**Online Supplemental Materials.**

This document includes supporting information for the paper **Phylogeny and divergence times of lemurs inferred with recent and ancient fossils in the tree** byJames P. Herrera, Liliana M. Dávalos. First, a list describing files and figures included in the Dryad data submission is given. Next, supplemental description of methods are given to expand on methodology presented in main text. Supplemental results follow, giving details of results not elaborated on in the main text. Supplementary data tables follow, and finally descriptions of the morphological characters and the states of each character are given.

**Online Supplemental Material File S1.** Morphological data matrix in Mesquite format. See separate data file.

**Online Supplemental Material File S2.** R code to run the Gower dissimilarity analysis used to identify characters that were potentially non-independent.

**Online Supplemental Material File S3.** Reduced morphological dataset after excluding characters that were potentially non-independent from the Gower dissimilarity analysis.

**Online Supplemental Material File S4.** Data sources, including morphological partition and GenBank accession numbers for each species and gene used in the analyses, as well as tabulations of the number of datasets for each species and number of species for each dataset. See separate data file.

**Online Supplemental Material File S5.** Concatenated partitioned molecular data alignment. See separate data file.

**Online Supplemental Material File S6.** MrBayes block of code to run fossilized birth-death process and tip-dating analyses. See separate file.

**Online Supplemental Material File S7.** 1000 trees from the posterior distribution of trees inferred from the total evidence dataset (full morphological dataset) under the fossilized birth-death model in MrBayes.

**Online Supplemental Material File S8.** 1000 trees from the posterior distribution of trees inferred from the total evidence dataset (reduced morphological dataset) under the fossilized birth-death model in MrBayes.

**Online Supplemental Material File S9.** 1000 trees from the posterior distribution of trees inferred from the total evidence dataset (full morphological dataset) using tip-dating under the uniform clock model in MrBayes.

**Online Supplemental Material File S10.** 1000 trees from the posterior distribution of trees inferred from the mtDNA dataset in MrBayes.

**Online Supplemental Material File S11.** 1000 trees from the posterior distribution of trees inferred from the nDNA dataset in MrBayes.

**Online Supplemental Material File S12.** 1000 trees from the posterior distribution of trees inferred from the morphological dataset in MrBayes.

**Online Supplemental Material File S13.** The primary concordance tree inferred using Bayesian concordance analysis (BUCKy) of the posterior distributions of trees inferred from individual analysis of the mtDNA, nDNA and morphology.

**Online Supplemental Material File S14.** Tree topology inferred from total evidence dataset and reduced morphological dataset using maximum likelihood (RaxML).

**Online Supplemental Material File S15.** 55 most parsimonious tree topologies inferred from total evidence dataset and reduced morphological dataset using the parsimony ratchet (TNT).

**Online Supplemental Material File S16.** Mean clade credibility tree from FBD analysis of full morphological and full molecular dataset.

**Online Supplemental Material File S17.** Mean clade credibility tree from FBD analysis of reduced morphological and full molecular dataset.

**Online Supplemental Material File S18.** Mean clade credibility tree from TD analysis of full morphological and full molecular dataset.

**Online Supplemental Material File S19.** Mean clade credibility tree from TD analysis of reduced morphological and full molecular dataset.

**Online Supplemental Material Figure S1.** Maximum clade credibility tree from fossilized birth-death process with 421 morphological characters and 5767 molecular characters. Posterior probabilities of nodes are labelled.

**Online Supplemental Material Figure S2.** Maximum clade credibility tree from fossilized birth-death process with 369 morphological characters and 5767 molecular characters. Posterior probabilities of nodes are labelled.

**Online Supplemental Material Figure S3.** Maximum clade credibility tree from tip-dating method with 421 morphological characters and 5767 molecular characters posterior probabilities of nodes are labelled.

**Online Supplemental Material Figure S4.** Maximum clade credibility tree from tip-dating method with 369 morphological characters and 5767 molecular characters posterior probabilities of nodes are labelled.

**Online Supplemental Material Figure S5.** Comparison of node age estimates from the fossilized-birth-death process analyses with the full (421) and reduced (369) morphological matrices and wide uniform or fixed point estimate age priors on fossils, as well as the tip-dating analyses with full and reduced morphological datasets.

**Online Supplemental Material Figure S6.** Maximum clade credibility tree topology for unconstrained (non-clock) Bayesian analysis of mtDNA in MrBayes. Circles on nodes represent the posterior probability of that node. The tree was rooted for drawing purposes only.

**Online Supplemental Material Figure S7.** Maximum clade credibility tree topology for unconstrained (non-clock) Bayesian analysis of nDNA in MrBayes. Circles on nodes represent the posterior probability of that node. The tree was rooted for drawing purposes only.

**Online Supplemental Material Figure S8.** Maximum clade credibility tree topology for unconstrained (non-clock) Bayesian analysis of the reduced morphological dataset (369 characters) in MrBayes. Circles on nodes represent the posterior probability of that node. The tree was rooted for drawing purposes only.

**Online Supplemental Material Figure S9.** The primary concordance tree topology inferred using Bayesian concordance analysis (BUCKy) of the posterior distributions of trees inferred from individual analysis of the mtDNA, nDNA and morphology. Numbers on branches indicate the concordance factor, a measure of the average number of data types that support the given branch. The tree was rooted for drawing purposes only.

**Online Supplemental Material Figure S10.** Box plots of Robinson-Foulds distances (RF) from the primary concordance tree (PCT) for tree sets inferred from different data types. mtDNA = mitochondrial DNA, nDNA = nuclear DNA, TE = total evidence, Null1 and Null2 = randomized trees to generate null distributions. See main text for further details.

**Online Supplemental Material Figure S11.** The tree topology with the highest likelihood found by RaxML with the bootstrap support values from 1000 pseudoreplicates indicated on branches.

**Online Supplemental Material Figure S12.** 50% majority rule consensus of 55 most parsimonious tree topologies inferred from the total evidence dataset (reduced morphological dataset) using the parsimony ratchet (TNT).

**Online Supplemental Material Figure S13.** Box plots of Robinson-Foulds distances (RF) among trees inferred from the total evidence dataset using different tree inference techniques. ML = maximum likelihood (using RaxML), parsimony = maximum parsimony (using TNT, 55 most parsimonious trees), Bayes = Bayesian inference (using MrBayes v3.2.6).

**Online Supplemental Material Methods**

***Topology comparison***

Alternate phylogenetic topologies were compared using stepping-stone analyses. First, for a subset of taxa (n=36) for which mtDNA, nDNA and morphological data were all available, we inferred non-clock total evidence trees from each dataset separately using MrBayes and inferred the primary concordance tree using BUCKy. The marginal likelihood of the total evidence dataset for the 36 taxa was compared with topology constraints to enforce relationships inferred from analysis of the 1) mtDNA, 2) nDNA, and 3) morphology alone, 4) a primary concordance analysis of the trees inferred from the three separate data types, and 5) an unconstrained total evidence analysis. Then, using the full set of taxa and the total evidence dataset, we compared marginal likelihoods under the following topology constraints: 1) PCT of taxa with all three datatypes was used as a partial backbone constraint, 2) the position of *Megaladapis* was constrained to be sister to Lemuridae, as found in other studies, e.g., Kistler et al. 2015, 3) a negative constraint on *Plesiopithecus* + *Daubentonia,* thus preventing that sister relationship, and 4) a backbone constraint of family-level relationships inferred from the original FBD analysis.

***Phylogenetic inference using maximum likelihood and parsimony***

In addition to the Bayesian tree inference procedures outlined in the main text, we performed tree searches using maximum likelihood in RaxML v8.2.3 (Stamatakis 2014) run on the CIPRES Science Gateway (Miller et al. 2010). For the RaxML analysis, we performed a rapid bootstrap (1000 pseudoreplicates) and a search for the tree with the maximum likelihood (*-f a* commands), defining the two molecular and one morphological partition as described in the main text for the Bayesian analysis and Table S2. The models for the partitions were set to GTRGAMMA and an ascertainment bias correction (Lewis) was applied.

Maximum parsimony tree search was performed using TNT (Goloboff et al. 2008). The New Technology toolkit was used implementing the parsimony ratchet, with 100 substitutions made during the perturbation phase, up- and down-weighting probabilities set to 10, the total number of iterations set to 100, and initial trees generated by 100 random addition sequences. Before analysis, the default number of trees held in memory (100) was increased to 1000.

**Online Supplemental Material Results**

***Results of topology comparisons***

The marginal likelihood of the total evidence data for the 36 taxa with mtDNA, nDNA, and morphology data in common was highest for the topology in which the primary concordance tree was enforced (log likelihood = -54169.89), which was a moderately better fit to the data than the total evidence topology (log likelihood difference = 1.90, Bayes factor = 6.66), and a significantly better fit than topology constraints based on trees from any one data type alone (Table S8).

The results of topology comparisons for the concatenated dataset (reduced 369 character morphological dataset) with the full taxon set suggest that the tree topology inferred using the FBD analysis was the best supported topology, with a marginal likelihood of -89598.96, while topology constraints reflecting other inferred relationships had significantly worse fits to the data (Bayes factors >1090 Table S8). These results lend strong support for the FBD topology over other possible topologies.

***Results of age-range prior calibrations versus fixed age calibrations***

We assessed the impact of using a fixed age prior calibration compared to wide uniform distributions of age ranges for calibrations on divergence time estimation under the FBD model. We found that the 95% highest probability density (HPD) of divergence time estimates for 21 key nodes in the tree overlapped among analyses of the concatenated molecular and morphological dataset under the FBD model with the full and reduced morphological dataset and with fixed or wide uniform age priors (OSM Fig S5). One surprising result, however, is that for several nodes deep in the lemur phylogeny (e.g., the lemuriforms, Megaladapidae, Lemuridae/Indroidea, Cheirogaleidae, Asian/African Lorisidae), the 95% HPD was wider with the fixed age priors than with the wide uniform distributions of ages. The mean estimates were similar among analyses.

***Phylogenetic inference using maximum likelihood and parsimony***

Here we describe results of the maximum likelihood and parsimony tree searches. The maximum likelihood tree had a score of -88440.538 and the bootstrap supports for nodes of the maximum likelihood tree are illustrated in OSM Figure S11. In general, the tree is in strong agreement with the tree from the Bayesian analysis (see main text), but low bootstrap supports, especially for some fossils, suggest that perturbation of the dataset leads to different topologies.

The 55 most parsimonious trees had a length of 19794 steps. The 50% majority rule tree is consistent with trees from maximum likelihood and Bayesian techniques (Figure S12).

Trees from maximum likelihood and parsimony were similar to the Bayesian analysis of the total evidence dataset, but the maximum likelihood tree had the lowest Robinson-Foulds distances from the total evidence trees (mean=80.22, SE=0.21), while the most parsimonious trees had greater distances from the total evidence tree (mean=89.15, SE=0.02). Both maximum likelihood and parsimony trees had distances that were outside the range of distances observed within the posterior distribution of total evidence trees (mean=52.69, SE=0.008), indicating that the variation among trees from different methods was greater than the variation within the Bayesian sample of total evidence trees. These differences are mostly among the tips with low posterior probabilities (e.g., *Microcebus* species), rather than among deep nodes, suggesting the overall ‘skeleton’ of the tree is stable and robust to the phylogenetic inference technique, while the power to resolve some relationships among closely related, recently diverged taxa is low.

Goloboff P.A., Farris J.S., Nixon K.C. 2008. TNT, a free program for phylogenetic analysis. Cladistics 24:774-786.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30:1312-1313.

