Zoological Research

Supplementary Materials

Improved mammalian family phylogeny using gap-rare multiple sequence alignment: A timetree of extant placentals and marsupials

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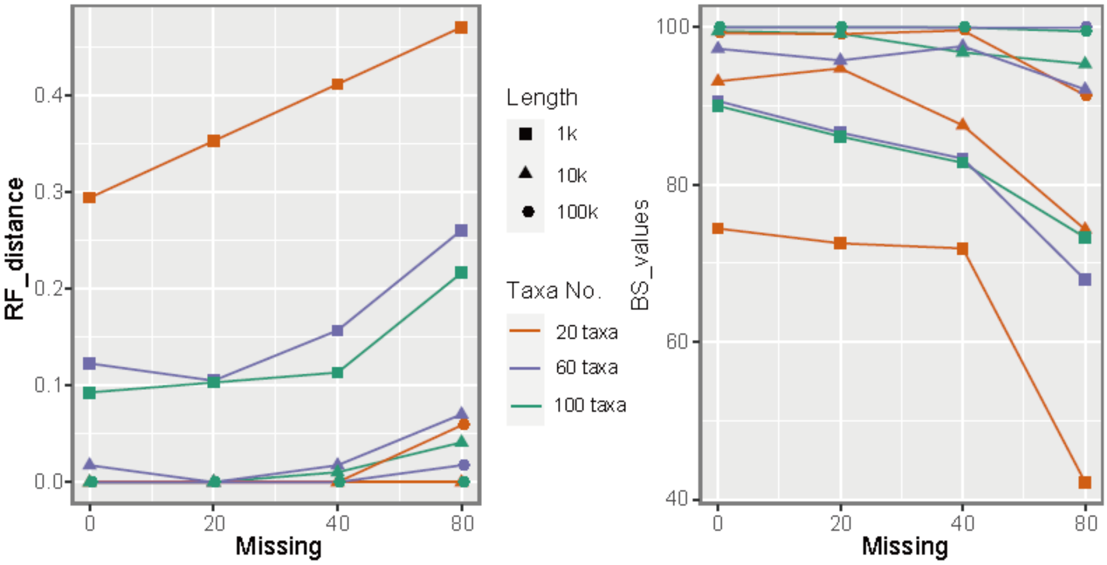
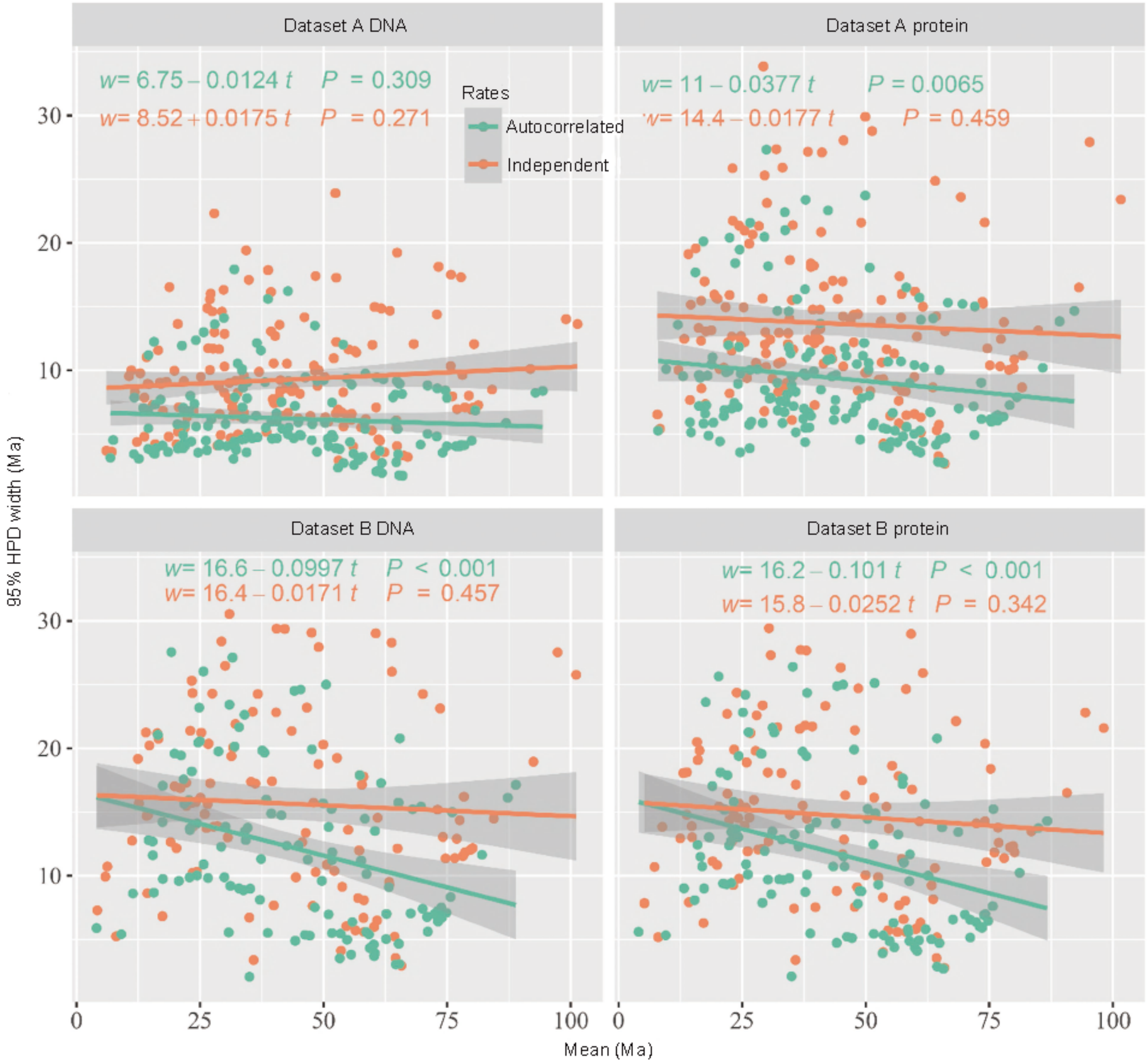


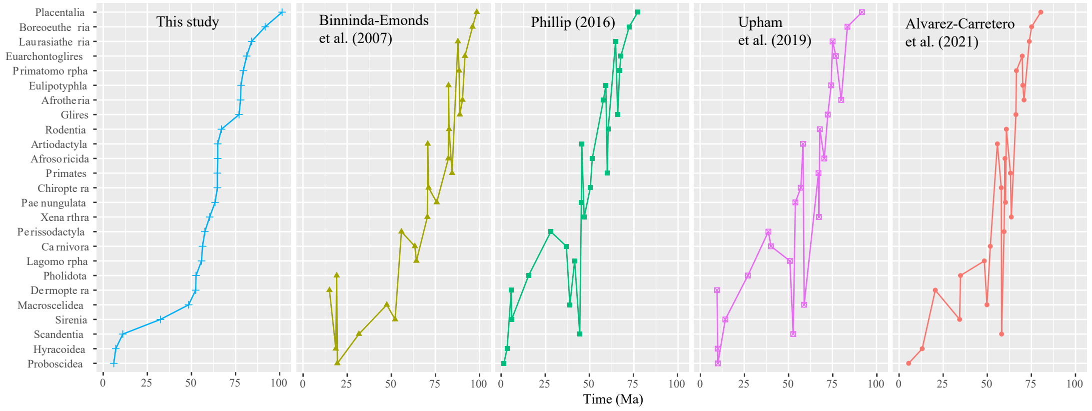
Supplementary Figure S1 RF distance and BS value under different percentages of missing data

Different line colors indicate different number of taxa and different shape indicates different alignment lengths.

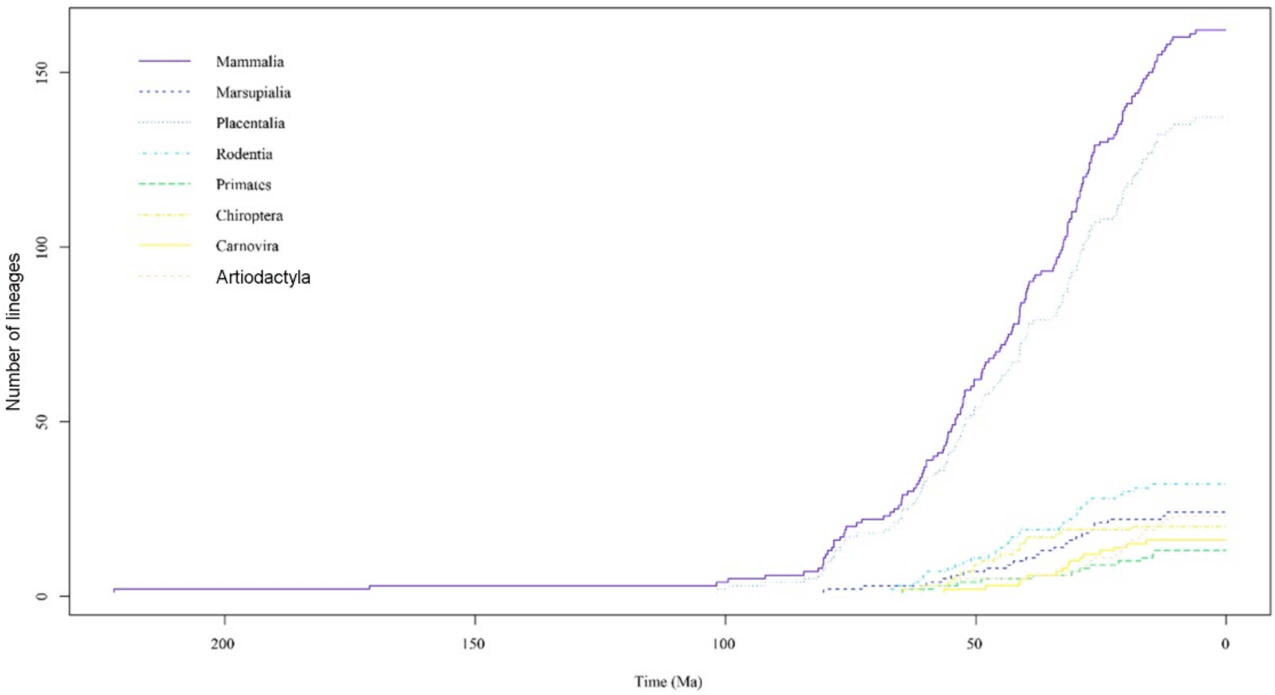


Supplementary Figure S2 Posterior 95% HPD width plots against mean posterior divergence times for two datasets under AR and IR clocks

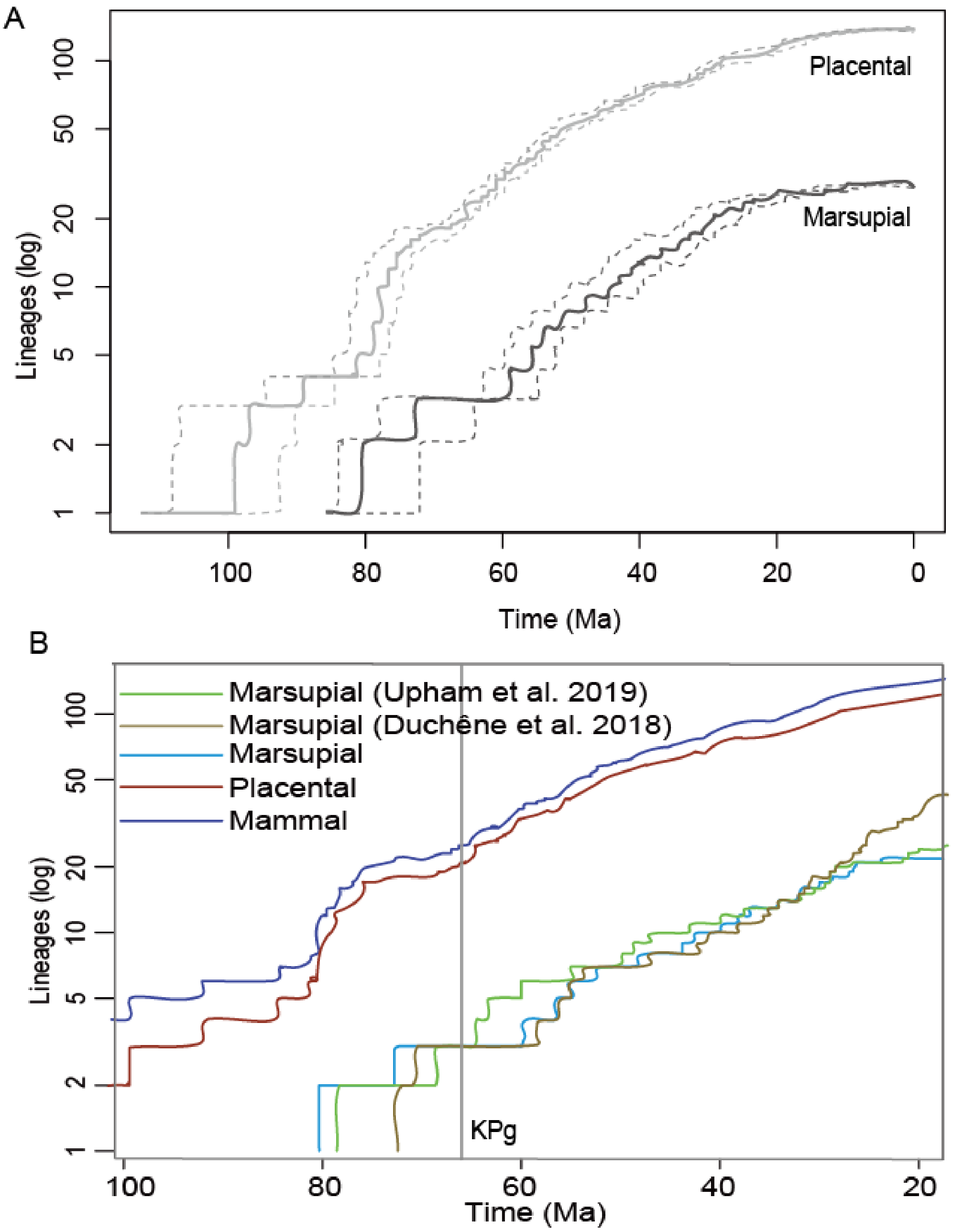
Fitted solid line with confidence interval (CI) (gray shadow) is the regression between posterior mean and 95% HPD width.



Supplementary Figure S3 Vital internode divergence time comparison between this and other studies

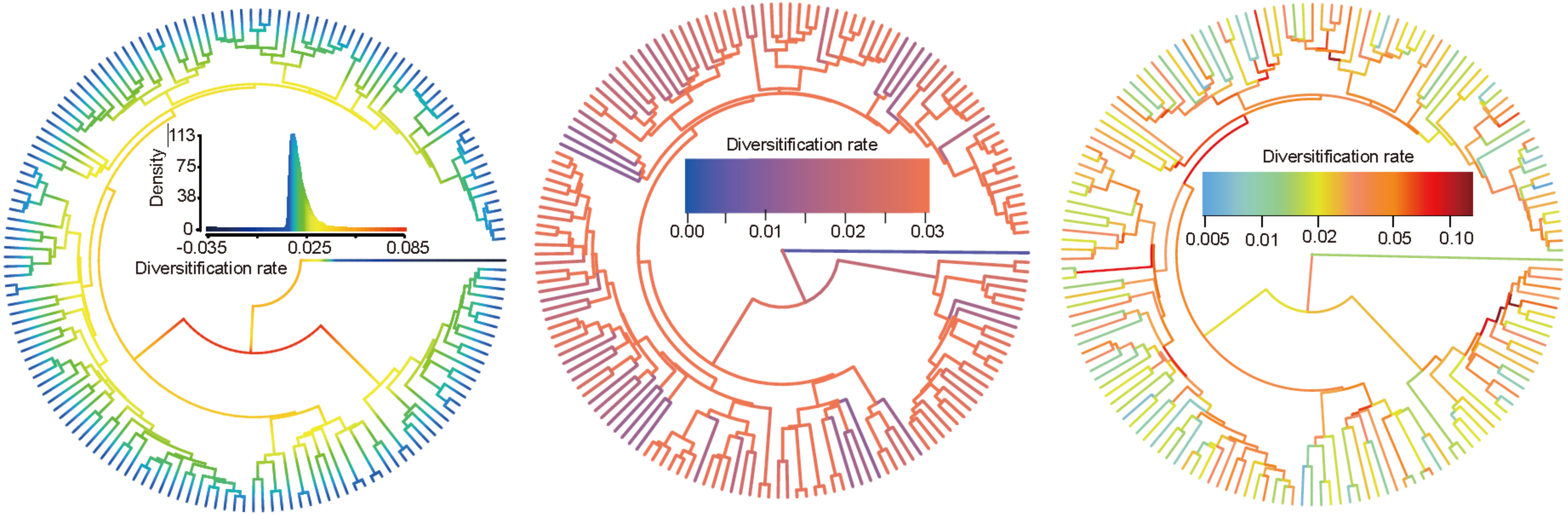


Supplementary Figure S4 Lineage-through-time (LTT) plot of mammalian and large group lineages
Different colors indicate timetree of different mammalian lineages.

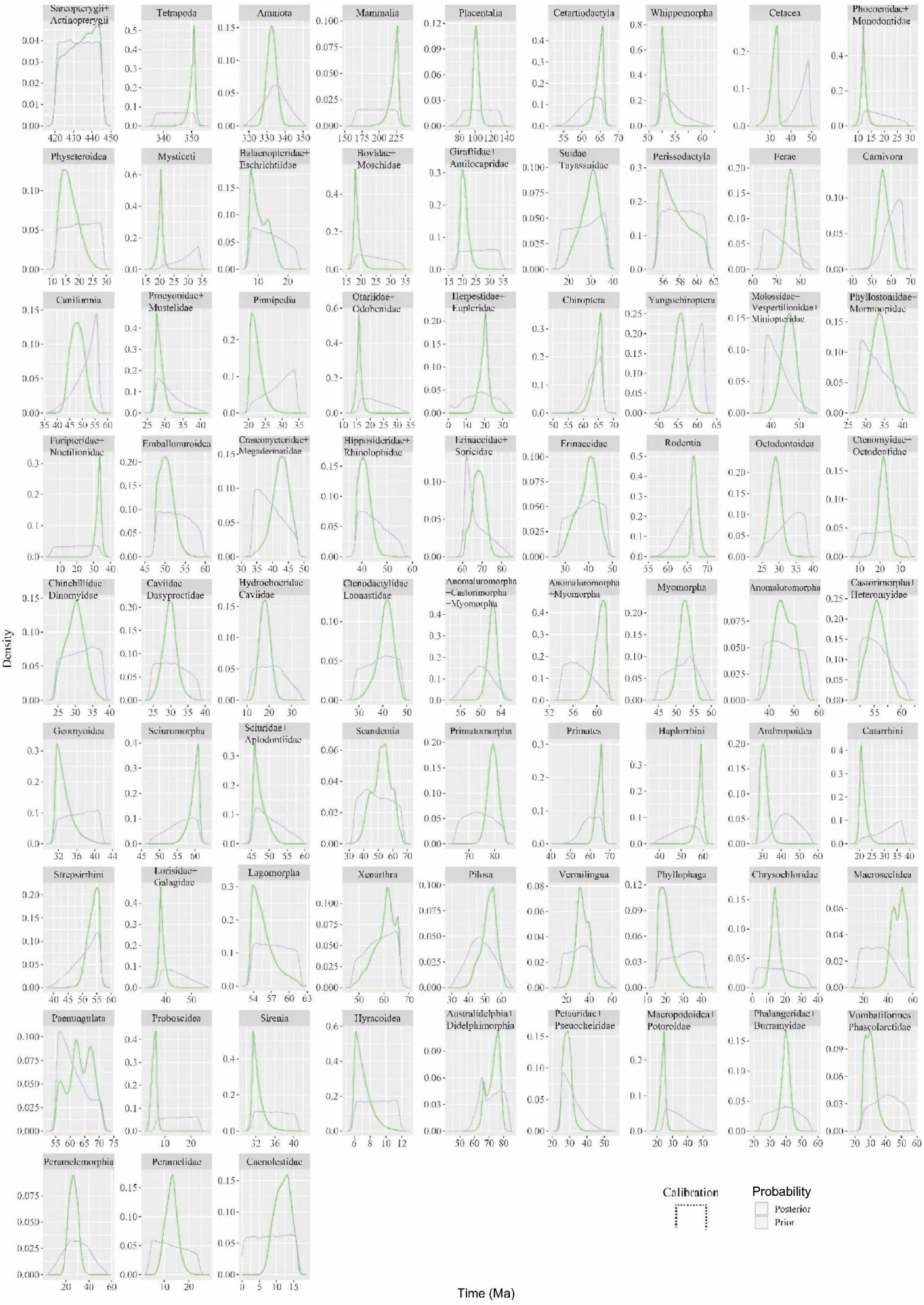


Supplementary Figure S5 Lineage-through-time (LTT) plots of placentals and marsupials

A: Mean and 95% CI of LTTs of placentals and marsupials. B: LTT plots for mammals, placentals, and marsupials with different sources.

