Materials and Methods

Phylogenetic inference using the MP and NJ methods

The MP (Fitch, 1971) and NJ (Saitou and Nei, 1987) methods were also applied with PAUP* ver. 4.0b4a (Swofford, 2002) and MEGA ver. 5 (Tamura et al., 2011), respectively. In applying the NJ, two distance measures, Maximum Composite Likelihood (NJ_MCL) (Tamura et al., 2004) and Tamura-Nei (NJ_TN) (Tamura and Nei, 1993) distances, were used with 1,000 bootstrap replications. The MP analysis was done with 500 bootstrap replications.

Results

Phylogenetic relationships

MP and NJ phylogenetic trees are shown in Supplementary Figs. S8–S10.

Subsequently, we also evaluated the performance of dense taxon sampling and models with respect to the positions of Pholidota (Manis, pangolins) and Physeteridae (sperm whale family). Pholidota was placed as a sister group to Carnivora by all ML analyses except ML_3, consistent with the nuclear gene analyses (Murphy et al., 2001; Zhou et al., 2012), but MP and NJ trees are apparently in conflict with the well-established tree concerning the position of Pholidota (Table 1 and Supplementary Table S5). Within Cetacea, Physeteridae was placed at the basal position of Odontoceti (toothed whales) by all ML analyses except ML_aa, consistent with the traditional taxonomy of the Odontoceti monophyly, but was placed as a sister group to a clade formed by Mysticeti (baleen whales), Platanista (Indian river dolphins) and Ziphiidae (beaked whales) by NJ_MCL (as high as 100% BP), NJ_TN (99% BP), and MP (67%). Although a similar relationship to the latter (i.e., paraphyly of Odontoceti) was suggested in early molecular studies (Milinkovitch et al., 1993; Hasegawa et al., 1997), it was rejected later by more extensive analyses of nuclear DNA including retroposon insertions (Nikaido et al., 2001; Steeman et al., 2009; Zhou et al., 2011). Thus, the ML analyses of mitogenomes at the nucleotide level are again better than the NJ and MP in this respect.

Comparison of the standard and rapid bootstrap methods

We also compared the rapid bootstrap method (Stamatakis et al., 2008) and standard bootstrap method based on the Euarchontoglires dataset (Supplementary Figs. S3 and S11). Although the algorithm of the rapid bootstrap method is directly related to the tree search algorithm, we found that these two methods gave little difference in both tree topology and log-likelihood score. However, nodal support values with the standard bootstrap method were slightly higher than those with the rapid bootstrap method.

Discussion

Bias of phylogenetic inference and importance of taxon sampling

Increasing the total number of characters can reduce sampling error and accordingly can increase phylogenetic resolution. However, as demonstrated by Nishihara et al. (2007) in resolving the basal branchings in Eutheria using genome-scale sequence data, a small bias of phylogenetic inference due to model mis-specification can be exaggerated in such a large dataset with respect to the number of characters and can give an incorrect tree with high statistical confidence. Systematic errors due to model mis-specification can be caused by several factors such as the LBA (Felsenstein, 1978), heterogeneous nucleotide or amino acid composition among lineages (Phillips et al., 2004), heterotachy (site-specific evolutionary rates that vary across the tree) (Lopez et al., 2002), and others (Philippe et al., 2011). By using ML, the increase of taxon sampling contributes to revealing undetected substitutions with additional internal nodes, which cut long branches, and helps to improve the estimation of branch lengths. This contributes to relieving misleading phylogenetic signals.

Position of Scandentia in Euarchontoglires

In Fig. 2 with the ML_CodonPartition model, Scandentia (tree shrews), represented only by *Tupaia belangeri*, is placed as a sister group to Lagomorpha. Since the BP for this relationship is only 19%, this placement is very uncertain from the dataset we analyzed. After we completed our major analyses, Xu et al. (2012) published four new sequences of *T. belangeri chinensis*, and we reanalyzed the boreotherian part by adding these new sequences to our dataset (123 sequences in total). Fixing the tree topology of Supplementary Fig. S1 except the position of Scandentia, seven possible trees for Scandentia relative to the four orders of Euarchontoglires were examined by the ML method with PAML ver. 4 (Yang, 2007). With the codon-substitution + Γ model (Yang, 1996; Yang et al., 1998) (amino acid distance calculated by Miyata et al.'s distance with geometric formula (Miyata et al., 1979)), Tree-1 with the Lagomorpha/Scandentia clade is the ML tree consistent with Fig. 2, but the Scandentia-basal tree in Euarchontoglires (Tree-2) has a log-likelihood score that is almost indistinguishable from the ML tree (lower by 3.4) (Supplementary Table S6). With the GTR + Γ + partition model (since the Γ + I model is not implemented in PAML, the model without I was applied), Tree-2 is the ML tree, but Tree-1 has an almost indistinguishablelog-likelihood score (lower by 8.4).