Yang Z. 2006. Computational molecular evolution. Oxford University Press Oxford. p113-114

**Online Supplemental Material Table S1**. Percent missing data in the complete (421) morphological character matrix, the mitochondrial DNA and the nuclear DNA datasets. Extinct taxa are in **bold**.

|  |  |  |  |
| --- | --- | --- | --- |
| **Binomial name** | **% missing morphology** | **% missing mtDNA** | **% missing nDNA** |
| ***Adapis parisiensis*** | 12% | 100% | 100% |
| ***Aegyptopithecus zeuxis*** | 28% | 100% | 100% |
| *Allenopithecus nigroviridis* | 13% | 0% | 7% |
| *Allocebus trichotis* | 100% | 0% | 100% |
| *Alouatta seniculus* | 11% | 55% | 100% |
| ***Altiatlasius koulchii*** | 90% | 100% | 100% |
| ***Anchomomys frontanyensis*** | 69% | 100% | 100% |
| *Aotus trivirgatus* | 10% | 0% | 8% |
| ***Archaeoindris fontoynontii*** | 71% | 100% | 100% |
| ***Archaeolemur edwardsi*** | 55% | 92% | 100% |
| ***Archaeolemur majori*** | 88% | 87% | 100% |
| *Arctocebus calabarensis* | 12% | 55% | 39% |
| *Avahi betsileo* | 100% | 45% | 100% |
| *Avahi cleesei* | 100% | 0% | 100% |
| *Avahi laniger* | 58% | 0% | 72% |
| *Avahi meridionalis* | 100% | 0% | 100% |
| *Avahi occidentalis* | 75% | 0% | 100% |
| *Avahi peyrierasi* | 100% | 0% | 100% |
| *Avahi ramanantsoavanai* | 100% | 0% | 100% |
| *Avahi unicolor* | 100% | 45% | 100% |
| ***Babakotia radafolia*** | 60% | 100% | 100% |
| ***Branisella boliviana*** | 67% | 100% | 100% |
| ***Cantius abditus*** | 40% | 100% | 100% |
| ***Carpolestes simpsoni*** | 21% | 100% | 100% |
| *Cheirogaleus crossleyi* | 100% | 55% | 89% |
| *Cheirogaleus lavasoaensis* | 100% | 55% | 89% |
| *Cheirogaleus major* | 1% | 55% | 89% |
| *Cheirogaleus medius* | 100% | 0% | 9% |
| *Cheirogaleus sibreei* | 100% | 55% | 89% |
| *Daubentonia madagascariensis* | 58% | 0% | 9% |
| ***Daubentonia robustus*** | 91% | 100% | 100% |
| ***Djebelemur martinezi*** | 65% | 100% | 100% |
| ***Donrussellia provincialis*** | 71% | 100% | 100% |
| *Eulemur albifrons* | 57% | 0% | 11% |
| *Eulemur cinereiceps* | 100% | 0% | 100% |
| *Eulemur collaris* | 100% | 0% | 65% |
| *Eulemur coronatus* | 100% | 0% | 42% |
| *Eulemur flavifrons* | 100% | 0% | 58% |
| *Eulemur fulvus* | 57% | 0% | 77% |
| *Eulemur macaco* | 100% | 0% | 8% |
| *Eulemur mongoz* | 100% | 0% | 24% |
| *Eulemur rubriventer* | 100% | 0% | 73% |
| *Eulemur rufifrons* | 100% | 0% | 100% |
| *Eulemur rufus* | 57% | 55% | 9% |
| *Eulemur sanfordi* | 100% | 0% | 64% |
| *Euoticus elegantulus* | 100% | 89% | 77% |
| *Galago alleni* | 100% | 89% | 100% |
| *Galago matschiei* | 100% | 55% | 65% |
| *Galago moholi* | 11% | 55% | 13% |
| *Galago senegalensis* | 78% | 0% | 10% |
| *Galago thomasi* | 100% | 100% | 88% |
| *Galagoides cocos* | 100% | 100% | 65% |
| *Galagoides demidoff* | 1% | 55% | 66% |
| *Galagoides zanzibaricus* | 100% | 89% | 65% |
| ***Hadropithecus stenognathus*** | 62% | 51% | 100% |
| *Hapalemur alaotrensis* | 100% | 86% | 100% |
| *Hapalemur aureus* | 100% | 0% | 100% |
| *Hapalemur griseus* | 56% | 0% | 8% |
| *Hapalemur meridionalis* | 100% | 55% | 100% |
| *Hapalemur occidentalis* | 100% | 31% | 19% |
| *Hapalemur simus* | 56% | 31% | 100% |
| *Homo sapiens* | 100% | 0% | 48% |
| *Indri indri* | 54% | 0% | 100% |
| ***Karanisia clarki*** | 69% | 100% | 100% |
| ***Komba robustus*** | 61% | 100% | 100% |
| *Lemur catta* | 1% | 0% | 20% |
| *Lepilemur aeeclis* | 100% | 0% | 100% |
| *Lepilemur ankaranensis* | 100% | 0% | 8% |
| *Lepilemur dorsalis* | 57% | 0% | 8% |
| *Lepilemur edwardsi* | 56% | 0% | 67% |
| *Lepilemur hubbardorum* | 100% | 55% | 100% |
| *Lepilemur jamesi* | 100% | 55% | 8% |
| *Lepilemur leucopus* | 55% | 0% | 100% |
| *Lepilemur manasamody* | 100% | 86% | 100% |
| *Lepilemur microdon* | 100% | 0% | 100% |
| *Lepilemur mittermeieri* | 100% | 55% | 100% |
| *Lepilemur mustelinus* | 4% | 0% | 100% |
| *Lepilemur otto* | 100% | 86% | 100% |
| *Lepilemur randrianasoloi* | 100% | 0% | 100% |
| *Lepilemur ruficaudatus* | 56% | 0% | 66% |
| *Lepilemur sahamalazensis* | 100% | 0% | 100% |
| *Lepilemur seali* | 100% | 45% | 100% |
| *Lepilemur septentrionalis* | 100% | 0% | 41% |
| *Leptadapis magnus* | 20% | 100% | 100% |
| *Loris tardigradus* | 2% | 0% | 8% |
| ***Megaladapis edwardsi*** | 59% | 0% | 100% |
| ***Megaladapis grandidieri*** | 84% | 100% | 100% |
| ***Megaladapis madagascariensis*** | 74% | 100% | 100% |
| ***Mesopropithecus dolichobrachion*** | 68% | 100% | 100% |
| ***Mesopropithecus pithecoides*** | 67% | 100% | 100% |
| *Microcebus arnholdi* | 100% | 55% | 88% |
| *Microcebus berthae* | 100% | 0% | 65% |
| *Microcebus bongolavensis* | 100% | 88% | 100% |
| *Microcebus danfossi* | 100% | 88% | 100% |
| *Microcebus gerpi* | 100% | 88% | 100% |
| *Microcebus griseorufus* | 75% | 55% | 88% |
| *Microcebus jollyae* | 100% | 45% | 100% |
| *Microcebus lehilahytsara* | 100% | 55% | 88% |
| *Microcebus macarthurii* | 100% | 88% | 100% |
| *Microcebus mamiratra* | 100% | 33% | 100% |
| *Microcebus margotmarshae* | 100% | 45% | 100% |
| *Microcebus marohita* | 100% | 55% | 88% |
| *Microcebus mittermeieri* | 100% | 0% | 88% |
| *Microcebus murinus* | 10% | 0% | 2% |
| *Microcebus myoxinus* | 100% | 55% | 88% |
| *Microcebus ravelobensis* | 100% | 0% | 64% |
| *Microcebus rufus* | 56% | 0% | 88% |
| *Microcebus sambiranensis* | 100% | 55% | 88% |
| *Microcebus simmonsi* | 100% | 45% | 88% |
| *Microcebus tanosi* | 100% | 55% | 88% |
| *Microcebus tavaratra* | 100% | 0% | 88% |
| *Mirza coquereli* | 57% | 0% | 14% |
| *Mirza zaza* | 100% | 0% | 89% |
| ***Notharctus pugnax*** | 95% | 100% | 100% |
| ***Notharctus tenebrosus*** | 55% | 100% | 100% |
| ***Nycticeboides simpsoni*** | 67% | 100% | 100% |
| *Nycticebus bengalensis* | 78% | 55% | 21% |
| *Nycticebus coucang* | 8% | 0% | 19% |
| *Nycticebus javanicus* | 100% | 83% | 100% |
| *Nycticebus menagensis* | 100% | 83% | 100% |
| *Nycticebus pygmaeus* | 100% | 55% | 8% |
| *Otolemur crassicaudatus* | 2% | 0% | 8% |
| *Otolemur garnetti* | 78% | 100% | 100% |
| *Otolemur garnettii* | 100% | 55% | 36% |
| ***Pachylemur jullyi*** | 75% | 8% | 100% |
| ***Palaeopropithecus ingens*** | 72% | 0% | 100% |
| ***Palaeopropithecus maximus*** | 63% | 13% | 100% |
| *Pan troglodytes* | 12% | 0% | 8% |
| *Perodicticus potto* | 3% | 0% | 12% |
| *Phaner furcifer* | 57% | 55% | 100% |
| ***Plesiadapis tricuspidens*** | 19% | 100% | 100% |
| ***Plesiopithecus teras*** | 59% | 100% | 100% |
| ***Pronycticebus gaudryi*** | 54% | 100% | 100% |
| *Propithecus candidus* | 58% | 100% | 100% |
| *Propithecus coquereli* | 58% | 0% | 2% |
| *Propithecus coronatus* | 58% | 0% | 100% |
| *Propithecus deckenii* | 58% | 0% | 100% |
| *Propithecus diadema* | 59% | 0% | 8% |
| *Propithecus edwardsi* | 61% | 0% | 39% |
| *Propithecus perrieri* | 64% | 55% | 100% |
| *Propithecus tattersalli* | 63% | 0% | 10% |
| *Propithecus verreauxi* | 3% | 0% | 8% |
| ***Purgatorius unio*** | 70% | 100% | 100% |
| ***Saharagalago misrensis*** | 90% | 100% | 100% |
| *Saimiri sciureus* | 10% | 0% | 13% |
| *Tarsius bancanus* | 11% | 0% | 11% |
| *Tarsius syrichta* | 100% | 0% | 39% |
| ***Teilhardina americana*** | 67% | 100% | 100% |
| *Varecia rubra* | 100% | 0% | 65% |
| *Varecia variegata* | 2% | 0% | 13% |
| ***Wadilemur elegans*** | 70% | 100% | 100% |

**Online Supplemental Material Table S2**. Molecular data partitioning scheme from PartitionFinder. Note that where PartitionFinder indicated that the best model included both a parameter for a gamma-distributed rate (G) and a parameter for the proportion of invariant sites (I), we did not include I in our models because there is strong correlation between G and I, the G parameter encompasses different rates among sites such that sites with low substitution or invariant sites are already modeled by G, and including both I and G in phylogenetic analyses can be pathological (Yang 2006; Stamatakis 2014).

model selection : bic

search : greedy

Best partitioning scheme

Scheme lnL : -75411.1184

Scheme BIC : 155074.251281

Number of params : 491

Number of sites : 5767

Number of subsets : 2

|  |  |  |
| --- | --- | --- |
| **Subset** | **Best Model** | **Subset Partitions** |
| 1 | SYM+I+G | ADORA posa1, ADORA pos2, ADORA pos3, CNR pos1, CNR pos2, CNR pos3, ND4 pos2, ND4 pos3, RAG1 pos1, RAG1 pos2, RAG1 pos3, RAG2 pos1, RAG2 pos2, RAG2 pos3, cytb pos1, cytb pos2 |
| 2 | GTR+I+G | ND4 pos1, cytb pos3 |

aPos: codon position 1, 2, or 3.