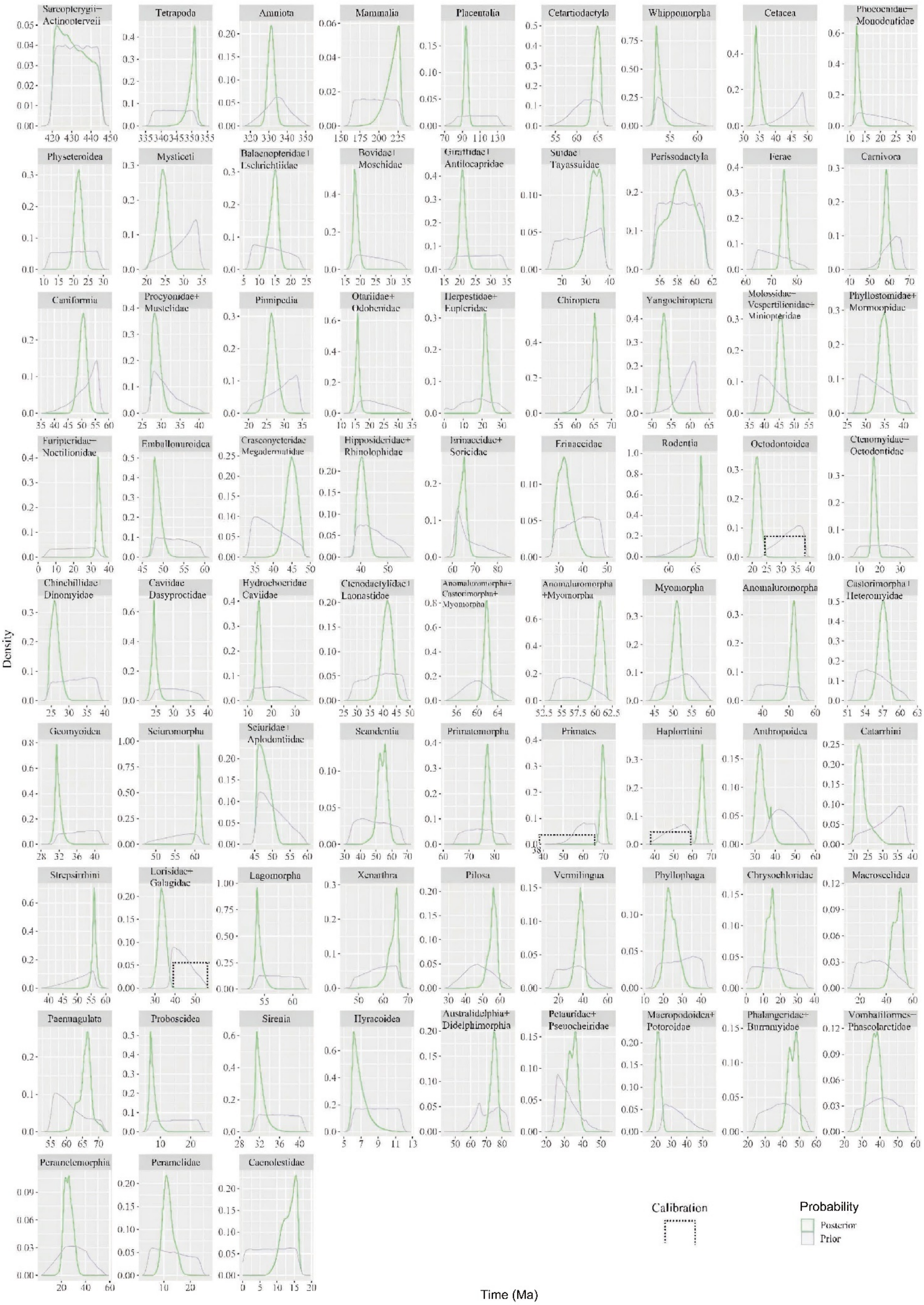


Supplementary Figure S6 Branch-specific rate of mammalian lineages inferred from BAMMtools (left), RevBayes (middle), and RPANDA (rights)
Diversification rate is represented by varying colors. Central left portion displays density of the diversification rate, while color gradient in the central and right portions indicates diversification rate from low to high..


Sarcopterygii+Actinopterygii
Tetrapoda
Amniota
Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae+Monodontidae
Physeteroidea
Mysticeti
Balaenopteridae+Eschrichtiidae
Bovidae–Moschidae
Giraffidae+Antilocapridae
Suidae–Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Procyonidae+Mustelidae
Pinnipedia
Otariidae–Odobenidae
Herpestidae+Eupleridae
Chiroptera
Yangochiroptera
Molossidae–Vespertilionidae+Miniopteridae
Phyllostomidae–Mormoopidae
Furipteridae–Noctilionidae
Emballonuroidea
Craseonycteridae+Megadermatidae
Hipposideridae+Rhinolophidae
Erinaceidae+Soricidae
Erinaceidae
Rodentia
Octodontoidea
Ctenomyidae–Octodontidae
Chinchillidae–Dinomyidae
Caviidae–Dasyproctidae
Hydrochoeridae–Caviidae
Ctenodactylidae–Laonastidae
Anomaluromorpha–Castorimorpha–Myomorpha
Anomaluromorpha+Myomorpha
Myomorpha
Anomaluromorpha
Castorimorpha+Heteromyidae
Geomyoidea
Sciuromorpha
Sciuridae+Aplodontiidae
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Catarrhini
Strepsirrhini
Lorisidae–Galagidae
Lagomorpha
Xenarthra
Pilosa
Vermilingua
Phyllophaga
Chrysochloridae
Macroscelidea
Paenungulata
Proboscidea
Sirenia
Hyracoidea
Australidelphia+Didelphimorphia
Petauridae+Pseudocheiridae
Macropodoidea+Potoroidae
Phalangeridae+Burramyidae
Vombatiformes+Phascolarctidae
Peramelemorphia
Peramelidae
Caenolestidae
Density
Time (Ma)
Calibration
Probability
Posterior
Prior

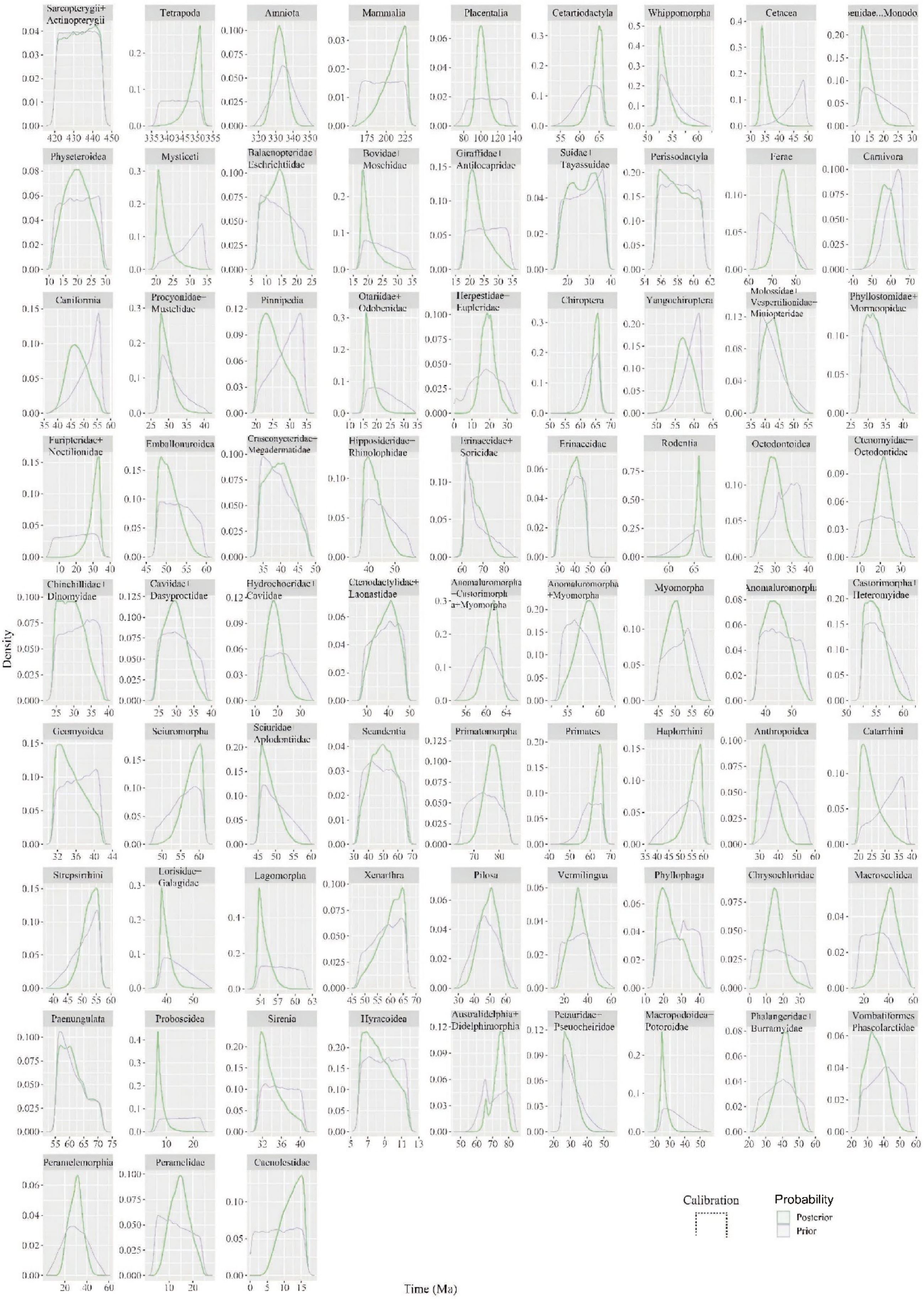
Supplementary Figure S7 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from DNA alignments of Dataset A under an IR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.


Sarcopterygii–Actinopterygii
Tetrapoda
Amniota
Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae–Monodontidae
Physeteroidea
Mysticeti
Balaenopteridae+Eschrichtiidae
Bovidae+Moschidae
Giraffidae+Antilocapridae
Suidae+Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Procyonidae+Mustelidae
Pinnipedia
Otariidae+Odobenidae
Herpestidae+Eupleridae
Chiroptera
Yangochiroptera
Molossidae–Vespertilionidae+Miniopteridae
Phyllostomidae+Mormoopidae
Furipteridae–Noctilionidae
Emballonuroidea
Craseonycteridae+Megadermatidae
Hipposideridae+Rhinolophidae
Erinaceidae+Soricidae
Erinaceidae
Rodentia
Octodontoidea
Ctenomyidae–Octodontidae
Chinchillidae+Dinomyidae
Caviidae+Dasyproctidae
Hydrochoeridae+Caviidae
Ctenodactylidae+Diatomyidae
Anomaluromorpha+Castorimorpha+Myomorpha
Anomaluromorpha+Myomorpha
Myomorpha
Anomaluromorpha
Castorimorpha+Heteromyidae
Geomyoidea
Sciuromorpha
Sciuridae+Aplodontiidae
Scandentia
Primatomorpha
Primates
Haplorhini
Anthropoidea
Catarrhini
Strepsirrhini
Lorisidae+Galagidae
Lagomorpha
Xenarthra
Pilosa
Vermilingua
Phyllophaga
Chrysochloridae
Macroscelidea
Paenungulata
Proboscidea
Sirenia
Hyracoidea
Australidelphia+Didelphimorphia
Petauridae+Pseudocheiridae
Macropodoidea+Potoroidae
Phalangeridae+Burramyidae
Vombatiformes–Phascolarctidae
Peramelemorphia
Peramelidae
Caenolestidae
Density
Time (Ma)
Calibration
Probability
Posterior
Prior

Supplementary Figure S8 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from DNA alignments of Dataset A under an AR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.


Sarcopterygii+ Actinopterygii
Tetrapoda
Amniota
Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
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Mysticeti
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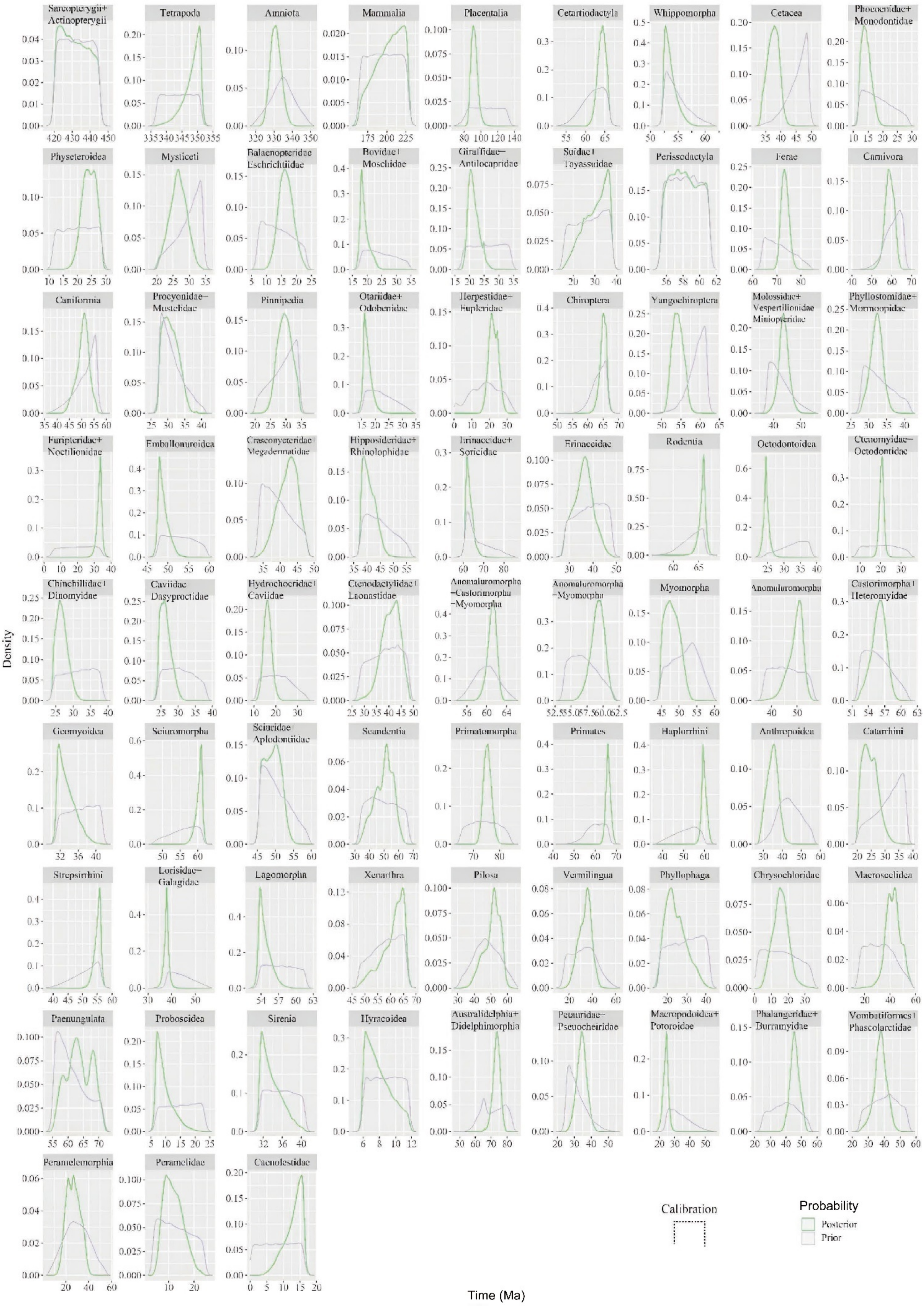
Bovidae+ Moschidae
Giraffidae+ Antilocapridae
Suidae+ Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Procyonidae–Mustelidae
Pinnipedia
Otariidae+ Odobenidae
Herpestidae–Eupleridae
Chiroptera
Yangochiroptera
Molossidae+ Vespertilionidae–Miniopteridae
Phyllostomidae+ Mormoopidae
Furipteridae+ Noctilionidae
Emballonuroidea
Craseonycteridae–Megadermatidae
Hipposideridae–Rhinolophidae
Erinaceidae+ Soricidae
Erinaceidae
Rodentia
Octodontoidea
Ctenomyidae–Octodontidae
Chinchillidae+ Dinomyidae
Caviidae+ Dasyproctidae
Hydrochoeridae+ Caviidae
Ctenodactylidae+ Laonastidae
Anomaluromorpha –Castorimorpha–Myomorpha
Anomaluromorpha +Myomorpha
Myomorpha
Anomaluromorpha
Castorimorpha+ Heteromyidae
Geomyoidea
Sciuromorpha
Sciuridae Aplodontiidae
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Catarrhini
Strepsirrhini
Lorisidae–Galagidae
Lagomorpha
Xenarthra
Pilosa
Vermilingua
Phyllophaga
Chrysochloridae
Macroscelidea
Paenungulata
Proboscidea
Sirenia
Hyracoidea
Australidelphia+ Didelphimorphia
Petauridae–Pseudocheiridae
Macropodoidea–Potoroidae
Phalangeridae+ Burramyidae
Vombatiformes Phascolarctidae
Peramelemorphia
Peramelidae
Caenolestidae
Density
Time (Ma)
Calibration
Probability
Posterior
Prior

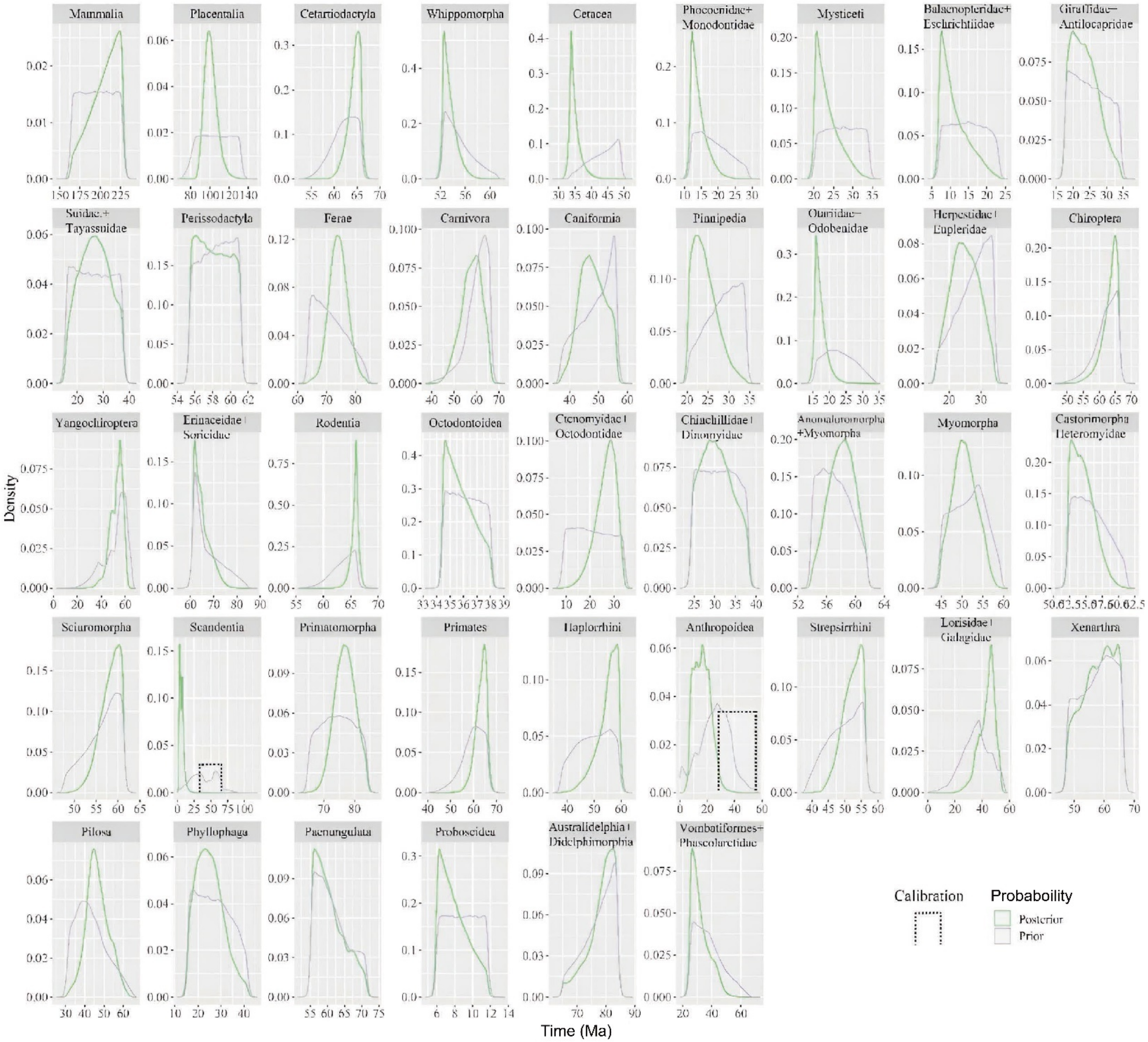
Supplementary Figure S9 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from Dataset A protein sequences under an IR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.