Table S1. Mitochondrial genome data used in this study

Scientific name	Accession Number	Super Order	Order	Family
Chrysochloris asiatica	AB096866	Afrotheria	Afrosoricida	Chrysochloridae
Eremitalpa granti	NC 010304	Afrotheria	Afrosoricida	Chrysochloridae
Dendrohyrax dorsalis	NC 010301	Afrotheria	Hyracoidea	Procaviidae
Procavia capensis	AB096865	Afrotheria	Hyracoidea	Procaviidae
Elephantulus sp. VB001	AB096867	Afrotheria	Macroscelidea	Macroscelididae
Macroscelides proboscideus	NC 004026	Afrotheria	Macroscelidea	Macroscelididae
Elephas maximus	DQ316068	Afrotheria	Proboscidea	Elephantidae
Loxodonta africana	NC 000934	Afrotheria	Proboscidea	Elephantidae
Mammut americanum	NC 009574	Afrotheria	Proboscidea	Mammutidae
Mammuthus columbi	JF912199	Afrotheria	Proboscidea	Mammuthus
Mammuthus primigenius	JF912200	Afrotheria	Proboscidea	Mammuthus
Dugong dugon	NC 003314	Afrotheria	Sirenia	Dugongidae
Trichechus manatus	NC 010302	Afrotheria	Sirenia	Trichechidae
Echinops telfairi	NC 002631	Afrotheria	Tenrecidea	Tenrecidae
Orycteropus afer	NC 002078	Afrotheria	Tubuildentata	Orycteropodidae
Galeopterus variegatus	NC 004031	Euarchontoglires	Dermoptera	Cynocephalidae
Lepus capensis	GU937113	Euarchontoglires	Lagomorpha	Leporidae
Lepus europaeus	NC 004028	Euarchontoglires	Lagomorpha	Leporidae
Ochotona collaris	NC 003033	Euarchontoglires	Lagomorpha	Ochotonidae
Ochotona curzoniae	NC 011029	Euarchontoglires	Lagomorpha	Ochotonidae
Ochotona princeps	NC 005358	Euarchontoglires	Lagomorpha	Ochotonidae
Oryctolagus cuniculus	AJ001588	Euarchontoglires	Lagomorpha	Leporidae
Aotus lemurinus	FJ785421	Euarchontoglires	Primates	Ceboidae
Ateles belzebuth	FJ785422	Euarchontoglires	Primates	Ceboidae
Callicebus donacophilus	FJ785423	Euarchontoglires	Primates	Ceboidae
Cebus albifrons	NC 002763	Euarchontoglires	Primates	Ceboidae
Cebus apella	NC 016666	Euarchontoglires	Primates	Ceboidae
Chlorocebus aethiops	NC 007009	Euarchontoglires	Primates	Cercopithecinae
Chlorocebus pygerythrus	NC 009747	Euarchontoglires	Primates	Cercopithecinae
Chlorocebus sabaeus	NC 008066	Euarchontoglires	Primates	Cercopithecinae
Chlorocebus tantalus	NC 009748	Euarchontoglires	Primates	Cercopithecinae
Colobus guereza	NC 006901	Euarchontoglires	Primates	Colobinae
Daubentonia madagascariensis	AB371085	Euarchontoglires	Primates	Daubentoniidae
Eulemur fulvus fulvus	NC 012766	Euarchontoglires	Primates	Lemuridae
Eulemur fulvus mayottensis	AB371087	Euarchontoglires	Primates	Lemuridae
Eulemur macaco macaco	AB371088	Euarchontoglires	Primates	Lemuridae
Eulemur mongoz	NC 010300	Euarchontoglires	Primates	Lemuridae
Galago senegalensis	AB371092	Euarchontoglires	Primates	Galagidae
Gorilla gorilla	NC 001645	Euarchontoglires	Primates	Hominidae
Homo sapiens	D38112	Euarchontoglires	Primates	Hominidae
Homo sp. Altai	NC 013993	Euarchontoglires	Primates	Hominidae
Hylobates agilis	AB504748	Euarchontoglires	Primates	Hylobatidae
Hylobates lar	HQ622775	Euarchontoglires	Primates	Hylobatidae
Hylobates pileatus	NC 014045	Euarchontoglires	Primates	Hylobatidae
Lemur catta	AJ421451	Euarchontoglires	Primates	Lemuridae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Lepilemur hubbardorum	NC 014453	Euarchontoglires	Primates	Megaladapidae
Loris tardigradus	AB371094	Euarchontoglires	Primates	Loridae
Macaca fascicularis	NC 012670	Euarchontoglires	Primates	Cercopithecinae
Macaca mulatta	NC 005943	Euarchontoglires	Primates	Cercopithecinae
Macaca sylvanus	NC 002764	Euarchontoglires	Primates	Cercopithecinae
Macaca thibetana	NC 011519	Euarchontoglires	Primates	Cercopithecinae
Nasalis concolor	JF293095	Euarchontoglires	Primates	Colobinae
Nasalis larvatus	NC 008216	Euarchontoglires	Primates	Colobinae
Nomascus gabriellae	HQ622806	Euarchontoglires	Primates	Hylobatidae
Nomascus siki	AB504751	Euarchontoglires	Primates	Hylobatidae
Nycticebus coucang	NC 002765	Euarchontoglires	Primates	Loridae
Otolemur crassicaudatus	AB371093	Euarchontoglires	Primates	Galagidae
Pan paniscus	NC 001644	Euarchontoglires	Primates	Hominidae
Pan troglodytes	NC 001643	Euarchontoglires	Primates	Hominidae
Papio hamadryas	NC 001992	Euarchontoglires	Primates	Cercopithecinae
Perodicticus potto	NC 012764	Euarchontoglires	Primates	Loridae
Piliocolobus badius	DQ355301	Euarchontoglires	Primates	Colobinae
Pongo abelii	NC 002083	Euarchontoglires	Primates	Hominidae
Pongo pygmaeus	NC 001646	Euarchontoglires	Primates	Hominidae
Presbytis melalophos	NC 008217	Euarchontoglires	Primates	Colobinae
Procolobus verus	JF293092	Euarchontoglires	Primates	Colobinae
Propithecus coquereli	NC 011053	Euarchontoglires	Primates	Indriidae
Pygathrix nemaeus	NC 008220	Euarchontoglires	Primates	Colobinae
Rhinopithecus avunculus	NC 015485	Euarchontoglires	Primates	Colobinae
Rhinopithecus bieti	HM125579	Euarchontoglires	Primates	Colobinae
Rhinopithecus roxellana	DQ355300	Euarchontoglires	Primates	Colobinae
Saimiri boliviensis	HQ644339	Euarchontoglires	Primates	Ceboidae
Saimiri oerstedii citrinellus	HQ644336	Euarchontoglires	Primates	Ceboidae
Saimiri oerstedii oerstedii	HQ644337	Euarchontoglires	Primates	Ceboidae
Saimiri sciureus	FJ785425	Euarchontoglires	Primates	Ceboidae
Saimiri sciureus macrodon	HQ644338	Euarchontoglires	Primates	Ceboidae
Semnopithecus entellus	NC 008215	Euarchontoglires	Primates	Colobinae
Symphalangus syndactylus	AB504750	Euarchontoglires	Primates	Hylobatidae
Tarsius bancanus	NC 002811	Euarchontoglires	Primates	Tarsiidae
Tarsius syrichta	NC 012774	Euarchontoglires	Primates	Tarsiidae
Theropithecus gelada	FJ785426	Euarchontoglires	Primates	Cercopithecinae
Trachypithecus obscurus	AY863425	Euarchontoglires	Primates	Colobinae
Varecia variegata variegata	AB371089	Euarchontoglires	Primates	Lemuridae
Acomys cahirinus	JN571154	Euarchontoglires	Rodentia	Muridae
Anomalurus sp. GP-2005	NC 009056	Euarchontoglires	Rodentia	Anomaluridae
Apodemus agrarius	HM034866	Euarchontoglires	Rodentia	Muridae
Apodemus chejuensis	NC 016662	Euarchontoglires	Rodentia	Muridae
Apodemus peninsulae	HQ660074	Euarchontoglires	Rodentia	Muridae
Castor canadensis	NC 015108	Euarchontoglires	Rodentia	Castoridae
Castor fiber	NC 015072	Euarchontoglires	Rodentia	Castoridae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Cavia porcellus	NC 000884	Euarchontoglires	Rodentia	Caviidae
Cricetulus griseus	NC 007936	Euarchontoglires	Rodentia	Cricetidae
Ctenomys leucodon	HM544131	Euarchontoglires	Rodentia	Ctenomyidae
Ctenomys sociabilis	HM544129	Euarchontoglires	Rodentia	Ctenomyidae
Eothenomys chinensis	NC 013571	Euarchontoglires	Rodentia	Cricetidae
Glis glis	NC 001892	Euarchontoglires	Rodentia	Gliridae
Heterocephalus glaber	NC 015112	Euarchontoglires	Rodentia	Bathyergidae
Jaculus jaculus	NC 005314	Euarchontoglires	Rodentia	Dipodidae
Leggadina lakedownensis	NC 014696	Euarchontoglires	Rodentia	Muridae
Mesocricetus auratus	NC 013276	Euarchontoglires	Rodentia	Cricetidae
Microtus fortis calamorum	JF261175	Euarchontoglires	Rodentia	Cricetidae
Microtus fortis fortis	NC 015241	Euarchontoglires	Rodentia	Cricetidae
Microtus kikuchii	NC 003041	Euarchontoglires	Rodentia	Cricetidae
Microtus levis	DQ015676	Euarchontoglires	Rodentia	Cricetidae
Mus musculus	NC 005089	Euarchontoglires	Rodentia	Muridae
Mus terricolor	NC 010650	Euarchontoglires	Rodentia	Muridae
Myodes regulus	NC 016427	Euarchontoglires	Rodentia	Cricetidae
Nannospalax ehrenbergi	NC 005315	Euarchontoglires	Rodentia	Spalacidae
Nannospalax galili	JN571130	Euarchontoglires	Rodentia	Spalacidae
Nannospalax judaei	JN571135	Euarchontoglires	Rodentia	Spalacidae
Neodon irene	NC 016055	Euarchontoglires	Rodentia	Cricetidae
Octodon degus	HM544134	Euarchontoglires	Rodentia	Octodontidae
Proechimys longicaudatus	HM544128	Euarchontoglires	Rodentia	Echimyidae
Proedromys liangshanensis	FJ463038	Euarchontoglires	Rodentia	Cricetidae
Pseudomys chapmani	NC 014698	Euarchontoglires	Rodentia	Muridae
Rattus exulans	NC 012389	Euarchontoglires	Rodentia	Muridae
Rattus fuscipes	NC 014867	Euarchontoglires	Rodentia	Muridae
Rattus leucopus	NC 014855	Euarchontoglires	Rodentia	Muridae
Rattus lutreolus	NC 014858	Euarchontoglires	Rodentia	Muridae
Rattus norvegicus	AC 000022	Euarchontoglires	Rodentia	Muridae
Rattus praetor	EU273708	Euarchontoglires	Rodentia	Muridae
Rattus sordidus	NC 014871	Euarchontoglires	Rodentia	Muridae
Rattus tanezumi	NC 011638	Euarchontoglires	Rodentia	Muridae
Rattus tunneyi	NC 014861	Euarchontoglires	Rodentia	Muridae
Rattus villosissimus	NC 014864	Euarchontoglires	Rodentia	Muridae
Sciurus vulgaris	NC 002369	Euarchontoglires	Rodentia	Sciuridae
Spalacopus cyanus	HM544133	Euarchontoglires	Rodentia	Octodontidae
Spalax carmeli	JN571137	Euarchontoglires	Rodentia	Spalacidae
Thryonomys swinderianus	NC 002658	Euarchontoglires	Rodentia	Thryonomyidae
Tscherskia triton	NC 013068	Euarchontoglires	Rodentia	Cricetidae
Tympanoctomys barrerae	HM544132	Euarchontoglires	Rodentia	Octodontidae
Tupaia belangeri	AF217811	Euarchontoglires	Scandentia	Tupaiidae
Ailuropoda melanoleuca	EF212882	Laurasiatheria	Carnivora	Ursidae
Ailurus fulgens	NC 011124	Laurasiatheria	Carnivora	Ailuridae
Ailurus fulgens styani	NC 009691	Laurasiatheria	Carnivora	Ailuridae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Arctocephalus forsteri	NC 004023	Laurasiatheria	Carnivora	Otariidae
Arctocephalus pusillus	NC 008417	Laurasiatheria	Carnivora	Otariidae
Arctocephalus townsendi	NC 008420	Laurasiatheria	Carnivora	Otariidae
Arctodus simus	NC 011116	Laurasiatheria	Carnivora	Ursidae
Arctonyx collaris	HM106329	Laurasiatheria	Carnivora	Mustelidae
Callorhinus ursinus	NC 008415	Laurasiatheria	Carnivora	Otariidae
Canis latrans	DQ480510	Laurasiatheria	Carnivora	Canidae
Canis lupus	AB499824	Laurasiatheria	Carnivora	Canidae
Canis lupus familiaris	NC 002008	Laurasiatheria	Carnivora	Canidae
Enhydra lutris	AB291077	Laurasiatheria	Carnivora	Mustelidae
Erignathus barbatus	NC 008426	Laurasiatheria	Carnivora	Phocidae
Eumetopias jubatus	NC 004030	Laurasiatheria	Carnivora	Otariidae
Gulo gulo	NC 009685	Laurasiatheria	Carnivora	Mustelidae
Halichoerus grypus	NC 001602	Laurasiatheria	Carnivora	Phocidae
Helarctos malayanus	NC 009968	Laurasiatheria	Carnivora	Ursidae
Hydrurga leptonyx	NC 008425	Laurasiatheria	Carnivora	Phocidae
Leptonychotes weddellii	NC 008424	Laurasiatheria	Carnivora	Phocidae
Lobodon carcinophaga	NC 008423	Laurasiatheria	Carnivora	Phocidae