**RaxML-style partition definitions:**

DNA, p1 = 1-1139\3, 2-1139\3, 1141-2518\3, 1142-2518\3, 2519-2931\3, 2520-2931\3, 2521-2931\3, 2932-3931\3, 2933-3931\3, 2934-3931\3, 3932-5008\3, 3933-5008\3, 3934-5008\3, 5009-5767\3, 5010-5767\3, 5011-5767\3

DNA, p2 = 3-1139\3, 1140-2518\3

**Online Supplemental Material Table S3**. Mitochondrial DNA sequence partitioning scheme from PartitionFinder:

model\_selection: aicc

search: greedy

Best partitioning scheme

Scheme lnL : -59057.38086

Scheme AICc : 118773.106733

Number of params : 291

Number of sites : 2518

Number of subsets : 5

|  |  |  |
| --- | --- | --- |
| **Subset** | **Best Model** | **Subset Partitions** |
| 1 | GTR + I + G | cytb pos1 |
| 2 | GTR + I + G | ND4 pos3, cytb pos2 |
| 3 | GTR + I + G | Cytb pos3 |
| 4 | GTR + I + G | ND4 pos 1 |
| 5 | GTR + I + G | ND4 pos 2 |

Pos: codon position 1, 2, or 3.

**RaxML-style partition definitions:**

DNA, p1 = 1-1139\3

DNA, p2 = 2-1139\3, 1142-2518\3

DNA, p3 = 3-1139\3

DNA, p4 = 1140-2518\3

DNA, p5 = 1141-2518\3

**Online Supplemental Material Table S4**. Nuclear DNA sequence partitioning scheme from PartitionFinder. Note that this scheme was highly partitioned with 9 subsets on a sequence alignment of 3249 sites and we reduced the number of subsets from this scheme to 5, including sites that were initially included in different subsets into subsets with the same models (see below).

model\_selection: aicc

search: greedy

Scheme lnL : -13961.38881

Scheme AICc : 28376.5246556

Number of params : 212

Number of sites : 3249

Number of subsets : 9

|  |  |  |
| --- | --- | --- |
| **Subset** | **Best Model** | **Subset Partitions** |
| 1 | GTR+G | ADORA pos1, RAG2 pos1 |
| 2 | HKY+G | ADORA pos2, RAG1 pos2 |
| 3 | K80+G | ADORA pos3 |
| 4 | GTR+G | CNR pos1 |
| 5 | GTR+I+G | CNR pos2, RAG1 pos3 |
| 6 | GTR+I | CNR pos3 |
| 7 | HKY+I | RAG1 pos1 |
| 8 | GTR+G | RAG2 pos2 |
| 9 | HKY+G | RAG2 pos3 |

Pos: codon position 1, 2, or 3.

**RaxML-style partition definitions:**

DNA, p1 = 1-413\3, 2491-3249\3

DNA, p2 = 2-413\3, 1415-2490\3

DNA, p3 = 3-413\3

DNA, p4 = 414-1413\3

DNA, p5 = 415-1413\3, 1416-2490\3

DNA, p6 = 416-1413\3

DNA, p7 = 1414-2490\3

DNA, p8 = 2492-3249\3

DNA, p9 = 2493-3249\3

**Reduced partitioning scheme to minimize the number of subsets:**

|  |  |  |
| --- | --- | --- |
| **Subset** | **Best Model** | **Subset Partitions** |
| 1 | GTR+G | ADORA pos1, RAG2 pos1 |
| 2 | HKY+G | ADORA pos2, RAG1 pos2 |
| 3 | K80+G | ADORA pos3 |
| 4 | GTR+G | CNR pos1, CNR pos2, CNR pos3, RAG1 pos3 |
| 5 | GTR+G | RAG1\_pos1 RAG2\_pos2 RAG2\_pos3 |

Pos: codon position 1, 2, or 3.

**Online Supplemental Material Table S5**. Combined DNA sequence with reduced taxon sampling (36 species) partitioning scheme from PartitionFinder.

model\_selection: bic

search: greedy

Scheme lnL : -44576.85691

Scheme BIC : 91846.9449883

Number of params : 311

Number of sites : 5767

Number of subsets : 4

|  |  |  |
| --- | --- | --- |
| **Subset** | **Best Model** | **Subset Partitions** |
| 1 | GTR+I+G | ND4 pos2, ND4 pos3, cytb pos1, cytb pos2 |
| 2 | GTR+I+G | ND4 pos1, cytb pos3 |
| 3 | GTR+I+G | ADORA pos1, ADORA pos3, CNR pos2, CNR pos3, RAG1 pos1, RAG1 pos3, RAG2 pos1, RAG2 pos2, RAG2 pos3 |
| 4 | HKY+G | ADORA pos2, CNR pos1, RAG1 pos2 |

**RaxML-style partition definitions**

DNA, p1 = 1-1139\3, 2-1139\3, 1141-2518\3, 1142-2518\3

DNA, p2 = 3-1139\3, 1140-2518\3

DNA, p3 = 2519-2931\3, 2521-2931\3, 2933-3931\3, 2934-3931\3, 3932-5008\3, 3934-5008\3, 5009-5767\3, 5010-5767\3, 5011-5767\3

DNA, p4 = 2520-2931\3, 2932-3931\3, 3933-5008\3

**Online Supplemental Material Table S6**

Robinson-Foulds distances from the primary concordance tree (PCT) among trees inferred from different data types. mtDNA = mitochondrial DNA, nDNA = nuclear DNA, TE = total evidence, Null1 and Null2 = randomized trees to generate null distributions. See main text for further details.

|  |  |  |
| --- | --- | --- |
| **Comparison** | **Mean** | **Standard error** |
| PCT vs. TE | 6.04 | 0.05 |
| PCT vs. mtDNA | 7.56 | 0.04 |
| PCT vs nDNA | 20.89 | 0.04 |
| PCT vs morphology | 40.75 | 0.08 |
| PCT vs. Null2 | 65.53 | 0.03 |
| PCT vs. Null1 | 68.00 | 0.00 |

**Online Supplemental Material Table S7**

Robinson-Foulds distances among total evidence trees inferred using different optimality criteria. ML = maximum likelihood (using RaxML), parsimony = maximum parsimony (using TNT, 55 most parsimonious trees), Bayes = Bayesian inference (using MrBayes v3.2.6). See main text for further details.

|  |  |  |
| --- | --- | --- |
| **Comparison** | **Mean** | **Standard error** |
| Within parsimony | 37.94 | 0.14 |
| Within Bayes | 52.69 | 0.01 |
| ML vs. Bayes | 80.22 | 0.21 |
| Parsimony vs. Bayes | 89.15 | 0.02 |

**Table S8.** Results of topology and model comparison using stepping stone analysis in MrBayes. (A) Results of stepping-stone analysis of reduced taxon set (36 taxa) for which mitochondrial DNA (mtDNA), nuclear DNA (nDNA) and morphological data were all available. The marginal likelihood of the data was compared using topology constraints reflecting the primary concordance tree (PCT), the topology from an unconstrained total evidence analysis (TE), the topology inferred for the mtDNA alone, the nDNA alone, and the morphology alone. (B) The results of stepping-stone analysis of the full taxon set and the combined morphological (reduced 369 morphological character set), mtDNA and nDNA datasets with topology constraints reflecting the family-level relationships inferred from the unconstrained analysis of the data under the fossilized birth-death process (FBD), the PCT, enforcing *Megaladapis* to be sister to Lemuridae, and enforcing *Plesiopithecus* to not be sister to *Daubentonia.* (C) model comparison of the full taxon combined data analysis under the tip-dating (TD) and FBD models.

|  |  |  |  |
| --- | --- | --- | --- |
| **A)** |  |  |  |
| **Topology** | **likelihood** | **difference** | **BF** |
| **PCT** | **-54169.89** |  |  |
| TE | -54171.78 | 1.90 | 6.664233878 |
| MtDNA | -54213.76 | 43.87 | 1.13206E+19 |
| NDNA | -54213.76 | 43.87 | 1.13206E+19 |
| Morphology | -55698.64 | 1528.76 | >E+150 |
|  |  |  |  |
| **B)** |  |  |  |
| **Topology** | **likelihood** | **difference** | **BF** |
| **FBD constraints** | **-89598.96** | **-** |  |
| PCT | -89814.83 | 215.88 | 5.69187E+93 |
| *Megaladapis*+Lemuridae | -89881.07 | 282.11 | 3.3032E+122 |
| no *Plesiopithecus* + *Daubentonia* | -89944.50 | 345.55 | 1.1727E+150 |
| **C)** |  |  |  |
| **Model** | **likelihood** | **difference** | **BF** |
| **FBD** | **-89950.87** | - |  |
| TD | -89984.41 | 33.54 | 3.68269E+14 |

**Online Supplemental Material Table S9.**

Synapomorphies that link *Plesiopithecus teras* with *Daubentonia* and with strepsirrhines.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Character** | **Description** | **State shared** | **Posterior probability** | **State Transition** |
| Synapomorphies supporting *Plesiopithecus* + *Daubentonia* | | |  |  |
| 62 | m1 cristid obliqua terminus | runs to base of trigonid | 0.83 | 2 -> 0 |
| 70 | m1 trigonid height | trigonid and talonid of similar height | 0.88 | 2->4 |
| 73 | m2 cristid obliqua development | weak (rounded) | 0.91 | 2->0 |
| 75 | m2 cristid obliqua terminus | runs to base of trigonid | 0.84 | 2->0 |
| 79 | m2 length / m3 length | m3 slightly shorter than m2 | 0.84 | 4->6 |
| 85 | m3 hypoconulid | not lobate | 0.83 | 0->2 |
| Synapomorphies supporting *Plesiopithecus* as a strepsirrhine | | |  |  |
| 12 | lower canine cross sectional shape | mesiodistally compressed | - | 2->1 |
| 14 | lower canine height | high crowned but very procumbent | - | 0->4 |
| 32 | lower p3 root orientation | mesial root placed lateral to distal root | - | 0->2 |
| 33 | number of lower p3 roots | two |  | 2->0 |
| 36 | lower p4 cristid obliqua development | absent |  | 2->0 |

**Online Supplemental Material.** Character and state descriptions for 421 morphological characters indicating the partition (cranial, mandibular, dental, postcranial, soft tissue, physiological). Characters that were omitted based on 0 Gower dissimilarity are shaded in grey. For dental characters, lower case letters denote the mandibular teeth (e.g., m1 = lower first molar) and upper case denotes the maxillary teeth (e.g., M1 = upper first molar). Polymorphisms are coded as an intermediate state (e.g., state 1 is coded ‘0/2’, meaning individuals of a species have state 0 or state 2).