Sarcopterygii+ Actinopterygii
Tetrapoda
Amniota
Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae+ Monodontidae
Physeteroidea
Mysticeti
Balaenopteridae Eschrichtiidae
Bovidae+ Moschidae
Giraffidae– Antilocapridae
Suidae+ Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Procyonidae– Mustelidae
Pinnipedia
Otariidae+ Odobenidae
Herpestidae– Eupleridae
Chiroptera
Yangochiroptera
Molossidae+ Vespertilionidae Miniopteridae
Phyllostomidae+ Mormoopidae
Furipteridae+ Noctilionidae
Emballonuroidea
Craseonycteridae+ Megadermatidae
Hipposideridae+ Rhinolophidae
Erinaceidae+ Soricidae
Erinaceidae
Rodentia
Octodontoidea
Ctenomyidae– Octodontidae
Chinchillidae+ Dinomyidae
Caviidae Dasyproctidae
Hydrochoeridae+ Caviidae
Ctenodactylidae+ Laonastidae
Anomaluromorpha –Castorimorpha –Myomorpha
Anomaluromorpha –Myomorpha
Myomorpha
Anomaluromorpha
Castorimorpha+ Heteromyidae
Geomyoidea
Sciuromorpha
Sciuridae+ Aplodontiidae
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Catarrhini
Strepsirrhini
Lorisidae– Galagidae
Lagomorpha
Xenarthra
Pilosa
Vermilingua
Phyllophaga
Chrysochloridae
Macroscelidea
Paenungulata
Proboscidea
Sirenia
Hyracoidea
Australidelphia+ Didelphimorphia
Petauridae– Pseudocheiridae
Macropodoidea+ Potoroidae
Phalangeridae+ Burramyidae
Vombatiformes+ Phascolarctidae
Peramelemorphia
Peramelidae
Caenolestidae
Density
Time (Ma)
Calibration
Probability
Posterior
Prior

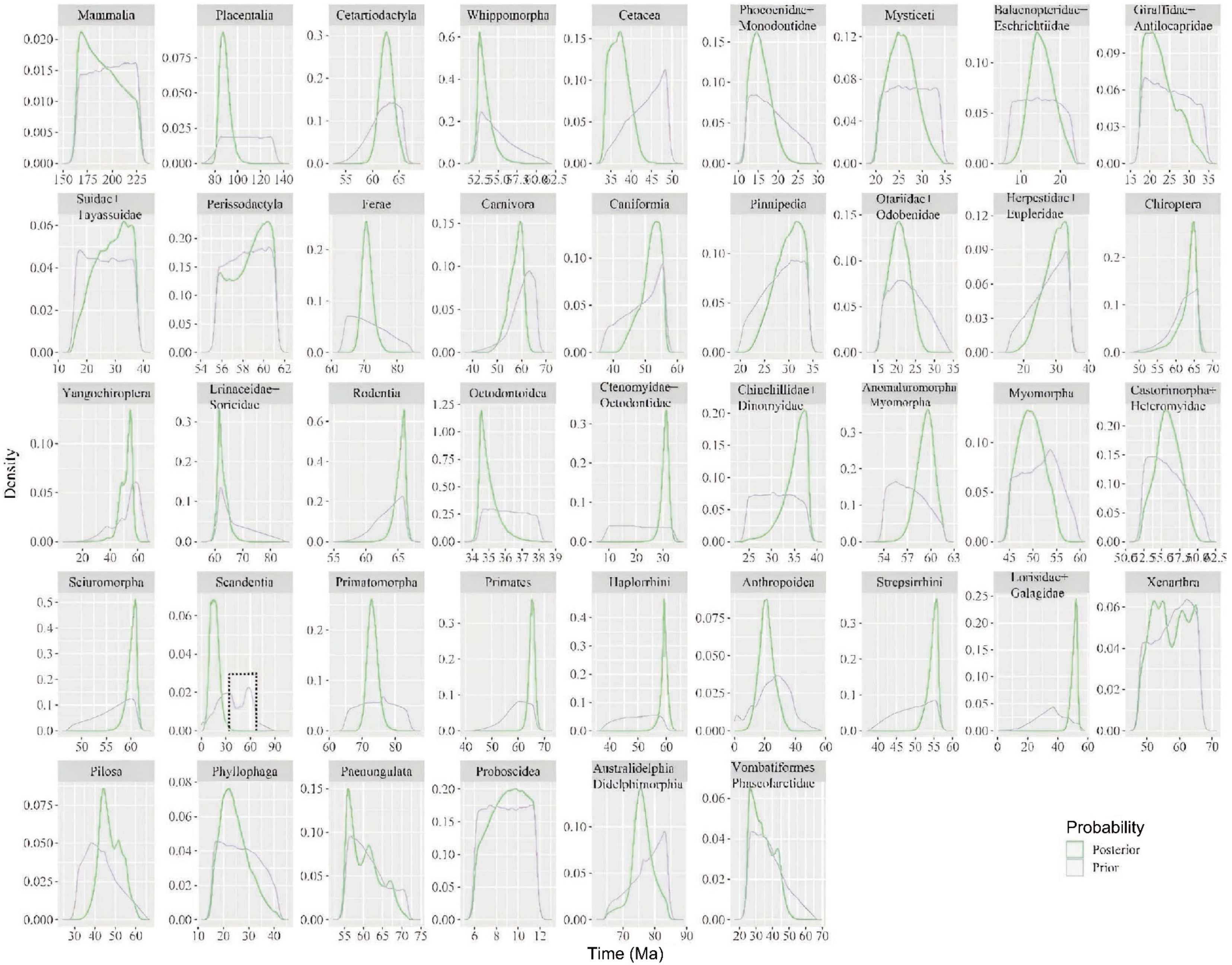
Supplementary Figure S10 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from protein sequences of Dataset A under an AR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.


Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae+ Monodontidae
Mysticeti
Balaenopteridae+ Eschrichtiidae
Giraffidae− Antilocapridae
Suidae+ Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Pinnipedia
Otariidae− Odobenidae
Herpestidae+ Eupleridae
Chiroptera
Yangochiroptera
Erinaceidae+ Soricidae
Rodentia
Octodontoidea
Ctenomyidae+ Octodontidae
Chinchillidae+ Dinomyidae
Anomaluromorpha +Myomorpha
Myomorpha
Castorimorpha Heteromyidae
Sciuromorpha
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Strepsirrhini
Lorisidae+ Galagidae
Xenarthra
Pilosa
Phyllophaga
Paenungulata
Proboscidea
Australidelphia+ Didelphimorphia
Vombatiformes+ Phascolarctidae
Density
Time (Ma)
Calibration
Probaboility
Posterior
Prior

Supplementary Figure S11 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from DNA sequences of Dataset B under an IR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.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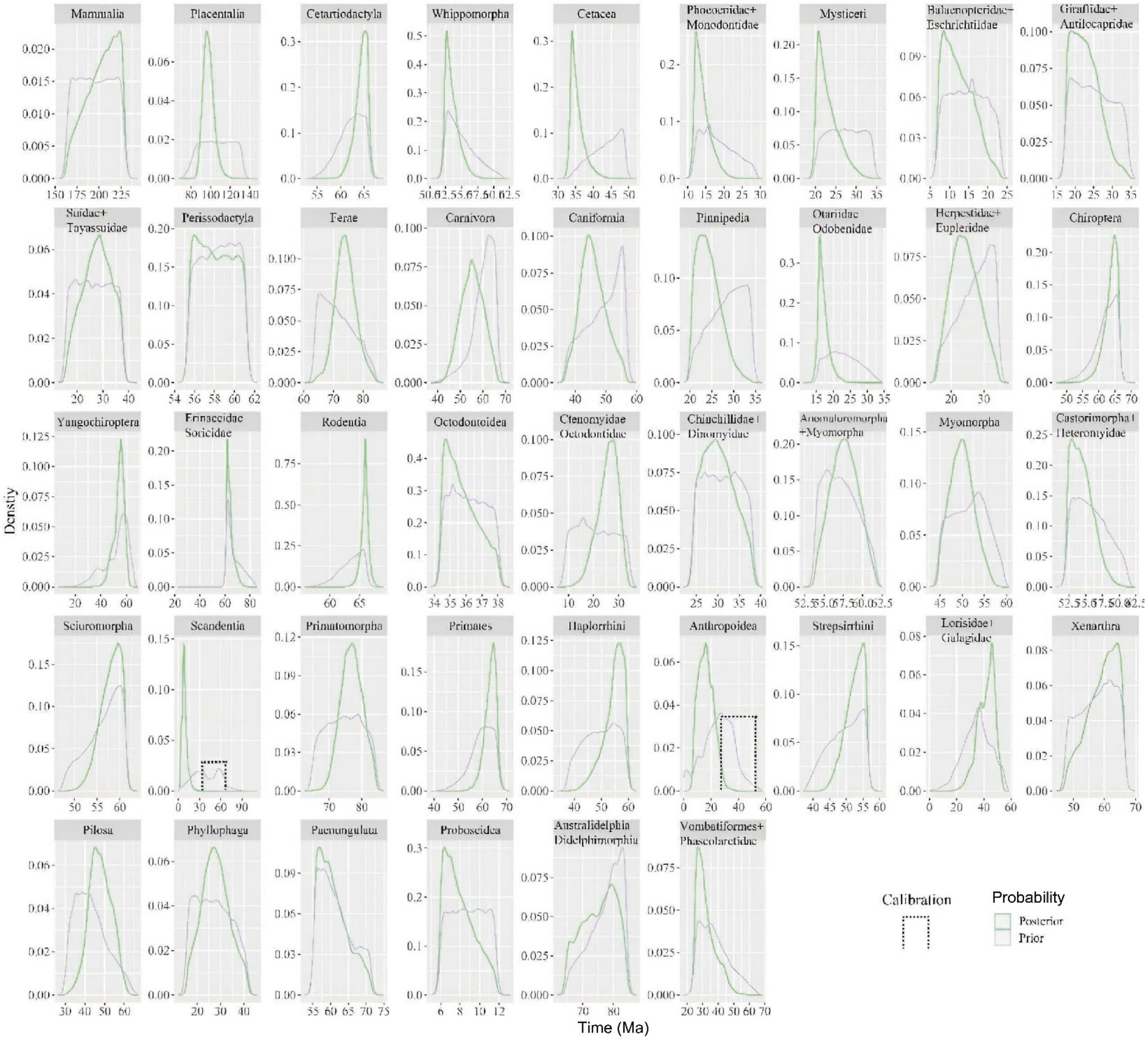
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae–Monodontidae
Mysticeti
Balaenopteridae–Eschrichtiidae
Giraffidae–Antilocapridae
Suidae+Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Pinnipedia
Otariidae+Odobenidae
Herpestidae+Eupleridae
Chiroptera
Yangochiroptera
Erinaceidae–Soricidae
Rodentia
Octodontoidea
Ctenomyidae–Octodontidae
Chinchillidae+Dinomyidae
Anomaluromorpha+Myomorpha
Myomorpha
Castorimorpha+Heteromyidae
Sciuromorpha
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Strepsirrhini
Lorisidae+Galagidae
Xenarthra
Pilosa
Phyllophaga
Paenungulata
Proboscidea
Australidelphia Didelphimorphia
Vombatiformes Phascolarctidae
Density
Time (Ma)
Probability
Posterior
Prior

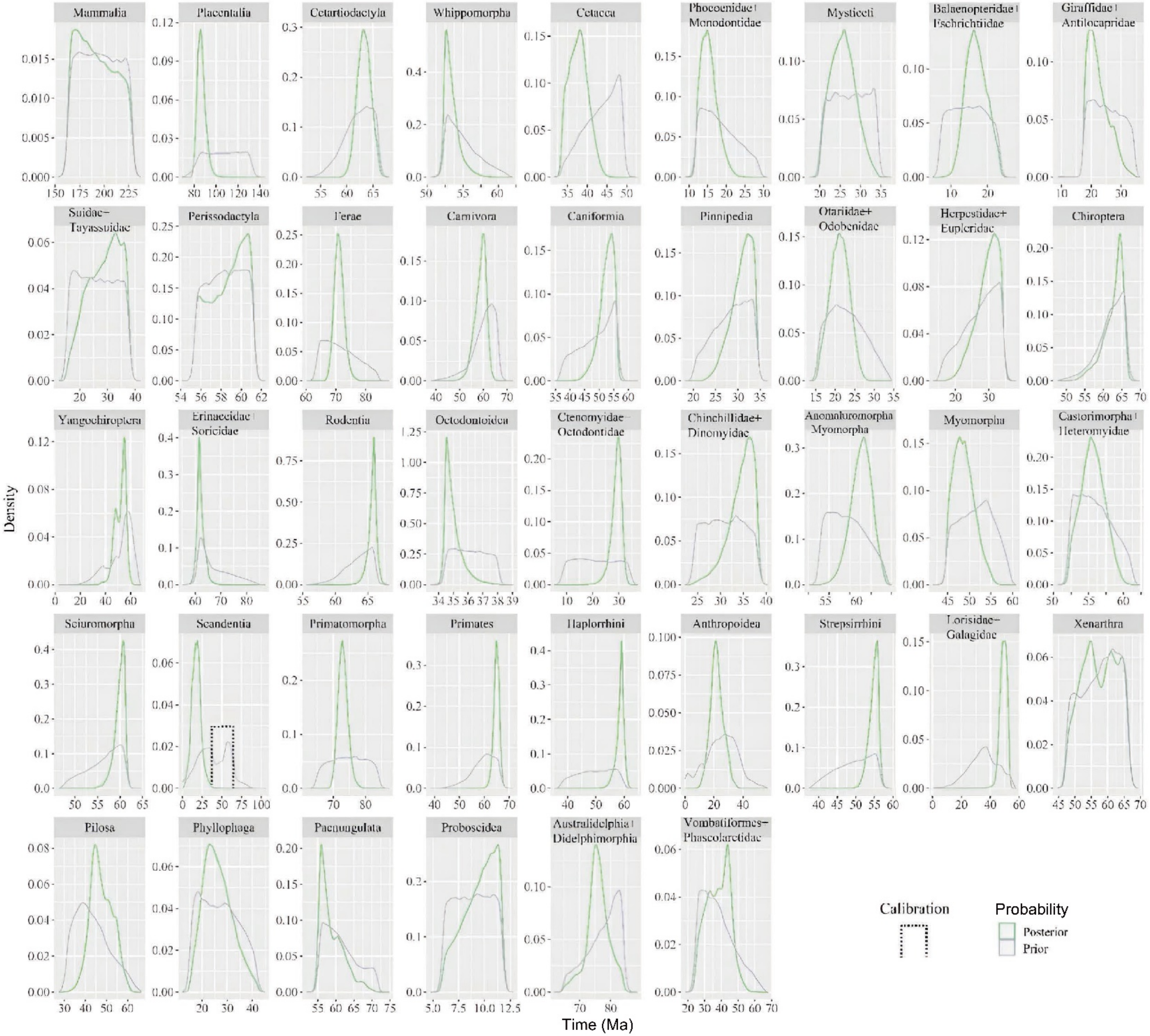
Supplementary Figure S12 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from DNA sequences of Dataset B under an AR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.


Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae+ Monodontidae
Mysticeti
Balaenopteridae+ Eschrichtiidae
Giraffidae+ Antilocapridae
Suidae+ Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Pinnipedia
Otariidae Odobenidae
Herpestidae+ Eupleridae
Chiroptera
Yangochiroptera
Erinaceidae Soricidae
Rodentia
Octodontoidea
Ctenomyidae Octodontidae
Chinchillidae+ Dinomyidae
Anomaluromorpha +Myomorpha
Myomorpha
Castorimorpha+ Heteromyidae
Sciuromorpha
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Strepsirrhini
Lorisidae+ Galagidae
Xenarthra
Pilosa
Phyllophaga
Paenungulata
Proboscidea
Australidelphia Didelphimorphia
Vombatiformes+ Phascolarctidae
Density
Time (Ma)
Calibration
Probability
Posterior
Prior

Supplementary Figure S13 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from protein sequences of Dataset B under an IR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.


Mammalia
Placentalia
Cetartiodactyla
Whippomorpha
Cetacea
Phocoenidae+
Monodontidae
Mysticeti
Balaenopteridae+
Eschrichtiidae
Giraffidae+
Antilocapridae
Suidae–
Tayassuidae
Perissodactyla
Ferae
Carnivora
Caniformia
Pinnipedia
Otariidae+
Odobenidae
Herpestidae+
Eupleridae
Chiroptera
Yangochiroptera
Erinaceidae+
Soricidae
Rodentia
Octodontoidea
Ctenomyidae–
Octodontidae
Chinchillidae+
Dinomyidae
Anomaluromorpha+
Myomorpha
Myomorpha
Castorimorpha+
Heteromyidae
Sciuromorpha
Scandentia
Primatomorpha
Primates
Haplorrhini
Anthropoidea
Strepsirrhini
Lorisidae–
Galagidae
Xenarthra
Pilosa
Phyllophaga
Paenungulata
Proboscidea
Australidelphia+
Didelphimorphia
Vombatiformes–
Phascolarctidae
Density
Time (Ma)
Calibration
Probability
Posterior
Prior

Supplementary Figure S14 Prior (purple) and posterior (green) distribution of fossil calibration (dashed line) nodes from protein sequences of under an AR clock

Purple and green lines indicate prior and posterior distribution, respectively. Black dotted line indicates fossil calibration.

Supplementary Table S1. Sequence origins and gap information of 162 mammalian lineages in dataset A.