Lutra lutra	FJ236015	Laurasiatheria	Carnivora	Mustelidae
Martes americana	HM106324	Laurasiatheria	Carnivora	Mustelidae
Martes flavigula	HM106326	Laurasiatheria	Carnivora	Mustelidae
Martes foina	HM106325	Laurasiatheria	Carnivora	Mustelidae
Martes melampus	NC 009678	Laurasiatheria	Carnivora	Mustelidae
Martes pennanti	HQ705180	Laurasiatheria	Carnivora	Mustelidae
Martes zibellina	NC 011579	Laurasiatheria	Carnivora	Mustelidae
Meles anakuma	NC 009677	Laurasiatheria	Carnivora	Mustelidae
Meles meles	NC 011125	Laurasiatheria	Carnivora	Mustelidae
Melogale moschata	HM106328	Laurasiatheria	Carnivora	Mustelidae
Melursus ursinus	NC 009970	Laurasiatheria	Carnivora	Ursidae
Mephitis mephitis	HM106332	Laurasiatheria	Carnivora	Mustelidae
Mirounga leonina	NC 008422	Laurasiatheria	Carnivora	Phocidae
Monachus schauinslandi	NC 008421	Laurasiatheria	Carnivora	Phocidae
Mustela frenata	HM106321	Laurasiatheria	Carnivora	Mustelidae
Mustela kathiah	HM106320	Laurasiatheria	Carnivora	Mustelidae
Mustela nivalis	HM106319	Laurasiatheria	Carnivora	Mustelidae
Mustela sibirica	HM106317	Laurasiatheria	Carnivora	Mustelidae
Nasua nasua	HM106331	Laurasiatheria	Carnivora	Mustelidae
Neophoca cinerea	NC 008419	Laurasiatheria	Carnivora	Otariidae
Neovison vison	HM106322	Laurasiatheria	Carnivora	Mustelidae
Nyctereutes procyonoides	GU256221	Laurasiatheria	Carnivora	Canidae
Odobenus rosmarus rosmarus	NC 004029	Laurasiatheria	Carnivora	Odobenidae
Phoca fasciata	NC 008428	Laurasiatheria	Carnivora	Phocidae
Phoca groenlandica	NC 008429	Laurasiatheria	Carnivora	Phocidae
Phoca largha	NC 008430	Laurasiatheria	Carnivora	Phocidae
Phoca vitulina	NC 001325	Laurasiatheria	Carnivora	Phocidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Phocarctos hookeri	NC 008418	Laurasiatheria	Carnivora	Otariidae
Procyon lotor	NC 009126	Laurasiatheria	Carnivora	Mustelidae
Pusa caspica	NC 008431	Laurasiatheria	Carnivora	Phocidae
Pusa hispida	NC 008433	Laurasiatheria	Carnivora	Phocidae
Pusa sibirica	NC 008432	Laurasiatheria	Carnivora	Phocidae
Spilogale putorius	NC 010497	Laurasiatheria	Carnivora	Mustelidae
Taxidea taxus	HM106330	Laurasiatheria	Carnivora	Mustelidae
Tremarctos ornatus	NC 009969	Laurasiatheria	Carnivora	Ursidae
Ursus americanus	NC 003426	Laurasiatheria	Carnivora	Ursidae
Ursus arctos	NC 003427	Laurasiatheria	Carnivora	Ursidae
Ursus maritimus	AF303111	Laurasiatheria	Carnivora	Ursidae
Ursus spelaeus	NC 011112	Laurasiatheria	Carnivora	Ursidae
Ursus thibetanus	NC 009971	Laurasiatheria	Carnivora	Ursidae
Ursus thibetanus formosanus	EF076773	Laurasiatheria	Carnivora	Ursidae
Ursus thibetanus mupinensis	DQ402478	Laurasiatheria	Carnivora	Ursidae
Ursus thibetanus ussuricus	EF681884	Laurasiatheria	Carnivora	Ursidae
Vulpes vulpes	GQ374180	Laurasiatheria	Carnivora	Canidae
Zalophus californianus	NC 008416	Laurasiatheria	Carnivora	Otariidae
Acinonyx jubatus	AY463959	Laurasiatheria	Carnivora	Felidae
Felis catus	NC 001700	Laurasiatheria	Carnivora	Felidae
Herpestes javanicus	AY873843	Laurasiatheria	Carnivora	Herpestidae
Lynx rufus	NC 014456	Laurasiatheria	Carnivora	Felidae
Neofelis nebulosa	NC 008450	Laurasiatheria	Carnivora	Felidae
Panthera pardus	NC 010641	Laurasiatheria	Carnivora	Felidae
Panthera tigris	EF551003	Laurasiatheria	Carnivora	Felidae
Panthera tigris altaica	JF357974	Laurasiatheria	Carnivora	Felidae
Panthera tigris amoyensis	HM589215	Laurasiatheria	Carnivora	Felidae
Panthera tigris sumatrae	JF357969	Laurasiatheria	Carnivora	Felidae
Panthera tigris tigris	JF357967	Laurasiatheria	Carnivora	Felidae
Prionailurus bengalensis	HM185183	Laurasiatheria	Carnivora	Felidae
Prionailurus bengalensis euptilurus	JN392459	Laurasiatheria	Carnivora	Felidae
Puma concolor	JN999997	Laurasiatheria	Carnivora	Felidae
Uncia uncia	NC 010638	Laurasiatheria	Carnivora	Felidae
Balaena mysticetus	NC 005268	Laurasiatheria	Cetartiodactyla	Balaenidae
Balaenoptera acutorostrata	NC 005271	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera bonaerensis	AP006466	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera borealis	NC 006929	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera brydei	AP006469	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera edeni	NC 007938	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera musculus	NC 001601	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera omurai	NC 007937	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Balaenoptera physalus	NC 001321	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Berardius bairdii	NC 005274	Laurasiatheria	Cetartiodactyla	Ziphiidae
Caperea marginata	AP006475	Laurasiatheria	Cetartiodactyla	Neobalaenidae
Cephalorhynchus heavisidii	JN632624	Laurasiatheria	Cetartiodactyla	Delphinidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Delphinus capensis	EU557094	Laurasiatheria	Cetartiodactyla	Delphinidae
Eschrichtius robustus	NC 005270	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Eubalaena australis	NC 006930	Laurasiatheria	Cetartiodactyla	Balaenidae
Eubalaena japonica	NC 006931	Laurasiatheria	Cetartiodactyla	Balaenidae
Feresa attenuata	JF289172	Laurasiatheria	Cetartiodactyla	Delphinidae
Globicephala macrorhynchus	JF339976	Laurasiatheria	Cetartiodactyla	Delphinidae
Globicephala melas	HM060334	Laurasiatheria	Cetartiodactyla	Delphinidae
Grampus griseus	EU557095	Laurasiatheria	Cetartiodactyla	Delphinidae
Hyperoodon ampullatus	NC 005273	Laurasiatheria	Cetartiodactyla	Ziphiidae
Inia geoffrensis	NC 005276	Laurasiatheria	Cetartiodactyla	Iniidae
Kogia breviceps	NC 005272	Laurasiatheria	Cetartiodactyla	Physeteridae
Lagenorhynchus albirostris	NC 005278	Laurasiatheria	Cetartiodactyla	Delphinidae
Lipotes vexillifer	AY789529	Laurasiatheria	Cetartiodactyla	Lipotidae
Megaptera novaeangliae	AP006467	Laurasiatheria	Cetartiodactyla	Balaenopteridae
Monodon monoceros	NC 005279	Laurasiatheria	Cetartiodactyla	Monodontidae
Orcaella brevirostris	JF289177	Laurasiatheria	Cetartiodactyla	Delphinidae
Orcaella heinsohni	JF339977	Laurasiatheria	Cetartiodactyla	Delphinidae
Orcinus orca	GU187219	Laurasiatheria	Cetartiodactyla	Delphinidae
Peponocephala electra	JF289176	Laurasiatheria	Cetartiodactyla	Delphinidae
Phocoena phocoena	NC 005280	Laurasiatheria	Cetartiodactyla	Phocoenidae
Physeter catodon	NC 002503	Laurasiatheria	Cetartiodactyla	Physeteridae
Platanista minor	NC 005275	Laurasiatheria	Cetartiodactyla	Physeteridae
Pontoporia blainvillei	NC 005277	Laurasiatheria	Cetartiodactyla	Iniidae
Pseudorca crassidens	HM060332	Laurasiatheria	Cetartiodactyla	Delphinidae
Sousa chinensis	NC 012057	Laurasiatheria	Cetartiodactyla	Delphinidae
Stenella attenuata	EU557096	Laurasiatheria	Cetartiodactyla	Delphinidae
Stenella coeruleoalba	NC 012053	Laurasiatheria	Cetartiodactyla	Delphinidae
Tursiops aduncus	NC 012058	Laurasiatheria	Cetartiodactyla	Delphinidae
Tursiops truncatus	EU557093	Laurasiatheria	Cetartiodactyla	Delphinidae
Addax nasomaculatus	JN632591	Laurasiatheria	Cetartiodactyla	Bovidae
Aepyceros melampus	JN632592	Laurasiatheria	Cetartiodactyla	Bovidae
Alcelaphus buselaphus	JN632594	Laurasiatheria	Cetartiodactyla	Bovidae
Alces alces	JN632595	Laurasiatheria	Cetartiodactyla	Cervidae
Ammotragus lervia	FJ207522	Laurasiatheria	Cetartiodactyla	Bovidae
Antidorcas marsupialis	JN632596	Laurasiatheria	Cetartiodactyla	Bovidae
Antilocapra americana	JN632597	Laurasiatheria	Cetartiodactyla	Antilocapridae
Antilope cervicapra	NC 012098	Laurasiatheria	Cetartiodactyla	Bovidae
Axis axis	JN632599	Laurasiatheria	Cetartiodactyla	Cervidae
Axis porcinus	JN632600	Laurasiatheria	Cetartiodactyla	Cervidae
Bison bison	JN632601	Laurasiatheria	Cetartiodactyla	Bovidae
Bison bonasus	NC 014044	Laurasiatheria	Cetartiodactyla	Bovidae
Blastocerus dichotomus	JN632603	Laurasiatheria	Cetartiodactyla	Cervidae
Bos gaurus	JN632604	Laurasiatheria	Cetartiodactyla	Bovidae
Bos grunniens	GQ464314	Laurasiatheria	Cetartiodactyla	Bovidae
Bos indicus	NC 005971	Laurasiatheria	Cetartiodactyla	Bovidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Bos javanicus	JN632605	Laurasiatheria	Cetartiodactyla	Bovidae
Bos primigenius	NC 013996	Laurasiatheria	Cetartiodactyla	Bovidae
Bos taurus	NC 006853	Laurasiatheria	Cetartiodactyla	Bovidae
Boselaphus tragocamelus	EF536350	Laurasiatheria	Cetartiodactyla	Bovidae
Bubalus bubalis	JN632607	Laurasiatheria	Cetartiodactyla	Bovidae
Bubalus depressicornis	EF536351	Laurasiatheria	Cetartiodactyla	Bovidae
Budorcas taxicolor	NC 013069	Laurasiatheria	Cetartiodactyla	Bovidae
Capra caucasica	JN632609	Laurasiatheria	Cetartiodactyla	Bovidae
Capra falconeri	FJ207525	Laurasiatheria	Cetartiodactyla	Bovidae
Capra hircus	NC 005044	Laurasiatheria	Cetartiodactyla	Bovidae
Capra ibex	FJ207526	Laurasiatheria	Cetartiodactyla	Bovidae
Capra nubiana	FJ207527	Laurasiatheria	Cetartiodactyla	Bovidae
Capra pyrenaica	FJ207528	Laurasiatheria	Cetartiodactyla	Bovidae
Capra sibirica	FJ207529	Laurasiatheria	Cetartiodactyla	Bovidae
Capreolus capreolus	JN632610	Laurasiatheria	Cetartiodactyla	Cervidae
Capricornis crispus	AP003429	Laurasiatheria	Cetartiodactyla	Bovidae
Capricornis sumatraensis	FJ207534	Laurasiatheria	Cetartiodactyla	Bovidae
Capricornis swinhoei	NC 010640	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus adersi	JN632611	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus callipygus	JN632613	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus dorsalis	JN632615	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus jentinki	JN632616	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus leucogaster	JN632617	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus natalensis	JN632618	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus nigrifrons	JN632619	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus ogilbyi	JN632620	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus rufilatus	JN632621	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus silvicultor	JN632622	Laurasiatheria	Cetartiodactyla	Bovidae
Cephalophus spadix	JN632623	Laurasiatheria	Cetartiodactyla	Bovidae
