer osteoderms than later cingulates'; an alternative interpretation is that the presence of only a small number of osteoderms is plesiomorphic for Xenarthra as a whole. The two astragali described by Cifelli [171] and Bergqvist et al. [167] also cannot be confidently referred to a crown-xenarthran clade. In the absence of a comprehensive phylogenetic analysis of xenarthrans that includes *Riostegotherium*, we consider the evidence that *Riostegotherium* is crown-xenarthran to be equivocal, particularly given that Bergqvist et al. [167] failed to demonstrate that *Riostegotherium* possesses crown-group apomorphies. We have similar concerns/doubts about other records of astegotheriin 'dasypodids' (e.g. [172]).

If the Itaboraian material is discounted, the oldest definitive dasypodid appears to be the Casamayoran *Utaetus* (which is known from fairly well-preserved skeletal material [134]), while the oldest glyptodont is the slightly younger, namely the Mustersan *Glyptatelus* [134]. The minimum age of the Casamayoran (Barrancan) is 39.0 Ma [135], which therefore is a suitable hard minimum bound for this divergence. As discussed above, a maximum is difficult to assign, as it is dependent on the precise affinities of the Itaboraian xenarthran material but, based on the apparent absence of xenarthrans (even putative stem-forms) in either North American Lancian faunas or

South American Alamitian faunas [158], we agree with Meredith et al. [10] that 72.1 Ma is probably a reasonable upper bound.

Clade: 'Paenungulata'

Included taxa: *Procavia*, *Moeritherium*, *Trichechus*, *Pezosiren*

Hard minimum bound: 56.001 Ma

Hard maximum bound: 145.0 Ma

Justification: 56.0 Ma (the minimum age of the Thanetian [11]) is a conservative minimum bound for this clade, based on the age of the oldest known (stem-) proboscidean, *Eritherium*, which is from the Selandian-Thanetian Ouled Abdoun Phosphate basin [173]. Given that Paenungulata probably originated in Africa [174], assigning a maximum is difficult, because the African Late Cretaceous record is almost non-existent [158]. The youngest well-preserved Mesozoic mammal-bearing locality in Africa is the ?Berriasian Synclinal d'Anoual in Morocco [158, 175], in which there is one fully tribosphenic mammal (*Tribotherium africanum* [176]), but definitive eutherians and metatherians have not been identified. The Berriasian has a maximum age of 145.0 Ma [11], which has been used as the maximum bound for this divergence in this study. Such an ancient maximum might be viewed as unduly conservative, but using a date younger than this is begging the question: we simply have no fossil evidence of mammalian evolution in Africa during the Late Cretaceous. Assuming that it is indeed a eutherian, *Juramaia* indicates a minimum for the Eutheria-Metatheria split of 160 Ma. It is therefore possible (although admittedly unlikely [177]) that Afrotheria could have already begun diversifying during the Cretaceous; certainly, the oldest Cenozoic mammal fossils from Africa, from the Ouled Abdoun Phosphate Basin, already indicate considerable diversification within

Afrotheria, including the presence of crown-forms such as *Eritherium* [173, 178, 179]. Given our reliance on hard bounds, we err on the side of caution here and use 145.0 Ma as a (very) conservative maximum bound.

Clade: 'Artiodactyla'

Included taxa: *Diacodexis*, *Gujaratia*

Hard minimum bound: 54.201 Ma

Hard maximum bound: 66.0 Ma

Justification: The minimum bound is very slightly older than the age of *Diacodexis* (the older of the two included terminal taxa) assumed here (see above). *Diacodexis* and *Gujaratia* are morphologically very similar, with *Gujaratia* often synonymised with *Diacodexis* [180], suggesting a relatively short divergence time from each other. Furthermore, The oldest putative stem-member of Artiodactyla is *Ganungulatum* from the Nongshanian (Selandian [103, 104]), and is reported to be more plesiomorphic than both *Diacodexis* and *Gujaratia* [181]; there is no evidence of either crown- or stem-artiodactyls in the Cretaceous. We therefore use the K-Pg boundary as a maximum bound on this divergence.

Clade: 'Primates'

Included taxa: *Notharctus*, *Adapis*, *Plesiadapis*, *Purgatorius*

Hard minimum bound: 64.431 Ma

Hard maximum bound: 83.6 Ma

Justification: Although *Purgatorius* was recovered as a stem-eutherian by Wible et al. [6] and in unconstrained analyses of subsequent versions of this matrix [1, 2], we follow the current consensus view that *Purgatorius* is a (stem-) primate [182, 183].