1. lower incisor # (Ross et al. 1998 character i1)

0 three in each quadrant

1 two in each quadrant

2 one in each quadrant

3 no incisors

2. lower incisor occlusal arrangement (Ross et al. 1998 character i2)

0 arcuate battery "U"

1 cusp tips staggered "V"

3. lower incisor crown height

0 low

1 0/2

2 moderate

3 2/4

4 high

4. lower incisor crown orientation

0 erect or vertical

1 0/2

2 procumbent

3 2/4

4 very procumbent

5. lower incisor root orientation (Ross et al. 1998 character i11)

0 erect or vertical

1 0/2

2 slightly procumbent

3 2/4

4 very procumbent

6. first lower incisor shape

0 spatulate

1 pointed or lanceolate

7. i1:i2 (Ross et al. 1998 character i6)

0 i1:i2 ratio <0.65

1 0/2

2 ratio=>0.65, <0.82

3 2/4

4 ratio =>0.83, <1

5 4/6

6 ratio =>1.01,<1.25

7 6/8

8 ratio =>1.25

8. i1-2 area relative to m1

0 small (=<0.69)

1 intermediate (=>0.70, =<1.07)

2 large (>0.70)

9. i1 to m1 area (Ross et al. 1998 character i19)

0 i1 area << m1 area

1 0/2

2 i1 area < or = m1 area

3 2/4

4 i1 > m1

10. i1 lingual cingulum

0 absent or weak

1 0/2

2 strong incomplete

3 2/4

4 strong complete

11. i2 cross sectional shape (Ross et al. 1998 character i8)

0 ratio =>0.64

1 <0.64

12. i2 heel development (Ross et al. 1998, character i15)

0 heel absent

1 heel present

13. female canine maximum cross-sectional area relative to first lower molar area (Ross et al. 1998 character c1, modified)

0 c1 area/m1 area < 0.40

1 0/2

2 c1 area/m1 area =>0.4, <0.8

3 2/4

4 c1 area/m1 area =>0.8, <=1.2

14. lower canine cross-sectional shape

0 rounded oval

1 mesiodistally compressed

2 buccolingually compresed

15. canine in toothcomb (modified from Marigo et al., which was modified from Ross et al. 1998 character i13)

0 lower canine not incorporated into a toothcomb

1 lower canine incorporated into toothcomb

16. lower canine height

0 low, squat

1 0/2

2 narrow,short

3 tall, at or above toothrow

4 high crowned but very procumbent

5 no lower canine

17. lower canine paracristid

0 oblique to occlusal plane

1 nearly horizontal

2 forms part of a cropping mechanism with i1-2

3 oriented in line with buccal face of adjacent incisor

18. lower canine lingual crest

0 rounded

1 0/2

2 sharp

19. orientation of lower canine root

0 oriented in line with long axis of crown

1 mesially inflected

20. lower premolar crowding (Ross et al. 1998 character p5)

0 no crowding

1 0/2

2 slightly crowded

3 2/4

4 very crowded

21. lower premolar inflation (Ross et al. 1998 character p29)

0 not basally inflated

1 0/2

2 slightly basally inflated

3 2/4

4 very basally inflated

22. premolar orientation

0 crown bases vertical

1 0/2

2 slightly oblique

3 2/4

4 strongly oblique, projecting mesially

23. p1 presence

0 present

1 0/2

2 absent

24. p2 buccal cingulum development

0 absent

1 0/2

2 incomplete, broken at protoconid and hypoconid

3 2/4

4 complete

25. p2 metaconid

0 metaconid absent or indistinct

1 0/2

2 metaconid small

3 2/4

4 large

26. p2 protoconid height and shape

0 extremely short, shorter than p3

1 0/2

2 not projecting, in line with p3

3 2/4

4 slender, projects above protoconids of p3-4

5 4/6

6 massive projects above protoconids of p3-4

27. p2 roots/presence

0 two

1 0/2

2 one

3 2/4

4 absent

28. p3:p4 area

0 <0.45

1 0/2

2 0.45-0.59

3 2/4

4 0.60-0.69

5 4/6

6 0.70-0.79

7 6/8

8 >0.80

29. p3-4 protoconid height

0 p3 much lower than p4

1 0/2

2 p3 slightly lower than p4

3 2/4

4 p3 equal in height to p4

5 4/6

6 p3 higher than p4

30. p3 entoconid and lingual talonid

0 absent

1 0/2

2 lingual talonid crest present but an entoconid does not stand out above it

3 2/4

4 entoconid is small discrete cusp

31. p3 lateral protocristid orientation

0 transverse

1 0/2

2 distal or distolingual

3 2/4

4 absent

32. p3 lingual cingulum

0 present

1 0/2

2 absent

33. p3 metaconid size

0 absent

1 0/2

2 present small

3 2/4

4 present, large

34. p3 paraconid

0 present, large

1 0/2

2 present small

3 2/4

4 negligible or absent

35. p3 root orientation (contains information similar to Ross et al. 1998 character p45)

0 mesial root placed directly mesial to distal root

1 0/2

2 mesial root placed lateral to distal root

36. p3 roots

0 one

1 0/2

2 two

37. p4:m1 area

0 <0.62

1 0/2

2 >0.63,<0.72

3 2/4

4 >0.73, <0.82

5 4/6

6 >0.83,<0.92

7 6/8

8 >0.93

38. p4 buccal cingulum

0 absent or indistinct

1 0/2

2 present and distinct

39. p4 cristid obliqua

0 absent

1 0/2

2 weak

3 2/4

4 strong

40. p4 entoconid and lingual talonid

0 absent or trace

1 0/2

2 lingual talonid crest present but entoconid does not stand out above it

3 2/4

4 entoconid is small discrete cusp

41. p4 exodaenodonty (Ross et al. 1998 character p30)

0 not exodaenodont

1 slightly exodaenodont

2 very exodaenodont

42. p4 hypocristid shearing development (Ross et al. 1998 character p27)

0 absent

1 0/2

2 weak

3 2/4

4 strong

43. p4 lateral protocristid morphology (contains information similar to Rp21-42 and Rp23-44)

0 protocristid poorly developed or absent

1 0/2

2 distolingually oriented protocristid present

3 2/4

4 trenchant and tranversely oriented protocristid present

44. height of p4 talonid

0 no aspect of talonid is at level of m1 trigonid

1 0/2

2 hypoconid extends to level of m1 trigonid

3 2/4

4 entire talonid basin extends to level of m1 trigonid

45. p4 lingual cingulum

0 absent or discontinuous

1 0/2

2 present and distinct

46. p4 md length/bl width (Ross et al. 1998 character p43)

0 <0.95

1 0/2

2 >0.96, <1.14

3 2/4

4 >1.15, <1.35

5 4/6

6 >1.36, <1.46

7 6/8

8 >1.47

47. p4 metaconid

0 absent or indistinct

1 0/2

2 small

3 2/4

4 large

48. p4 metaconid and protoconid space

0 close to protoconid

1 0/2

2 widely spaced from protoconid

49. p4 paraconid

0 p4 paraconid present and large

1 0/2

2 present small

3 2/4

4 very small/absent

50. p4 paraconid position

0 mesial to protoconid

1 mesiolingual, between proto and metaconid

2 mesial to metaconid but widely spaced from it

51. p4 postmetacristid (contains information similar to Ross et al. 1998 character p37)

0 weak or absent

1 0/2

2 moderate

3 2/4

4 very strong

52. p4 postprotocristid (Ross et al. 1998 character p36)

0 weak or absent

1 0/2

2 moderate

3 2/4

4 very strong

53. p4 premetacristid (Ross et al. 1998 character p18, modified)

0 premetacristid absent or poorly developed

1 0/2

2 premetacristid present

54. p4 root number

0 one

1 two

55. length of p4 talonid

0 =>1.27,<1.61

1 0/2

2 =>0.92,<1.27

3 2/4

4 <0.9

56. mesiodistal postion of p4 meta and protoconid

0 metaconid distal to protoconid

1 0/2

2 metaconid is transverse to protoconid

57. position of p4 hypoconid or distal terminus of p4 cristid obliqua

0 buccal to protoconid

1 0/2

2 distal to protoconid

3 2/4

4 between protoconid and metaconid

5 4/6

6 distal to metaconid

58. lower molar metastylids (Ross et al. 1998 character m12)

0 absent

1 0/2

2 trenchant postmetacristid or incipient metastylid

3 2/4

4 present, large

59. m1-2 basal cusp inflation

0 crestiform

1 0/2

2 moderate basal inflation

3 2/4

4 cusp bases bulbous

60. m1-2 buccal cingulum

0 absent to trace

1 0/2

2 partial, discontinuous

3 2/4

4 complete

61. m1-2 hypocristid development (Ross et al. 1998 character m38)

0 absent or indistinct

1 0/2

2 weak

3 2/4

4 strong

62. m1-2 talonid lingual configuration

0 open

1 0/2

2 notched lingually or closed

63. m1 area (Ross et al. 1998 character m54)

0 1.10-3.00 mm

1 0/2

2 3.10-5.00 mm

3 2/4

4 5.10-7.00 mm

5 4/6

6 7.10-9.00 mm

7 6/8

8 >9.10 mm

64. m1 cristid obliqua

0 reaches trigonid wall at point distal to protoconid

1 0/2

2 reaches trigonid wall at point distolingual to protoconid

3 2/4

4 reaches trigonid wall at a point distal to metaconid

65. m1 cristid obliqua development

0 weak (rounded)

1 0/2

2 strong(trenchant)

66. m1 cristid obliqua terminus

0 runs to base of trigonid

1 0/2

2 runs part way up the distal talonid wall

3 2/4

4 connects with protoconid tip or protocrstid

5 4/6

6 connects with metaconid

67. m1 hypoconulid

0 large

1 0/2

2 moderate

3 2/4

4 small

5 4/6

6 absent

68. m1 length/width

0 1.0-1.15

1 0/2

2 1.16-1.22

3 2/4

4 1.23-1.32

5 4/6

6 >1.33

69. m1 metaconid position

0 approximately transverse to protoconid

1 0/2

2 distal to protoconid

70. m1 paraconid

0 absent or crestiform

1 0/2

2 present, small

3 2/4

4 present, large

71. m1 paraconid position

0 mesial to protoconid

1 mesiolingual

2 1/3

3 mesial to metaconid but widely spaced

4 twinned with metaconid

72. m1 parastylid (Ross et al. 1998 character m11)

0 absent

1 0/2

2 present

73. m1 premetacristid (contains information similar to Ross et al. 1998 character m18)

0 premetacristid absent or indistinct

1 0/2

2 premetacristid present

74. m1 trigonid height

0 higher than talonid

1 0/2

2 slightly higher than talonid

3 2/4

4 trig and tal of similar height

75. hypoconulid position on m1 (contains information similar to Ross et al. 1998 character m30)

0 twinned with, or most closely situated next to, entoconid

1 0/2

2 central

3 2/4

4 closer to hypoconid than to entoconid

76. sulcus between metaconid and protoconid on m1-2 (contains information similar to Ross et al. 1998 character m22 and m23)

0 absent

1 0/2

2 present; protocristids poorly developed or absent

77. m2 cristid obliqua development

0 weak(rounded)

1 0/2

2 strong(trenchant)

78. m2 cristid obliqua orientation

0 reaches trigonid wall distal to protoconid

1 0/2

2 reaches trigonid wall distolingual protoconid

3 2/4

4 reaches trigonid distal to metaconid

79. m2 cristid obliqua terminus

0 runs to base of trigonid

1 0/2

2 runs part way up distal trigonid

3 connects to protoconid tip

4 3/5

5 connects with metaconid

80. m2 entoconid relative to hypoconid

0 mesial to hypoconid

1 0/2

2 transverse to hypoconid

3 2/4

4 distal to hypoconid

81. m2 hypoconulid position

0 twinned with or closest to entoconid

1 0/2

2 central

3 2/4

4 closer to hypoconid than to entoconid

82. m2 hypoconulid size

0 large

1 0/2

2 moderate

3 2/4

4 small

5 4/6

6 absent

83. m2 length/m3 length

0 m3 much longer than m2 (0.71-0.8)