Cervus elaphus	AB245427	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus elaphus songaricus	NC 014703	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus elaphus xanthopygus	NC 013836	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus elaphus yarkandensis	GU457435	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus nippon centralis	NC 006993	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus nippon hortulorum	HQ191428	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus nippon kopschi	HQ832482	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus nippon taiouanus	NC 008462	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus nippon yakushimae	AB218689	Laurasiatheria	Cetartiodactyla	Cervidae
Cervus nippon yesoensis	NC 006973	Laurasiatheria	Cetartiodactyla	Cervidae
Connochaetes gnou	JN632626	Laurasiatheria	Cetartiodactyla	Bovidae
Connochaetes taurinus	JN632627	Laurasiatheria	Cetartiodactyla	Bovidae
Dama dama	JN632629	Laurasiatheria	Cetartiodactyla	Cervidae
Dama mesopotamica	JN632630	Laurasiatheria	Cetartiodactyla	Cervidae
Damaliscus pygargus	FJ207530	Laurasiatheria	Cetartiodactyla	Bovidae
Dorcatragus megalotis	JN632631	Laurasiatheria	Cetartiodactyla	Bovidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Elaphodus cephalophus	NC 008749	Laurasiatheria	Cetartiodactyla	Cervidae
Elaphurus davidianus	JN632632	Laurasiatheria	Cetartiodactyla	Cervidae
Eudorcas rufifrons	JN632633	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella bennettii	JN632635	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella cuvieri	JN632636	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella dorcas	JN632637	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella erlangeri	JN632639	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella gazella	JN632640	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella leptoceros	JN632641	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella spekei	JN632642	Laurasiatheria	Cetartiodactyla	Bovidae
Gazella subgutturosa	JN632643	Laurasiatheria	Cetartiodactyla	Bovidae
Giraffa camelopardalis	AP003424	Laurasiatheria	Cetartiodactyla	Giraffidae
Hemitragus jayakari	FJ207523	Laurasiatheria	Cetartiodactyla	Bovidae
Hemitragus jemlahicus	FJ207531	Laurasiatheria	Cetartiodactyla	Bovidae
Hippocamelus antisensis	JN632646	Laurasiatheria	Cetartiodactyla	Cervidae
Hippotragus equinus	JN632647	Laurasiatheria	Cetartiodactyla	Bovidae
Hippotragus niger	JN632648	Laurasiatheria	Cetartiodactyla	Bovidae
Hyemoschus aquaticus	JN632650	Laurasiatheria	Cetartiodactyla	Tragulidae
Kobus ellipsiprymnus	JN632651	Laurasiatheria	Cetartiodactyla	Bovidae
Kobus leche	JN632652	Laurasiatheria	Cetartiodactyla	Bovidae
Litocranius walleri	JN632653	Laurasiatheria	Cetartiodactyla	Bovidae
Madoqua kirkii	JN632654	Laurasiatheria	Cetartiodactyla	Bovidae
Madoqua saltiana	JN632655	Laurasiatheria	Cetartiodactyla	Bovidae
Mazama americana	JN632656	Laurasiatheria	Cetartiodactyla	Cervidae
Mazama gouazoupira	JN632658	Laurasiatheria	Cetartiodactyla	Cervidae
Mazama nemorivaga	JN632660	Laurasiatheria	Cetartiodactyla	Cervidae
Mazama rufina	JN632661	Laurasiatheria	Cetartiodactyla	Cervidae
Moschus berezovskii	NC 012694	Laurasiatheria	Cetartiodactyla	Moschidae
Moschus moschiferus	JN632662	Laurasiatheria	Cetartiodactyla	Moschidae
Muntiacus crinifrons	NC 004577	Laurasiatheria	Cetartiodactyla	Cervidae
Muntiacus muntjak	NC 004563	Laurasiatheria	Cetartiodactyla	Cervidae
Muntiacus reevesi	AF527537	Laurasiatheria	Cetartiodactyla	Cervidae
Muntiacus reevesi micrurus	EF035447	Laurasiatheria	Cetartiodactyla	Cervidae
Muntiacus vuquangensis	NC 016920	Laurasiatheria	Cetartiodactyla	Cervidae
Naemorhedus baileyi	JN632663	Laurasiatheria	Cetartiodactyla	Bovidae
Naemorhedus caudatus	NC 013751	Laurasiatheria	Cetartiodactyla	Bovidae
Naemorhedus griseus	JN632664	Laurasiatheria	Cetartiodactyla	Bovidae
Nanger dama	JN632665	Laurasiatheria	Cetartiodactyla	Bovidae
Nanger granti	JN632666	Laurasiatheria	Cetartiodactyla	Bovidae
Nanger soemmerringii	JN632667	Laurasiatheria	Cetartiodactyla	Bovidae
Neotragus batesi	JN632668	Laurasiatheria	Cetartiodactyla	Bovidae
Neotragus moschatus	JN632669	Laurasiatheria	Cetartiodactyla	Bovidae
Odocoileus hemionus	JN632670	Laurasiatheria	Cetartiodactyla	Cervidae
Odocoileus virginianus	JN632672	Laurasiatheria	Cetartiodactyla	Cervidae
Okapia johnstoni	JN632674	Laurasiatheria	Cetartiodactyla	Giraffidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Oreamnos americanus	FJ207535	Laurasiatheria	Cetartiodactyla	Bovidae
Oreotragus oreotragus	JN632675	Laurasiatheria	Cetartiodactyla	Bovidae
Oryx beisa	JN632676	Laurasiatheria	Cetartiodactyla	Bovidae
Oryx dammah	JN632677	Laurasiatheria	Cetartiodactyla	Bovidae
Oryx gazella	NC 016422	Laurasiatheria	Cetartiodactyla	Bovidae
Oryx leucoryx	JN632679	Laurasiatheria	Cetartiodactyla	Bovidae
Ourebia ourebi	JN632680	Laurasiatheria	Cetartiodactyla	Bovidae
Ovibos moschatus	FJ207536	Laurasiatheria	Cetartiodactyla	Bovidae
Ovis ammon	HM236188	Laurasiatheria	Cetartiodactyla	Bovidae
Ovis aries	NC 001941	Laurasiatheria	Cetartiodactyla	Bovidae
Ovis aries musimon	HM236185	Laurasiatheria	Cetartiodactyla	Bovidae
Ovis canadensis	NC 015889	Laurasiatheria	Cetartiodactyla	Bovidae
Ovis vignei	HM236189	Laurasiatheria	Cetartiodactyla	Bovidae
Ozotoceros bezoarticus	JN632681	Laurasiatheria	Cetartiodactyla	Cervidae
Pantholops hodgsonii	NC 007441	Laurasiatheria	Cetartiodactyla	Bovidae
Pelea capreolus	JN632684	Laurasiatheria	Cetartiodactyla	Bovidae
Philantomba maxwellii	JN632685	Laurasiatheria	Cetartiodactyla	Bovidae
Philantomba monticola	JN632686	Laurasiatheria	Cetartiodactyla	Bovidae
Procapra gutturosa	JN632689	Laurasiatheria	Cetartiodactyla	Bovidae
Procapra przewalskii	GU386355	Laurasiatheria	Cetartiodactyla	Bovidae
Przewalskium albirostris	NC 016707	Laurasiatheria	Cetartiodactyla	Cervidae
Pseudois nayaur	FJ207537	Laurasiatheria	Cetartiodactyla	Bovidae
Pseudois schaeferi	JQ040802	Laurasiatheria	Cetartiodactyla	Bovidae
Pseudoryx nghetinhensis	EF536352	Laurasiatheria	Cetartiodactyla	Bovidae
Pudu mephistophiles	JN632691	Laurasiatheria	Cetartiodactyla	Cervidae
Pudu puda	JN632692	Laurasiatheria	Cetartiodactyla	Cervidae
Rangifer tarandus	AB245426	Laurasiatheria	Cetartiodactyla	Cervidae
Raphicerus campestris	JN632693	Laurasiatheria	Cetartiodactyla	Bovidae
Redunca arundinum	JN632694	Laurasiatheria	Cetartiodactyla	Bovidae
Redunca fulvorufula	JN632695	Laurasiatheria	Cetartiodactyla	Bovidae
Rucervus duvaucelii	JN632696	Laurasiatheria	Cetartiodactyla	Cervidae
Rucervus eldi	JN632697	Laurasiatheria	Cetartiodactyla	Cervidae
Rupicapra pyrenaica	FJ207538	Laurasiatheria	Cetartiodactyla	Bovidae
Rupicapra rupicapra	FJ207539	Laurasiatheria	Cetartiodactyla	Bovidae
Rusa alfredi	JN632698	Laurasiatheria	Cetartiodactyla	Cervidae
Rusa timorensis	JN632699	Laurasiatheria	Cetartiodactyla	Cervidae
Rusa unicolor swinhoei	DQ989636	Laurasiatheria	Cetartiodactyla	Cervidae
Saiga tatarica	JN632700	Laurasiatheria	Cetartiodactyla	Bovidae
Sylvicapra grimmia	JN632701	Laurasiatheria	Cetartiodactyla	Bovidae
Syncerus caffer	EF536353	Laurasiatheria	Cetartiodactyla	Bovidae
Tetracerus quadricornis	EF536355	Laurasiatheria	Cetartiodactyla	Bovidae
Tragelaphus angasii	JN632702	Laurasiatheria	Cetartiodactyla	Bovidae
Tragelaphus imberbis	EF536356	Laurasiatheria	Cetartiodactyla	Bovidae
Tragelaphus oryx	JN632704	Laurasiatheria	Cetartiodactyla	Bovidae
Tragelaphus scriptus	JN632706	Laurasiatheria	Cetartiodactyla	Bovidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Tragelaphus spekii	EF536357	Laurasiatheria	Cetartiodactyla	Bovidae
Tragelaphus strepsiceros	JN632708	Laurasiatheria	Cetartiodactyla	Bovidae
Tragulus kanchil	JN632709	Laurasiatheria	Cetartiodactyla	Tragulidae
Camelus bactrianus	EF212037	Laurasiatheria	Cetartiodactyla	Camelidae
Camelus dromedarius	JN632608	Laurasiatheria	Cetartiodactyla	Camelidae
Camelus ferus	NC 009629	Laurasiatheria	Cetartiodactyla	Camelidae
Hexaprotodon liberiensis	JN632625	Laurasiatheria	Cetartiodactyla	Hippopotamidae
Hippopotamus amphibius	AJ010957	Laurasiatheria	Cetartiodactyla	Hippopotamidae
Hydropotes inermis	JN632649	Laurasiatheria	Cetartiodactyla	Cervidae
Lama glama	AP003426	Laurasiatheria	Cetartiodactyla	Camelidae
Lama guanicoe	NC 011822	Laurasiatheria	Cetartiodactyla	Camelidae
Pecari tajacu	NC 012103	Laurasiatheria	Cetartiodactyla	Tayassuidae
Phacochoerus africanus	DQ409327	Laurasiatheria	Cetartiodactyla	Suidae
Potamochoerus porcus	JN632688	Laurasiatheria	Cetartiodactyla	Suidae
Sus scrofa	AJ002189	Laurasiatheria	Cetartiodactyla	Suidae
Sus scrofa domesticus	NC 012095	Laurasiatheria	Cetartiodactyla	Suidae
Sus scrofa taiwanensis	NC 014692	Laurasiatheria	Cetartiodactyla	Suidae
Taurotragus derbianus	EF536354	Laurasiatheria	Cetartiodactyla	Bovidae
Vicugna pacos	NC 002504	Laurasiatheria	Cetartiodactyla	Camelidae
Vicugna vicugna	FJ456892	Laurasiatheria	Cetartiodactyla	Camelidae
Artibeus jamaicensis	NC 002009	Laurasiatheria	Chiroptera	Phyllostomidae
Artibeus lituratus	JN209840	Laurasiatheria	Chiroptera	Phyllostomidae
Chalinolobus tuberculatus	AF321051	Laurasiatheria	Chiroptera	Vespertilionidae
Lasiurus borealis	NC 016873	Laurasiatheria	Chiroptera	Vespertilionidae
Myotis formosus	NC 015828	Laurasiatheria	Chiroptera	Vespertilionidae
Mystacina tuberculata	NC 006925	Laurasiatheria	Chiroptera	Mystacinidae
Pipistrellus abramus	AB061528	Laurasiatheria	Chiroptera	Vespertilionidae
Plecotus auritus	NC 015484	Laurasiatheria	Chiroptera	Vespertilionidae
Plecotus rafinesquii	JN209841	Laurasiatheria	Chiroptera	Vespertilionidae
Pteropus dasymallus	NC 002612	Laurasiatheria	Chiroptera	Pteropodidae
Pteropus scapulatus	NC 002619	Laurasiatheria	Chiroptera	Pteropodidae
Rhinolophus ferrumequinum korai	NC016191	Laurasiatheria	Chiroptera	Rhinolophidae
Rhinolophus formosae	EU166918	Laurasiatheria	Chiroptera	Rhinolophidae
Rhinolophus monoceros	NC 005433	Laurasiatheria	Chiroptera	Rhinolophidae
Rhinolophus pumilus	AB061526	Laurasiatheria	Chiroptera	Rhinolophidae
Rousettus aegyptiacus	NC 007393	Laurasiatheria	Chiroptera	Pteropodidae
Crocidura russula	NC 006893	Laurasiatheria	Insectivora	Soricidae
Episoriculus fumidus	AF348081	Laurasiatheria	Insectivora	Soricidae
Galemys pyrenaicus	NC 008156	Laurasiatheria	Insectivora	Talpidae
Mogera wogura	AB099482	Laurasiatheria	Insectivora	Talpidae
Sorex unguiculatus	NC 005435	Laurasiatheria	Insectivora	Soricidae
Talpa europaea	NC 002391	Laurasiatheria	Insectivora	Talpidae
Urotrichus talpoides	NC 005034	Laurasiatheria	Insectivora	Talpidae
Ceratotherium simum	NC 001808	Laurasiatheria	Perissodactyla	Rhinocerotidae
Coelodonta antiquitatis	FJ905813	Laurasiatheria	Perissodactyla	Rhinocerotidae