The minimum bound is very slightly older than the age of *Purgatorius* (the oldest of these three taxa) assumed here (see above). It seems highly likely that Primates originated in Laurasia [174, 182, 184-186], and have not been found in Laurasian Late Cretaceous fossil deposits [158]; their oldest record is early Palaeocene [185]. Given the poor Maastrichtian mammal record in Asia [158] (see 'Glires' above), we use the maximum age of the Campanian as the maximum bound here.

Clade: 'Carnivoramorpha'

Included taxa: *Vulpavus*, *Miacis*, *Protictis*

Hard minimum bound: 63.651 Ma

Hard maximum bound: 83.6 Ma

Justification: The minimum bound is very slightly older than the age of *Protictis* (the oldest of the three included terminal taxa) assumed here (see above). As for Primates (see above), combined fossil and phylogenetic evidence indicates that Carnivoramorpha probably originated in Laurasia [174, 187], and their oldest putative fossil record is from the early Palaeocene [188, 189]; there is no evidence of fossil carnivoramorphians in the Late Cretaceous of Laurasia [158]. Given the poor Maastrichtian mammal record in Asia [158] (see 'Glires' above), we use the maximum age of the Campanian as the maximum bound here.

Clade: 'Sirenia'

Included taxa: *Trichechus*, *Pezosiren*

Hard minimum bound: 50.001 Ma

Hard maximum bound: 66.0 Ma

Justification: The minimum bound is very slightly older than the age of *Pezosiren* (the older of these two taxa) assumed here (see above). We use the K-Pg boundary as a maximum bound here.

Clade: 'Notoungulata'

Included taxa: *Henricosbornia*, *Simpsonotus*, *Thomashuxleya*, *Pyrotherium*

Hard minimum bound: 52.001 Ma

Hard maximum bound: 72.1 Ma

Justification: The minimum bound is very slightly older than the age of *Henricosbornia* and *Simpsonotus* (the oldest of the four included terminal taxa) assumed here (see above). With one possible exception [21, 190], notoungulates appear to be absent from the early or middle Palaeocene Tiupampa fauna in Bolivia [191] and the early or middle Palaeocene Punta Peligro fauna in Argentina [192], despite the presence of a diverse range of eutherian 'condylarths' at both sites, suggesting that this clade did not begin to diversify until well after the K-Pg boundary. However, given the poor latest Cretaceous record of mammals in South America, we use the maximum age of the Campanian as a maximum bound here.

Clade: 'Euarchonta'

Included taxa: *Ptilocercus Cynocephalus Notharctus Adapis Plesiadapis Purgatorius*

Hard minimum bound: 64.432 Ma

Hard maximum bound: 161.0 Ma

Justification: The minimum bound is very slightly older than the age of *Purgatorius* (the oldest of the six included terminal taxa) assumed here (see above). Unlike Primates (for which a Laurasian origin seems likely – see above), it is possible that

the more inclusive clade Euarchonta evolved in poorly sampled geographical regions, particularly given the general lack of fossils of stem-members of Dermoptera (depending on the affinities of plagiomenids and mixodectids, which remain controversial; [186, 193-195]) and Scandentia prior to the middle Eocene [196-198]. We therefore specify a very conservative maximum bound here, based on the age of the oldest putative eutherian, *Juramaia* (see above).

Clade: '*Erinaceus+Blarina*'

Included taxa: *Erinaceus*, *Blarina*

Hard minimum bound: 61.983 Ma

Hard maximum bound: 83.6 Ma

Justification: Among living eulipotyphlan 'insectivores', molecular phylogenies consistently support a sister-taxon relationship between erinaceids and soricids to the exclusion of *Solenodon* (e.g. [10]). According to Scott [199], *Litolestes* and *Cedrocherus* represent the probable oldest erinaceids, but he did not provide a phylogenetic analysis to support this. Scott's unpublished thesis [200] does, however, include a phylogenetic analysis of relevant taxa; based on his results, the split between Erinaceidae and Soricidae must have occurred by the middle Torrejonian (To2). The end of To2 appears to correlate with the base of C27n, which is 61.983 Ma [11]; we use this date as a minimum bound here. Eulipotyphla almost certainly evolved in Laurasia (all evidence points to their presence in South America and Africa as the result of much later dispersal), and recent phylogenies place all included Laurasian late Cretaceous eutherians outside crown-Placentalia [1, 2, 6]. Given the poor Maastrichtian mammal record in Asia [158] (see 'Glires' above), we use the maximum age of the Campanian as the maximum bound here.