1 0/2

2 m3 longer than m2 (0.81-0.9)

3 2/4

4 slightly longer or equal to m2 (0.91-1)

5 4/6

6 m3 slightly shorter than m2 (1.01-1.12)

7 6/8

8 m3 much shorter than m2 (=>1.13) or absent

84. m2 paraconid

0 absent

1 0/2

2 present, small

3 2/4

4 present, large

85. m2 paraconid position

0 mesial to protoconid

1 0/2

2 equidistance between proto and metaconid

3 2/4

4 mesial to metaconid but widely spaced

5 twinned with metaconid

86. m2 trigonid width (ratio of buccolingual breadths of trigonid and talonid) (Ross et al. 1998 character m6)

0 much wider than talonid (=>1.11)

1 0/2

2 width similar (<1.11,>0.90)

3 2/4

4 much narrower than talonid (=<0.90)

87. morphology of distolingual aspect of m2 (contains information similar to Ross et al. 1998 characters m26 and m41)

0 no postentoconid sulcus

1 hypoconulid closely situated next to entoconid and postentoconid sulcus present, entoconid confluent with distal talonid wall

2 distolingual fovea present, entoconid confluent with posterior talonid wall

3 distolingual fovea present, entoconid mesiodistally abbreviated and not confluent with posterior talonid wall

88. accessory cusps on distolingual aspect of m2

0 absent

1 variably present

89. m3 cristid obliqua terminus

0 absent or indistinct

1 runs to base of trigonid

2 runs part way up distal trigonid wall

3 connects with protoconid tip

4 connects with metaconid

90. m3 entoconid

0 present and distinct

1 0/2

2 greatly reduced or absent

91. m3 hypoconulid

0 lobate

1 0/2

2 not lobate

92. m3 paraconid position

0 mesial to protoconid

1 0/2

2 mesiolingual, between proto and meta

3 2/4

4 mesial to metaconid but widely spaced from it

5 4/6

6 twinned with metaconid

93. m3 paraconid size

0 absent

1 0/2

2 present, small

3 2/4

4 present large

94. m3 root number

0 one

1 two

95. m3 trigonid width (based on relative buccolingual breadths) (Ross et al. 1998 character m7)

0 =>1.20

1 0/2

2 <1.20->1.05

3 2/4

4 <1.05

96. position of m3 hypoconulid

0 centrally located

1 twinned with or next to entoconid

2 bucally located closer to hypoconid

97. molar centroconids (contains information similar to Ross et al. 1998 character m37)

0 absent

1 present

98. molar enamel crenulation

0 smooth

1 0/2

2 slightly crenulated

3 2/4

4 highly crenulated

99. interincisal diastema

0 very broad

1 narrow

100. upper incisor #

0 three

1 two

2 one

3 zero

101. I1:I2

0 areas approximately equal or I1 smaller than I2

1 0/2

2 I1 slightly arger than I2

3 2/4

4 I1 much larer than I2

102. I1:M1

0 small (<0.5)

1 moderate (0.5-.56)

2 large (>0.56)

103. I1 basal lingual cusp (RI12-125)

0 absent

1 present

104. I1 crown shape

0 spatulate

1 0/2

2 semispatulate

3 2/4

4 central occlusal cusp pointed, occlusal edges steep

105. I1-I2 buccal cingulum (RI13-126)

0 absent

1 present

106. I1I2 interincisal contact

0 absent, teeth widely spaced

1 0/2

2 present as a narrow contact

3 2/4

4 tightly packed against I1

107. I1 occlusal edge orientation

0 occlusal edge approximately orthoganol to long axis of root

1 occlusal edge wears at a steep angle to long axis of root

2 crown with pronounced mesial asymmetry

108. I1 occlusal shape (mesiodistal length/buccolingual breadth) (RI6-119)

0 rounded\_oval\_(<1.05)

1 0/2

2 buccolingually\_compressed\_(>1.05,\_<1.30)

3 2/4

4 extremely compressed\_(>1.30)

109. I2-C diastema

0 present

1 0/2

2 absent

110. I2 occlusal shape (mesiodistal length/buccolingual breadth) (RI7-120)

0 rounded oval (=<1.05)

1 0/2

2 slightly buccolingually compressed (>1.05, <1.30)

3 2/4

4 extremely\_buccolingually\_compressed\_(=>1.30)

111. C1 lingual cingulum (RC4-130)

0 weak or absent

1 0/2

2 strong

3 2/4

4 very strong

112. C1 mesial groove (females) (RC3-129)

0 shallow or absent

1 deep

113. upper canine occlusion (RC2-128)

0 wears\_against\_p1-2

1 0/2

2 wears against p2

3 2/4

4 wears\_against\_p2-3

5 4/6

6 wears against p3

114. rotation of upper canine

0 long axis oriented in line with premolar

1 slightly rotated internally

2 strongly rotated internally

3 absent

115. upper canine shape (contains information similar to RC1-127)

0 round in cross-section

1 0/2

2 oval

3 2/4

4 strongly compressed buccolingually

116. canine dimorphism (square root of male lower canine area / square root of female lower canine area)

0 <1.07

1 >=1.07, < 1.17

2 >=1.17

117. P1 presence

0 present

1 absent

118. height of P2 relative to P3

0 smaller than or subequal in height

1 0/2

2 P2 slightly taller than P3

3 2/4

4 P2 much taller than P3

119. P2:P3 area

0 much smaller than P3 (<=0.85)

1 0/2

2 app. same size, or slightly smaller than P3

3 2/4

4 larger than P3

120. P2 occlusal outline (RP6-136)

0 triangular

1 suboval with the long axis buccolingual

2 suboval with the long axis mesiodistal

3 round

121. P2 protocone (RP12-142, modified)

0 present

1 absent

122. P2 root #/presence

0 three

1 two

2 one

3 P2 absent

123. P3-4 buccal cingulum

0 absent or weak

1 0/2

2 strong

124. P3 distal crown margin

0 smoothly rounded

1 0/2

2 waisted between buccal and lingual cusps

125. P3 metacone

0 absent

1 0/2

2 present

126. P3 hypocone

0 absent

1 0/2

2 present

127. P3 protocone

0 absent

1 0/2

2 present small

3 2/4

4 present distinct

128. P3-4 trigon/talon proportions (RP8-138)

0 trigon>=talon

1 trigon<talon

129. P3 root number

0 one

1 0/2

2 two

3 2/4

4 three

5 absent

130. P4 area:M1 area

0 P4<<M1 (<=0.66)

1 0/2

2 P4<M1 (0.66-0.76)

3 2/4

4 P4=M1

5 4/6

6 P4>M1

131. P4 lingual cingulum

0 absent

1 0/2

2 present

132. P4 hypocone

0 absent

1 0/2

2 present

133. P4 metacone

0 absent

1 0/2

2 present

134. P4 metaconules

0 absent

1 0/2

2 present

135. P4 occlusal outline

0 triangular

1 suboval

2 1/3

3 squared

136. P4 pericone

0 absent

1 present

137. P4 postprotocrista

0 absent

1 0/2

2 weak, short

3 2/4

4 strong

5 4/6

6 strong, secondary postprotocrista directed towards metacone

138. P4 protocone

0 low relative to paracone

1 high rel to paracone

2 absent

139. P4 root number (RP3-133)

0 one

1 two

2 three

140. P4 styles

0 absent

1 parastyles present

2 metastyles present

3 both present

141. upper premolar paraconules (contains information similar to RP14-144)

0 absent or indistinct

1 transverse crest connecting protocone to paracone

2 present

142. M1:M2

0 M1>M2\_(<1.40,>1.0)

1 0/2

2 M1=<M2\_(=<1.0)

143. M1-2 buccal cingulum

0 absent

1 0/2

2 present poorly developed

3 2/4

4 present, distinct

5 4/6

6 extensive buccal shelf

144. M1-2 hypocone

0 large

1 0/2

2 small

3 2/4

4 absent

145. M1-2 hypocone position (RM12-162)

0 distal, slightly lingual to protocone

1 0/2

2 distal,\_far\_lingual\_to\_protocone

146. M1-2 lateral posterior transverse crista development (RM19-169)

0 sharp

1 0/2

2 indistinct

147. M1-2 metaconule size

0 absent

1 0/2

2 small

3 2/4

4 large

148. M1-2 Nannopithex fold (RM5-156)

0 absent

1 0/2

2 weak

3 2/4

4 strong

149. M1-2 paraconule

0 absent

1 0/2

2 small, moderate

3 2/4

4 large, as large as protocone

150. M1-2 paraconule position (RM15-165)

0 attached to preprotocrista

1 0/2

2 not attached to preprotocrista

151. M1-2 pericone

0 absent

1 0/1

2 present

152. M1-2 postmetaconule cristae (RM28-174)\*

0 absent or weak

1 0/2

2 strong

153. M1-2 postprotocrista

0 strong runs to base of metaconule or metacone

1 0/2

2 strong but short

3 2/4

4 absent

154. M1-2 premetaconule cristae (RM27-173)

0 absent or weak

1 strong

155. M1-2 root number (RM1-152)

0 three\_or\_more,\_three\_or\_more

1 three,\_two

156. M1-2 styles

0 absent

1 parastyles present

2 metastyles present

3 both present

157. M1-3 anterior cingulum

0 strong, compelte, long

1 0/2

2 strong, short

3 2/4

4 weak, absent

158. M1-3 lingual cingulum

0 absent

1 0/2

2 weak, broken

3 2/4

4 strong, complete

159. convex distal lobe for M1-2 hypocone

0 absent

1 0/2

2 present, distal crown margin weakly concave

3 2/4

4 present,\_distal\_crown\_margin\_deeply\_notched

160. molar protocone lingual inflation (RM31-176)

0 not inflated

1 0/2

2 slightly inflated

3 2/4

4 very inflated

161. lingual extension of M1 hypocone lobe

0 lobe does not extend lingually far beyond protocone

1 0/2

2 lobe does extend far lingually past protocone

162. M1 mesiobuccal fovea delimited by trenchant parahypocrista

0 absent

1 0/2

2 present

163. M2 buccal expansion of paracone (RM33-177)

0 no expansion

1 0/2

2 slight expansion

3 2/4

4 considerable expansion

164. M2 postmetacrista

0 short,\_indistinct,\_or\_absent

1 long,\_trenchant,\_and\_labially\_extended

165. M2 prehypocrista development (RM13-163)

0 absent

1 0/2

2 weak

3 2/4

4 strong\_--\_reaches\_to\_postprotocrista,\_encloses\_the\_talon\_lingually

166. M2 shape (bl/md)

0 very broad (>1.65)

1 0/2

2 broad\_(<1.65,>1.30)

3 2/4

4 squared\_(=<1.30)

167. shape of M2 centrocrista

0 straight, aligned with mesiodistal plane

1 0/2

2 crests are more buccally oriented, meet at an angle

3 2/4

4 crests meet at a sharp angle or form a mesostyle

168. M3 hypocone

0 absent or small

1 0/2

2 small

3 2/4

4 larage

169. M3 metacone

0 absent or very small

1 0/2

2 moderate (but smaller than paracone)

3 2/4

4 large (equal to paracone)

170. M3 paraconule (RM30-175)

0 absent

1 0/2

2 small-moderate

3 2/4

4 large

171. M3 relative to M1

0 very small (half or less of M1)