Table S1. Continued

Scientific name	Accession Number	Super Order	Order	Family
Dicerorhinus sumatrensis	NC 012684	Laurasiatheria	Perissodactyla	Rhinocerotidae
Diceros bicornis	FJ905814	Laurasiatheria	Perissodactyla	Rhinocerotidae
Equus asinus	NC 001788	Laurasiatheria	Perissodactyla	Equidae
Equus caballus	AY584828	Laurasiatheria	Perissodactyla	Equidae
Equus hemionus	HM118851	Laurasiatheria	Perissodactyla	Equidae
Equus przewalskii	HQ439484	Laurasiatheria	Perissodactyla	Equidae
Rhinoceros sondaicus	FJ905815	Laurasiatheria	Perissodactyla	Rhinocerotidae
Rhinoceros unicornis	NC 001779	Laurasiatheria	Perissodactyla	Rhinocerotidae
Manis pentadactyla	NC 016008	Laurasiatheria	Pholidota	Manidae
Dasypus novemcinctus	NC 001821	Xenarthra	Cingulata	Dasypodidae
Bradypus tridactylus	NC 006923	Xenarthra	Pilosa	Bradypodidae
Choloepus didactylus	NC 006924	Xenarthra	Pilosa	Megalonychidae
Tamandua tetradactyla	AJ421450	Xenarthra	Pilosa	Myrmecophagidae
Manis tetradactyla	NC 004027	Laurasiatheria	Pholidota	Manidae
Tupaia belangeri	NC 002521	Euarchontoglires	Scandentia	Tupaiidae
Tupaia belangeri	JN800724	Euarchontoglires	Scandentia	Tupaiidae
Tupaia belangeri	JN800723	Euarchontoglires	Scandentia	Tupaiidae
Tupaia belangeri	JN800722	Euarchontoglires	Scandentia	Tupaiidae
Galeopterus variegatus	JN800721	Euarchontoglires	Dermoptera	Cynocephalidae

Table S2. Bootstrap probabilities of each branch for different samples

Sample Size		¥50+5(1T1C)			Sample Size		*50+8(2T3C)		
No.	*Colugo	Tarsius	Manis	Whale	No.	*Colugo	Tarsius	Manis	Whale
#1	41(81)	46	85	–	1	56(74)	51	80	–
2	×	×	60	50	2	×	×	52	40
3	×	×	94	×	3	×	×	85	×
4	58(75)	49	95	×	4	61(63)	52	88	×
5	×	×	91	–	5	×	×	85	–
6	–	–	52	×	6	–	–	63	×
7	×	×	78	48	7	×	×	76	57
8	×	×	92	×	8	×	×	90	×
9	×	×	88	×	9	×	×	81	×
10	×	×	76	×	10	×	×	80	×
Sample Size		100+5(1T1C)			Sample Size		100+8(2T3C)		
No.	*Colugo	Tarsius	Manis	Whale	No.	*Colugo	Tarsius	Manis	Whale
1	×	×	82	84	1	41(93)	45	80	88
2	47(99)	33	81	53	2	50(99)	38	71	50
3	53(83)	35	72	77	3	61(83)	52	73	69
4	×	×	75	×	4	×	×	79	×
5	61(99)	28	64	71	5	63(100)	50	74	68
6	×	×	84	71	6	×	×	84	65
7	×	×	95	×	7	42(100)	29	97	62
8	×	×	53	84	8	×	×	59	92