Species_famalily	ADORA3	ADRB2	APP	ATP7A	BCHE
Ailurus fulgens_Ailuridae	+	+	+	+	+
Chrysochloridae_Chrysochloridae	+	+	+	+	+
Aplodontia rufa_Aplodontiidae	+	+	+	+	GCA_004027875.1
Arctocephalus forsteri_Otariidae	+	+	+	+	+
Bradypus tridactylus_Bradypodidae	+	+	+	+	+
Capromys pilorides_Capromyidae	+	+	GCA_004027915.1	+	+
Ceratotherium simum_Rhinocerotidae	+	+	+	+	+
Chinchilla lanigera_Chinchillidae	-	GCF_000276665.1	+	+	+
Chrysochloris asiatica_Chrysochloridae	+	+	+	+	+
Craseonycteris thonglongyai_Craseonycteridae	+	+	+	+	GCA_004027555.1
Cricetus cricetus_Cricetidae	+	+	+	+	GCF_000223135.1
Dasyprocta punctata_Dasyproctidae	+	+	+	+	+
Dasyuridae_Dasyuridae	+	+	+	+	+
Didelphidae_Didelphidae	+	+	+	+	+
Dinomys branickii_Dinomyidae	+	+	+	+	+
Dipodomys_Heteromyidae	+	+	+	+	GCF_000151885.1
Elephas maximus_Elephantidae	+	GCA_014332765.1	+	+	+
Emballonuridae_Emballonuridae	+	+	+	+	-
Eschrichtius robustus_Eschrichtiidae	+	+	GCA_002189225.1	+	+
Viverridae_Viverridae	+	GCA_004024585.1	+	+	+
Gliridae_Gliridae	+	+	+	+	+
Heterocephalus glaber_Bathyergidae	+	+	+	+	+
Jaculus jaculus_Dipodidae	+	+	+	GCA_000280705.1	+
Peramelidae_Peramelidae	GCA_904811065.1	+	+	+	GCA_904811065.1
Manis pentadactyla_Manidae	+	+	AY011374.1	+	+
Manis tricuspis_Manidae	+	+	+	+	+
Mustelidae_Mustelidae	+	+	+	+	+
Miniopterus_Vespertilionidae	+	+	+	+	GCF_001595765.1

Myocastor coypus_Myocastoridae	+	+	GCA_004027025.1	+	+
Myotis lucifugus_Vespertilionidae	+	+	GCF_000147115.1	+	+
Myzopoda aurita_Myzopodidae	+	+	+	+	-
Nandinia binotata_Nandiniidae	+	-	+	+	+
Noctilio_Noctilionidae	+	+	+	+	GCA_004026585.1
Ochotona_Ochotonidae	+	+	+	+	+
Ctenomyidae_Ctenomyidae	+	GCA_004027165.1	+	+	+
Odobenus rosmarus_Odobenidae	+	GCF_000321225.1	+	+	GCF_000321225.1
Ornithorhynchus anatinus_Ornithorhynchidae	+	-	-	+	+
Nesomyidae_Nesomyidae	+	+	GCA_004027575.1	+	-
Erinaceidae_Erinaceidae	+	+	+	+	GCF_000296755.1
Viverridae_Viverridae	+	+	+	+	+
Procyon lotor_Procyonidae	+	+	+	+	+
Rhinopoma hardwickii_Rhinopomatidae	+	+	+	+	-
Solenodon paradoxus_Solenodontidae	+	+	+	+	+
Sorex_Soricidae	+	+	+	+	+
Spalacidae_Spalacidae	+	+	GCF_000622305.1	+	GCF_000622305.1
Suricata suricatta_Herpestidae	+	+	+	+	+
Talpidae_Talpidae	+	+	+	+	+
Tapirus indicus_Tapiridae	+	+	+	+	+
Thryonomys swinderianus_Thryonomyidae	+	GCA_004025085.1	+	+	+

Sample gap information (continuous)

Species_famalily	BDNF	BMI1	BRCA1	CNR1	CREM
Ailurus fulgens_Ailuridae	+	+	+	+	+
Chrysochloridae_Chrysochloridae	+	+	+	+	+
Aplodontia rufa_Aplodontiidae	+	GCA_004027875.1	+	+	+
Arctocephalus forsteri_Otariidae	+	+	+	+	+
Bradypus tridactylus_Bradypodidae	+	+	+	+	+
Capromys pilorides_Capromyidae	GCA_004027915.1	GCA_004027915.1	+	+	GCA_004027915.1
Ceratotherium simum_Rhinocerotidae	+	GCF_000283155.1	+	+	+

Chinchilla lanigera_Chinchillidae	GCF_000276665.1	+	+	+	+
Chrysochloris asiatica_Chrysochloridae	+	+	+	+	GCF_000296735.1
Craseonycteris thonglongyai_Craseonycteridae	+	+	+	+	+
Cricetus cricetus_Cricetidae	+	+	+	+	+
Dasyprocta punctata_Dasyproctidae	GCA_004363535.1	+	+	+	+
Dasyuridae_Dasyuridae	+	+	+	+	+
Didelphidae_Didelphidae	+	+	+	+	+
Dinomys branickii_Dinomyidae	+	+	+	GCA_004027595.1	+
Dipodomys_Heteromyidae	+	+	+	+	+
Elephas maximus_Elephantidae	+	+	+	+	+
Emballonuridae_Emballonuridae	+	+	+	+	+
Eschrichtius robustus_Eschrichtiidae	+	+	+	+	+
Viverridae_Viverridae	+	+	+	+	+
Gliridae_Gliridae	+	GCA_004027185.1	+	GCA_004027185.1	-
Heterocephalus glaber_Bathyergidae	GCA_000247695.1	+	+	+	+
Jaculus jaculus_Dipodidae	GCA_000280705.1	GCA_000280705.1	+	+	+
Peramelidae_Peramelidae	+	+	+	+	+
Manis pentadactyla_Manidae	+	+	+	+	+
Manis tricuspis_Manidae	+	+	+	GCA_004765945.1	+
Mustelidae_Mustelidae	+	GCA_000215625.1	+	+	+
Miniopterus_Vespertilionidae	+	+	+	GCF_001595765.1	+
Myocastor coypus_Myocastoridae	+	+	+	+	+
Myotis lucifugus_Vespertilionidae	+	+	+	+	+
Myzopoda aurita_Myzopodidae	+	+	AY834649.1	-	+
Nandinia binotata_Nandiniidae	+	+	+	+	-
Noctilio_Noctilionidae	+	+	+	+	+
Ochotona_Ochotonidae	+	+	+	+	+
Ctenomyidae_Ctenomyidae	-	GCA_004027165.1	+	+	+
Odobenus rosmarus_Odobenidae	+	+	+	+	+
Ornithorhynchus anatinus_Ornithorhynchidae	+	GCA_004115215.4	-	+	GCA_004115215.4

Nesomyidae_Nesomyidae	+	+	+	+	+
Erinaceidae_Erinaceidae	+	+	+	+	+
Viverridae_Viverridae	+	GCA_004024585.1	+	+	+
Procyon lotor_Procyonidae	+	+	+	+	+
Rhinopoma hardwickii_Rhinopomatidae	+	+	+	+	+
Solenodon paradoxus_Solenodontidae	+	+	+	+	+
Sorex_Soricidae	+	+	+	+	+
Spalacidae_Spalacidae	+	+	+	+	+
Suricata suricatta_Herpestidae	+	GCA_006229205.1	+	+	+
Talpidae_Talpidae	+	+	+	+	+
Tapirus indicus_Tapiridae	+	+	+	+	+
Thryonomys swinderianus_Thryonomyidae	GCA_004025085.1	+	+	+	-

Sample gap information (continuous)

Species_famalily	DMP1	EDG1	FBN1	GHR	PLCB4
Ailurus fulgens_Ailuridae	+	GCA_002007465.1	+	+	GCA_002007465.1
Chrysochloridae_Chrysochloridae	+	+	GCF_000296735.1	+	+
Aplodontia rufa_Aplodontiidae	+	+	+	+	+
Arctocephalus forsteri_Otariidae	+	+	GU931076.1	+	+
Bradypus tridactylus_Bradypodidae	+	GCA_004027775.1	+	+	+
Capromys pilorides_Capromyidae	+	+	+	+	+
Ceratotherium simum_Rhinocerotidae	+	+	+	+	+
Chinchilla lanigera_Chinchillidae	+	GCF_000276665.1	+	+	+
Chrysochloris asiatica_Chrysochloridae	+	+	+	+	+
Craseonycteris thonglongyai_Craseonycteridae	GCA_004027555.1	+	+	+	+
Cricetus cricetus_Cricetidae	+	+	+	+	+
Dasyprocta punctata_Dasyproctidae	+	+	+	+	+
Dasyuridae_Dasyuridae	+	+	+	+	+
Didelphidae_Didelphidae	+	+	+	GCF_000002295.2	+
Dinomys branickii_Dinomyidae	+	GCA_004027595.1	+	+	+
Dipodomys_Heteromyidae	+	+	+	+	+

Elephas maximus_Elephantidae	+	+	+	+	+
Emballonuridae_Emballonuridae	+	AY834563.1	+	+	+
Eschrichtius robustus_Eschrichtiidae	+	+	+	+	+
Viverridae_Viverridae	+	+	GCA_004024585.1	+	+
Gliridae_Gliridae	+	+	+	+	+
Heterocephalus glaber_Bathyergidae	+	+	+	+	+
Jaculus jaculus_Dipodidae	+	GCA_000280705.1	+	+	+
Peramelidae_Peramelidae	+	+	+	+	+
Manis pentadactyla_Manidae	+	+	+	+	+
Manis tricuspis_Manidae	+	+	+	+	+
Mustelidae_Mustelidae	+	+	+	+	+
Miniopterus_Vespertilionidae	+	GCF_001595765.1	+	+	+
Myocastor coypus_Myocastoridae	+	+	+	+	+
Myotis lucifugus_Vespertilionidae	+	+	+	+	+
Myzopoda aurita_Myzopodidae	+	+	-	+	+
Nandinia binotata_Nandiniidae	+	-	GU931063.1	+	+
Noctilio_Noctilionidae	+	+	GCA_004026585.1	GCA_004026585.1	+
Ochotona_Ochotonidae	+	+	+	+	GCF_000292845.1
Ctenomyidae_Ctenomyidae	+	GCA_004027165.1	+	+	+
Odobenus rosmarus_Odobenidae	+	+	+	+	+
Ornithorhynchus anatinus_Ornithorhynchidae	+	+	GCA_004115215.4	+	-
Nesomyidae_Nesomyidae	+	+	+	+	+
Erinaceidae_Erinaceidae	+	+	GCF_000296755.1	+	+
Viverridae_Viverridae	+	+	+	+	+
Procyon lotor_Procyonidae	+	+	+	+	GCA_015708975.1
Rhinopoma hardwickii_Rhinopomatidae	+	AY834561.1	-	+	+
Solenodon paradoxus_Solenodontidae	+	+	GCA_004363575.1	+	+
Sorex_Soricidae	+	+	+	+	+
Spalacidae_Spalacidae	+	+	+	+	+
Suricata suricatta_Herpestidae	+	+	+	+	+

Talpidae_Talpidae	+	+	GCF_000260355.1	+	+
Tapirus indicus_Tapiridae	+	+	+	+	+
Thryonomys swinderianus_Thryonomyidae	+	+	+	+	+

Sample gap information (continuous)

Species_famalily	PNOC	RAG2	TYR1	VWF
Ailurus fulgens_Ailuridae	+	+	GCA_002007465.1	+
Chrysochloridae_Chrysochloridae	+	+	+	+
Aplodontia rufa_Aplodontiidae	+	+	+	+
Arctocephalus forsteri_Otariidae	+	+	+	+
Bradypus tridactylus_Bradypodidae	+	+	-	+
Capromys pilorides_Capromyidae	+	+	-	+
Ceratotherium simum_Rhinocerotidae	+	+	+	+
Chinchilla lanigera_Chinchillidae	-	GCF_000276665.1	GCF_000276665.1	+
Chrysochloris asiatica_Chrysochloridae	+	+	+	+
Craseonycteris thonglongyai_Craseonycteridae	+	+	GCA_004027555.1	+
Cricetus cricetus_Cricetidae	GCF_000223135.1	+	+	+
Dasyprocta punctata_Dasyproctidae	-	+	GCA_004363535.1	+
Dasyuridae_Dasyuridae	GCF_902635505.1	+	+	+
Didelphidae_Didelphidae	+	+	+	+
Dinomys branickii_Dinomyidae	+	+	+	+
Dipodomys_Heteromyidae	+	+	+	+
Elephas maximus_Elephantidae	GCA_014332765.1	+	+	+
Emballonuridae_Emballonuridae	AY834587.1	+	+	+
Eschrichtius robustus_Eschrichtiidae	+	+	+	+
Viverridae_Viverridae	+	+	+	+
Gliridae_Gliridae	-	+	+	+
Heterocephalus glaber_Bathyergidae	+	+	+	+
Jaculus jaculus_Dipodidae	+	GCA_000280705.1	+	+
Peramelidae_Peramelidae	+	+	+	+
Manis pentadactyla_Manidae	+	+	-	+

Manis tricuspis_Manidae	+	GCA_004765945.1	+	+
Mustelidae_Mustelidae	GCA_000215625.1	+	+	+
Miniopterus_Vespertilionidae	GCF_001595765.1	+	+	+
Myocastor coypus_Myocastoridae	+	+	+	+
Myotis lucifugus_Vespertilionidae	+	+	+	+
Myzopoda aurita_Myzopodidae	+	+	-	-
Nandinia binotata_Nandiniidae	+	+	+	+
Noctilio_Noctilionidae	+	+	GCA_004026585.1	+
Ochotona_Ochotonidae	+	+	+	+
Ctenomyidae_Ctenomyidae	-	+	GCA_004027165.1	+
Odobenus rosmarus_Odobenidae	+	+	+	+
Ornithorhynchus anatinus_Ornithorhynchidae	-	+	+	+
Nesomyidae_Nesomyidae	+	GCA_004027575.1	+	+
Erinaceidae_Erinaceidae	-	+	+	+
Viverridae_Viverridae	+	+	+	+
Procyon lotor_Procyonidae	+	+	+	+
Rhinopoma hardwickii_Rhinopomatidae	+	+	+	+
Solenodon paradoxus_Solenodontidae	+	+	+	+
Sorex_Soricidae	GCF_000181275.1	+	+	GCF_000181275.1
Spalacidae_Spalacidae	+	+	+	+
Suricata suricatta_Herpestidae	+	+	+	+
Talpidae_Talpidae	-	+	+	+
Tapirus indicus_Tapiridae	+	+	GCA_004024905.1	+
Thryonomys swinderianus_Thryonomyidae	-	+	+	+

Note: #, the sample sequence has been used in Meredith *et al.* (6); -, the sample sequence is still gap.

Supplementary Table S2. The species name, tissue and origin of sample.

Sample name	Tissue or blood	Origin	Donated or collected	Accession No.
Nycticebus sp.	blood	Shijiazhuang ZOO, China	donated	OR503106,OR503119,OR503153,OR503165,OR503182,OR503193,OR503203,OR503216,OR503229,OR503240,OR503252,OR503265,OR503290,OR503297,OR503315,OR503330,OR503341,OR503421,OR503432,OR503444,OR503457,OR503466,OR503486,OR503499,OR503518,OR503530,OR503548,OR503559,OR503569,OR503577,OR503587,OR503599,OR503611,OR503631,OR503639,OR503650,OR503660,OR503671,OR503680,OR503691,OR503703,OR503710,OR503720,OR503729,OR503739,OR503750,OR503757,OR503769,OR503779,OR503790,OR503800,OR503812,OR503822,OR503830,OR503850,OR503859,OR503868,OR503880,OR503888,OR503898,OR503911,OR503920,OR503930,OR503940,OR503950,OR503961,OR503968,OR503978,OR503988,OR503998,OR504009,OR504022,OR504032,OR504042,OR504053,OR504060
Paguma larvata	blood	Shijiazhuang ZOO, China	donated	OR503110,OR503123,OR503132,OR503144,OR503155,OR503168,OR503186,OR503196,OR503207,OR503220,OR503232,OR503244,OR503256,OR503269,OR503285,OR503300,OR503307,OR503322,OR503334,OR503344,OR503355,OR503372,OR503384,OR503391,OR503400,OR503407,OR503424,OR503435,OR503447,OR503460,OR503468,OR503478,OR503489,OR503502
Ateles geoffroyi	muscle	Beijing ZOO, China	collected	OR503107,OR503120,OR503129,OR503141,OR503154,OR503166,OR503173,OR503183,OR503194,OR503204,OR503217,OR503241,OR503253,OR503266,OR503282,OR503291,OR503298,OR503316,OR503320,OR503331,OR503342,OR503352,OR503365,OR503381,OR503405,OR503414,OR503422,OR503433,OR503445,OR503458,OR503467,OR503476,OR503487,OR503500,OR503511,OR503519,OR503531,OR503541,OR503549,OR503560,OR503570,OR503578,OR503588,OR503600,OR503612,OR503622,OR503632,OR503640,OR503651,OR503661,OR503672,OR503681,OR503692,OR503704,OR503711,OR503721,OR503730,OR503740,OR503751,OR503758,OR503770,OR503780,OR503791,OR503801,OR503813,OR503831,OR503841,OR503851,OR503860,OR503869,OR503881,OR503889,OR503899,OR503912,OR503921,OR503931,OR503941,OR503951,OR503962,OR503969,OR503979,OR503989,OR503999,OR504010,OR504023,OR504033,OR504043,OR504054,OR504061
Chiropotes israelita	muscle	Beijing ZOO, China	collected	OR503108,OR503121,OR503130,OR503142,OR503167,OR503174,OR503184,OR503195,OR503205,OR503218,OR503230,OR503242,OR503254,OR503267,OR503277,OR503283,OR503299,OR503