Clade: 'Tenrecidae'

Included taxa: *Microgale*, *Potamogale*

Hard minimum bound: 15.0 Ma

Hard maximum bound: 61.6 Ma

Justification: The fossil tenrec *Parageogale* is known from multiple early Miocene sites in east Africa [201], including the Kulu Formation on Rusinga Island in Kenya, which has a minimum age of 15.0 Ma [202]. Published phylogenetic analyses typically recover *Parageogale* as the sister-taxon of the extant species *Geogale aurita* [117, 203], and because *Microgale* is closer to *Geogale* than to *Potamogale* [203, 204], it provides a minimum on the *Microgale-Potamogale* split. *Afrodon chleuhi* (see above) and *Todralestes* from the late Palaeocene Ouarzazate Basin in Morocco have been suggested to be stem-afrosoricids or stem-tenrecids, but are dentally far more plesiomorphic than crown-tenrecids [115], and so we use the Selandian-Danian boundary as a maximum bound here.

Clade: 'Ferae'

Included taxa: *Vulpavus*, *Miacis*, *Protictis*, *Patriomanis*

Hard minimum bound: 63.652 Ma

Hard maximum bound: 83.601 Ma

Justification: The minimum bound is very slightly older than the age of *Protictis* (the oldest of the four included terminal taxa) assumed here (see above). Ferae appears to have had a Laurasian origin [174], as do its subclades Carnivoramorpha (see above) and Pholidota [205]. There is no evidence of fossil members of Ferae in the Late Cretaceous of Laurasia [158]. Given the poor Maastrichtian mammal record in Asia

[158] (see 'Glires' above), we use the maximum age of the Campanian as the maximum bound here.

5. *Clock and Substitution Models*

Only 13 of the 421 characters in the matrix (3.1%) are parsimony-uninformative, of which eight concern autapomorphic states in a single taxon (the stem-therian *Vincelestes*), strongly implying that the original studies (see above) focused heavily on only parsimony-informative characters; thus, we assumed that only parsimony-informative characters were scored, using the 'coding=inf' command (which leads to the 13 autapomorphic and invariable characters being ignored).

We investigated two clock models in MrBayes for the morphological data: the independent gamma rates (IGR) model [206, 207] and the Thorne-Kishino (TK) model [208]. The IGR model is an uncorrelated model, which assumes rates for each branch are drawn independently from a common underlying gamma distribution. The TK model, by contrast, assumes autocorrelation of rates across adjacent branches, and is implemented for molecular data in the commonly-used dating program multidivtime. The IGR model is most appropriate when there is little systematic variation in rates across clades, while the TK model is most appropriate when certain clades exhibit consistently higher or lower evolutionary rates. Clock analyses of the TE dataset were as for the morphological matrix only (i.e. using either the IGR or TK model), except that two separate clocks were specified: one for the morphological partition and one for the combined molecular partition.

Clock model comparisons used Bayes Factors, calculated as twice the difference in marginal log-likelihoods as estimated via stepping-stone analyses [209]. These comparisons focused on the IGR analysis with internal topological and age

constraints, which was compared to the corresponding model with an alternative clock model (TK or strict).

The best partition scheme and models for the molecular sequences were determined using were determined using PartitionFinder [210]. Sequences were initially partitioned by gene and codon position. The 'greedy' algorithm and Bayesian Information Criterion were used in PartitionFinder, testing only molecular substitution models implemented by MrBayes (e.g. JC, HKY, GTR, with and without invariant sites and/or gamma).

As noted in the main text, our study employed the widely-used Mk model for discrete morphological data, which has a number of limitations. First, it assumes equal rates of change among all character states (for unordered characters) or all adjacent character states (for ordered characters). Modelling unequal rates of change between character states (e.g. using a complex substitution matrix and/or differential equilibrium state frequencies) is more straightforward in molecular compared to morphological data: nucleotide states (A, T, C and G) are comparable across DNA characters, whereas state labels (e.g. 0, 1 and 2) are usually not comparable across morphological characters. Second, it assumes characters are all independent from each other. Again, modelling correlation is easier in molecular rather than morphological data: in a DNA sequence, adjacency of nucleotide position is a tractable potential proxy for degree of correlation, whereas in a list of morphological characters adjacency is largely meaningless since the order is somewhat arbitrary (although morphological characters are often grouped by general anatomical region). More realistic substitution models for morphology might dramatically reduce the inferred dates and make them more compatible with the molecular and fossil evidence.