Table S2. Continued

Sample Size		100+5(1T1C)			Sample Size		100+8(2T3C)		
No.	*Colugo	Tarsius	Manis	Whale	No.	*Colugo	Tarsius	Manis	Whale
9	×	×	×	75	9	45(100)	37	×	69
10	60(90)	47	68	×	10	71(87)	74	71	×
Sample Size		150+5(1T1C)			Sample Size		150+8(2T3C)		
No.	*Colugo	Tarsius	Manis	Whale	No.	*Colugo	Tarsius	Manis	Whale
1	×	×	84	75	1	50(86)	46	85	63
2	×	×	66	61	2	36(91)	32	68	51
3	×	×	66	61	3	32(88)	12	81	66
4	×	×	80	61	4	×	×	81	45
5	52(100)	43	90	×	5	44(89)	30	85	×
6	63(99)	38	83	72	6	65(90)	52	78	68
7	38(100)	29	78	72	7	42(89)	18	80	63
8	×	×	93	63	8	35(90)	29	83	65
9	44(100)	46	86	60	9	37(90)	26	81	26
10	42(100)	50	80	83	10	42(86)	33	77	75
Sample Size		200+5(1T1C)			Sample Size		200+8(2T3C)		
No.	*Colugo	Tarsius	Manis	Whale	No.	*Colugo	Tarsius	Manis	Whale
1	33(84)	18	78	32	1	42(83)	37	81	42
2	×	×	55	48	2	34(83)	20	54	57
3	×	×	75	46	3	34(91)	13	73	53
4	×	×	66	49	4	39(89)	27	74	54
5	47(91)	10	79	56	5	41(88)	26	80	62
6	×	×	78	36	6	44(88)	20	84	43
7	×	×	65	73	7	28(88)	21	69	72
8	37(84)	12	74	×	8	47(83)	21	74	×
9	44(90)	17	66	50	9	44(89)	38	70	56
10	×	×	79	43	10	47(88)	31	48	84
Sample Size		240+5(1T1C)			Sample Size		240+8(2T3C)		
No.	*Colugo	Tarsius	Manis	Whale	No.	*Colugo	Tarsius	Manis	Whale
1	×	×	84	56	1	×	×	74	50
2	52(100)	35	87	41	2	41(84)	22	77	48
3	44(100)	32	81	×	3	40(85)	27	70	35
4	×	×	77	59	4	32(85)	22	81	54
5	×	×	83	65	5	37(88)	18	75	56
6	45(99)	41	82	60	6	44(87)	23	78	50
7	49(100)	41	77	69	7	44(88)	27	74	58
8	×	×	76	54	8	37(85)	23	73	57
9	41(99)	39	74	62	9	39(88)	24	76	57
10	51(98)	43	76	65	10	45(83)	29	76	55

× indicates wrong position of this taxon.

¥ T1C1 samples include one tarsier and one colugo sequence, while T2C3 samples include two tarsier and three colugo sequences.

* First number (outside brackets) indicates BPs of monophyly of Primates, and second number (inside brackets) indicates BPs that colugo is sister group of Primates.

Samples in same rows are the same except for the number of sequences of tarsiers and colugos.

However, both trees are likely to be wrong, because the placement of Scandentia with Dermoptera and Primates in the grouping Euarchonta has been supported by nuclear DNA evidence including retroposon-insertion analysis (Kriegs et al., 2007; McCormack et al., 2012; Song et al., 2012). Although colugo was not included, recently published genome-scale analyses by Fan et al. (2013) strongly support the monophyly of Primates and tree-shrew. On the other hand, the relationship among Scandentia, Dermoptera and Primates within the monophyletic Euarchonta was left as an unresolved trichotomy. While nuclear sequence analysis including indels (Janečka et al., 2007) supported the basal Euarchonta postion of Scandentia (Nie et al., 2008), cytogenetic analysis supported the Scandentia/Dermoptera grouping called Sundatheria, and the relationship among Scandentia, Dermoptera and Primates thus still awaits resolution (Martin, 2008).

The basal-Euarchonta position of Scandentia (Tree-4) (Janečka et al., 2007) was rejected only marginally with both the codon-substitution and GTR models by the AU test, and the Dermoptera/Scandentia tree (Tree-6) (Nie et al., 2008) was not rejected with the codon-substitution model (P = 0.067) but was rejected with the GTR model, which performed worse than the codon-substitution model as shown later (P = 0.003). These trees were not rejected by the more conservative test of wSH, except Tree-6 with the GTR model (P = 0.002). While the GTR + Γ + codon partition model has more parameters than the codon-substitution + Γ model, the log-likelihood score of the latter is much higher (by 5,700) than that of the former, indicating a much lower AIC of the codon-substitution model than the GTR model, and therefore the codon-substitution model better approximates our dataset than the GTR model. Among the trees supporting the Euarchonta hypothesis, support for Tree-4 and

Table S3. Bootstrap probabilities of each branch for different samples of out-group

Sample Size	10		20		30		40	
	Colugo	Tarsier	Colugo	Tarsier	Colugo	Tarsier	Colugo	Tarsier
1	*59(94)	50	58(92)	19	48(92)	24	56(93)	11
2	81(85)	28	57(93)	13	43(92)	20	47(92)	19
3	67(93)	64	50(93)	28	50(91)	20	42(93)	11
4	69(94)	38	36(93)	13	61(92)	25	52(93)	20
5	70(92)	29	×	×	×	×	43(91)	12
6	44(82)	12	43(93)	12	61(93)	13	58(92)	26
7	31(81)	21	54(89)	34	×	×	51(92)	16
8	74(94)	37	56(89)	26	68(93)	29	56(93)	11
9	40(92)	28	53(87)	32	61(92)	27	59(92)	30
10	47(94)	41	49(93)	17	53(93)	13	51(91)	8

× indicates wrong position of this taxon.
* First number (outside brackets) indicates BPs of monophyly of Primates, and second number (inside brackets) indicates BPs that colugo is sister group of Primates.

Table S4. Bootstrap probabilities of each branch for different samples of in-group

Sample Size	10		20		30		40		50	
	Colugo	Tarsier	Colugo	Tarsier	Colugo	Tarsier	Colugo	Tarsier	Colugo	Tarsier
1	*×	×	51(89)	26	55(91)	24	33(92)	8	46(91)	19
2	×	×	×	×	41(93)	14	51(93)	19	40(92)	14
3	×	×	×	×	37(90)	11	49(92)	17	53(93)	16
4	×	×	×	×	35(91)	15	60(93)	22	54(90)	24
5	×	×	×	×	58(93)	18	37(91)	12	46(92)	16
6	×	×	44(90)	9	45(92)	9	42(91)	21	53(92)	16

× indicates wrong position of this taxon.
* First number (outside brackets) indicates BPs of monophyly of Primates, and second number (inside brackets) indicates BPs that colugo is sister group of Primates.

Tree-6 is almost identical with the codon-substitution model and near the marginal level of 5% significance. A drawback in this analysis is inclusion of only *T. belangeri* and *Galeopterus variegates* from Scandentia and Dermoptera, respectively. Actually, Scandentia is a diversified order including groups that are distant from *Tupaia*, such as *Ptilocercus* and *Dendrogale* (Roberts et al., 2011), and Dermoptera has another genus *Cynocephalus* distant from *Galeopithecus* (Janečka et al., 2007). Inclusion of these additional taxa in the mitogenome analysis should contribute to resolving the phylogenetic relationships among orders in Euarchonta.

Position of Erinaceidae

We did not include Erinaceidae such as hedgehogs and moon rats in our analysis, because the position of Erinaceidae has not been settled, as noted below. Early mitogenomic analyses (Krettek et al., 1995; Mouchaty et al., 2000; Arnason et al., 2002) suggested a basal-eutherian position of Erinaceidae separate from other Eulipotyphla families such as Soricidae (shrews) and Talpidae (moles). This relationship is again in contradiction of the nuclear DNA tree, which suggests a position for Erinaceidae in a monophyletic Eulipotyphla within Laurasiatheria (Murphy et al., 2001; Douady et al., 2002; Hallström et al., 2011; Zhou et al., 2012). The aberrant placement of Erinaceidae was attributed to their distinct nucleotide compositions and rapid rate of mitogenome evolution, particularly in hedgehogs (Lin et al., 2002; Nikaido et al., 2003). Nikaido et al. (2003) showed that, by using an appropriate model, the placement of Erinaceidae in Eulipotyphla represents the best tree (when only moonrat is included) or a tree with a log-likelihood score indistinguishable from that of the best tree (when both hedgehogs and moonrat are included). More recently, (Arnason et al., 2008) mitogenome analysis including another moonrat species also gave the Erinaceidae-Eulipotyphla tree. However, all mitogenome analyses to date indicating the Erinaceidae-Eulipotyphla tree are still contradictory to the nuclear DNA tree with respect to the within-Eulipotyphla relationships: while the nuclear tree supports the Erinaceidae/Soricidae clade

Table S5. Phylogenetic positions estimated by various methods and models

	tarsier Tarsiiformes	colugo Dermoptera	Pangolin Pholidota	sperm whale Physeteridae
MP	Sister to Dermoptera + Simiiformes (<u>34</u>)	Sister to Simiiformes (56)	Sister to Tylopoda (48)	Sister to *Platanista* + Ziphiidae + Mysticeti (67)
NJ_MCL	Basal Primates (89)	Sister to Simiiformes (90)	Basal Laurasiatheria (86)	Sister to *Platanista* + Ziphiidae+Mysticeti (100)
NJ_TN	Sister to Sciuromorpha in Rodentia (19)	Sister to Simiiformes (97)	Basal Laurasiatheria next to Eulipotyphla and Chiroptera (36)	Sister to *Platanista* + Ziphiidae+ Mysticeti (99)

The numbers in parentheses indicate BP in %.

