**Figure S1. Relationship of solenodon mitochondrial genomes to those of other mammals.** The maximum likelihood tree of laurasiatherian mammals showing the position of solenodons was generated in RAxML version 8.2.4 (Stamatakis 2014), using the GTR+I+G substitution model and 1000 rapid bootstrap replicates. Full mitochondrial genome sequences (excluding control region and regions of poor alignment) from the taxa on the tree were used to generate the phylogeny. Letters indicate the nodes for which fossil calibration dates and inferred molecular dates are described in Table S3.

**Figure S2.** **Phylogeny of laurasiatherian mammals showing the position of *Solenodon paradoxus*.** The tree was generated using the full mitogenome sequences except that regions of poor alignment were excluded, as was the control region, which is unreliable for the deep time scales involved (Ingman et al. 2000). The relationships among taxa were not constrained to those established using the fossil record or nuclear genetic relationships, since in some circumstances mitogenomic relationships may be incongruent with the true species tree (Petit and Excoffier 2009). For molecular dating, previously well-established fossil calibrations (Meredith et al. 2011) were incorporated into an analysis conducted using the software BEAST v1.8.2 software (Drummond et al. 2012). At eulipotyphlan nodes, the Bayesian posterior probability and maximum likelihood bootstrap support are listed above, while below are listed dates of divergence with 95% credibility intervals in parentheses. The time at which the solenodon mitogenome diverged from that of other mammals was estimated as 78.2 Mya (95% CI: 62.1-98.6 Mya). The point estimate for the divergence time between solenodons and other mammals is similar to previous estimates ranging from 73-76 Mya, based upon analysis of datasets largely comprised of nuclear sequences (Roca et al. 2004, Meredith et al. 2011).



|  |
| --- |
| **Table S1.** Radical mutations in mitochondrial protein coding genes of *S. paradoxus* in comparison to those of reference species. Mutations are shown in this format: position, amino acid in the reference mitogenome, amino acid in *S. paradoxus*. Scores were calculated with PROVEAN using a stringent threshold for listing the radical mutations of -4.1. Entries are vertically aligned with regard to preceding insertion and deletion events. |
| **Gene** | **Reference species** |
|  | ***Talpa europaea*** | ***Sorex araneus*** | ***Felis catus*** | ***Homo sapiens*** |
| *ATP6* | 125,L,T  | -4.525 | 125,L,T | -4.478 | 125,L,T | -4.537 | 33,T,H125,L,T | -4.310-4.453 |
| *ATP8* | 27,K,A 34,P,T 62,L,H  | -5.702-4.805-5.634 | 27,K,A34,P,T62,L,H | -5.677-4.792-5.016 | 24,F,L27,K,A34,P,T39,P,L62,L,H | -4.253-5.755-4.690-4.293-4.682 | 27,K,A 34,H,T | -5.993-4.171 |
| *COX1* | — | — | — | — | — | — | — | — |
| *COX2* | 39,H,G | -7.301 |  |  | 39,H,G | -7.099 | 151,P,T | -5.157 |
| *COX3* | — | — | — | — | — | — | — | — |
| *CYTB* | — | — | — | — | — | — | — | — |
| *ND1* | 252,P,S308,P,H | -4.615-6.980 | 252,P,S308,P,H | -5.249-7.014 | 252,P,S308,P,H | -5.008-6.881 | 250,P,S306,P,H | -5.384-7.051 |
| *ND2* | 46,M,T243,W,G244,N,S254,L,T313,M,T314,F,L | -4.480-10.996-4.510-4.230-4.258-4.986 | 20,G,S41,M,T96,P,I147,Y,M202,P,Q238,W,G239,N,S308,M,T309,F,L | -4.458-4.937-5.200-5.460-6.613-10.116-4.366-4.449-5.164 | 25,G,S101,P,I152,Y,M207,P,Q243,W,G244,N,S313,M,T314,F,L | -4.367-5.685-6.104-6.447-10.578-4.544-4.215-5.218 | 22,G,S43,M,T149,Y,M153,P,N204,P,Q240,W,G241,N,S295,N,S | -5.039-4.721-5.543-5.191-6.187-10.553-4.500-4.223 |
| *ND3* | 27,L,P | -4.797 | 27,L,P | -5.226 | 27,L,P | -4.965 | 27,L,P | -5.285 |
| *ND4* |  |  |  |  |  |  | 4,H,M5,S,Y185,G,S | -4.380-4.341-4.427 |
| *ND4L* | — | — | — | — | — | — | — | — |
| *ND5* | 62,S,Y154,G,S349,N,A431,G,K435,F,S446,P,K450,N,K469,N,Y510,K,M578,Q,N | -4.845-4.377-6.467-4.196-5.564-5.870-4.681-4.690-4.121-4.282 | 62,S,Y154,G,S349,N,A431,G,K446,P,K450,N,K469,N,Y510,K,M514,P,K578,Q,N | -4.857-4.401-6.734-4.371-5.925-4.558-4.226-4.451-4.402-4.335 | 62,S,Y154,G,S349,N,A435,F,S450,N,K469,N,Y510,K,M514,P,K578,Q,N | -4.745-4.377-6.467-5.562-4.681-4.560-4.244-4.325-4.282 | 60,S,Y347,N,A429,G,K433,F,S444,P,K448,N,K467,N,Y508,K,M512,P,K576,Q,N | -4.623-6.667-4.393-5.628-5.883-4.691-4.369-4.423-4.544-4.294 |
| *ND6* | 106,Y,C138,E,G | -4.909-4.758 | 106,Y,C | -4.378 | 106,Y,C138,E,G | -4.945-4.775 | 106,W,C162,F,V | -5.745-5.011 |