				306,OR503317,OR503321,OR503332,OR503343,OR503353,OR503366,OR503382,OR503406,OR503423,OR503434,OR503446,OR503459,OR503477,OR503488,OR503501,OR503512,OR503520,OR503532,OR503542,OR503550,OR503561,OR503571,OR503579,OR503589,OR503601,OR503613,OR503623,OR503633,OR503641,OR503652,OR503662,OR503673,OR503682,OR503693,OR503705,OR503712,OR503722,OR503731,OR503741,OR503752,OR503759,OR503771,OR503781,OR503792,OR503802,OR503814,OR503823,OR503832,OR503842,OR503852,OR503861,OR503870,OR503882,OR503890,OR503900,OR503906,OR503913,OR503922,OR503932,OR503942,OR503952,OR503963,OR503970,OR503980,OR503990,OR504000,OR504011,OR504018,OR504024,OR504034,OR504044,OR504055,OR504062
Suricata suricatta	muscle	Beijing ZOO, China	collected	OR503117,OR503139,OR503151,OR503163,OR503191,OR503201,OR503214,OR503227,OR503238,OR503250,OR503263,OR503275,OR503280,OR503304,OR503313,OR503328,OR503339,OR503350,OR503363,OR503379,OR503397,OR503412,OR503442,OR503455,OR503484,OR503497,OR503509,OR503516,OR503528,OR503539,OR503557,OR503567,OR503585,OR503597,OR503609,OR503620,OR503630,OR503648,OR503658,OR503669,OR503678,OR503689,OR503701,OR503727,OR503737,OR503748,OR503767,OR503777,OR503788,OR503810,OR503821,OR503839,OR503857,OR503866,OR503878,OR503918,OR503938,OR503948,OR503959,OR503966,OR503986,OR503996,OR504007,OR504041,OR504051
Herpestes sp.	muscle	Beijing ZOO, China	collected	OR503118,OR503128,OR503140,OR503152,OR503164,OR503181,OR503192,OR503202,OR503215,OR503228,OR503239,OR503251,OR503264,OR503276,OR503281,OR503296,OR503305,OR503314,OR503329,OR503340,OR503351,OR503364,OR503380,OR503389,OR503398,OR503404,OR503413,OR503431,OR503443,OR503456,OR503475,OR503485,OR503498,OR503510,OR503517,OR503529,OR503540,OR503558,OR503568,OR503586,OR503598,OR503610,OR503621,OR503649,OR503659,OR503670,OR503679,OR503690,OR503702,OR503719,OR503728,OR503738,OR503749,OR503768,OR503778,OR503789,OR503799,OR503811,OR503840,OR503858,OR503867,OR503879,OR503887,OR503897,OR503905,OR503919,OR503929,OR503939,OR503949,OR503960,OR503967,OR503977,OR503987,OR503997,OR504008,OR504017,OR504031,OR504052,OR504059,OR504069
Typhlomys daloushanensis	muscle	Sichuan Academy of Forestry, China	donated	OR503109,OR503122,OR503131,OR503143,OR503175,OR503185,OR503206,OR503219,OR503231,OR503243,OR503255,OR503268,OR503284,OR503333,OR503354,OR503383,OR503390,OR503399
Taphozous	muscle	Xishuangbanna	collecte	OR503111,OR503133,OR503145,OR503156,OR503176,OR503197,OR503208,OR503221,OR50323

melanopogon		National Nature Reserve, China	d	3,OR503257,OR503270,OR503286,OR503292,OR503301,OR503318,OR503323,OR503345,OR503356,OR503367,OR503373,OR503385,OR503392,OR503401,OR503415,OR503448,OR503461,OR503469,OR503479,OR503490,OR503503,OR503521,OR503533,OR503543,OR503551,OR503562,OR503572,OR503580,OR503590,OR503602,OR503614,OR503624,OR503634,OR503642,OR503653,OR503663,OR503674,OR503683,OR503694,OR503706,OR503723,OR503732,OR503742,OR503753,OR503760,OR503772,OR503782,OR503803,OR503815,OR503833,OR503843,OR503862,OR503871,OR503923,OR503933,OR503943,OR503953,OR503971,OR503981,OR503991,OR504001,OR504012,OR504025,OR504035,OR504045,OR504063
Aselliscus stoliczkanus	muscle	Xishuangbanna National Nature Reserve, China	collected	OR503112,OR503124,OR503134,OR503146,OR503157,OR503169,OR503177,OR503187,OR503209,OR503222,OR503234,OR503245,OR503258,OR503271,OR503278,OR503293,OR503302,OR503308,OR503324,OR503346,OR503357,OR503368,OR503374,OR503386,OR503393,OR503402,OR503416,OR503425,OR503436,OR503449,OR503470,OR503480,OR503491,OR503504,OR503522,OR503534,OR503552,OR503563,OR503573,OR503591,OR503603,OR503615,OR503625,OR503635,OR503643,OR503654,OR503664,OR503675,OR503684,OR503695,OR503713,OR503733,OR503743,OR503754,OR503761,OR503783,OR503793,OR503804,OR503816,OR503824,OR503834,OR503844,OR503872,OR503891,OR503901,OR503907,OR503914,OR503924,OR503934,OR503944,OR503954,OR503972,OR503982,OR504002,OR504013,OR504026,OR504036,OR504046,OR504064
Chaerephon plicatus	muscle	Xishuangbanna National Nature Reserve, China	collected	OR503113,OR503135,OR503147,OR503158,OR503170,OR503178,OR503188,OR503198,OR503210,OR503223,OR503235,OR503246,OR503259,OR503272,OR503287,OR503294,OR503303,OR503309,OR503319,OR503325,OR503335,OR503347,OR503358,OR503369,OR503375,OR503387,OR503394,OR503403,OR503408,OR503417,OR503426,OR503437,OR503450,OR503462,OR503471,OR503481,OR503492,OR503505,OR503513,OR503523,OR503535,OR503544,OR503553,OR503564,OR503574,OR503581,OR503592,OR503604,OR503616,OR503626,OR503636,OR503644,OR503655,OR503665,OR503676,OR503685,OR503696,OR503707,OR503714,OR503734,OR503744,OR503755,OR503762,OR503773,OR503784,OR503794,OR503805,OR503817,OR503825,OR503835,OR503845,OR503853,OR503863,OR503873,OR503883,OR503892,OR503902,OR503908,OR503915,OR503925,OR503935,OR503945,OR503955,OR503964,OR503973,OR503983,OR503992,OR504003,OR504014,OR504019,OR504027,OR504037,OR504047,OR504056,OR504065
Hipposideros larvatus	muscle	Xishuangbanna National Nature Reserve, China	collected	OR503114,OR503125,OR503136,OR503148,OR503159,OR503171,OR503179,OR503199,OR503211,OR503224,OR503247,OR503260,OR503288,OR503310,OR503326,OR503359,OR503370,OR503376,OR503395,OR503409,OR503418,OR503427,OR503438,OR503451,OR503463,OR503472,OR5

				03482,OR503493,OR503506,OR503524,OR503536,OR503545,OR503554,OR503565,OR503575,OR503582,OR503593,OR503605,OR503617,OR503627,OR503637,OR503645,OR503656,OR503666,OR503677,OR503686,OR503697,OR503708,OR503715,OR503724,OR503735,OR503745,OR503756,OR503763,OR503774,OR503785,OR503795,OR503806,OR503818,OR503826,OR503836,OR503846,OR503854,OR503864,OR503874,OR503884,OR503893,OR503903,OR503909,OR503916,OR503926,OR503936,OR503946,OR503956,OR503974,OR503984,OR503993,OR504004,OR504015,OR504020,OR504028,OR504038,OR504048,OR504057,OR504066
Myocastor coypus	muscle	Pet market, China	collected	OR503115,OR503126,OR503137,OR503149,OR503160,OR503189,OR503212,OR503225,OR503236,OR503248,OR503261,OR503273,OR503279,OR503289,OR503311,OR503327,OR503336,OR503348,OR503360,OR503377,OR503388,OR503396,OR503410,OR503419,OR503428,OR503439,OR503452,OR503464,OR503473,OR503494,OR503514,OR503525,OR503537,OR503546,OR503555,OR503566,OR503576,OR503583,OR503594,OR503606,OR503618,OR503628,OR503646,OR503657,OR503667,OR503687,OR503698,OR503709,OR503716,OR503725,OR503746,OR503764,OR503775,OR503786,OR503796,OR503807,OR503819,OR503827,OR503837,OR503847,OR503855,OR503865,OR503875,OR503885,OR503894,OR503910,OR503917,OR503927,OR503937,OR503947,OR503957,OR503975,OR503985,OR503994,OR504005,OR504016,OR504021,OR504029,OR504039,OR504049,OR504058,OR504067
Petaurus breviceps	muscle	Pet market, China	collected	OR503116,OR503127,OR503138,OR503150,OR503161,OR503172,OR503180,OR503190,OR503200,OR503213,OR503226,OR503237,OR503249,OR503262,OR503274,OR503295,OR503312,OR503337,OR503349,OR503361,OR503371,OR503378,OR503411,OR503420,OR503429,OR503440,OR503453,OR503495,OR503507,OR503526,OR503556,OR503584,OR503595,OR503607,OR503699,OR503717,OR503747,OR503765,OR503797,OR503808,OR503828,OR503848,OR503876,OR503886,OR503895,OR503904,OR503928,OR503958,OR503965,OR503976,OR503995,OR504006,OR504030,OR504040,OR504050,OR504068
Graphiurus kelleni	muscle	Pet market, China	collected	OR503162,OR503338,OR503362,OR503430,OR503441,OR503454,OR503465,OR503474,OR503483,OR503496,OR503508,OR503515,OR503527,OR503538,OR503547,OR503596,OR503608,OR503619,OR503629,OR503638,OR503647,OR503668,OR503688,OR503700,OR503718,OR503726,OR503736,OR503766,OR503776,OR503787,OR503798,OR503809,OR503820,OR503829,OR503838,OR503849,OR503856,OR503877,OR503896

Supplementary Table S3. The designed PCR primers information in this study.

No.	Marker	Forward Primer（5`→3`）	Reverse Primer（5`→3`）	PL (bp)	AT (℃)
1*	ANKHD1	AACAGATYCGGCATCCTC	GGTGGYAAAGAYTTATTTGCTGG	1011	61
2*	ZNF281	CTAGTGCRGAACCTGGGTC	TGGCAACACTGAGGTAACAG	1063	59
3*	KLHL25	ATGTGYGACAAGATYTACCAGG	GTGGGGATGAGBGARTARGG	817	61
4*	TAB2	CATCTTTGCACATACATGGTGTACC	CAGGKGGYTTATTDGGAGAAAC	848	59
5*	ADNP	GCACCTTACATAGCAAAGGC	GATGTGCAAGTGCATCAGA	1359	59
6*	ARHGAP35	GAGCGGTACATTMGAGAT	TGACATTSCCYTCTATTGG	1314	55
7*	LRRC8A	TGGARCACTTTGTBTCTATCC	TGCTGGAARCTGATGATCTC	1452	59
8*	PROX1	CGAAAAGAACAGAAGCGAGAGGAG	TGRGATGACATCTTGGTCCTCAGACT	910	59
9*	RBBP6	GTTCCAAACGDAGAGATGAAAGG	TGTTTTTGGCTYTTTTCCAATTCT	849	61
10*	FZD4	ATGTGCCAATGTGCACRGAGAAGATCAAC	GCMGACCARATCCACATGCC	910	59
11*	ZBTB6	CTGCTTGYTCHACTTTCATGAGAG	TGYTTYTTGAGRGCAGATTTGTG	1044	61
12*	SP3	CAAGTCCAGGTTCAGGGAGTTRCAATTGGTGG	TGTAGATTTGGCAACTGACCAGTGCTTAGAC	877	55
13*	TRIM13	AACAARATCAARRTCTCTCCCAAAATGCC	TCCCAYTGACTRGTATCAAARTTYTT	613	61
14*	TTC30B	GTSACCYTGCACAACCAGGC	GAARCATCTTTTGGCRTARTACCAGG	908	61
15*	NR3C1	ATTYCCWCARCAGGGCCAAA	TCATCKCCAGATCCYTGGCA	827	57
16*	GJC1	GGYTATGCCATYCAYAAGATTGCC	GAYTTGCTRCTRGCACTGCT	886	61
17*	MARCH7	CARGGAGCRAGACCAAAAGA	AGAAATCKAAATCCYTGAG	514	53
18*	NFE2L2	GCTTCAGYGATTCTGARATGGAAG	AGCATGCTGAASACYTCDAGAT	594	61
19*	GJA1	CAGTGGTACATCTAYGGMTTCAGC	GCTGGCTCTRCTKGAAGG	589	61
20*	CEBPZ	ACARARCHTTGGCTCAGAA	AGKGCACTDAGCATTTTWGA	846	57
21*	DET1	TACCAGGGCTGCCARGCA	AGSAGGTCATCCTCATAGC	538	59
22*	PLXNB2	CAGCCTCTTCAAGGGCATCTG	TGGCACTSCAGGTCCAYCTC	479	61
23*	HIPK2	CCTTCAATCAAGTGCCTTCTGTAGTGTGAAG	CCTTCAATCAAGTGCCTTCTGTAGTGTGAAG	475	61
24*	HIPK3	ATGTTGCARACMAACATGGGAAATCCAGTGAC	TTCTCTGGTTTRAGGTCAGCATGAATTAAACCAAG	523	61
25*	TMEM168	GGATTTGCYATTGCYAGYAC	CGCATYCCTTTRGATGCCAT	559	61
26*	WDR89	ATTTGTGCTGGYACWGAAAAAKTTG	TGTGCATCYTCTCCWCCAG	643	59
27*	ACKR4	TCTGGRATGCAGTTTCTGGC	TGKATGGCVACATCYATGCG	484	57
28*	Fbxo42	GATYTGAATTGGGAYCTRAA	GGATAGTACTTCACATTCTGYTTCTTGTCCATGAG	613	57

29*	1 EDG1	CGCTAYATCACSATGCTSAAGATG	GTGTARATGATGGGGTTGG	511	61
30*	MAPK6	CAAAGCAAAGAAAARTCTGATAAGARAGGCAAGTC	GGGAYGCCTATRGAYTCAAGCTGC	598	61
31*	RNF146	AAAGGTAAAAAGARCACTGAAATGTTAATTGCYGG	ATCCTCACTATCACTACTVGCRTCTG	554	61
32*	ZNF768	GGYATCTGYGGRAAGAGCTT	GGRCACTTRAAGGGCTTYTC	505	61
33#	CASR	TCCGYTGGAACTGGGTGGGCACMATTGCAGC	CTGCCAVGCCTCAACYTTCTTGATGTCTGCACAGG	770	63/55
34#	KERA	GAGCTAGAGGAGGTACCTTCTCCATTGCCAAGAAG	AAGGTGCTGCAGRTKAGCAYTGATT	468	63/55
35#	KLHL28	CCCCGACCTACATGCTTGCTAACTTAACCCACT	GGAGCACAGCGAGGTCGTGTCATCAAGACTGTCTG	832	63/55
36#	BCHE2	TGGAATGCCACAAAATATGCAAATTC	TCATARCCATGCATCACTCCCATCCAT	1175	63/55
37#	BTBD3	ATCTATTGTGATGAAATTGAYTTGGCTGCYGACAC	GAGAAGTACTTGCTBARGTTCTGCCC	794	63/55
38#	MYPN	AGTCGAGCDGARCCYTCCTCCAACCCT	GGTGGAATTCCTACCACTATRCAATCCAACTG	824	63/55
39#	STON2	ACATCATGTCCTCYAGGCACTGGGGACC	CCAAAACTYGCCCCCCGGTTCACTTTGGCTTTC	976	63/55
40#	ZNF318	GAGAGAGCTAGCCAGGAYGGCAGTGG	GCTGCATATGCCATGTARTGCCTATAKGCATCA	938	63/55
41#	MED13L	CCAAGAACTCCCAGAGGWGGGGGCACTGCYAGTGG	TGRTTCTGVARGAGGAGGAGRAGGCT	539	63/55
42#	KCNJ2	CGCTGGMGGTGGATGCTGGTYATCTTCTG	CTGGGCTCTAGAGGYACRCTKGCCTGGTTGTG	1022	63/55
43#	ZNFX1	TGAGRGCCTCTGGKGTTRACATARAAG	AGGCTTCCATYTGRGAGTCATCCAGC	987	63/55
44#	BMP2	CACCGAATTAATATTTATGAAATYATAAARCCTGC	CCCTCSACRACCATGTCCTGAT	671	63/55
45#	PLAGL2	TGGCCACCCACTCAGCCCAGAAACCCCACCAGTG	GGCCGCAGCTGCYGCCGGCTGAGGTGAG	905	63/55
46#	CHRNA6	GACAAAGCTGAAATTGAYCTTCTMATCATTGG	TCTTCATGTTTTCYGCTATGA	802	63/55
47#	ZC3H12C	GGCCTTCCATCTGGAGTTCAYTTCCCASCTCAGG	TGGCKGCRGCSAGCTGCTGGGCRTC	1018	63/55
48#	KCNJ1	GGAAGGTGYAACATHGARTTTGGCA	TGGGARCAAAVCGGTARCCCCARAGCAC	844	63/55
49#	SETBP1	CTCCAGCCCATCAGTGCTCTTCCAACCAAAACCC	TGGCTGGAGAAGCCWGTGGCTTTGCCTGC	1130	63/55
50#	KCNJ6	GTGGCCATYCACCAGCCWAAGTTGCCTAAGC	TTGGAGATCTCCCAGAARGGACTCTG	809	63/55
51#	BMP10	GGAACCAACAGTGAGTGGGAGAC	AGGTGACGACRCCYTTRTCTAAATAGAGGATGGAG	652	63/55
52#	ZNF691	CCYTGGAGAGTGGATGRCTCHRAGG	AGCTGGARCTGTTGCTRAAGCTCT	574	63/55
53#	FRMD7	TGTGAATGGAGTGCACGC	AGGTCAGCTTTACGACTSAGAGYAGGRCAAGGCCC	792	63/55
54#	KIAA0355	AARCTGACMTCCCGSTTCACMAAGAA	AGCTGCTCACYAGACCCAAGCTGTAYAAGTCAG	793	63/55
55#	CDKN2AIP	TGTTGAAAKCMAGTRTGAATAGTCA	TTGCTTTTTCCACAGCCRGTGCCCAAAT	832	63/55
56#	NP_689653.3	GGAGGRCAGTCTCAGAAGGCYGTKCAGCC	AGGAARGAAATAAARTGGGAGTCTCT	545	63/55
57#	DMRTA1	TGGAATCAGGAAATGAAAGTGAGTGG	CCYGAAAAGGCATAATCCARAGCWGG	532	63/55
58#	C3orf59	TGCGCCACTCAGCCTTRTGYCACTCTTGGC	GCTCCAGCGTCAGCCKGTTGGCYGCCTTGACGTGC	870	63/55
59#	GRIN2A	CCAAAGSGAGCTCSCCCAGGGACAAGATCTACACC	AGGCATTTTCTTGTACACRCGTCTAYTGCTGCAGG	1073	63/55

60#	COG8	GCATTGTGAAYGAAGTGCGCCARTCCATGCAGCTG	GGGCAGCARAGRCGCAGATCA	778	63/55
61#	ENPP4	TCCTTYGAYGGYTTCAGAGCTGACT	GARCACTGGGTCATCCCRTGRTCRCT	620	63/55
62#	FAM135A	GCCTAAATCTYTGTGCAAATTTGTCCATTTCAGG	GTCCAAGTTAGGTTTGGAG	1052	63/55
63#	FBX040	CATGTCCCGCCACAAGCTGGCCAAGC	CGAGCCCGCTTYCCACAGTAGCTCAC	867	63/55
64#	FZD6	TGGTGTCCMAGGCATCTYAAGACTTCTGG	AGGCCACTRAAGACTCCWATKCGAATCAT	791	63/55
65#	MET	CTGTGCTTRCACCTGGCRTYCTTGTGCTTCTG	GCMCCAGGCTTACTGACATABGCAGCTTG	970	63/55
66#	KIAA010	TGGAGCCCMCCAGATCACATG	GCCCGGCGCATRGGYGTGTTGCCATAGAGACGACG	878	63/55
67#	CASR2	AGTGCCCHGATGACTTCTGGTCCAATGARAACCAC	CTGCAGCGCACCTCCTCGATGGTG	874	63/55
68#	GPRC5C	CTGCTGGGGACCCTGGGCCTCTTCTGCCTCG	GAGGCTGGCTCRTCCATGGAAAABGCCTTG	788	63/55
69#	NPAS4	GAGGCTGTGCYTTCCTCTTYAGCCTCCAYGAGCCC	AGGGGAATGCTGAGACACCTGTCTCAAAGGCGG	1023	63/55
70#	PAPPA	CGTGACCGAGGATGGGTYGTGGGMATTCACACC	GCCAGCTGCYGGTGCTGGAAGTCRATCTGCTG	713	63/55
71#	POLR1B	CTCTGCCAYGATGCBACMCCCTTCA	TGTTCATAGCTGCCAGYTCRGCTACAAAATACCG	556	63/55
72#	SCN8A	TGGCCCGTATTGGGCGCATCYTGCGTCTGATC	GCCACGAACCKCTCCTCCATCTG	763	63/55
73#	STOX2	CGCCSTCTGCCTCAGGCTGCRTCAGGGAAAG	CGGTCCTGGGTATGGCTGTGGCTTCGGTG	898	63/55
74#	SYT11	GTRCTGGTGGTGTGYGTSTCRGTGAC	TGCAGSACCAGGTCYTGSAGCTGGCTG	656	63/55
75#	C60RF60	TGATGAGCAYGAATCTGCAATTCAAGCCCTCA	CCTATGGTTTTTCGYAAAATTGCTTCTTG	723	63/55
76#	NEDD9	AAGCCYGTGGAGAAYGACATCTC	TCTTGAGCTGYTCGCABAGCTGGTTGCTGGAG	334	63/55
77#	KL	GCTCAYGCCAAAATCTGGCATCTCTAC	TCTTGGTGGTCCCKGARACRAACCAGC	454	63/55
78#	GGPS1	ATTGAAGTGACDGARATGTTRCATA	CTTTTGTTTTCRCTRTATTCTTTGGAGTG	461	63/55
79#	MRPL16	TGAAATGATGCGCCTGACRATCAACCGCT	AGCATGTTGGCRGTGRCKATGCGCTC	366	63/55
80#	SIPA1L1-exon8	GTGGCYGTSACCAGGTCCAGAG	GTCCACCCKATCACRTCTCTGCAGG	467	63/55
81#	GPR987-intro6	ATTCAACTGAAAAGTGTRGAAGGAGGAGCTG	GCCAACATCTGCCCTTGTGCAAAATGSAGAACTCC	966	63/55
82#	HAS3	AGCGGGCYTGCCAGTCCTACTTTGGCTGYGTGCAG	AAGCTATACTGYTCTGGCTTCTTCCC	835	63/55
83#	MED13	GATCAAGAATATGGYCCTGCTTAYACACCTCA	TGACGYCCATGTTCTAATGCAAGGTAGCA	818	63/55
84#	PPARGC1A	TCCACCCACAACTCCTCCTCAYAAAGCCAACCAAG	GATCTACTGCCTGGGGACCKWGATCTTGACCTGG	912	63/55
85#	EHBP1	TCTCTATCAAATMAGRGCACATTTCAGYGGCCAAG	TCTGRATCAGAYTCTGTYTGCCTCAGGG	765	63/55
86#	NR4A2	AGGCGCAGTATGGGTCCTCGCCTCAAGGAGCCAGC	AGCAGCTGCGACGCGTGGCCGATCTGCAG	718	63/55
87#	TRIP12	CCACARCCASAGGAYCCAGACAGAGCC	GATGTYTCTGACTTAGAAGACCCTGGAAGAGACAG	743	63/55
88#	C17orf71	TGAACCAAGTACTCCAGATCCTGCWCCTGC	AAAGGAGCATCRGGAACYACAACAAAMAGCCTCAT	798	63/55
89#	GRM5	GAGCCCATTGCWGCWGTGGTGTTTGCCTGCCT	GTGGTGAAGGCGCTGCGYAC	782	63/55
90#	HAS2	CCTGGATCTCYTTCCTCAGCAGTGTGAGATACTGG	ATGGTTTTCCTTCCAGATGTGCCCCACCCAGC	664	63/55

91#	VCPIP1	TCTGCCTGGCAAAACMTTTGTCTATAATGCTTCTG	CAGCATCTTGRCTATCCATCTCTTCRGGCTCCTCC	803	63/55
92#	ZNF192	AGGCAGCGRGGRAATCCCACCCARGAGAGACG	AGGCCAGTGTTCCCATTGAARGCTTTCCCACATTC	668	63/55
93#	ZNF652	AGCAGGRATGGCACAAGA	CTTCTCCTTYTTCTTCTGCCT	499	63/55
94#	TRPS1	AGCCATTCTGCTCAGCAGCCRGTCCTGGTCAGCC	TGTCCGTGCAAAGATGCTGGCATATGCTGCACTG	727	63/55
95#	PCDH9	TCTGAGAATCTGCCAAAGTATAGTACTGTGGGGG	AGCCTCCTTGGGAACTGCACTCTGAGGCACTGAAG	1261	63/55
96#	KLHL15	TCAAGCCGCATCCGYTCTGCCAAACC	GAATCGCTGTAATGACCRTTGTAGCAAAGGCCTCC	863	63/55
97#	KLHL23	TTTCTGGATGCATTCAGAACATTTTACTTGGATGG	TGGGKCCCAAACAYGTAACRCCATAGCTCTCCC	898	63/55
98#	HDX	ACGTGGGTYGGCAATAARAGAAGAAAAATGAG	TCATCARCATCTCCAGTCTCCATTGCA	788	63/55

Note: *, newly designed primers in this study. #, the primers from the Zhou et al. (Zhou et al., 2011).