Table S6. Tests of alternative positions of Scandentia in Euarchontoglires (codon-substitution + Γ model and GTR + Γ with the partition model among codon positions) with CONSEL (Shimodaira and Hasegawa, 2001)

Tree: Position of Scandentia	Codon-substitution + Γ			GTR+Γ: CodonPartition		
	$\Delta\ell$	AU	wSH	$\Delta\ell$	AU	wSH
1. Sister to Lagomorpha	<–1,045,635.9>	0.632	0.824	–8.4	0.403	0.597
2. Basal Euarchontoglires	–3.4	0.550	0.752	<–1,051,428>	0.778	0.931
3. Sister to Glires	–18.1	0.107	0.479	–9.7	0.196	0.571
4. Basal Euarchonta	–25.5	<u>**0.049**</u>	0.212	–15.9	<u>**0.050**</u>	0.191
5. Sister to Rodentia	–29.7	<u>**0.016**</u>	0.071	–12.1	0.249	0.490
6. Sister to Dermoptera	–31.5	0.067	0.229	–47.7	<u>**0.003**</u>	<u>**0.002**</u>
7. Sister to Primates	–51.0	<u>**0.001**</u>	<u>**0.019**</u>	–54.0	<u>**10^{-53}**</u>	<u>**0.007**</u>

AU and wSH refer to P-values of the Approximate Unbiased test (Shimodaira, 2002) and the weighted Shimodaira-Hasegawa test (Shimodaira and Hasegawa, 1999), respectively. P-values with 5% level of significance are bold-faced and underlined.
$\Delta\ell$: log-likelihood difference from the ML tree. Numbers in angled brackets are log-likelihood scores of the ML tree. Tree-4, -6 and -7 represent the Euarchonta hypothesis.

(Murphy et al., 2001; Douady et al., 2002), the mitogenome tree supports the Talpidae/Soricidae clade (Arnason et al., 2008; Hallström et al., 2011). Furthermore, there is no consensus in this respect in morphological studies: while (McKenna and Bell, 1997) suggested the Talpidae/Erinaceidae clade, (Butler, 1988) suggested the Talpidae/Soricidae. The position of Erinaceidae in Eulipotyphla therefore remains to be settled.

Cytb tree

Among the protein-encoding genes in mitogenomes, cytochrome b (cytb) sequences have been used extensively in the molecular phylogeny of eutherians since (Irwin et al., 1991). Agnarsson and colleagues advocated using cytb sequences in reconstructing the eutherian tree (Agnarsson and May-Collado, 2008; Agnarsson et al., 2010, 2011; Kuntner et al., 2010), and their studies showed that even a single cytb gene can perform unexpectedly well in reconstructing the eutherian tree if the taxon sampling is sufficiently dense.

Using cytb sequences, (Adachi and Hasegawa, 1996) demonstrated the instability of phylogenetic inference with only four species in analyzing the relationships among Cetacea, Ruminantia, Suiformes and out-group eutherians. One representative species was selected from each group, and ML analyses were then carried out for every combination of the selected quartets. Quartets of species providing a high BP for each of the three possible trees could be found, indicating that analyses with sparse taxon sampling can be highly misleading. Later, with highly dense taxon sampling of cytb sequences from Cetartiodactyla, (Agnarsson and May-Collado, 2008) could show with high support values that Ruminantia is closer to Cetacea than to Suiformes and that Hippopotamidae is even closer to Cetacea than Ruminantia, consistent with the tree established by nuclear DNA analyses (Nikaido et al., 1999). It is evident that extensive taxon sampling can overcome some of the shortcomings of using mitogenomes, and that even a single gene (cytb) can be used at this taxonomic level.

Because of their very small sample size in terms of the number of characters, Agnarsson and colleagues' analyses of cytb sequences inevitably differ somewhat from both our tree and the well-established nuclear DNA tree, as listed below. (Agnarsson et al., 2011) suggested monophyly for the Microchiroptera, which contradicts our tree and nuclear gene analyses (Eick et al., 2005; Teeling et al., 2005). However, the support for Microchiroptera monophyly by Agnarsson et al. (2011) was very weak (0.50 or 0.75 posterior probabilities depending on the dataset), and therefore the discrepancy was not substantial. In their analysis of Carnivora, Agnarsson et al. (2010) placed *Ailurus fulgens* (red panda) as a sister group to Canidae, whereas red panda is a sister group to Musteloidea *sensu stricto* in previous studies (Yonezawa et al., 2007; Eizirik et al., 2010) as well as in our tree (Supplementary Fig. S1). They further placed Pinnipedia as a sister group to Ursidae, while it was a sister group to Musteloidea *sensu lato* including Ailuridae in our tree and in the well-established nuclear tree (Eizirik et al., 2010). The support for these relations in (Agnarsson et al., 2010) was not high, and can be attributed simply to a small sample size with respect to the number of characters. Despite these discrepancies, the overall consistency of their trees with our tree is quite remarkable.

Power and pitfalls of using mitogenomes

The rapid pace of mitogenome nucleotide substitutions compared to those of nuclear DNA, coupled with the special mode of maternal non-recombining inheritance, offers advantages of using this marker for phylogenetic analyses, particularly at lower taxonomic levels, that cannot be matched easily by any nuclear markers (Avise et al., 1987). Because of this high rate, substitution saturation was a concern in using mitogenomes for deep phylogeny. However, our analysis indicates that dense taxon sampling with an appropriate method can reduce and overcome this potential problem. Because of their maternal inheritance and the haploid nature of mitochondria, the effective population size of mitogenomes is 1/4 that of nuclear autosomal genes (Birky et al., 1989), and incomplete lineage sorting of ancestral polymorphism is less of a concern for mitochondrial than for nuclear gene trees, providing an additional advantage of using a mitogenome tree as an estimate of a species tree (Avise et al., 1987). Indeed, compared to mitogenome analyses, the analysis of nuclear genes, among which there exist differences in phylogenetic history, is complicated, and the concatenated analysis of such genes may lead to well-resolved relationships that are not concordant with the species tree (Song et al., 2012; Nakagome et al., 2013; Ting and Sterner, 2013). On the other hand, the smaller effective population size of mitogenomes may facilitate fixation of an introgressed haplotype in a foreign population when hybridization occurs (Takahata and Slatkin, 1984). Therefore, a combination of mitogenomes with several nuclear markers may become a major approach in reconstructing a comprehensive tree of eutherian mammals in the future.

References

Adachi, J. and Hasegawa, M., 1996. Instability of quartet analyses of molecular sequence data by the maximum likelihood method: the Cetacea/Artiodactyla relationships. Mol Phylogenet Evol. 6, 72–6.

Agnarsson, I. and May-Collado, L.J., 2008. The phylogeny of Cetartiodactyla: the importance of dense taxon sampling, missing data, and the remarkable promise of cytochrome *b* to provide reliable species-level phylogenies. Mol Phylogenet Evol. 48, 964–85.

Agnarsson, I., Kuntner, M. and May-Collado, L.J., 2010. Dogs, cats, and kin: a molecular species-level phylogeny of Carnivora. Mol Phylogenet Evol. 54, 726–45.

Agnarsson, I., Zambrana-Torrelio, C.M., Flores-Saldana, N.P. and May-Collado, L.J., 2011. A time-calibrated species-level phylogeny of bats (Chiroptera, Mammalia). PLoS Curr. 3, RRN1212.

Arnason, U., Adegoke, J.A., Bodin, K., Born, E.W., Esa, Y.B., Gullberg, A., Nilsson, M., Short, R.V., Xu, X. and Janke, A., 2002. Mammalian mitogenomic relationships and the root of the eutherian tree. Proc Natl Acad Sci USA. 99, 8151–6.

Arnason, U., Adegoke, J.A., Gullberg, A., Harley, E.H., Janke, A. and Kullberg, M., 2008. Mitogenomic relationships of placental mammals and molecular estimates of their divergences. Gene 421, 37–51.

Avise, J.C., Arnold, J., Ball, R.M., Bermingham, E., Lamb, T., Neigel, J.E., Reef, C. and Saunders, N., 1987. Intraspecific phylogeography: The mitochondrial DNA bridge between population genetics and systematics. Ann Rev Ecol Syst. 18, 489–522.

Birky, C.W.Jr., Fuerst, P. and Maruyama, T., 1989. Organelle gene diversity under migration, mutation, and drift: equilibrium expectations, approach to equilibrium, effects of heteroplasmic cells, and comparison to nuclear genes. Genetics 121, 613–27.

Butler, P.M., 1988. Phylogeny of the insectivores. In The Phylogeny and the Classification of the Tetrapods, Mammals. Edited by Benton MJ. Clarendon Press, Oxford, pp. 117–141.

Douady, C.J., Chatelier, P.I., Madsen, O., de Jong, W.W., Catzeflis, F., Springer, M.S. and Stanhope, M.J., 2002. Molecular phylogenetic evidence confirming the Eulipotyphla concept and in support of hedgehogs as the sister group to shrews. Mol Phylogenet Evol. 25, 200–9.

Eick, G.N., Jacobs, D.S. and Matthee, C.A., 2005. A nuclear DNA phylogenetic perspective on the evolution of echolocation and historical biogeography of extant bats (Chiroptera). Mol Biol Evol. 22, 1869–86.

Eizirik, E., Murphy, W.J., Koepfli, K.P., Johnson, W.E., Dragoo, J.W., Wayne, R.K. and O'Brien, S.J., 2010. Pattern and timing of diversification of the mammalian order Carnivora inferred from multiple nuclear gene sequences. Mol Phylogenet Evol. 56, 49–63.

Fan, Y., Huang, Z.Y., Cao, C.C., Chen, C.S., Chen, Y.X., Fan, D.D., He, J., Hou, H.L., Hu, L., Hu, X.T., Jiang, X.T., Lai, R., Lang, Y.S., Liang, B., Liao, S.G., Mu, D., Ma, Y.Y., Niu, Y.Y., Sun, X.Q., Xia, J.Q., Xiao, J., Xiong, Z.Q., Xu, L., Yang, L., Zhang, Y., Zhao, W., Zhao, X.D., Zheng, Y.T., Zhou, J.M., Zhu, Y.B., Zhang, G.J., Wang, J. and Yao, Y.G., 2013. Genome of the Chinese tree shrew. Nat Commun. 4, 1426.