**Table S2. Taxa used for comparison of *S. paradoxus* to other mammals.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Order** | **Family** | **Taxon** | **GenBank accession code** |
| Eulipotyphla | Solenodontidae | SPA-1 | KU697358 |
| Eulipotyphla | Solenodontidae | SPA-K | KU697359 |
| Eulipotyphla | Solenodontidae | SPA-L | KU697360 |
| Eulipotyphla | Solenodontidae | SPA-M | KU697361 |
| Eulipotyphla | Solenodontidae | SPA-N | KU697362 |
| Eulipotyphla | Solenodontidae | SPA-O | KU697363 |
| Eulipotyphla | Soricidae | European shrew | NC\_027963 |
| Eulipotyphla  | Talpidae | European mole | NC\_002391 |
| Cetartiodactyla | Antilocapridae | Pronghorn | NC\_020679  |
| Cetartiodactyla | Balaenidae  | Southern right whale | NC\_006930  |
| Cetartiodactyla | Balaenopteridae 1 | Pygmy Bryde's whale | NC\_007938 |
| Cetartiodactyla | Balaenopteridae 2 | Humpback whale | NC\_006927 |
| Cetartiodactyla | Bovidae | Domestic cattle | NC\_006853 |
| Cetartiodactyla | Camelidae  | Bactrian camel | NC\_009628  |
| Cetartiodactyla | Cervidae | Reindeer | NC\_007703 |
| Cetartiodactyla | Delphinidae | Heaviside's dolphin | NC\_020696 |
| Cetartiodactyla | Eschrichtiidae | Grey whale | NC\_005270  |
| Cetartiodactyla | Giraffidae | Giraffe | NC\_024820  |
| Cetartiodactyla | Hippopotamidae  | Pygmy hippopotamus | NC\_020697 |
| Cetartiodactyla | Iniidae  | Amazon river dolphin | NC\_005276 |
| Cetartiodactyla | Kogiidae | Pygmy sperm whale | NC\_005272 |
| Cetartiodactyla | Monodontidae | Narwhal | NC\_005279 |
| Cetartiodactyla | Moschidae 1 | Anhui musk deer | NC\_020017  |
| Cetartiodactyla | Moschidae 2 | Siberian musk deer | NC\_013753 |
| Cetartiodactyla | Neobalaenidae | Pygmy right whale | NC\_005269 |
| Cetartiodactyla | Phocoenidae | Finless porpoise | NC\_026456  |
| Cetartiodactyla | Physeteridae | Sperm whale | NC\_002503 |
| Cetartiodactyla | Platanistidae  | Indus River dolphin | NC\_005275 |
| Cetartiodactyla | Pontoporiidae | La Plata dolphin | NC\_005277 |
| Cetartiodactyla | Suidae | Domestic pig | NC\_000845 |
| Cetartiodactyla | Tayassuidae | Collared peccary | NC\_012103 |
| Cetartiodactyla | Tragulidae | Water chevrotain | NC\_020714 |
| Cetartiodactyla | Ziphiidae | Ginkgo-toothed beaked whale | NC\_027593 |
| Perissodactyla | Equidae | Horse | NC\_001640  |
| Perissodactyla | Rhinocerotidae  | White rhinoceros | NC\_001808 |
| Perissodactyla | Tapiridae | Malayan tapir | NC\_023838 |
| Carnivora | Ailuridae | Red panda | NC\_009691 |
| Carnivora | Canidae | Domestic dog | NC\_002008 |