Supplementary Table S4. Likelihood ratio test of alternative topologies for dataset A DNA alignments as implemented in CONSENL package.

Tree topology	ln L	Δ ln L	SH probability	AU probability
Laurastheria				
(Chroptera, (Artiodactyla, (Perissodactyle, Ferae)))	-1243820.9	Best	0.894	0.763
(Ferae, (Chiroptera, (Perissodactyle, Artiodactyla)))	-1243828.1	7.2	0.506	0.433
(Chiroptera, ((Perissodactyle, Artiodactyla), Ferae))	-1243830.0	9.1	0.480	0.240
(Chroptera, (Perissodactyle, (Artiodactyla, Ferae)))	-1243834.6	13.7	0.279	0.102
((Chiroptera, Perissodactyle), (Artiodactyla, Ferae))	-1243835.0	14.1	0.294	0.189
Paenungulata				
(Sirenia, (Proboscidea, Hyracoidea))	-1243819.9	Best	0.783	0.703
(Proboscidea, (Sirenia, Hyracoidea))	-1243823.7	3.7	0.499	0.421
(Hyracoidea, (Proboscidea, Sirenia))	-1243830.0	10.0	0.238	0.130
Placentia root				
Afrotheria	-1243828.5	Best	0.722	0.618
Atlantogenata	-1243830.0	1.5	0.571	0.510
Xenartheria	-1243835.2	6.7	0.291	0.150
Rodentia				
(Sciuromorpha, (Mouse-related clade, Hystricomorpha))	-1243817.5	Best	0.806	0.810
(Mouse-related clade, (Sciuromorpha, Hystricomorpha))	-1243830.0	12.5	0.194	0.190
Scandentia				
Sister to Glires	-1243830.0	Best	0.791	0.788
Sister to Primatomorpha	-1243838.2	8.2	0.209	0.212

Abbreviations: ln L, log-likelihood; Δ ln L, the difference between best topology and other topology; SH probability, Shimodaira-Hasegawa probability; AU probability, approximately unbiased probability.

Supplementary Table S5. Likelihood ratio test of alternative topologies for dataset A protein sequences as implemented in CONSENL package.

Tree topology	ln L	Δ ln L	SH probability	AU probability
Laurastheria				
(Ferae, (Chiroptera, (Perissodactyle, Artiodactyla)))	-660387.6	Best	0.951	0.858
(Chiroptera, ((Perissodactyle, Artiodactyla), Ferae))	-660400.0	12.4	0.354	0.134
(Chroptera, (Artiodactyla, (Perissodactyle, Ferae)))	-660401.7	14.4	0.299	0.244
(Chroptera, (Perissodactyle, (Artiodactyla, Ferae)))	-660413.3	25.7	0.052	**0.041**
((Chiroptera, Perissodactyle), (Artiodactyla, Ferae))	-660416.1	28.5	**0.047**	**0.022**
Paenungulata				
(Sirenia, (Proboscidea, Hyracoidea))	-660393.7	Best	0.787	0.683
(Hyracoidea, (Proboscidea, Sirenia))	-660400.0	6.3	0.505	0.434
(Proboscidea, (Sirenia, Hyracoidea))	-660405.5	11.8	0.364	0.242
Placentia root				
Atlantogenata	-660400.0	Best	0.931	0.883
Afrotheria	-660414.0	14.0	0.186	0.165
Xenartheria	-660414.6	14.6	0.171	0.154
Rodentia				
(Sciuromorpha, (Mouse-related clade, Hystricomorpha))	-660385.6	Best	0.783	0.801
(Mouse-related clade, (Sciuromorpha, Hystricomorpha))	-660400.0	14.4	0.217	0.199
Scandentia				
Sister to Glires	-660400.0	Best	0.699	0.699
Sister to Primatomorpha	-660405.7	5.7	0.301	0.301

Abbreviations: ln L, log-likelihood; Δ ln L, the difference between best topology and other topology; SH probability, Shimodaira-Hasegawa probability; AU probability, approximately unbiased probability.

Supplementary Table S6. Likelihood ratio test of alternative topologies for dataset B DNA sequences as implemented in CONSENL package.

Tree topology	ln L	Δ ln L	SH probability	AU probability
Laurastheria				
(Chroptera, (Perissodactyle, (Artiodactyla, Ferae)))	-1120805.2	Best	0.965	0.895
(Chroptera, (Artiodactyla, (Perissodactyle, Ferae)))	-1120823.9	18.7	0.323	0.191
(Chiroptera, ((Perissodactyle, Artiodactyla), Ferae))	-1120825.4	20.2	0.275	0.144
((Chiroptera, Perissodactyle), (Artiodactyla, Ferae))	-1120829.8	24.6	0.218	0.211
(Ferae, (Chiroptera, (Perissodactyle, Artiodactyla)))	-1120832.2	27.0	0.168	0.192
Paenungulata				
(Sirenia, (Proboscidea, Hyracoidea))	-1120813.3	Best	0.844	0.774
(Proboscidea, (Sirenia, Hyracoidea))	-1120820.7	7.4	0.419	0.348
(Hyracoidea, (Proboscidea, Sirenia))	-1120825.4	12.1	0.272	0.166
Placentia root				
Xenartheria	-1120820.6	Best	0.734	0.632
Atlantogenata	-1120822.5	1.9	0.579	0.475
Afrotheria	-1120825.4	4.8	0.453	0.298
Rodentia				
Sciuromorpha, (Mouse-related clade, Hystricomorpha)	-1120825.4	Best	0.580	0.602
Mouse-related clade, (Sciuromorpha, Hystricomorpha)	-1120828.1	2.7	0.420	0.398
Scandentia				
Sister to Glires	-1120825.3	Best	0.680	0.681
Sister to Primatomorpha	-1120829.2	3.9	0.320	0.319

Abbreviations: ln L, log-likelihood; Δ ln L, the difference between best topology and other topology; SH probability, Shimodaira-Hasegawa probability; AU probability, approximately unbiased probability.

Supplementary Table S7. Likelihood ratio test of alternative topologies for dataset B protein sequences as implemented in CONSENL package.

Tree topology	ln L	Δ ln L	SH probability	AU probability
Laurastheria				
(Ferae, (Chiroptera, (Perissodactyle, Artiodactyla)))	-413317.4	Best	0.974	0.948
(Chiroptera, ((Perissodactyle, Artiodactyla), Ferae))	-413326.9	9.5	0.522	0.106
((Chiroptera, Perissodactyle), (Artiodactyla, Ferae))	-413339.0	21.6	0.230	0.113
(Chroptera, (Perissodactyle, (Artiodactyla, Ferae)))	-413343.6	26.2	0.162	0.133
(Chroptera, (Artiodactyla, (Perissodactyle, Ferae)))	-413366.9	49.5	**0.006**	**<0.001**
Paenungulata				
(Proboscidea, (Sirenia, Hyracoidea))	-413296.2	Best	0.835	0.753
(Sirenia, (Proboscidea, Hyracoidea))	-413306.9	10.7	0.393	0.287
(Hyracoidea, (Proboscidea, Sirenia))	-413326.9	30.7	**0.046**	**0.021**
Placentia root				
Xenartheria	-413309.5	Best	0.690	0.565
Afrotheria	-413311.0	1.5	0.603	0.477
Atlantogenata	-413326.9	17.4	0.086	**0.020**
Rodentia				
(Sciuromorpha, (Mouse-related clade, Hystricomorpha))	-413326.9	Best	0.763	0.738
(Mouse-related clade, (Sciuromorpha, Hystricomorpha)	-413337.8	10.9	0.237	0.262
Scandentia				
Sister to Glires	-413326.9	Best	0.809	0.825
Sister to Primatomorpha	-413335.4	8.5	0.191	0.175

Abbreviations: ln L, log-likelihood; Δ ln L, the difference between best topology and other topology; SH probability, Shimodaira-Hasegawa probability; AU probability, approximately unbiased probability.

Supplementary Table S8. Guanine-cytosine (GC) along with the third position of codon (GC3) content of two datasets.

Dataset A	GC	GC3
A2AB	0.6005	0.8393
ADORA3	0.4569	0.6664
ADRB2	0.5325	0.7666
ApoB	0.4315	0.4610
APP	0.3691	None
ATP7A	0.4063	0.3453
BCHE	0.4134	0.3506
BDNF	0.5558	0.6688
BMI1	0.3259	None
BRCA1	0.4180	0.3435
BRCA2	0.3488	0.2666
CNR1	0.5304	0.7352
CREM	0.4333	None
DMP1	0.5136	0.5250
EDG1	0.5624	0.8367
ENAM	0.4470	0.3444
FBN1	0.3425	None
GHR	0.4886	0.4779
IRBP	0.6099	0.7530
PLCB4	0.4013	None
PNOC	0.6150	0.7479
RAG1	0.5192	0.6270
RAG2	0.4391	0.4105
TTN	0.4175	0.3156
TYR1	0.4746	0.5678
vWF	0.5928	0.7890

Dataset B	GC	GC3
000_comb	0.4931	0.3702
001_comb	0.4128	0.4109
002_comb	0.6337	0.8548
003_comb	0.4792	0.4463
004_comb	0.4735	0.4631
005_comb	0.4604	0.5287
006_comb	0.5860	0.9082
007_comb	0.5861	0.6485
009_comb	0.4273	0.3854
010_comb	0.4955	0.5893
011_comb	0.4076	0.3877
012_comb	0.4276	0.3033
013_comb	0.4251	0.4938
014_comb	0.4419	0.5364
015_comb	0.4454	0.4221
016_comb	0.4475	0.4880
017_comb	0.3919	0.2313
018_comb	0.4295	0.3975
019_comb	0.5035	0.5634
020_comb	0.4164	0.4259
021_comb	0.5378	0.6734
022_comb	0.6303	0.8764
023_comb	0.5581	0.6454
025_comb	0.3907	0.3433
027_comb	0.3514	0.3303
028_comb	0.4066	0.3498
029_comb	0.4472	0.5570
030_comb	0.5737	0.5662
031_comb	0.5905	0.8931
033_comb	0.4212	0.4365
034_comb	0.4896	0.3402
036_comb	0.6333	0.8130
037_comb	0.5145	0.6142
038_comb	0.4224	0.4587
039_comb	0.4061	0.3468
040_comb	0.4177	0.3308
041_comb	0.5418	0.6467
042_comb	0.4768	0.4351
043_comb	0.5217	0.6665
044_comb	0.5045	0.4279
045_comb	0.5056	0.5874
046_comb	0.4854	0.5952
047_comb	0.4792	0.5621
048_comb	0.5171	0.6304
049_comb	0.5744	0.6951
050_comb	0.4497	0.5605
051_comb	0.5272	0.5658
052_comb	0.4583	0.5487
053_comb	0.5249	0.6360
054_comb	0.4963	0.6716
055_comb	0.5111	0.6163
056_comb	0.5756	0.7108
057_comb	0.4699	0.4320
058_comb	0.5409	0.5392
059_comb	0.4541	0.4197
060_comb	0.4879	0.6157
061_comb	0.4611	0.3475
062_comb	0.5448	0.7562
063_comb	0.5478	0.7229
064_comb	0.5608	0.6771
065_comb	0.4205	0.4961
066_comb	0.3715	0.2407
067_comb	0.4993	0.5357
068_comb	0.4200	0.4622
069_comb	0.4514	0.4466
070_comb	0.5213	0.5479
071_comb	0.5799	0.8603
072_comb	0.6199	0.8567
073_comb	0.5756	0.6338
074_comb	0.5848	0.7557
075_comb	0.5019	0.5387
076_comb	0.5268	0.7368
077_comb	0.5055	0.5739
078_comb	0.5471	0.6794
079_comb	0.4292	0.4432
080_comb	0.5544	0.7640
082_comb	0.4432	0.4759
084_comb	0.4148	0.3861
085_comb	0.5590	0.6301
086_comb	0.4919	0.6069
087_comb	0.3504	0.2900
089_comb	0.5390	0.7256
090_comb	0.4343	0.2972
091_comb	0.4901	0.5122
092_comb	0.4177	0.3546
093_comb	0.5911	0.8014
094_comb	0.4950	0.4067
095_comb	0.4465	0.3198
096_comb	0.4781	0.6368
097_comb	0.4645	0.5763
098_comb	0.4488	0.3124
099_comb	0.4831	0.5193
100_comb	0.4601	0.5153

101_comb	0.4527	0.4038
102_comb	0.4708	0.5108
103_comb	0.4582	0.4770
104_comb	0.3819	0.3596
105_comb	0.4059	0.3703

Supplementary Table S9. The Robinson-Foulds (RF) distance between the tree without GC-rich genes and the trees under multiple partition strategies.

Dataset A - DNA	①concatenation	②gene	③coding+ noncoding	④codon1/2+ codon3+ noncoding	⑤gene+codon1/2 + codon3 + noncoding	⑥Partition-Finder2
GC-rich	0.0061	0.0061	0.0061	0.0183	0.0183	0.0000
0		0.0000	0.0000	0.0183	0.0183	0.0061
②			0.0000	0.0183	0.0183	0.0061
③				0.0183	0.0183	0.0061
④					0.0000	0.0183
⑤						0.0183

Dataset B - DNA	①concatenation	②gene	③codon1/2 + codon3	④gene+ codon1/2 + codon3	⑤PartitionFinder2
GC-rich	0.0342	0.00855	0.0513	0.0256	0.0256
①	0.0000	0.0256	0.0427	0.0256	0.0427
②		0.000	0.0427	0.0171	0.0171
③			0.0000	0.0513	0.0598
④				0.0000	0.0171

Supplementary Table S10. Calibrations used in molecular dating analyses.

Number	Clade	MinAge	MaxAge	References
1	Caenolestidae	0	15.97	Meredith et al., 2011
2	Peramelidae	4.36	23.8	Meredith et al., 2011
3	Peramelemorphia	4.36	54.65	Meredith et al., 2011
4	Phalangeridae+Burramyidae	25	54.65	Meredith et al., 2011
5	Petauridae+Pseuocheiridae	25.5	54.65	Meredith et al., 2011
6	Macropodoidea+Potoroidae	24.7	54.65	Meredith et al., 2011
7*	Placentalia	65.2	131.5	Meredith et al., 2011
8*	Vombatiformes	25.5	54.65	Springer et al., 2017
9*	Australidelphia +Didelphimorphia	65.18	83.8	Springer et al., 2017
10	Vermilingua	15.97	61.1	Meredith et al., 2011
11*	Phyllophaga	15.97	41.3	Springer et al., 2017
12*	Pilosa	31.5	66	Springer et al., 2017
13*	Xenarthra	47.8	66	Springer et al., 2017
14	Proboscidea	6.8	23.03	Meredith et al.,

				2011
15*	Hyracoidea	6.08	11.62	Springer et al., 2017
16	Sirenia	31.4	40.6	Meredith et al., 2011
17	Macroscelidea	15.97	56	Meredith et al., 2011
18	Chrysochloridae	1.7	33.9	Meredith et al., 2011
19*	Paenungulata	55.6	71.2	Springer et al., 2017
20	Lagomorpha	53.7	61.6	Meredith et al., 2011
21	Emballonuroidea	47.8	59.2	Meredith et al., 2011
22	Hipposideridae+Rhinolophidae	38	56	Meredith et al., 2011
23	Craseonycteridae+Megadermatidae	33.9	47.8	Meredith et al., 2011
24	Molossidae+Vespertilionidae+Miniopteridae	38	56	Meredith et al., 2011
25	Phyllostomidae+Mormoopidae	28.1	41.3	Meredith et al., 2011
26	Furipteridae+Noctilionidae	5.332	33.9	Meredith et al., 2011
27*	Chiroptera	47.8	66	Springer et al., 2017
28*	Yangochiroptera	47.8	61.6	Springer et al., 2017
29*	Caniformia	37.1	56	Springer

				et al., 2017
30	Procyonidae+Mustelidae	27.6	40.6	Meredith et al., 2011
31*	Otariidae+Odobenidae	15.97	34	Springer et al., 2017
32*	Pinnipedia	20.43	34	Springer et al., 2017
33	Felidae+Prionodontidae	28.1	41.3	Meredith et al., 2011
34*	Herpestidae+Eupleridae	15.97	34	Springer et al., 2017
35*	Ferae	64	83.8	Springer et al., 2017
36*	Carnivora	38	66	Springer et al., 2017
37*	Lorisidae+Galagidae	38	56	Springer et al., 2017
38*	Haplorrhini	38	59.2	Springer et al., 2017
39*	Anthropoidea	28.3	56	Meredith et al., 2011
40*	Primatomorpha	65.2	83.8	Springer et al., 2017
41*	Primates	38	66	Springer et al., 2017
42	Catarrhini	20.55	37.3	Meredith et al., 2011
43*	Strepsirrhini	38	56	Springer et al., 2017

44*	Scandentia	34	66	Meredith et al., 2011
45*	Perissodactyla	55.5	61.1	Springer et al., 2017
46*	Erinaceidae+Soricidae	61.6	83.8	Springer et al., 2017
47	Erinaceidae	28.1	47.8	Meredith et al., 2011
48*	Artiodactyla	52.5	65.8	Springer et al., 2017
49*	Giraffidae+Antilocapridae	17.8	34	Springer et al., 2017
50*	Balaenopteridae+Eschrichtiidae	7.3	23.03	Springer et al., 2017
51	Bovidae+Moschidae	18	34	Meredith et al., 2011
52*	Suidae+Tayassuidae	15.97	37.3	Springer et al., 2017
53*	Whippomorpha	52.5	61.1	Springer et al., 2017
54*	Cetacea	33.8	48.8	Springer et al., 2017
55*	Mysticeti	20.43	34	Springer et al., 2017
56	Physeteroidea	11.608	28.5	Meredith et al., 2011
57*	Phocoenidae+Monodontidae	12.1	28.5	Springer et al., 2017
58*	Rodentia	56	66	Springer et al.,

				2017
59	Sciuridae+Aplodontiidae	45.7	59.2	Springer et al., 2017
60*	Sciuromorpha	47.8	61.1	Springer et al., 2017
61*	Octodontoidea+Ctenomyidae+Octodontidae	24.5	38	Springer et al., 2017
62*	Ctenomyidae+Octodontidae	9.07	33.9	Springer et al., 2017
63*	Chinchillidae+Dinomyidae	24.5	38	Springer et al., 2017
64	Hydrochoeridae+Caviidae	11.8	34	Meredith et al., 2011
65	Caviidae+Dasyproctidae	24.5	38	Meredith et al., 2011
66*	Anomaluromorpha+Myomorpha	54	61.6	Springer et al., 2017
67	Anomaluromorpha	37.1	56	Meredith et al., 2011
68	Geomyoidea	31.4	41.3	Meredith et al., 2011
69*	Castorimorpha+Heteromyidae	52.4	61.1	Springer et al., 2017
70*	Myomorpha	45	59.2	Springer et al., 2017
71	Ctenodactylidae	28.3	47.8	Meredith et al., 2011
72	Anomaluromorpha+Castorimorpha+Myomorpha	54	66	Meredith et al., 2011
73*	Mammalia	164.9	227	Springer

				et al., 2017
74	Amniota	318	332.9	Meredith et al., 2011
75	Tetrapoda	337	351	Meredith et al., 2011
76	Sarcopterygii + Actinopterygii	420.7	444.9	Meredith et al., 2011

Note: *, the shared calibration fossil record between two datasets

Supplementary Table S11. Bayesian selection of molecular clocks for dataset A and B amino acid alignments.