Rate heterogeneity across morphological characters was assessed using Bayes Factors to asertain the improvement that results from inclusion of the gamma parameter. These tests again focused on the IGR analysis with internal topological and age constraints: stepping-stone analyses were employed with and without the gamma parameter.

Eeach MrBayes analysis comprised four independent runs of four chains (increased to six chains in certain analyses to improve convergence), run for 50 million generations, and sampling every 5000 generations. Convergence of parameters across runs was assessed by potential scale reduction factors (PSRF) approaching unity, and convergence of topology across runs was assessed by low standard deviations of split (i.e. clade) frequencies. A burnin of 10 million generations was used, unless (as in a few analyses) convergence parameters suggested a longer required burnin; in the latter case, an appropriate burnin was determined manually using Tracer 1.5. Trees were summarised in MrBayes 3.2 using majority-rule consensus with all compatible partitions included. The exact MrBayes commands used, and the consensus tree from each analysis, are provided in ESM.

6. *Rates of Evolution Along Stem vs Crown branches.*

Preliminary qualitative examination of estimated rates of morphological evolution suggested that morphological rates are consistently higher along branches ancestral to or within Placentalia than along other branches within Eutheria. To investigate this further, we classified the ingroup internal branches from each analysis as either 'stem-crown' (ancestral to or within Placentalia) or 'side' branches (all other branches), and binned them according to geological stage, using the midpoint age of each branch, and stage durations from the 2012 Stratigraphic Chart

(http://www.stratigraphy.org/ICSchart/ChronostratChart2012.pdf). Median rates of morphological evolution along the 'stem-crown' and 'side' branches were then compared for each analysis using a one-tailed Mann–Whitney U test [211], with the comparison restricted to the range of geological stages in which 'stem-crown' and 'side' branches co-occur; 'stem-crown' branches from younger geological stages in which 'side' branches are not present (due to the complete extinction of stem-eutherians) were excluded from these comparisons.

Within Eutheria, morphological rates along 'stem-crown' branches (internal branches leading directly to, or within, Placentalia) are consistently and significantly higher (one tailed Mann Whitney U test $p < 0.05$; see supplementary table 5) than rates along contemporaneous 'side' branches (all other internal branches); this pattern is observed with both the IGR and TK clock models, and even when no topological or node age constraints (apart from root age) were enforced (see supplementary table 5). This pattern is not an artefact of failure to sample autapomorphies, since terminal branches were excluded from these comparisons, nor is it simply the result of enforcing topological or temporal constraints on clades within Placentalia (which might result in inflated rates along branches adjacent to constrained nodes), because it was observed even without topological constraints or temporal constraints. There are at least two remaining explanations. The prosaic one is that mammal systematists have focused particularly on innovations that evolved along the placental stem and thus over-sampled traits changing on those branches, relative to extinct side branches that are not ancestral to Placentalia. A more exciting explanation is that rates of evolution were genuinely faster along the placental stem lineage, and this consistent innovation might have contributed to that lineage being the longest-lived and most

successful. These two possibilities are not mutually exclusive, and morphological

analyses that explicitly avoid "stem-crown bias" during trait sampling are required to

test these relative effects.

7. *Extended results.*

Supplementary table 1. Recent palaeontological and molecular estimates of divergence dates for Placentalia and selected placental subclades. Dates in bold represent point estimates, while values in brackets represent ranges or confidence intervals (where given in the original studies). In some studies, particular clades were not recovered, and hence ages were unavailable for those clades; this is indicated by 'n/a'. For full details of analyses, readers are referred to the original studies.