1 0/2

2 small (two thirds)

3 2/4

4 large (app same size)

172. M3 root number (RM2-153)

0 three

1 0/2

2 two

3 2/4

4 one

173. mandible fusion

0 absent

1 present

174. mandible angle

0 ventrally

1 postero-ventrally

2 hooks dorsally upward

3 widely expanded posteroventrally

4 mandibular angle very slight and low rugosity

5 0/1

175. mandibular depth (Y39,RCr45-227)

0 shallow\_(less\_than\_1.8\_times\_as\_deep\_@\_m2\_as\_md\_length\_of\_m2)

1 0/2

2 deep\_(>1.8\_times\_as\_deep\_@\_m2\_as\_md\_length\_of\_m2,\_<2.19)

3 2/4

4 very\_deep\_(more\_than\_2.2\_times\_as\_deep\_@\_m2\_as\_md\_length\_of\_m2)

176. genial fossa

0 absent

1 present

2 0/1

177. posterior surface of condylar process

0 broad and slightly angled inferiorly [funnel-like]

1 globular

2 resembling a clock-wise rotated L such that the medial and dorsal aspects are thickened and the postero-lateral aspect is indistinct

3 medio-laterally broad and dorso-ventrally short

4 posterior aspect does not show a clear articular surface

5 polymorphic

178. height of coronoid process relative to condyle (RCr43-225)

0 very high above

1 slightly above or equal

179. shape of masseteric fossa

0 shallow

1 deeply excavated

2 intermediate

3 polymorphic

180. mandibular foramina

0 absent

1 present, one under incisor

2 present multiple anterior most under incisor

3 present multiple anteriormost lateral to lateral incisor

4 present, one lateral to incisor

5 2/3

6 3/4

181. mandibular lamina

0 absent

1 slight protuberence present

2 distinct notch-like protuberance prresent

3 0/1

4 1/2

5 0/1/2

182. mandibular symphysis tubercle

0 indistinct

1 distint

2 0/1

183. condyle height relative to toothrow (RCr44-226)

0 at level of toothrow

1 slightly above

2 well above toothrow

184. facial profile (Masters & Brothers, 2002)\*

0 straight

1 0/2

2 dished

185. degree of orbital convergence (contains information similar to RCr32-214)

0 >89

1 0/2

2 90-104

3 2/4

4 105-119

5 4/6

6 120-134

7 6/8

8 >135

186. orbit size (contains information similar to RCr23-205)

0 small

1 large

2 hypertrophied

187. pronounced interorbital constriction (RCr27-209)

0 absent

1 present below CN I

188. infraorbital foramina

0 one

1 two

2 three

3 0/1

4 1/2

189. orbital orientation

0 greatly flared

1 acutely laterally flared

2 180 degrees to midline

3 acute lateral flare, dorsally oriented

190. length of infraorbital canal

0 one-third the length of rostrum

1 very short, almost just an opening through orbital rim from max to orbit

2 intermediate

3 1/2

191. ethmomaxillary fissure (Y13, modified following Cartmill 1978)

0 absent

1 present

2 0/1

192. anterior and posterior hiatus of ethmomaxillary fissure (Cartmill, 1978)

0 anterior hiatus variably present

1 0/2

2 posterior hiatus at least variably present

3 2/4

4 no hiatuses present

193. ascending wing of premaxilla

0 narrow

1 broad

2 0/1

194. rostral projection of premaxilla

0 absent

1 present

2 0/1

195. expansion of ethmoturbinals (YIP89)

0 no anteromedial expansion

1 anterior and medial expansion

196. transverse lamina/ethmoturbinal recess

0 extensive transverse lamina and ethmoturbinal recess present

1 extensive transverse lamina and ethmoturbinal recess absent

197. nasal morphology (Y62, contains information similar to R289)

0 lateral cleft between medial and lateral nasal processes

1 lateral cleft fused and rhinarium covered with dry hairy skin

198. nasal sinus swelling

0 absent

1 nasals swollen, causing inflated lacrimals

2 0/1

199. frontal-maxillary contact

0 present

1 0/2

2 absent due to intervening lacrimal

3 0/4

4 absent due to intervening premaxilla

5 absent due to orbital constriction

200. frontal-palatine contact (Cartmill 1978)

0 absent

1 present

2 0/1

201. lacrimal-palatine contact (RCr28-210)

0 present

1 no contact, separated by large front-max contact, or small os planum

2 no contact, separated by large os planum-maxillary contact

3 no contact, separated by ethmomaxillary fisure

4 0/1

202. zygomatic-lacrimal contact (Y6)

0 absent

1 present

2 0/1

203. lacrimal foramen (Y11)

0 surrounded by lacrimal bone

1 lies on lacrimal-maxillary suture

2 lac-max suture but is primarily surrounded by maxilla

204. position of lacrimal foramen (RCr30-212)

0 on\_rim,\_or\_outside\_of,\_orbit\_

1 inside the orbit

205. relation of infraorbital foramen to lacrimal (Tattersall and Schwartz 1999)

0 IOF lies in line with or posterior to LF

1 IOF anterior to LF

2 0/1

206. metopic fusion (RCr31-213)

0 absent

1 present

2 nearly fused, slight/faint suture

3 0/1

4 0/2

5 1/2

6 0/1/2

207. snout length (RCr37-219)

0 long snout

1 short snout

208. alisphenoid shape (Tattersall and Schwartz 1991)

0 concave

1 inflated

2 intermediate

3 0/2

209. ethmoid exposure in inner orbit (Cartmill 1978)

0 absent

1 present

2 0/1

210. exposure of maxilla laterally in orbital floor in superior view (Tattersall and Schwartz 1999)

0 extensively exposed laterally

1 moderately exposed

2 completely covered

3 maxilla drops off vertically in orbit so not exposed, but not covered

211. inflation of palatine in inner orbit (Tattersall and Schwartz 1999)

0 absent

1 present slight

2 present extreme

3 0/1

4 1/2

212. maxillary depth (RCr38-220)

0 deep

1 shallow

213. morphology of frontal segment of the postorbital bar (Y17, contains information similar to RCr24-25)

0 partial frontal process but no postorbital bar

1 slender and delicate

2 1/3

3 wide and robust

4 incorporated into postorbital septum

214. morphology of zygomatic portion of postorbital bar (Y18, contains information similar to RCr24-25)

0 no postorbital bar

1 slender and delicate

2 1/3

3 wide and robust

4 contributes to postorbital septum

215. inferior anterior zygomatic

0 thin and round

1 robust with flattened origin of masseter

2 intermediate

3 0/1

4 1/2

216. notch in inferior zygomatic

0 absent

1 present

2 0/1

217. nuchal crest development

0 absent

1 present weak

2 present marked

3 0/2

4 0/1

5 1/2

6 0/1/2

218. mastoid inflation (RCr3-185)

0 absent

1 present slight

2 present marked

3 0/1

4 1/2

219. parietal emissary foramina (Y33)

0 absent

1 0/2

2 present

220. sagittal cresting

0 temporal lines converge on frontal

1 0/2

2 temporal lines converge on parietals

3 temporal lines not confluent, subparallel, no crest

4 2/3

5 sag crest extensive, temporal lines converge on parietals

6 temporal lines not confluent, subparallel, no crest but temporal lines form raised distinct bony ridges

7 2/6

221. suprameatal foramen (RCr21-203)

0 absent

1 present,\_small,\_and\_in\_the\_posterior\_root\_of\_the\_zygomatic\_arch

2 present,\_large,\_and\_above\_the\_external\_auditory\_meatus

3 0/2

222. shape of external auditory meatus

0 tubular

1 0/2

2 not tubular

223. postorbital bar/septum

0 frontal/zygomatic do not contact, no bar

1 frontal/zygomatic contact form a postorbital bar no septum

2 zygomatic/frontal/parietal contact contributes to septum

224. zygomatic arch depth

0 slender

1 0/2

2 dorsoventrally deep

225. zygomaticofacial foramen

0 absent

1 present small

2 present large

3 0/1

4 1/2

226. thickness of zygomatic portion of postorbital bar (quant)

227. Frontal length (quant)

228. Nasal length (quant)

229. postorbital constriction (quant)

230. Skull height (quant)

231. Occipital length (quant)

232. basal skull length (quant)

233. breadth of central basicranium (quant)

234. choanal shape (Tattersall and Schwartz 1999)

0 broad

1 peaked

2 0/1

235. position of the anteriormost point on the palatine/maxillary suture of the palate (Y19)

0 medial to space between M1 and M2 or more posterior

1 0/2

2 medial to M1

3 2/4

4 medial to the space between P4 and M1

236. position of the posteromedial edge of the palate in relation to M3 (Y24)

0 anterior to

1 medial to

2 posterior to M3

3 0/1

4 1/2

237. maxillary palatine notch, slight groove between the maxilla and palatine at approximate level of M3

0 absent

1 present

238. position of anterior palatine foramina relative to incisors (Masters & Brothers, 2002)\*

0 foramina sit behind first incisors

1 0/2

2 foramina intrude between first incisors

239. cranial base behind hard palate

0 roof of nasal fossa and cranial base posterior to it form a continuous flat plane, the sphenoid continuing into the posterior part of the nasal fossa at the same level as sphenooccipital synchondrosis

1 roof of nasal fossa raised anterior to the level of the palatine, a steep plane forming in the sphenoid medially and palatine laterally

2 plane commences more posteriorly, such that ?post-choanal pits? are visibile posterior to the palate but mostly anterior to M3 and pterygoid plate

3 plane commences more posteriorly, at the level of the wing of the internal pterygoid plate

4 depression marked, with posterior excavation toward the occipital producing paired 'post-choanal pits'

5 0/1

6 1/2

240. posterior palatine flange

0 unextended posteriorly leaving the maxilla widely exposed in the posterior part of the orbital floor

1 short flange that extends slightly posteriorly, partly obscuring sphenopalatine foramen/maxilla

2 moderately to reach the edge of the temporal fossa

3 greatly intruding into the fossa

4 0/1

5 1/2

6 2/3

241. posterior palatine foramen

0 large, shallow and round

1 large, oval and canal-like

2 tiny/absent

3 moderate oval

4 1/3

5 0/2

6 2/3

242. number of palatine foramina

0 absent

1 one

2 two

3 three

4 polymorphic

243. posterior palatine torus

0 absent

1 present

2 0/1

244. basioccipital flange (contains information similar to RCr20-202)

0 absent or minimal

1 present,\_extensive

245. paroccipital processes

0 absent

1 0/2

2 present, small

3 2/4

4 present large

246. central stem of basicranium (D47)

0 narrow

1 broad

247. extent of contact between the lateral pterygoid plate and the bullar wall (RCr19-201)

0 slight

1 very extensive

248. lateral pterygoid-bulla

0 absent

1 abutting

2 laminar

3 0/1

4 1/2

5 0/2

6 0/1/2

249. composition of bulla

0 petrosal

1 entotympanic

250. auditory bulla deflation

0 inflated bony structures

1 deflated

251. epitympanic crest (RCr48-230)

0 absent

1 present

252. position of chorda tympani relative to m. tensor tympani (Maier, 2008)

0 ventral to m. tensor tympani

1 dorsal to m. tensor tympani

2 m. tensor tympani absent

253. position of ventral edge of tympanic bone (RCr14-196)

0 intrabullar

1 extrabullar

254. entoglenoid proess

0 indistinct absent

1 0/2

2 robust

255. encroachment of auditory bulla on pterygoid fossa (RCr17-199)