Data	Clocks	-logL	S.E.	BF	Pr(M|D)
Dataset A AA	CLK	5882.798	2.214	0.000	0.000
	IR	1195.989	2.220	4686.809	0.000
	AR	**1128.256**	**2.568**	**4754.542**	**1.000**
Dataset B DNA	CLK	10552.860	1.672	0.000	0.000
	IR	976.233	1.807	9576.627	0.000
	AR	**957.524**	**2.118**	**9595.336**	**1.000**
Dataset B AA	CLK	3012.954	1.707	0.000	0.000
	IR	**708.276**	**1.886**	**2304.678**	**0.976**
	AR	711.996	1.767	2300.958	0.024

Note: **BF**: Bayes factors, **CLK**： strict clock, **IR**: Independent-rates model under log-normal distribution, **AR**: Autocorrelated-rates model under geometric Brownian motion.

Supplementary Table S12. The divergence time difference between this study and Meredith et al. (2011) from DNA alignments.

Order	Class	Mean	Lower	Upper	Width	Class	Mean	Lower	Upper	Width	Δmean	Δwidth
Agreodontia	26DNA_new	55.04	49.69	61.33	11.64	26DNA_meredith	53.56	51.44	55.99	4.55	3.60	7.09
Eomarsupialia	26DNA_new	56.61	51.37	62.76	11.39	26DNA_meredith	54.02	51.95	56.44	4.49	2.59	6.9
Australidelphia	26DNA_new	59.88	54.40	66.39	11.99	26DNA_meredith	55.76	53.65	58.31	4.66	6.23	7.33
Xenarthra	26DNA_new	60.33	51.72	66.70	14.98	26DNA_meredith	61.57	58.43	66.79	8.36	-1.24	6.62
Paenungulata	26DNA_new	63.42	55.51	70.18	14.67	26DNA_meredith	63.60	59.04	68.78	9.74	4.38	4.93
Afroinsectivora	26DNA_new	73.25	61.51	79.63	18.12	26DNA_meredith	77.13	72.09	93.94	21.85	-3.88	-3.73
Afroinsectiphilia	26DNA_new	75.78	64.37	81.88	17.51	26DNA_meredith	78.29	73.19	95.18	21.99	2.59	-4.48
Ferae	26DNA_new	76.01	72.06	80.02	7.96	26DNA_meredith	78.63	73.57	81.40	7.83	-2.62	0.13
Glires	26DNA_new	76.99	73.59	80.54	6.95	26DNA_meredith	81.25	79.13	83.47	4.34	-2.14	2.61
Afrotheria	26DNA_new	77.80	66.45	83.76	17.31	26DNA_meredith	79.47	74.41	96.51	22.10	-1.67	-4.79
Primatomorpha	26DNA_new	79.40	75.65	83.63	7.98	26DNA_meredith	83.37	81.15	85.75	4.60	-1.75	3.38
Variamana	26DNA_new	80.39	76.93	83.84	6.91	26DNA_meredith	81.48	76.56	83.90	7.34	-1.09	-0.43

Marsupialia	26DNA_new	80.44	72.75	84.81	12.06	26DNA_meredith	71.68	67.93	75.33	7.40	12.51	4.66
Euarchontoglires	26DNA_new	81.30	77.78	85.05	7.27	26DNA_meredith	83.89	81.82	86.16	4.34	-2.59	2.93
Laurasiatheria	26DNA_new	84.09	80.01	88.50	8.49	26DNA_meredith	84.05	80.14	86.39	6.25	3.95	2.24
Boreoeutheria	26DNA_new	91.84	86.92	97.03	10.11	26DNA_meredith	91.67	89.23	94.67	5.44	0.17	4.67
Placentalia	26DNA_new	101.37	94.58	108.21	13.63	26DNA_meredith	100.99	97.20	114.66	17.46	4.17	-3.83
Eulipotyphla	26DNA_new	78.10	73.29	82.91	9.62	26DNA_meredith	76.89	72.48	79.91	7.43	1.21	2.19
Rodentia	26DNA_new	67.02	65.63	68.84	3.21	26DNA_meredith	72.95	71.15	74.80	3.65	-4.13	-0.44
Afrosoricida	26DNA_new	64.88	54.14	73.37	19.23	26DNA_meredith	70.75	65.36	87.96	22.6	-5.87	-3.37
Artiodactyla	26DNA_new	64.85	62.50	66.57	4.07	26DNA_meredith	64.90	62.34	66.34	4.00	2.51	0.07
Primates	26DNA_new	64.70	64.35	67.43	3.08	26DNA_meredith	71.90	67.04	75.35	8.31	-7.20	-5.23
Chiroptera	26DNA_new	64.69	61.49	66.95	5.46	26DNA_meredith	65.81	62.74	68.03	5.29	1.95	0.17
Perissodactyla	26DNA_new	57.62	55.33	60.85	5.52	26DNA_meredith	55.87	55.08	57.37	2.29	1.75	3.23
Carnivora	26DNA_new	56.28	50.73	62.25	11.52	26DNA_meredith	50.37	47.35	53.41	6.06	8.93	5.46
Lagomorpha	26DNA_new	55.69	53.21	59.80	6.59	26DNA_meredith	51.52	48.21	54.45	6.24	4.17	0.35

Pilosa	26DNA_new	52.56	43.32	60.59	17.27	26DNA_meredith	53.9	50.28	59.00	8.72	2.28	8.55
Scandentia	26DNA_new	52.40	40.20	64.10	23.90	26DNA_meredith	56.25	51.00	62.33	11.33	-3.85	12.57
Macroscelidea	26DNA_new	48.38	39.23	56.63	17.40	26DNA_meredith	52.32	46.29	56.99	10.70	2.09	6.70
Diprotodontia	26DNA_new	48.22	43.56	53.32	9.76	26DNA_meredith	45.13	42.42	47.85	5.43	3.09	4.33
Didelphimorphia	26DNA_new	38.78	29.84	47.71	17.87	26DNA_meredith	29.17	25.65	32.37	6.72	13.13	11.15
Sirenia	26DNA_new	32.40	30.58	35.21	4.63	26DNA_meredith	29.28	24.96	31.57	6.61	3.12	-1.98
Pholidota	26DNA_new	27.87	17.10	39.42	22.32	26DNA_meredith	20.15	16.91	24.96	8.05	10.96	14.27
Dasyuromorphia	26DNA_new	27.01	18.61	34.18	15.57	26DNA_meredith	25.66	22.15	29.64	7.49	1.35	8.08
Peramelemorphia	26DNA_new	26.47	19.18	34.06	14.88	26DNA_meredith	24.26	21.05	27.69	6.64	5.42	8.24
Paucituberculata	26DNA_new	11.81	7.70	16.00	8.30	26DNA_meredith	10.28	7.96	12.94	4.98	1.53	3.32
Dermoptera	26DNA_new	11.10	6.08	16.08	10.00	26DNA_meredith	7.32	5.91	8.96	3.05	3.78	6.22
Hyracoidea	26DNA_new	7.13	5.72	9.33	3.61	26DNA_meredith	4.91	3.87	6.07	2.20	2.22	1.41
Proboscidea	26DNA_new	6.04	4.04	7.73	3.69	26DNA_meredith	2.44	1.79	3.21	1.42	4.25	2.27
Sum											75.90 (p=4.56e-02)	123.79 (p=3.43e-04)

Note: Δmean represents the difference mean values of in this study and Meredith et al. (2011); Δwidth represents the difference width values of in this study and Meredith et al. (2011). P values was calculated by paired Wilcoxon signed rank test.

Supplementary Table S13. The divergence time difference between this study and Meredith et al. (2011) from protein sequences.

Order	Class	Mean	Lower	Upper	Width	Class	Mean	Lower	Upper	Width	Δmean	Δwidth
Agreodontia	21AA_new	59.84	54.7	65.11	10.41	21AA_meredith	65.10	60.01	70.22	10.21	-5.26	-0.20
Eomarsupialia	21AA_new	61.83	56.43	66.67	10.24	21AA_meredith	66.38	61.41	71.58	10.17	-4.55	-0.07
Australidelphia	21AA_new	64.89	59.83	69.83	10.00	21AA_meredith	68.36	61.41	71.58	10.17	-3.47	0.17
Xenarthra	21AA_new	60.89	51.30	67.00	15.70	21AA_meredith	68.42	63.11	71.50	8.39	-7.53	-7.31
Paenungulata	21AA_new	63.65	56.48	70.56	14.08	21AA_meredith	64.70	60.21	69.41	9.20	-1.05	-4.88
Afroinsectivora	21AA_new	66.63	59.07	74.38	15.31	21AA_meredith	76.75	71.44	80.90	9.46	-10.12	-5.85
Afroinsectiphilia	21AA_new	69.58	61.76	76.97	15.21	21AA_meredith	77.98	72.89	81.90	9.01	-8.40	-6.20
Ferae	21AA_new	73.42	70.41	76.59	6.18	21AA_meredith	80.56	78.03	82.98	4.95	-7.14	-1.23
Glires	21AA_new	72.00	69.61	75.54	5.93	21AA_meredith	78.70	79.13	94.12	14.99	-6.70	9.06
Afrotheria	21AA_new	72.08	64.51	79.52	15.01	21AA_meredith	81.77	77.31	85.30	7.99	-9.69	-7.02
Primatomorpha	21AA_new	75.38	72.38	78.35	5.97	21AA_meredith	81.74	79.33	84.14	4.81	-6.36	-1.16
Variamana	21AA_new	76.70	73.56	80.04	6.48	21AA_meredith	82.33	80.04	84.49	4.45	-5.63	-2.03
Marsupialia	21AA_new	80.58	76.48	84.38	7.90	21AA_meredith	87.87	81.57	96.45	14.88	-7.29	6.98

Euarchontoglires	21AA_new	77.88	74.72	81.08	6.36	21AA_meredith	83.26	81.02	85.46	4.44	-5.38	-1.92
Laurasiatheria	21AA_new	79.12	75.68	82.94	7.26	21AA_meredith	84.64	82.14	87.02	4.88	-5.52	-2.38
Boreoeutheria	21AA_new	85.81	80.79	90.99	10.20	21AA_meredith	91.34	88.83	93.85	5.02	-5.53	-5.18
Placentalia	21AA_new	92.22	85.11	99.78	14.67	21AA_meredith	100.74	97.37	104.11	6.74	-8.52	-7.93
Eulipotyphla	21AA_new	71.82	68.31	75.49	7.18	21AA_meredith	75.71	72.07	79.13	7.06	-3.89	-0.12
Rodentia	21AA_new	65.71	64.21	66.94	2.73	21AA_meredith	68.60	67.00	74.80	7.80	-2.89	5.07
Afrosoricida	21AA_new	58.20	50.07	66.57	16.5	21AA_meredith	64.78	57.83	69.8	11.97	-6.58	-4.53
Artiodactyla	21AA_new	64.23	62.06	66.21	4.15	21AA_meredith	66.11	64.64	67.98	3.34	-1.88	-0.81
Primates	21AA_new	66.19	63.89	68.59	4.70	21AA_meredith	75.77	73.02	78.43	5.41	-9.58	0.71
Chiroptera	21AA_new	64.98	62.58	67.12	4.54	21AA_meredith	66.39	63.34	69.48	6.14	-1.41	1.60
Perissodactyla	21AA_new	58.28	55.58	61.14	5.56	21AA_meredith	58.03	55.47	60.98	5.51	0.25	-0.05
Carnivora	21AA_new	58.91	54.41	63.43	9.02	21AA_meredith	57.12	53.68	60.64	6.96	1.79	-2.06
Lagomorpha	21AA_new	54.66	53.08	56.95	3.87	21AA_meredith	49.07	47.40	51.77	4.37	5.59	0.50
Pilosa	21AA_new	50.81	40.78	58.84	18.06	21AA_meredith	57.93	52.8	62.44	9.64	-7.12	-8.42

Scandentia	21AA_new	49.91	36.87	60.58	23.71	21AA_meredith	57.54	51.00	63.05	12.05	-7.63	11.66
Macroscelidea	21AA_new	42.37	31.84	54.39	22.55	21AA_meredith	45.70	38.44	53.25	14.81	-3.33	-7.74
Diprotodontia	21AA_new	54.51	49.24	59.92	10.68	21AA_meredith	56.32	51.52	61.30	9.78	-1.81	-0.90
Didelphimorphia	21AA_new	37.84	25.75	49.13	23.38	21AA_meredith	31.09	26.04	36.45	10.41	6.75	-12.97
Sirenia	21AA_new	33.82	30.77	38.26	7.49	21AA_meredith	31.86	30.52	34.09	3.57	1.96	-3.92
Pholidota	21AA_new	29.91	15.67	42.99	27.32	21AA_meredith	27.24	18.98	35.44	16.46	2.67	10.86
Dasyuromorphia	21AA_new	29.52	18.88	39.35	20.47	21AA_meredith	32.02	25.37	39.6	14.23	-2.50	-6.24
Peramelemorphia	21AA_new	26.62	16.18	37.76	21.58	21AA_meredith	29.35	24.59	35.06	10.47	-2.73	-11.11
Paucituberculata	21AA_new	13.02	7.30	16.84	9.54	21AA_meredith	13.32	8.55	16.18	7.63	-0.30	-1.91
Dermoptera	21AA_new	17.14	6.50	26.61	20.11	21AA_meredith	7.38	5.91	10.12	4.21	9.76	10.35
Hyracoidea	21AA_new	7.98	5.81	11.08	5.27	21AA_meredith	6.09	4.62	7.75	3.13	1.89	-2.14
Proboscidea	21AA_new	9.60	5.71	15.81	10.11	21AA_meredith	5.19	3.22	7.06	3.84	4.41	-6.26
Sum											-124.72 (p = 2.84e-04)	-65.58 (p=4.40e-05)

Note: Δmean represents the difference mean values of in this study and Meredith et al. (2011); Δwidth represents the difference width values of in this study and Meredith et al. (2011). P value is from paired Wilcoxon Signed Rank Test. P values was calculated by paired Wilcoxon signed rank test.

Supplementary Table S14. The comparation of the divergence time with different DNA datasets and fossil calibrations under the autocorrelated clock.

Order	Old_data_new_calibration		New_data_old_calibration		Old_data_old_calibration*		New_data_new_calibration	
	Mean	95% HPD	Mean	95% HPD	Mean	95%HPD	Mean	95%HPD
Agreodontia	61.03	55.27-66.40	60.97	56.14-65.07	63.03	61.71-68.28	61.00	55.99-65.06
Eomarsupialia	62.34	56.61-67.61	62.35	57.68-66.37	65.01	62.35-68.88	61.38	57.55-66.44
Australidelphia	64.87	55.34-70.16	65.03	60.51-69.08	66.69	63.88-70.66	65.05	60.42-69.16
Xenarthra	60.96	51.15-67.04	63.97	59.49-67.43	64.19	60.18-68.65	63.94	59.39-67.27
Paenungulata	63.39	56.21-70.78	65.90	61.65-69.87	65.63	62.77-69.12	65.64	61.16-69.63
Afroinsectivora	68.35	60.35-75.68	71.04	66.28-75.29	77.98	74.83-81.26	70.75	65.55-74.92
Afroinsectiphilia	70.33	62.51-77.79	73.03	68.54-77.28	79.10	76.02-82.33	72.78	67.59-76.95
Ferae	73.91	70.60-77.23	74.91	72.89-77.04	79.49	77.48-81.50	74.96	72.94-77.31
Glires	72.28	69.56-74.97	74.09	72.32-75.87	78.50	76.69-80.23	74.08	72.25-75.93
Afrotheria	71.98	64.10-79.44	74.64	70.20-78.81	80.66	77.70-83.78	74.40	69.26-78.69
Primatomorpha	75.24	72.18-78.45	77.11	75.11-79.14	81.69	79.90-83.45	77.09	74.96-79.14
Variamana	76.60	73.05-80.16	77.87	75.80-80.08	81.71	79.85-83.62	77.94	75.73-80.22
Marsupialia	79.13	74.71-84.03	80.76	77.40-84.11	82.21	78.81-86.72	80.78	77.28-84.27
Euarchontoglires	76.59	73.23-79.91	78.49	76.47-80.61	81.91	80.16-83.64	92.81	88.17-97.36
Laurasiatheria	78.53	74.53-82.29	79.94	77.60-82.19	83.81	81.85-85.81	80.00	77.52-82.45
Boreoeutheria	85.22	79.67-90.56	86.91	83.93-89.89	90.05	88.06-92.11	86.93	83.74-90.25
Placentalia	92.07	84.35-99.80	94.31	90.17-98.66	99.19	96.55-102.00	94.29	89.75-99.13
Eulipotyphla	71.88	68.14-75.93	72.90	70.44-75.26	77.02	74.58-79.45	72.98	70.39-75.51