Study	O'Leary et al. (2013)	Bininda-Emonds et al. (2007)	Meredith et al. (2011)	dos Reis et al. (2012)
Data	total evidence	supertree plus nuclear and mitochondrial sequences	nuclear sequences	nuclear and mitochondrial sequences
Dating method	palaeontological (minimisation of ghost lineages)	multiple local strict molecular clocks with fossil calibrations plus interpolation assuming a pure birth model	relaxed molecular (autocorrelated and independent rates) clocks with fossil calibrations	autocorrelated relaxed molecular clock with fossil calibrations
Program(s)	n/a	*relDate* and *chronoGrapher*	*MCMCTree*	*MCMCTree*
Clade age (Ma)				
Placentalia	**64.9**	**98.5** (93.2-108.1)	**101.3** (92.1–116.8)	**90.9** (87.9-93.8)
Glires	**63.4** (61.7–65.0)	**88.9** (87.8-90.1)	**79.5** (71.5–94.1)	**70.7** (69.4-71.8)
Euarchonta	**64.9**	**91.6** (89.2-93.6)	n/a	**74.0** (72.6-75.3)

Euarchontoglires	**64.9**	**91.8** (90.0-93.8)	**83.3** (74.1-97.8)	**75.6** (74.2-77.0)
Eulipotyphla	**58.3** (57.8-58.9)	**82.5** (79.8-85.3)	**77.3** (70.7-85.8)	**61.4** (60.6-62.1)
Ferae	**63.8**	**81.4** (78.2-84.7)	**79.6** (73.6-86.6)	n/a
Laurasiatheria	**64.9**	**87.8** (85.0-90.5)	**84.6** (78.5-93.0)	**75.8** (74.4-77.1)
Boreoeutheria	**64.9**	**96.1** (92.9-98.4)	**92.0** (82.9-107.6)	**82.8** (80.7-84.9)
Paenungulata	**61.8** (61.0-62.5)	**75.8** (72.4-79.2)	**64.3** (56.0-70.6)	**61.6** (57.7-66.2)
Afrotheria	**64.9**	**90.4** (87.3-93.6)	**80.9** (74.4-96.5)	**71.3** (68.5-74.8)
Pilosa	**36**	n/a	**56.4** (49.2-62.9)	n/a
Xenarthra	**58.3** (57.5–59.0)	**70.5** (65.6-75.4)	**65.4** (58.4-71.5)	**71.9** (66.5-77.3)
Atlantogeneta	n/a	n/a	**98.7** (96.7-100.1)	**87.5** (85.9-89.1)
number of lineages crossing KPg boundary	**1**	**43** (40-60)	**24-28**	**16** (15-20)

Supplementary table 2. Summary of divergence estimates of selected placental clades that result from our analyses with different datasets, clock models and assumptions. This represents an expanded version of Table 1 in the main text. Values in bold represent point estimates, whilst values in brackets represent 95% HPD intervals. All analyses enforced nine topological constraints within Placentalia to match the current consensus phylogeny.

Dataset	morph	morph	TE[1]	morph	morph	TE	morph	morph	TE	morph	morph	TE[2]
Clock model	TK	IGR	IGR	TK	IGR	IGR	TK	IGR	IGR	TK	IGR	IGR
Node age constraints	root only	root only	root only	root and internal	root and internal	root and internal	root, internal and Placentalia <93.8 MA	root, internal and Placentalia <93.8 MA	root, internal and Placentalia <93.8 Ma	root, internal and Placentalia <66 MA	root, internal and Placentalia <66 MA	root, internal and Placentalia <66.0 MA
Clade age (Ma)												
Placentalia	**136.2** (118.6-151.2)	**163.7** (146.9-181.3)	**164.5** (150.1-180.1)	**121.7** (108.6-134.5)	**141.5** (127.6-158.1)	**137.0** (124.0-151.7)	**92.9** (90.5-93.8)	**93.0** (90.6-93.8)	**92.2** (90.2-93.8)	**66.0** (65.9-66.0)	**65.9** (65.5-66.0)	**65.9** (65.6-66.0)
Glires	**79.7** (68.9-93.2)	**108.1** (84.8-135.3)	**110.6** (85.6-137.3)	**70.2** (63.8-78.9)	**79.7** (71.6-83.6)	**79.6** (70.9-83.6)	**65.9** (62.3-70.3)	**78.4** (69.9-83.6)	**78.4** (69.3-83.6)	**61.1** (60.7-61.9)	**65.3** (63.8-66.0)	**65.2** (63.1-65.9)
Euarchonta	**121.8** (101.4-141.3)	**135.1** (106.2-162.6)	**137.9** (113.2-163.4)	**100.6** (81.8-116.6)	**106.0** (78.6-134.1)	**109.3** (84.1-132.8)	**86.0** (79.1-92.3)	**86.3** (78.3-92.7)	**84.5** (77.2-91.4)	**65.4** (65.0-65.8)	**65.4** (64.8-65.9)	**65.4** (64.8-65.9)
Euarchontoglires	**128.0** (111.1-144.7)	**147.8** (125.5-170.5)	**150.0** (128.5-170.7)	**107.9** (94.4-122.2)	**124.9** (101.4-145.4)	**122.9** (101.6-142.8)	**88.7** (84.0-93.0)	**89.4** (94.3-93.2)	**88.7** (82.6-93.0)	**65.6** (65.2-65.9)	**65.7** (65.2-66.0)	**65.7** (65.2-66.0)