0 absent

1 present and formed by the AAC

2 present and formed by the tympanic cavity

3 1/2

256. postglenoid-auditory bullar relationship

0 not confluent

1 partially fused

2 postglenoid process fused to lateral aspect of bulla

3 0/1

4 1/2

257. postglenoid process

0 absent

1 present

258. position of postglenoid foramen relative to postglenoid process

0 posterior to postero-medial to postglenoid process

1 medial to postglenoid process, abutting bulla

2 foramen posteromedial to the postglenoid process but then surrounded by a bony lamina from the bulla

3 fusion of process and bulla extensive and foramen located medial to process such that it is totally surrounded by bone

4 0/1

5 foramen absent

259. foramen ovale

0 lateral side of lateral pterygoid

1 posterior to terminus of lat pterygoid

2 medial to lateral ptery

3 0/1

260. foramen rotundum

0 absent, confluent with superior orbital fissure

1 present

2 0/1

261. mediolateral position of carotid

0 medial

1 midline of bulla

2 lateral

3 1/2

262. basisphenoid foramen between pterygoid plate

0 absent

1 present

2 0/1

263. medial vs lateral pterygoid depth

0 shorter than

1 approximately equal to

2 deeper than

3 0/1

4 1/2

264. presence or absence of canal for internal carotid artery or nerves (RCr13-195)

0 absent

1 present

265. ventrodorsal position of posterior carotid foramen relative to fenestra cochleae (RCr7-189)

0 dorsal

1 ventral

266. rostrocaudal position of posterior carotid foramen with respect to fenestra cochleae (contains information similar to RCr8-190)

0 posterior to fenestra cochleae

1 ventral to fenestra cochleae

2 anterior to fenestra cochleae

267. morphology of promontory canal

0 absent

1 open trough

2 complete canal

268. morphology of annular bridge (RCr16-198)

0 linea semicircularis or partial anular bridge formed on an entotympanic bulla

1 linea semicircularis formed on a petrosal bulla

2 complete annular bridge

269. parotic fissure (RCr22-204)

0 patent

1 closed

270. perbullar pathway for internal carotid artery (RCr4-186)

0 absent

1 present

271. position of ectotympanic

0 ring-like ectotympanic lies within the bulla and is free at the bottom when looking inside EAM

1 ectotympanic ring-like and fused to lateral aspect of bulla

2 ectotympanic tube-like and fused to lateral aspect

272. position of infraorbital foramina (contains information similar to Y3)

0 above P2

1 0/2

2 above P3

3 2/4

4 above P4

5 4/6

6 above M1

273. position of pathway for internal carotid artery or nerve relative to fenestra cochleae (RCr9-191)

0 runs\_across\_ventral\_lip\_of\_fenestra\_cochleae,\_shielding\_it\_from\_ventral\_view

1 does not shield fenestra cochleae

274. position of pyramidal processes (RCr35-217)

0 medially placed

1 0/2

2 laterally placed

275. position of sphenopalatine foramen

0 within palatine

1 0/2

2 on ethmopalatine suture

276. transverse septum defining caudal wall of anterior accessory cavity (contains information similar to RCr1-183)

0 absent

1 present,\_forms\_lateral\_wall\_of\_AAC\_pneumatized\_from\_tympanic\_cavity

2 present,\_forms\_lateral\_wall\_of\_AAC\_pneumatized\_from\_epitympanic\_recess

277. trabeculated anterior accessory cavity

0 absent

1 present

278. shape of medial pterygoid plate (RCr36-218, contains information similar to Y22)

0 long\_medial\_pterygoid\_plate\_extending\_one-third\_to\_one\_half\_of\_the\_distance\_to\_the\_anterior\_surface\_of\_the\_bulla

1 0/2

2 short but distinct from lateral pterygoid plate for its entire dorsoventral extent

3 2/4

4 medial\_pterygoid\_plate\_entirely\_absent,\_or\_reduced\_to\_a\_low\_rugosity

279. Scapular morphology (mediolateral width/inferosuperior height)

0 <1.25

1 0/2

2 <1.5-1.25

3 2/4

4 >1.5,<1.75

5 4/6

6 >1.75

280. relative size of infra and supraspinous fossae

0 supraspinous fossa larger than infraspinous fossa

1 0/2

2 fossae roughly equivalent

3 2/4

4 infraspinous fossa approximately two times as large as the supraspinous fossa

5 4/6

6 infraspinous fossa approximately three times as large as the supraspinous fossa

281. teres major insertion

0 absent or poorly defined

1 0/2

2 elongate, well defined crest

3 2/4

4 well developed tubercle

282. shape of glenoid

0 wide and biconcave

1 anteroposteriorly oriented trough

283. shape of humeral trochlea

0 cylindrical,\_distomedial\_aspect\_of\_trochlea\_is\_straight

1 0/2

2 conical,\_medial\_aspect\_of\_trochlea\_flares\_distally

284. supinator crest

0 prominent

1 low

285. shape of dorsal aspect of distal humeral articulation (contains information similar to that of RH10-241)

0 no pronounced lips on dorsal trochlear edges

1 0/2

2 both medial and lateral edges pronounced

3 very pronounced lateral lip

286. brachialis flange

0 broad

1 0/2

2 moderate

3 2/4

4 narrow

287. morph of deltopectoral crest

0 prominent

1 0/2

2 low

288. dorsal placement of medial epicondyle

0 parallel

1 0/2

2 slight dorsal angle

3 2/4

4 large dorsal angle

289. dorsoepitrochlear fossa

0 present

1 0/2

2 small, shallow

3 2/4

4 absent

290. humeral head relative to tubercles

0 humeral head is expanded dorsal to tubercles

1 0/2

2 humeral head and tubercles are approximately equal in height

3 2/4

4 tubercles are expanded above humeral head

291. humerofemoral index

0 <59

1 0/2

2 60-69

3 2/4

4 70-79

5 4/6

6 80-89

7 6/8

8 90-100

292. length of scapular coracoid process (coracoid process length/glenoid fossa height)

0 <=0.9

1 0/2

2 >.9-1

3 2/4

4 >1, <1.1

5 4/6

6 >1.1

293. olecranon fossa morphology (Y78, contains information similar to RH12-243)

0 deep,\_open\_and\_unossified\_

1 0/2

2 moderately\_deep,\_thinly\_ossified\_and\_nearly\_transparent\_

3 2/4

4 shallow, robustly ossified

294. presence/mediolateral position entepicondylar

0 foramen is placed far proximal to trochlea

1 0/2

2 lateral wall of medial strut defining foramen is confluent with medial edge of the trochlea

3 foramen\_more\_medial,\_and\_lateral\_wall\_of\_medial\_strut\_defining\_foramen\_is\_not\_confluent\_with\_medial\_edge\_of\_the\_trochlea

4 absent

295. relative heights of medial and lateral edges of the humeral trochlea (RH2-233)

0 subequal

1 0/2

2 medial edge more flared than lateral edge

296. rotation of medial malleolus

0 none

1 0/2

2 slight

3 2/4

4 strong

297. second digit of hand

0 of normal length

1 drastically reduced

298. medial epicondyle

0 reduced

1 0/2

2 prominent

299. shape of the medial malleolar articular surface (RT5-266)

0 flat

1 0/2

2 anteriorly\_convex,\_posteriorly\_flat

3 2/4

4 all convex

300. ulnar-pisiform articulation

0 no\_ulnar-pisiform\_articulation

1 facet\_on\_pisiform\_for\_ulnar\_styloid\_process\_is\_smaller\_than,\_or\_roughly\_equal\_in\_size\_to,\_that\_for\_triquetrum

2 facet on pisiform for ulnar styloid process is much enlarged and deeply excavated

301. trochlear-capitular junction

0 trochlea\_and\_capitulum\_are\_confluent,\_with\_no\_distinct\_trochleo-capitular\_ridge

1 0/2

2 lateral aspect of trochlea is offset from capitulum by a weak ridge

3 2/4

4 lateral aspect of trochlea is separated from capitulum by a deep gutter

302. capitular shape

0 globular

1 0/2

2 ovoid

303. capitular tail

0 elongate and distinct

1 short or absent

2 1/3

3 proximodistally tall capitular flange is present

304. styloid process

0 no discernable styloid process

1 present but only moderately developed

2 long\_and\_well-developed\_

305. size of centrale, orientation of centrale trapezoid facet, and articulation with hamate (modified from RW1-249)

0 facet\_faces\_distally,\_no\_articulation\_with\_hamate

1 facet\_faces\_distoradially,\_articulation\_with\_hamate

2 centrale not present as an independent element

306. navicular length relative to width (contains information similar to RN1-278)

0 <100

1 100-150

2 >150% longer than wide

307. morphology of the naviculocuboid articulation (RN3-279)

0 cuboid facet contacts only the ectocuneiform

1 cuboid facet contacts the ectocuneiform and the mesocuneiform

308. three-pronged distal navicular articulation

0 absent

1 present

309. femoral head shape

0 spherical

1 semicylindrical

2 cylindrical

310. morphology of femoral head articular surface

0 restricted to femoral head

1 extends onto back of femoral head

311. fovea capitis

0 small insignificant

1 0/2

2 present, well developed

312. length of femoral neck

0 <=75

1 0/2

2 >75<120

3 2/4

4 >120

313. crista paratrochanterica

0 absent

1 0/2

2 present

314. anteroposterior angulation of proximal femur (contains information similar to RF8-258)

0 bent anteriorly

1 not bent anteriorly

315. triangular depression on medial side of proximal femur (Dagosto and Schmid, 1996)

0 absent

1 present

316. gluteal tuberosity

0 present, large

1 0/2

2 present, small reduced crest

3 2/4

4 absent

317. position of gluteal tuberosity

0 proximal to lesser trochanter

1 0/2

2 at level of lesser trochanter

3 2/4

4 distal to lesser trochanter

318. angle of femoral neck

0 <60

1 0/2

2 60-70

3 2/4

4 >70

319. angle of lesser trochanter (RF3-253)

0 medial\_(0-30\_degrees)

1 0/2

2 posterior\_(>30\_degrees)

320. greater trochanter

0 hook-shaped

1 0/2

2 rounded

321. intertrochanteric crest (RF10-260)

0 absent

1 present

322. knee index (contains information similar to RF5-255)

0 100 or higher

1 90-99

2 80-89

3 70-79

323. patellar margin asymmetry

0 absent

1 present

324. relative length of trochanteric fossa

0 >125 (long)

1 0/2

2 110-125 (moderate)

3 2/4

4 <110 (very short)

325. retroflexion of proximal tibial articulation

0 absent,\_articular\_surface\_of\_tibial\_condyles\_perpendicular\_to\_long\_axis\_of\_tibial\_shaft

1 moderate retroflexion present

2 proximal articular surface is strongly retroflexed

326. position of tibialis posterior groove (RT7-268)

0 on medial side of malleolus

1 0/2

2 on posterior side of malleolus

327. shape of distal surface of tibia

0 square

1 intermediate

2 triangular

328. tibial process for peroneus longus

0 absent or poorly developed

1 present and distinct

329. shape of distal tibial shaft (RT6-267)

0 no compression

1 anteroposteriorly compressed

330. fusion of tibia and fibula (RT1-263)

0 absent,\_small\_articulation

1 no\_fusion,\_moderate\_articulation

2 no fusion but extensive articulation

3 fusion

331. length of MT1 relative to MT3 (RMT2)