**Table S2. Continued.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Order** | **Family** | **Taxon** | **GenBank accession code** |
| Carnivora | Eupleridae | Narrow-striped mongoose | NC\_027828 |
| Carnivora | Felidae | Domestic cat | NC\_001700 |
| Carnivora | Herpestidae | Indian mongoose | NC\_006835 |
| Carnivora | Hyaenidae | Spotted hyena | NC\_020670  |
| Carnivora | Mephitidae | Striped skunk | NC\_020648  |
| Carnivora | Mustelidae | American marten | NC\_020642 |
| Carnivora | Nandiniidae | African palm civet | NC\_024567 |
| Carnivora | Odobenidae | Atlantic walrus | NC\_004029 |
| Carnivora | Otariidae | California sea lion | NC\_008416 |
| Carnivora | Phocidae 1 | Harp seal | NC\_008429 |
| Carnivora | Phocidae 2 | Weddell seal | NC\_008424 |
| Carnivora | Prionodontidae | Spotted linsang | NC\_024569 |
| Carnivora | Procyonidae | Raccoon | NC\_009126  |
| Carnivora | Ursidae | Giant short-faced bear | NC\_011116 |
| Carnivora | Viverridae | Servaline genet | NC\_024568 |
| Chiroptera | Hipposideridae  | Great roundleaf bat | NC\_018540  |
| Chiroptera | Phyllostomidae  | Common vampire bat | NC\_022423 |
| Chiroptera | Pteropodidae | Large flying fox | NC\_026542 |
| Chiroptera | Rhinolophidae | Big-eared horseshoe Bat | NC\_026460  |
| Chiroptera | Vespertilionidae | Red bat | NC\_016873 |
| Pholidota | Manidae 1 | Tree pangolin | NC\_026780 |
| Pholidota | Manidae 2 | Malayan pangolin | NC\_026781 |

**Table S3. Laurasiatherian fossil calibration dates and inferred molecular dating.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Group** | **Node** | **Fossil\*** | **Estimated** |  **(95% CI)** | **Posterior probability** | **Bootstrap node support (%)** |
| Base of *S. paradoxus* | A | - | 0.60 |  (0.33-0.94) | 1.00 | 100 |
| Megaptera-Eschrichtius | B | 7.3-23.03 | 10.74 |  (7.69-14.02) | 1.00 | 100 |
| Phocoenidae-Monodontidae | C | 12.1-28.5 | 16.10 |  (11.52-20.40) | 1.00 | 100 |
| Otariidae-Odobenidae | D | 15.97-34 | 20.84 |  (15.83-25.67) | 1.00 | 100 |
| Bovidae-Moschidae | E | 18-34 | 21.05 |  (16.49-25.54) | 1.00 | 31 |
| Herpestidae-Eupleridae | F | 15.97-34 | 23.43 |  (18.44-28.85) | 1.00 | 100 |
| Phocidae-(Otariidae+Odobenidae) | G | 20.43-34 | 29.36 |  (24.93-34.06) | 1.00 | 100 |
| Giraffidae-Antilocapridae | H | 17.8-34 | 30.55 |  (25.80-35.39) | 1.00 | 100 |
| Felidae-Prionodontidae | I | 28.3-40.6 | 32.27 |  (27.29-37.10) | 1.00 | 99 |
| Suidae-Tayassuidae | J | 15.97-37.3 | 32.37 |  (35.55-41.13) | 1.00 | 100 |
| Procyonidae-Mustelidae | K | 27.6-40.6 | 32.61 |  (27.50-37.43) | 1.00 | 96 |
| Cetacea | L | 33.8-48.8 | 37.80 |  (33.27-42.18) | 1.00 | 100 |
| Hipposideridae-Rhinolophidae | M | 37.1-56 | 43.28 |  (34.18-52.18) | 1.00 | 100 |
| Canidae-Arctoidea | N | 37.1-56 | 50.38 |  (45.25-55.75) | 1.00 | 100 |
| Whippomorpha | O | 52.5-61.1 | 54.80 |  (50.85-58.73) | 1.00 | 100 |
| Base of Perissodactyla | P | 55.5-61.1 | 57.33 |  (54.11-60.58) | 1.00 | 100 |
| Base of Carnivora | Q | 37.1-65.8 | 57.78 |  (52.11-63.57) | 1.00 | 100 |
| Talpidae-Soricidae | R | - | 67.96 |  (47.83-95.82) | 0.99 | 98 |
| Base of Cetartiodactyla | S | 52.5-65.8 | 67.46 |  (52.67-72.57) | 1.00 | 100 |
| Base of Chiroptera | T | - | 76.09 |  (66.57-85.48) | 1.00 | 100 |
| Base of Eulipotyphla | U | - | 78.16 |  (62.07-98.61) | 0.79 | 99 |
| Base of Laurasiatheria | V | - | 92.61 |  (80.06-119.48) | 1.00 | - |

\*Fossil calibration dates are as described previously (Meredith *et al.* 2011).