Eulipotyphla	**103.2** (83.4-122.7)	**110.6** (80.8-142.3)	**126.4** (104.9-148.9)	**91.2** (78.6-104.0)	**98.2** (76.7-121.2)	**99.0** (81.2-117.1)	**78.0** (72.1-83.8)	**77.0** (67.6-86.3)	**77.3** (68.6-85.8)	**64.2** [1] (63.1-65.3)	**64.7** [3] (63.0-65.8)	**64.7** [3] (63.0-65.7)
Ferae	**117.9** (95.3-137.5)	**137.9** (109.6-165.3)	**139.8** (111.8-165.7)	**82.0** (77.7-83.6)	**81.3** (74.9-83.6)	**81.3** (75.3-83.6)	**82.2** (78.4-83.6)	**81.7** (76.3-83.6)	**81.7** (76.3-83.6)	**65.3** (64.9-65.7)	**65.1** (64.3-65.8)	**65.2** (64.2-65.8)
Laurasiatheria	**133.0** (116.3-148.8)	**159.4** (143.0-177.2)	**160.2** (144.6-176.1)	**116.3** (105.6-127.8)	**136.2** (120.8-152.0)	**132.2** (117.2-147.8)	**91.4** (88.6-93.5)	**91.1** (87.8-93.4)	**91.0** (87.2-93.4)	**65.9** (65.7-66.0)	**65.6** (65.2-66.0)	**65.6** (65.2-66.0)
Boreoeutheria	**134.9** (117.9-150.5)	**161.3** (145.0-179.6)	**162.3** (146.9-177.3)	n/a	**138.7** (123.7-154.0)	**134.6** (121.5-149.3)	**92.3** (89.9-93.8)	**92.2** (89.5-93.7)	**92.0** (88.9-93.7)	**65.9** (65.9-66.0)	**65.8** (65.4-66.0)	**65.8** (65.5-66.0)
Paenungulata	**90.3** (71.4-113.4)	**107.7** (77.7-137.4)	**104.2** (79.9-131.0)	**77.0** (64.4-91.6)	**87.1** (63.9-111.8)	**80.5** (63.6-102.1)	**69.8** (60.8-79.1)	**70.3** (58.2-83.1)	**65.4** (56.0-75.4)	**58.4** (56.0-61.2)	**59.4** (56.0-63.2)	**58.0** (56.0-61.3)
Afrotheria	**130.4** (112.8-146.8)	**152.5** (130.7-175.3)	**149.3** (127.2-170.6)	**111.6** (98.1-125.9)	**132.8** (112.1-151.5)	**120.0** (101.2-137.6)	**88.8** (83.7-92.9)	**87.6** (79.8-93.1)	**82.9** (75.4-92.0)	**64.8** (63.4-65.8)	**63.8** (61.3-65.7)	**62.8** (61.0-65.0)
Pilosa	**37.6** (11.4-68.2)	**42.8** (12.8-78.2)	**62.6** (38.4-88.3)	**38.1** (26.0-55.2)	**38.3** (26.0-56.6)	**40.1** (28.8-63.9)	**38.2** (26.0-52.5)	**34.6** (26.0-50.6)	**39.1** (26.0-54.6)	**39.7** (27.2-51.0)	**36.0** (26.0-53.3)	**35.6** (27.3-48.3)
Xenarthra	**59.5** (28.3-90.0)	**71.6** (34.9-112.9)	**84.0** (56.2-112.5)	**57.5** (43.2-72.1)	**59.5** (43.5-72.1)	**59.7** (46.8-72.1)	**53.4** (39.8-65.4)	**53.3** (39.0-69.0)	**53.4** (40.5-68.9)	**51.2** (42.5-57.5)	**55.3** (41.3-66.0)	**47.3** (39.0-58.4)
Atlantogeneta	**130.9** (114.5-147.1)	**156.3** (135.4-177.5)	**156.7** (138.6-175.5)	**112.1** (99.2-126.4)	**136.2** (116.7-154.2)	**128.4** (105.8-146.2)	**89.8** (85.0-93.5)	**89.7** (83.1-93.7)	**88.5** (82.2-93.6)	**65.1** (63.8-66.0)	**64.9** (62.5-66.0)	**64.4** (62.2-66.0)
number of lineages crossing KPg boundary	**45** (31-50)	**53** (36-56)	**49** (35-52)	**37** (27-46)	**40** (28-46)	**40** (28-46)	**30** (23-37)	**35** (24-46)	**34** (22-46)	**1**	**1**	**1**