Felsenstein, J., 1978. Cases in which parsimony or compatibility methods will be positively misleading. Syst Zool. 27, 401–410.

Fitch, W., 1971. Toward defining the course of evolution: minimum change for a specific tree topology. Syst Zool. 20, 406–416.

Hallström, B.M., Schneider, A., Zoller, S. and Janke, A., 2011. A genomic approach to examine the complex evolution of Laurasiatherian mammals. PLoS One 6, e28199.

Hasegawa, M., Adachi, J. and Milinkovitch, M.C., 1997. Novel phylogeny of whales supported by total molecular evidence. J Mol Evol. 44 Suppl 1, S117–20.

Irwin, D.M., Kocher, T.D. and Wilson, A.C., 1991. Evolution of the cytochrome b gene of mammals. J Mol Evol. 32, 128–44.

Janečka, J.E., Miller, W., Pringle, T.H., Wiens, F., Zitzmann, A., Helgen, K.M., Springer, M.S. and Murphy, W.J., 2007. Molecular and genomic data identify the closest living relative of primates. Science 318, 792–4.

Krettek, A., Gullberg, A. and Arnason, U., 1995. Sequence analysis of the complete mitochondrial DNA molecule of the hedgehog, Erinaceus europaeus, and the phylogenetic position of the Lipotyphla. J Mol Evol. 41, 952–7.

Kriegs, J.O., Churakov, G., Jurka, J., Brosius, J. and Schmitz, J., 2007. Evolutionary history of 7SL RNA-derived SINEs in Supraprimates. Trends Genet. 23, 158–61.

Kuntner, M., May-Collado, L.J. and Agnarsson, I., 2010. Phylogeny and conservation priorities of afrotherian mammals (Afrotheria, Mammalia). Zoologica Scripta. 40, 1–15.

Lin, Y.H., McLenachan, P.A., Gore, A.R., Phillips, M.J., Ota, R., Hendy, M.D. and Penny, D., 2002. Four new mitochondrial genomes and the increased stability of evolutionary trees of mammals from improved taxon sampling. Mol Biol Evol. 19, 2060–70.

Lopez, P., Casane, D. and Philippe, H., 2002. Heterotachy, an important process of protein evolution. Mol Biol Evol. 19, 1–7.

Martin, R.D., 2008. Colugos: obscure mammals glide into the evolutionary limelight. J Biol. 7, 13.

McCormack, J.E., Faircloth, B.C., Crawford, N.G., Gowaty, P.A., Brumfield, R.T. and Glenn, T.C., 2012. Ultraconserved elements are novel phylogenomic markers that resolve placental mammal phylogeny when combined with species-tree analysis. Genome Res. 22, 746–54.

McKenna, M.C. and Bell, S.K., 1997. Classification of Mammals Above the Species Level. Columbia University Press, New York.

Milinkovitch, M.C., Orti, G. and Meyer, A., 1993. Revised phylogeny of whales suggested by mitochondrial ribosomal DNA sequences. Nature 361, 346–8.

Miyata, T., Miyazawa, S. and Yasunaga, T., 1979. Two types of amino acid substitutions in protein evolution. J Mol Evol. 12, 219–36.

Mouchaty, S.K., Gullberg, A., Janke, A. and Arnason, U., 2000. The phylogenetic position of the Talpidae within eutheria based on analysis of complete mitochondrial sequences. Mol Biol Evol. 17, 60–7.

Murphy, W.J., Eizirik, E., O'Brien, S.J., Madsen, O., Scally, M., Douady, C.J., Teeling, E., Ryder, O.A., Stanhope, M.J., de Jong, W.W. and Springer, M.S., 2001. Resolution of the early placental mammal radiation using Bayesian phylogenetics. Science 294, 2348–51.

Nakagome, S., Mano, S. and Hasegawa, M., 2013. Comment on "Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage". Science 339, 1522; discussion 1522.

Nie, W., Fu, B., O'Brien, P.C., Wang, J., Su, W., Tanomtong, A., Volobouev, V., Ferguson-Smith, M.A. and Yang, F., 2008. Flying lemurs--the 'flying tree shrews'? Molecular cytogenetic evidence for a Scandentia-Dermoptera sister clade. BMC Biol. 6, 18.

Nikaido, M., Cao, Y., Harada, M., Okada, N. and Hasegawa, M., 2003. Mitochondrial phylogeny of hedgehogs and monophyly of Eulipotyphla. Mol Phylogenet Evol. 28, 276–84.

Nikaido, M., Matsuno, F., Hamilton, H., Brownell, R.L., Jr., Cao, Y., Ding, W., Zuoyan, Z., Shedlock, A.M., Fordyce, R.E., Hasegawa, M. and Okada, N., 2001. Retroposon analysis of major cetacean lineages: the monophyly of toothed whales and the paraphyly of river dolphins. Proc Natl Acad Sci USA. 98, 7384–9.

Nikaido, M., Rooney, A.P. and Okada, N., 1999. Phylogenetic relationships among cetartiodactyls based on insertions of short and long interpersed elements: Hippopotamuses are the closest extant relatives of whales. Proc Natl Acad Sci USA. 96, 10261–6.

Nishihara, H., Okada, N. and Hasegawa, M., 2007. Rooting the eutherian tree: the power and pitfalls of phylogenomics. Genome Biol. 8, R199.

Philippe, H., Brinkmann, H., Lavrov, D.V., Littlewood, D. T., Manuel, M., Worheide, G. and Baurain, D., 2011. Resolving difficult phylogenetic questions: why more sequences are not enough. PLoS Biol. 9, e1000602.

Phillips, M.J., Delsuc, F. and Penny, D., 2004. Genome-scale phylogeny and the detection of systematic biases. Mol Biol Evol. 21, 1455–8.

Roberts, T.E., Lanier, H.C., Sargis, E.J. and Olson, L.E., 2011. Molecular phylogeny of treeshrews (Mammalia: Scandentia) and the timescale of diversification in Southeast Asia. Mol Phylogenet Evol. 60, 358–72.

Saitou, N. and Nei, M., 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol. 4, 406–25.

Shimodaira, H., 2002. An approximately unbiased test of phylogenetic tree selection. Syst Biol. 51, 492–508.

Shimodaira, H. and Hasegawa, M., 1999. Multiple comparisons of log-likelihoods with applications to phylogenetic inference. Mol Biol Evol. 16, 1114–1116.

Shimodaira, H. and Hasegawa, M., 2001. CONSEL: for assessing the confidence of phylogenetic tree selection. Bioinformatics 17, 1246–1247.

Song, S., Liu, L., Edwards, S.V. and Wu, S., 2012. Resolving conflict in eutherian mammal phylogeny using phylogenomics and the multispecies coalescent model. Proc Natl Acad Sci USA. 109, 14942–7.

Stamatakis, A., Hoover, P. and Rougemont, J., 2008. A rapid bootstrap algorithm for the RAxML Web servers. Syst Biol. 57, 758–71.

Steeman, M.E., Hebsgaard, M.B., Fordyce, R.E., Ho, S.Y., Rabosky, D.L., Nielsen, R., Rahbek, C., Glenner, H., Sorensen, M.V. and Willerslev, E., 2009. Radiation of extant cetaceans driven by restructuring of the oceans. Syst Biol. 58, 573–85.

Swofford, D.L., 2002. PAUP* Phylogenetic Analysis Using Parsimony (*and Other Methods), Version 4. Sinauer Associates, Sunderland, Massachusetts.

Takahata, N. and Slatkin, M., 1984. Mitochondrial gene flow. Proc Natl Acad Sci USA. 81, 1764–7.

Tamura, K. and Nei, M., 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol Biol Evol. 10, 512–26.

Tamura, K., Nei, M. and Kumar, S., 2004. Prospects for inferring very large phylogenies by using the neighbor-joining method. Proc Natl Acad Sci USA. 101, 11030–5.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. and Kumar, S., 2011. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol. 28, 2731–9.

Teeling, E.C., Springer, M.S., Madsen, O., Bates, P., O'Brien, S. J. and Murphy, W.J., 2005. A molecular phylogeny for bats illuminates biogeography and the fossil record. Science 307, 580–4.

Ting, N. and Sterner, K.N., 2013. Primate molecular phylogenetics in a genomic era. Mol Phylogenet Evol. 66, 565–8.

Xu, L., Chen, S.Y., Nie, W.H., Jiang, X.L. and Yao, Y.G., 2012. Evaluating the phylogenetic position of Chinese tree shrew (*Tupaia belangeri chinensis*) based on complete mitochondrial genome: implication for using tree shrew as an alternative experimental animal to primates in biomedical research. J Genet Genomics 39, 131–7.

Yang, Z., 1996. Among-site rate variation and its impact on phylogenetic analyses. Trends Ecol Evol. 11, 367–72.

Yang, Z., 2007. PAML 4: phylogenetic analysis by maximum likelihood. Mol Biol Evol. 24, 1586–91.

Yang, Z., Nielsen, R. and Hasegawa, M., 1998. Models of amino acid substitution and applications to mitochondrial protein evolution. Mol Biol Evol. 15, 1600–11.

Yonezawa, T., Nikaido, M., Kohno, N., Fukumoto, Y., Okada, N. and Hasegawa, M., 2007. Molecular phylogenetic study on the origin and evolution of Mustelidae. Gene 396, 1–12.

Zhou, X., Xu, S., Xu, J., Chen, B., Zhou, K. and Yang, G., 2012. Phylogenomic analysis resolves the interordinal relationships and rapid diversification of the Laurasiatherian mammals. Syst Biol. 61, 150–64.

Zhou, X., Xu, S., Yang, Y., Zhou, K. and Yang, G., 2011. Phylogenomic analyses and improved resolution of Cetartiodactyla. Mol Phylogenet Evol. 61, 255–64.