Rodentia	65.15	63.33-66.51	65.99	65.10-66.85	68.20	66.70-69.64	66.00	65.06-66.91
Afrosoricida	62.54	54.70-71.00	65.37	60.77-69.78	71.05	67.11-75.01	74.40	69.26-78.69
Artiodactyla	64.28	62.10-66.17	64.68	63.24-66.04	66.67	65.31-68.46	64.90	63.24-66.07
Primates	66.22	63.82-68.73	69.62	67.45-71.60	75.47	73.42-77.54	69.62	67.52-71.76
Chiroptera	71.88	68.14-75.93	72.90	70.44-75.26	66.98	64.96-68.91	65.13	63.29-66.57
Perissodactyla	58.37	55.60-61.12	58.45	55.69-61.09	56.07	55.14-57.81	58.38	55.47-60.84
Carnivora	59.43	55.04-63.70	58.32	55.40-61.41	57.68	55.29-60.02	58.35	55.29-61.43
Lagomorpha	54.89	53.12-57.47	54.03	52.91-55.57	49.11	47.49-51.78	54.05	52.88-55.62
Pilosa	52.38	42.13-59.93	55.60	50.72-59.71	56.50	18.84-32.41	55.55	50.53-59.72
Scandentia	49.98	37.14-60.57	54.00	47.78-59.90	56.30	51.51-60.77	53.91	47.29-60.24
Macroscelidea	44.34	34.43-56.01	48.25	41.14-54.59	48.02	38.44-53.25	47.89	40.50-54.57
Diprotodontia	55.50	50.13-61.09	54.93	50.37-59.11	55.74	51.52-61.30	54.92	50.45-59.03
Didelphimorphia	38.33	24.64-50.94	43.10	34.50-50.45	34.96	26.04-36.45	42.52	33.83-52.94
Sirenia	33.98	30.84-38.72	32.18	30.58-34.43	31.35	30.52-34.09	32.19	30.55-34.57
Pholidota	30.59	15.31-44.24	32.11	22.09-40.25	25.47	19.15-35.44	32.10	22.81-41.15
Dasyuromorphia	27.99	17.32-39.06	28.15	21.01-34.61	29.72	22.15-32.32	28.32	21.15-34.78
Peramelemorphia	28.32	17.21-39.74	25.71	19.95-32.61	28.92	21.05-30.36	25.63	19.33-32.79
Paucituberculata	12.81	7.00-16.93	13.49	9.57-16.67	12.49	7.96-13.71	13.47	9.38-16.57
Dermoptera	18.39	6.70-28.65	15.69	10.37-22.34	7.44	5.91-10.12	15.48	10.36-22.62
Hyracoidea	8.02	5.89-11.22	6.87	5.66-8.76	5.62	3.87-6.94	6.86	5.65-8.71
Proboscidea	10.26	5.85-16.99	7.45	5.46-9.99	2.92	1.79-7.21	7.45	5.40-9.96
P value	(Δmean-oldold/oldnew = 86.2; p=7.16e-03); (Δ95%HPD-oldold/oldnew = -233.46; p=3.64e-12);							

	(Δmean-newold/newnew = -12.81; p=0.283); (Δ95%HPD-newold/newnew = -16.1; p=6.141e-06); (Δmean-oldold/newold = 43.44; p=0.053); (Δ95%HPD-oldold/newold = -42.76; p=1.73e-03) (Δmean-oldnew/newnew = -55.57; p=5.70e-03);95%HPD-oldnew/newnew = 174.6; p=4.00e-10);

Old_data_new_calibration was the Meredith et al.'s (2011) DNA dataset and new (in this study we updated) fossil calibrations; New_data_old_calibration was the new DNA dataset generated in this study and Meredith et al.'s (2011) fossil calibrations; Old_data_old_calibration was Meredith et al.'s (2011) DNA dataset and fossil calibrations and the mean value and 95% was from the Meredith et al. (2011) study; New_data_new_calibration was new dataset and fossil calibration generated in this study. Δmean-oldold/oldnew and Δ95%HPD-oldold/oldnew was the comparation of the mean value and 95%HPD between Old_data_old_calibration and Old_data_new_calibration, respectively. The front part of the bracket was the different value and the latter part of the bracket was the p value calculated by paired Wilcoxon signed rank test. *: the results from Meredith et al. (2011) study.

Supplementary Table S15. The likelihood tests of rate-constant (RC) and rate-variable (RV) models of mammalian diversification from R packages.

Models	LH	AIC	*r*1	*r*2	*r*3	Package
PB	**-114.036**	**230.071**	**0.022**			laser
BD	-111.036	232.071	0.022			laser
DDX	-106.394	216.788	0.066			laser
DDL	-95.800	192.598	0.033			laser
yule2rate	-78.601	163.202	0.028	0.001		laser
yule3rate	**-69.722**	**149.444**	**0.036**	**0.014**	**0.002**	laser
Models	LH	AICc	Lamb_par	Mu_par		Package
PB	**-773.751**	**1549.528**	**0.022**	**0**		RPANDA
BD	-773.752	1551.578	0.022	1.310×10^{-08}		RPANDA
B-Exp	-767.392	1538.86	0.017,0.007	0		RPANDA
B-Exp_D	-767.392	1540.936	0.017,0.007	7.209×10^{-09}		RPANDA
B_D-Exp	-751.382	1508.916	0.039	8.136×10^{02}, 7.431×10^{02}	-	RPANDA
B-Exp_D-Exp	-747.715	1503.684	0.012,0.020	1.460×10^{-03}, 3.362×10^{-02}		RPANDA
B-Lin	-752.352	1508.778	0.002,0.001	0		RPANDA
B-Lin_D	-752.352	1510.855	0.002,0.001	4.557×10^{-09}		RPANDA
B_D-Lin	**-741.540**	**1489.232**	**0.059**	**1.398×10^{01},** **4.122×10^{01}**		RPANDA
B-Lin_D-Lin	-752.352	1512.958	0.002,0.001	-1.28×10^{-02}, 7.500×10^{-04}	-	RPANDA

Abbreviations: LH, log-likelihood; AIC, Aaike Information Criterion; AICc, corrected Akaike

Information Criterion; *r*1, *r*2, *r*3, net diversification rates, as applicable for models; Lamb_par, speciation rate λ parameter; Mu_par, extinction rate μ parameter; PB, pure birth model with constant speciation rate; BD, birth-death model with constant speciation and extinction rate; DDX, fit exponential variants of the density-dependent speciation rate model; DDL, fit logistic variants of the density-dependent speciation rate model; yule2rate, pure birth (Yule) model assumes that the clade has diversified under net diversification rate *r*1 until some time point *st*, at which point the diversification rate shifts to a new rate *r2*, yule3rate assumes diversification rate *r*1 until some time point *st1* shifts to a new rate *r2*, then to another time point *st2* shifts to a new rate *r2*; B-Exp, pure birth with exponential variation of the speciation rate; D-Exp, birth-death model with exponential variation of the extinction rate; B-Lin, pure birth with linear variation of speciation rate; D-Lin, birth-death model with linear variation of the extinction rate.

Supplementary Table S16. The zombie and ghost lineages implied from mammalian timetree.

Dataset	Molecular clock	Calibration clade	Fossil record from Minage to Maxage	95% HPD of divergence time	Lineages types
Dataset A DNAs	AR	Octodontoidea	(24.5, 38.0)	(19.6, 23.9)	ghost
		Lorisidae + Galagidae	(38.0, 56.0)	(30.2,37.3)	ghost
		Primates	(38.0, 66.0)	(67.5,71.7)	zombie
		Haplorrhini	(38.0, 59.2)	(62.2,67.5)	zombie
Dataset B DNAs	IR	Scandentia	(34.0, 66.0)	(1.4, 12.2)	ghost
		Anthropoidea	(28.3, 56.0)	(6.4, 27.5)	ghost
	AR	Scandentia	(34.0, 66.0)	(6.4, 27.5)	ghost
Dataset B proteins	IR	Scandentia	(34.0, 66.0)	(2.5, 16.3)	ghost
		Anthropoidea	(28.3, 56.0)	(6.9, 26.7)	ghost
	AR	Scandentia	(34.0, 66.0)	(5.0, 28.6)	ghost

Abbreviations: AR, autocorrelated rates model; IR, independent rates model; Minage, Minimum Age; MaxAge, Maximum Age; HPD, highest posterior density intervals.

Supplementary Table S17. The divergence time difference between all and partial calibrations from DNA alignments under the independent clock.

Order	Class	Mean	Lower	Upper	Width	Class	Mean	Lower	Upper	Width	Δmean	Δwidth
Agreodontia	26DNA_new	55.04	49.69	61.33	11.64	26DNA_recalibration	54.65	49.29	61.05	11.76	0.39	-0.12
Eomarsupialia	26DNA_new	56.61	51.37	62.76	11.39	26DNA_recalibration	56.19	50.87	62.44	11.57	0.42	-0.18
Australidelphia	26DNA_new	59.88	54.40	66.39	11.99	26DNA_recalibration	59.45	53.86	66.07	12.21	0.43	-0.22
Xenarthra	26DNA_new	60.33	51.72	66.70	14.98	26DNA_recalibration	60.58	51.97	66.83	14.86	-0.25	0.12
Paenungulata	26DNA_new	63.42	55.51	70.18	14.67	26DNA_recalibration	63.90	55.53	70.68	15.15	-0.48	-0.48
Afroinsectivora	26DNA_new	73.25	61.51	79.63	18.12	26DNA_recalibration	73.52	62.16	80.15	17.99	-0.27	0.13
Afroinsectiphilia	26DNA_new	75.78	64.37	81.88	17.51	26DNA_recalibration	76.07	65.25	82.50	17.25	-0.29	0.26
Ferae	26DNA_new	76.01	72.06	80.02	7.96	26DNA_recalibration	76.55	72.33	80.69	8.36	-0.54	-0.40
Glires	26DNA_new	76.99	73.59	80.54	6.95	26DNA_recalibration	77.68	74.15	81.31	7.16	-0.69	-0.21
Afrotheria	26DNA_new	77.80	66.45	83.76	17.31	26DNA_recalibration	78.10	67.08	84.31	17.23	-0.30	0.08
Primatomorpha	26DNA_new	79.40	75.65	83.63	7.98	26DNA_recalibration	80.44	76.63	84.19	7.56	-1.04	0.42
Variamana	26DNA_new	80.39	76.93	83.84	6.91	26DNA_recalibration	80.84	76.91	84.33	7.42	-0.45	-0.51
Marsupialia	26DNA_new	80.44	72.75	84.81	12.06	26DNA_recalibration	79.72	71.41	84.62	13.21	0.72	-1.15

Euarchontoglires	26DNA_new	81.30	77.78	85.05	7.27	26DNA_recalibration	82.19	78.44	85.86	7.42	-0.89	-0.15
Laurasiatheria	26DNA_new	84.09	80.01	88.50	8.49	26DNA_recalibration	84.46	80.03	88.83	8.80	-0.37	-0.31
Boreoeutheria	26DNA_new	91.84	86.92	97.03	10.11	26DNA_recalibration	92.33	87.39	97.48	10.09	-0.49	0.02
Placentalia	26DNA_new	101.37	94.58	108.21	13.63	26DNA_recalibration	101.68	94.67	108.58	13.91	-0.31	-0.28
Eulipotyphla	26DNA_new	78.10	73.29	82.91	9.62	26DNA_recalibration	78.21	72.87	83.09	10.22	-0.11	-0.60
Rodentia	26DNA_new	67.02	65.63	68.84	3.21	26DNA_recalibration	67.28	65.76	69.22	3.46	-0.26	-0.25
Afrosoricida	26DNA_new	64.88	54.14	73.37	19.23	26DNA_recalibration	65.46	54.51	73.61	19.10	-0.58	0.13
Artiodactyla	26DNA_new	64.85	62.50	66.57	4.07	26DNA_recalibration	64.95	62.76	66.64	3.88	-0.10	0.19
Primates	26DNA_new	64.70	64.35	67.43	3.08	26DNA_recalibration	69.74	63.09	78.18	15.09	-5.04	-12.01
Chiroptera	26DNA_new	64.69	61.49	66.95	5.46	26DNA_recalibration	64.83	61.81	67.06	5.25	-0.14	0.21
Perissodactyla	26DNA_new	57.62	55.33	60.85	5.52	26DNA_recalibration	57.57	55.33	60.81	5.48	0.05	0.04
Carnivora	26DNA_new	56.28	50.73	62.25	11.52	26DNA_recalibration	56.64	51.45	62.21	10.76	-0.36	0.76
Lagomorpha	26DNA_new	55.69	53.21	59.80	6.59	26DNA_recalibration	55.74	53.20	59.92	6.72	-0.05	-0.13
Pilosa	26DNA_new	52.56	43.32	60.59	17.27	26DNA_recalibration	52.76	43.39	60.82	17.43	-0.20	-0.16

Scandentia	26DNA_new	52.04	40.20	64.10	23.9	26DNA_recalibration	52.99	40.53	63.88	23.35	-0.95	0.55
Macroscelidea	26DNA_new	48.38	39.23	56.63	17.4	26DNA_recalibration	48.43	39.38	56.76	17.38	-0.05	0.02
Diprotodontia	26DNA_new	48.22	43.56	53.32	9.76	26DNA_recalibration	47.85	43.19	52.95	9.76	0.37	0
Didelphimorphia	26DNA_new	38.78	29.84	47.71	17.87	26DNA_recalibration	37.48	29.11	47.74	18.63	1.30	-0.76
Sirenia	26DNA_new	32.40	30.58	35.21	4.63	26DNA_recalibration	32.37	30.50	35.10	4.60	0.03	0.03
Pholidota	26DNA_new	27.87	17.10	39.42	22.32	26DNA_recalibration	27.90	17.48	40.86	23.38	-0.03	-1.06
Dasyuromorphia	26DNA_new	27.01	18.61	34.18	15.57	26DNA_recalibration	26.63	18.92	34.22	15.30	0.38	0.27
Peramelemorphia	26DNA_new	26.47	19.18	34.06	14.88	26DNA_recalibration	26.18	19.02	33.04	14.02	0.29	0.86
Paucituberculata	26DNA_new	11.81	7.70	16.00	8.30	26DNA_recalibration	11.78	7.72	16.07	8.35	0.03	-0.05
Dermoptera	26DNA_new	11.10	6.08	16.08	10.00	26DNA_recalibration	10.96	6.01	15.82	9.81	0.14	0.19
Hyracoidea	26DNA_new	7.13	5.72	9.33	3.61	26DNA_recalibration	7.09	5.73	9.23	3.50	0.04	0.11
Proboscidea	26DNA_new	6.04	4.04	7.73	3.69	26DNA_recalibration	5.96	4.02	7.66	3.64	0.08	0.05
Sum											-9.57 (p = 8.89e-01)	-14.59 (p=2.74e-01)

P values was calculated by paired Wilcoxon signed rank test.

Supplementary Table S18. The divergence time difference between all and partial calibrations from protein alignments under the autocorrelated clock.

Order	Class	Mean	Lower	Upper	Width	Class	Mean	Lower	Upper	Width	Δmean	Δwidth
Agreodontia	21AA_new	59.84	54.70	65.11	10.41	21AA_recalibration	60.11	54.74	65.51	10.77	-0.27	-0.36
Eomarsupialia	21AA_new	61.83	56.43	66.67	10.24	21AA_recalibration	62.20	56.81	67.32	10.51	-0.37	-0.27
Australidelphia	21AA_new	64.89	59.83	69.83	10.00	21AA_recalibration	65.37	60.30	70.31	10.01	-0.48	-0.01
Xenarthra	21AA_new	60.89	51.30	67.00	15.70	21AA_recalibration	62.05	53.09	67.30	14.21	-1.16	1.49
Paenungulata	21AA_new	63.65	56.48	70.56	14.08	21AA_recalibration	65.52	58.21	71.26	13.05	-1.87	1.03
Afroinsectivora	21AA_new	66.63	59.07	74.38	15.31	21AA_recalibration	68.73	60.88	75.32	14.44	-2.10	0.87
Afroinsectiphilia	21AA_new	69.58	61.76	76.97	15.21	21AA_recalibration	71.91	64.15	78.40	14.25	-2.33	0.96
Ferae	21AA_new	73.42	70.41	76.59	6.18	21AA_recalibration	74.92	71.91	78.12	6.21	-1.50	-0.03
Glires	21AA_new	72.00	69.61	75.54	5.93	21AA_recalibration	73.93	71.26	76.66	5.40	-1.93	0.53
Afrotheria	21AA_new	72.08	64.51	79.52	15.01	21AA_recalibration	74.61	66.90	81.20	14.3	-2.53	0.71
Primatomorpha	21AA_new	75.38	72.38	78.35	5.97	21AA_recalibration	78.28	75.11	81.60	6.49	-2.90	-0.52
Variamana	21AA_new	76.70	73.56	80.04	6.48	21AA_recalibration	78.54	75.30	81.78	6.48	-1.84	0

Marsupialia	21AA_new	80.58	76.48	84.38	7.90	21AA_recalibration	82.01	78.33	84.81	6.48	-1.43	1.42
Euarchontoglires	21AA_new	77.88	74.72	81.08	6.36	21AA_recalibration	80.58	77.31	83.96	6.65	-2.70	-0.29
Laurasiatheria	21AA_new	79.12	75.68	82.94	7.26	21AA_recalibration	81.18	77.68	84.88	7.20	-2.06	0.06
Boreoeutheria	21AA_new	85.81	80.79	90.99	10.20	21AA_recalibration	88.60	83.72	93.28	9.56	-2.79	0.64
Placentalia	21AA_new	92.22	85.11	99.78	14.67	21AA_recalibration	95.53	88.78	102.16	13.38	-3.31	1.29
Eulipotyphla	21AA_new	71.82	68.31	75.49	7.18	21AA_recalibration	73.01	69.37	76.60	7.23	-1.19	-0.05
Rodentia	21AA_new	65.71	64.21	66.94	2.73	21AA_recalibration	66.09	64.90	67.30	2.40	-0.38	0.33
Afrosoricida	21AA_new	58.20	50.07	66.57	16.5	21AA_recalibration	59.81	51.53	66.97	15.44	-1.61	1.06
Artiodactyla	21AA_new	64.23	62.06	66.21	4.15	21AA_recalibration	64.75	62.75	66.47	3.72	-0.52	0.43
Primates	21AA_new	66.19	63.89	68.59	4.70	21AA_recalibration	71.24	67.50	75.52	8.02	-5.05	-3.32
Chiroptera	21AA_new	64.98	62.58	67.12	4.54	21AA_recalibration	65.34	63.05	67.38	4.33	-0.36	0.21
Perissodactyla	21AA_new	58.28	55.58	61.14	5.56	21AA_recalibration	58.27	55.56	61.13	5.57	0.01	-0.01
Carnivora	21AA_new	58.91	54.41	63.43	9.02	21AA_recalibration	59.42	55.55	63.59	8.04	-0.51	0.98
Lagomorpha	21AA_new	54.66	53.08	56.95	3.87	21AA_recalibration	54.68	53.13	57.05	3.92	-0.02	-0.05

Pilosa	21AA_new	50.81	40.78	58.84	18.06	21AA_recalibration	51.45	42.07	58.62	16.55	-0.64	1.51
Scandentia	21AA_new	49.91	36.87	60.58	23.71	21AA_recalibration	52.99	40.53	63.88	23.35	-3.08	0.36
Macroscelidea	21AA_new	42.37	31.84	54.39	22.55	21AA_recalibration	48.43	39.38	56.76	17.38	-6.06	5.17
Diprotodontia	21AA_new	54.51	49.24	59.92	10.68	21AA_recalibration	47.85	43.19	52.95	9.76	6.66	0.92
Didelphimorphia	21AA_new	37.84	25.75	49.13	23.38	21AA_recalibration	37.48	29.11	47.74	18.63	0.36	4.75
Sirenia	21AA_new	33.82	30.77	38.26	7.49	21AA_recalibration	32.37	30.50	35.10	4.60	1.45	2.89
Pholidota	21AA_new	29.91	15.67	42.99	27.32	21AA_recalibration	27.90	17.48	40.86	23.38	2.01	3.94
Dasyuromorphia	21AA_new	29.52	18.88	39.35	20.47	21AA_recalibration	26.63	18.92	34.22	15.30	2.89	5.17
Peramelemorphia	21AA_new	26.62	16.18	37.76	21.58	21AA_recalibration	26.18	19.02	33.04	14.02	0.44	7.56
Paucituberculata	21AA_new	13.02	7.30	16.84	9.54	21AA_recalibration	11.78	7.72	16.07	8.35	1.24	1.19
Dermoptera	21AA_new	17.14	6.50	26.61	20.11	21AA_recalibration	10.96	6.01	15.82	9.81	6.18	10.3
Hyracoidea	21AA_new	7.98	5.81	11.08	5.27	21AA_recalibration	7.09	5.73	9.23	3.50	0.89	1.77
Proboscidea	21AA_new	9.60	5.71	15.81	10.10	21AA_recalibration	5.96	4.02	7.66	3.64	3.64	6.46
Sum											-25.22 (p=2.30e-02)	59.09 (p=4.46e-05)

P-values was calculated by paired Wilcoxon signed rank test.

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