Supplementary table 3. Summary of variation in rates of morphological evolution under different clock models and assumptions. All

analyses enforced nine topological constraints within Placentalia to match the current consensus phylogeny, and comparisons were restricted to

ingroup internal branches.

Dataset	morph	morph	TE	morph	morph	TE	morph	morph	TE	morph	morph	TE
Clock model	TK	IGR	IGR	TK	IGR	IGR	TK	IGR	IGR	TK	IGR	IGR
Node age constraints	root only	root only	root only	root and internal	root and internal	root and internal	root, internal and Placentalia <93.8 Ma	root, internal and Placentalia <93.8 Ma	root, internal and Placentalia <93.8 Ma	root, internal and Placentalia <66 Ma	root, internal and Placentalia <66 Ma	root, internal and Placentalia <66 Ma
Highest median rate of morphological evolution (% change/Ma)	1.12	11.34	3.15	1.29	7.14	1.27	1.93	4.22	1.37	15.26	129.21	30.84
Lowest median rate of morphological evolution (% change/Ma)	0.12	0.0087	0.0022	0.11	0.0073	0.0036	0.14	0.0064	0.0023	0.13	0.0085	0.0041
Range of rates (=highest median rate/lowest median rate)	10x	1299x	1456x	12x	984x	357x	14x	661x	584x	118x	15265x	7566x

Supplementary table 4. Summary of variation in rates of molecular evolution under different assumptions. All analyses enforced nine topological constraints within Placentalia to match the current consensus phylogeny, and comparisons were restricted to branches within Placentalia, but included both internal and terminal branches (see main text).

Dataset	TE	TE	TE	TE
Clock model	IGR	IGR	IGR	IGR
topological constraints?	yes	yes	yes	yes
Node age constraints	root only	root and internal	root, internal and Placentalia <93.8 Ma	root, internal and Placentalia <66 Ma
Highest median rate of molecular evolution (% change/Ma)	0.46	0.37	0.76	2.54
Lowest median rate of molecular evolution (% change/Ma)	0.0089	0.0074	0.020	0.019
Range of rates (=highest median rate/lowest median rate)	51x	51x	39x	137x

Supplementary table 5. Summary of Mann-Whitney U tests comparing rates of evolution in 'stem-crown' and 'side' branches. An online implementation of the Mann-Whitney U test (http://vassarstats.net/utest.html) was used. Comparisons were restricted to ingroup internal branches from the range of geological stages in which 'stem-crown' and 'side' branches co-occur (see main text). P-values are 1-tailed, comparing the alternative hypothesis that rates of morphological evolution are higher in 'stem-crown' branches than in 'side' branches (see Figure 2), versus the null hypothesis that there is no difference in rates. P-values <0.05 are highlighted in bold.

Clock model	TK	IGR	TK	IGR	TK	IGR	TK	IGR
topological constraints?	no	no	yes	yes	yes	yes	yes	yes
Age constraints	root only	root only	root only	root only	root and internal	root and internal	root, internal and Placentalia <66 MA	root, internal and Placentalia <66 MA
range of geological stages in which 'stem-crown' and 'side' branches co-occur	Toarcian-Turonian	Bathonian-Campanian	Toarcian-Campanian	Bajocian-Campanian	Bathonian-Coniacian	Oxfordian-Campanian	Oxfordian-Campanian	Kimmeridgian-Campanian
Number of 'stem-crown' branches in range	20	51	47	57	24	50	7	9
Number of 'side' branches in range	23	35	32	29	25	33	23	32
1-tailed Mann-Whitney U test p-value (H_1 = rates of morphological evolution are higher in 'stem-crown' than 'side' branches)	**<0.0001**	**<0.0001**	**<0.0001**	**0.0057**	**<0.0001**	**0.0001**	**0.0006**	**0.0049**

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