0 less than 70% the length of MT3

1 0/2

2 71-80%

3 2/4

4 81-90%

5 4/6

6 91-100%

7 6/8

8 >100%

332. metatarsus length (MT3 length/proximal phalanx of digit III) (contains information similar to that of RO4-285)

0 <1.0

1 0/2

2 >1.01,\_<1.5

3 2/4

4 >1.51,\_<2.0

5 4/6

6 >2.01

333. MTI distal articular surface midline keel

0 single

1 bifurcate

334. MTI distal epicondyle asymmetry in distal and dorsal views

0 medial epicondyle larger

1 epicondyles symmetrical

2 lateral epicondyle larger

335. MTI dorsal extension of proximal articular surface

0 present

1 absent

336. MTI dorsal notch located proximal to the distal articular surface in dorsal or lateral view

0 deep

1 intermediate

2 shallow

337. MTI dorsoplantar axis of head orientation relative to long axis of diaphysis in plantar view, with respect to the distal end of the bone

0 medial

1 intermediate

2 lateral

338. MTI head distal projection in dorsal view

0 short

1 long

339. MTI head shape in distal view

0 ovoid

1 rectangular

340. MTI medial proximally projecting tubercle size

0 smaller or equal in size to peroneal process

1 larger than peroneal process

341. MTI medial side of proximal articular surface with respect to the proximal end of the bone

0 rounded or weak keel

1 strong keel

342. MTI peroneal process dorsoplantar thickness in dorsolateral view with respect to the proximal end of the bone

0 flat

1 shallow

2 deep

343. MTI proximal articular surface angle, in dorsolateral view with respect to the proximal end of the bone

0 <=105

1 >105

344. MTI proximal articular surface notch location

0 absent

1 medioplantar

2 lateroplantar

345. MTI proximal articular surface orientation in proximal view (i.e., torsion)

0 dorsoventral

1 0/2

2 intermediate

3 2/4

4 mediolateral

346. MTI proximal articular surface shape in dorsolateral view

0 slight concavity

1 deep concativty, saddle-shaped

347. MTI relative dorsoplantar diaphysis midshaft breadth

0 wide

1 narrow

348. peroneal tubercle shape

0 discrete tubercle with clearly defined borders

1 tubercle gradually slopes into body (substantially longer proximodistally relative to mediolateral width)

349. position of distal terminus of ectal facet relative to anterior calcaneal segment

0 dorsally positioned on body

1 intermediate condition

2 sunk into body plantarly

350. position of groove for flexor fibularis (RA1-269)

0 lateral to astragalar trochlea

1 plantar to astragalar trochlea

351. position of peroneal process relative to sustentaculum

0 below

1 lower half

2 upper half

352. morphology of groove for flexor fibularis under sustentaculum

0 no noticeable groove present

1 deep medially with distinct groove or wall

353. size of lateral tubercle buttressing flexor fibularis

0 poorly developed

1 0/2

2 small

3 2/4

4 large

354. level of distal plantar tubercle (tubercle to cuboid facet/calcaneal length)

0 distal, near cuboid facet (0-0.19)

1 more proximal (>0.20)

355. fibular facet angle

0 79 degrees or less

1 0/2

2 80-89

3 2/4

4 90-99

5 4/6

6 100-109

7 6/8

8 110+

356. foot axis (R01-282)

0 mesaxonic

1 paraxonic

2 ectaxonic

357. concavity of cuboid facet

0 flat (>=160

1 shallow (>=150, <160

2 deep (<150)

358. development of distal plantar tubercle on calcaneus

0 small,\_poorly\_developed

1 0/2

2 well-developed

359. dorsal extension of bone supporting cuboid facet

0 absent

1 present

360. dorsal heel process

0 tucked under ectal facet in lateral view

1 level with ectal facet in lateral view

2 projects dorsal to ectal facet

361. ectal facet flange development

0 absent

1 intermediate

2 present

362. ectal facet radius of curvature

0 <120 degrees

1 >=120 degrees

363. shape of medial edge of sustentaculum in plantar view

0 triangular or beak-like

1 rounded

364. relative length of ectal facet (ectal facet width/ectal facet length)

0 <50

1 0/2

2 >50,\_<60

3 2/4

4 >60

365. facet anterior to the anterior extension of the sustentacular facet (navicular or otherwise)

0 prominent

1 very small or absent

366. form of medial margin between sustentaculum and anterior calcaneal facet (viewed dorsally)

0 waisted into body

1 relatively linear medial margin

367. angle between sustentaculum and ectal facet

0 <140

1 140-160

2 >160-<180

3 >180

368. position of the peroneal tubercle relative to ectal facet (RC2-276)

0 maximum width of peroneal tubercle is placed distal to distal terminus of ectal facet

1 maximum width of peroneal tubercle is placed approximately at the distal terminus of the ectal facet

2 maximum width of peroneal tubercle is placed proximal to the distal terminus of the ectal facet, closer to the distal terminus of the ectal facet than the proximal

3 maximum width of peroneal tubercle is placed proximal to distal terminus of the ectal facet, closer to the proximal terminus of the ectal facet than distal

369. lateral process of entocuneiform (RE2-281)

0 small

1 hypertrophied

370. nail/claw on second pedal digit (Y82,RO2-283)

0 nail present

1 claw present

371. prehallux

0 present

1 absent

372. shape of intertubercular sulcus (contains information similar to RH15-246)

0 narrow and deep

1 0/2

2 narrow and shallow

3 2/4

4 shallow and wide

373. relative width of capitulum (contains information similar to RH5-236)

0 ventral\_articular\_width/capitular\_width\_>2.5

1 0/2

2 <2.5,\_>2.0

3 2/4

4 <2.0

374. number of "peaks" on calcaneal peroneal tubercle

0 single tubercle present

1 two "peaks" present

375. proximal calcaneal elongation (length from proximal border of ectal facet to proximal end of calcaneus/calcaneus length) from Gebo et al. 2001

0 .10-.15

1 0/2

2 .16-.20

3 2/4

4 .21-.25

5 4/6

6 .26-.30

7 6/8

8 >.31

376. orientation of long axis of calcaneocuboid joint

0 dorsoventral

1 oblique

2 mediolateral

377. posterior (plantar) calcaneal bowing

0 absent

1 present, moderately developed

2 present, extreme bowing

378. mediolateral bowing of calcaneal tuber

0 absent

1 present, moderate bowing

2 present, extreme bowing

379. anterior calcaneal elongation (length of calcaneus distal to ectal facet/total calcaneal length x 100) (modified from RC1-275, scoring from D22 addendum)

0 >30,<40

1 0/2

2 >41,<50

3 2/4

4 >51,<60

5 4/6

6 >61,<70

7 6/8

8 >71

380. bony distinction between plantar edge of ectal facet and body

0 no well-defined border

1 well-defined border present

381. calcaneal sustentacular facet configuration

0 single continuous sustentacular facet present

1 0/2

2 separate anterior and posterior sustentacular facets present

382. calcaneal width/length

0 <35

1 0/2

2 >35<40

3 2/4

4 40-45

5 4/6

6 45-50

7 6/8

8 >50

383. calcaneocuboid joint shape

0 oval

1 fan-shaped noth is articular

2 fan-shaped notch is non-articular

3 oval but longest in dorsoplantar direction

384. shape of tuber calcanei

0 oval

1 square/rectangular

2 uneven walls/trapezoidal

3 proximally projecting medial wall

385. size of tuber calcanei

0 relatively small (sliver, oval, no clear insertion for tendo calcanei)

1 medium (large in one direction, insertion for tendo calcanei present but not robust)

2 relatively large

386. size of calcaneal peroneal tubercle (100\*widest point on peroneal tubercle to ectal facet, measured perpendicular to long axis of bone/calcaneal width)

0 massive, extends far laterally (>=21)

1 medium (<21)

2 highly reduced or too small to measure

387. astragalar body height

0 <100

1 0/2

2 100-120

3 2/4

4 >120

388. astragalar cotylar fossa (Seiffert & Simons, 2001)

0 shallow

1 0/2

2 moderate

3 2/4

4 deep,\_medially\_projecting

389. astragalar neck angle

0 <20 degrees

1 0/2

2 20-30 degrees

3 2/4

4 >30 degrees

390. astragalar neck length

0 <100

1 0/2

2 >100<120

3 2/4

4 >120

391. astragalar width/astragalar length

0 <50

1 0/2

2 >50<60

3 2/4

4 >60<70

5 4/6

6 >70

392. elevated lateral trochlear margin of astragalus

0 absent

1 0/2

2 present

393. plantarflexion of astragalar head\*

0 absent

1 present

394. relative astragalar head width

0 head\_width/head\_height\_x\_100\_<115

1 0/2

2 head\_width/head\_height\_x\_100\_>115,\_<130

3 2/4

4 head\_width/head\_height\_x\_100\_>130

395. posterior astragalar shelf (D20; contains information similar to RA4-272)

0 absent

1 0/2

2 present small

3 2/4

4 present large

396. shape of proximal aspect of medial tibial facet on astragalus (RA6-274, modified)

0 dorsoventrally\_deep,\_extends\_to\_plantar\_aspect\_of\_astragalus

1 0/2

2 dorsoventrally\_restricted,\_confined\_to\_dorsal\_half\_of\_astragalar\_body

397. number of thoraco-lumbar vertebrae

0 17 or fewer

1 0/2

2 18

3 2/4

4 19

5 4/6

6 20

7 6/8

8 21 or more

398. anticlinal vertebra

0 T10

1 T11

2 T12

3 L1

4 no anticlinal vertebra

399. spinous process reduction on thoraco-lumbar vertebrae

0 distinct, elongate processes, no reduction

1 reduced and indistinct

400. transpedicular foramina

0 absent

1 present

401. shape of manubrium

0 sternal head elongate

1 shortened and triangular

402. sacral vertebrae

0 2-3

1 4-5

2 >5

403. pubic bone flaring

0 absent

1 present

404. ilium shape

0 narrow

1 0/2

2 markedly flared

405. anterior inferior iliac spine

0 tuberosity not expressed

1 small tubercle

2 well developed tuberosity present

406. ischial flaring

0 absent

1 present

407. tail length (Y86)

0 long tail

1 reduced

2 absent

408. ascorbic acid synthesis

0 absent

1 present

409. tapetum lucidum (Y59, R290)

0 present

1 absent

410. retinal fovea (Y60, R288)

0 absent

1 present

411. allantois development (KPL6)

0 large,\_vesicular

1 rudimentary

412. amniotic cavity (KPL3)

0 primordial cavity absent

1 primordial cavity present

413. presence/absence of choriovitelline placenta (Y58, KPL4)

0 choriovitelline placenta

1 no choriovitelline placenta

414. embryonic body stalk (KPL5)

0 absent

1 present

415. epitheliochorial vs. hemochorial placentation (KPL1)

0 epitheliochorial

1 diffuse,\_hemochorial

416. ascending pharyngeal artery (Y52)

0 if present is poorly developed

1 present and enlarged

417. blastocyst attachment (KPL2)

0 invasive

1 non-invasive

418. stapedial

0 extremely small undetectable

1 present

419. relative size of stapedial and promontory arteries (contains information similar to RCr11-193)

0 equal size

1 stapedial smaller than promontory

2 stapedial absent or reduced

3 promontories present, stapedials larger

4 both absent

5 1/2

6 1/3

420. retia mirabilia of the proximal limb vessels (YIP87)

0 absent

1 present

421. vascular plexus associated with ascending pharyngeal artery (Y53)

0 absent

1 present