Supplementary Information:

Title: Higher speciation and Lower extinction influence mammal diversity gradients in Asia
Authors: Krishnapriya Tamma and Uma Ramakrishnan

1. How Asian are the Asian species?
There are 457 mammalian genera that have distribution in Asia. There are 1863 species of mammals in Asia [1]. If all species in each of these genera, irrespective of their geographic distribution is considered, there are 2549 species. Thus overall, Asian genera have 25% of their species outside the Asian boundaries as defined by this study.

The figure shows the distribution of different proportions of Asian species across the 457 genera. Most genera have species that are restricted in Asia, while few have more than 50% of their species distributed outside this study’s definition of Asia. Thus, we consider this dataset to be reflective of processes occurring in Asia and to be an accurate representation of the same.

Figure 1: Distribution of the proportion of Asian species across the 457 genera considered in this study that have predominantly Asian presence.

2. How do missing species affect the patterns?
We have three analysis that rely on the phylogeny heavily – Phylogenetic diversity, LTT and Stadler’s method for temporal patterns and GeoSSE for spatial patterns. Both Stadler’s algorithm and the GeoSSE method can account for missing species while estimating diversification rates.
In total, 405 mammal species are not represented in the supertree. Of these, 275 have geographical ranges described by the IUCN (which is the source of range-data in our study). The remaining 129 have no range data described in the IUCN. Of the 275 species whose ranges are described in the IUCN, 75 species have ranges in Asia. The 75 species include 1 Monotreme, 6 marsupials, 2 primates, 3 lagomorphs, 2 Erinaceomorphs, 14 soricomorphs, 21 bats, 6 Artiodactyls and 20 rodents. Most of these species are from South and Southeast Asia and Western mountains of the Himalayan system (Supplementary Figure 2). Of the 129 species with no range data in IUCN, 9 are from Asia (whose locations fall within our study area). Most of these species have gone extinct.

Figure 2: South and Southeast Asia (Biomes 1 and 2) along with Biome 4 show the most number of mammal species with missing data. These regions already show the highest phylogenetic diversity in Asia, and adding these missing species to the mammal supertree will only make the patterns of species and phylogenetic diversity recovered by the study only more conspicuous/prominent.
3. How does unrecognized or unknown diversity impact the patterns?

Previous studies have predicted that the highest number of undiscovered mammal species will be from the tropical forests [2]. Given this, and the fact that there have been new species of rodents and shrews described from tropical forests in Asia, it is conceivable that a high proportion of unsampled diversity is hidden tropical regions. Some of the recently discovered mammal species from these regions include - *Leonastus aenigmamus* (striped rabbit) [3], *Saxatilomys pailinae* [4], *Tonkinomys daovantiens* [5], *Hylomys megalotis*, *Chodsigoa caovansungu* [6], *Crocidura kegoensis*, among others [7]. Accounting for this ‘hidden’ diversity will only accentuate the patterns we observe.

Most this hidden diversity is non-randomly distributed across clades and space. Small mammal orders - such as Chiroptera, Rodentia and Sorcimorpha are witnessing high species discovery. Apart from genetic species, new morpho-species are also being described. Many regions of tropical Asia still remain poorly surveyed and the diversity poorly documented. Species and phylogenetic diversity of this region will increase, and the estimates of diversification rates may subsequently increase for the tropical biome. Given that for Rodentia, Chiroptera and Soricimorpha we recovered higher speciation rates in the tropical biomes, discovery of new species will only increase the estimates of speciation rates.

4. What is the relationship between species richness (SR) and Phylogenetic diversity (PD)?

Figure 3: The relationship between PD and SR for all mammals in Asia. The quadratic spatial regression model best fit the relationship.
5. What is the relationship between SR and PD for different orders and across biomes?

Figure 4: Panel showing the relationship between PD and SR for different orders across biomes. Each point represents a cell, and the colour denotes the biome it belongs to.

6. Pull of the present and LTT plots:

Inferring speciation and extinction rates solely from LTT plots may be incorrect as they suffer from the 'pull of the present' effects. The pull of the present refers to the apparent increase in diversification rate towards the present, arising from the fact that lineages that have arisen recently are less likely to go extinct and thus are represented in the phylogeny. In our study, we do not estimate diversification rate changes from the LTT, and use the LTT plots as indicators of the overall temporal patterns of lineage diversifications. The diversification shift-times were estimated using the method developed by Stadler et al 2011, which is unaffected by the 'pull of the present'.

7. LTT plots for each of the orders

Figure 5: LTT plots for the individual mammalian orders in Asia.
8. What are the patterns of species richness for each of the orders?

Figure 6: Species Richness per order. The lighter shades of blue depict higher species richness and the darker shades depict lower species richness.

a) Artiodactyla, b) Carnivora, c) Chiroptera, d) Lagomorpha, e) Primates, f) Rodentia, and g) Soricomorpha

9. Calculation of Sampling frequency:

For all global mammals:

The GeoSSE algorithm can account for missing species by incorporating the sampling frequency of the phylogeny in the likelihood estimations. Sampling frequency refers to the proportion of the species in each geographic region present in our phylogeny. Out of the total of
5416 global mammals, 3959 species were included in our phylogeny. This included 2718 which belonged to both regions, 638 that belonged to tropical biomes and 603 that belonged to non-tropical biomes. Initially, we able to ascribe geographic state for 3038 species belonging to both regions, 804 belonging to tropical regions and 671 belonging to non-tropical regions. We then estimated the sampling frequencies to be as follows: 0.741 for species spanning both biome types, 0.66 for species restricted in the tropical biomes and 0.747 for species restricted to the non-tropical biomes.

E.g., Sampling frequency, for species belonging to both biomes = 2718 / (5416 * 3038 / 4505)

For all Asian mammals:
Out of the total of 2549 mammals that had Asian affinities or sisters distributed in Asia (of which 1863 are restricted to Asia), 1670 species were included in our phylogeny. 75 out of 1863 species have no genetic data and hence are excluded from the mammal supertree. The 1670 species included included 782, which belonged to both regions, 488 that belonged to tropical biomes, and 394 that belonged to non-tropical biomes. Initially, we were able to ascribe geographic state for 841 species belonging to both regions, 578 belonging to tropical regions and 432 belonging to non-tropical regions. To calculate the sampling frequency, we did consider the total species to be 2549 in order to incorporate the entire evolutionary history of every genus found in Asia (that is the complete monophyletic lineage). We thus estimated the sampling frequencies to be as follows: 0.67 for species spanning both biome types, 0.613 for species restricted in the tropical biomes and 0.662 for species restricted to the non-tropical biomes.

The inclusion of all species in a genus even if they were not distributed in Asia was inevitable to take into consideration the entire evolutionary history of the genus. If we ignored some species in every genus, it would be an underestimate of the number of evolutionary events that have occurred in the genus, thus resulting in lower speciation estimates. But this results in a decrease in the sampling frequency fed into the algorithm, leading the algorithm to assume that the missing species are also found in the corresponding biomes in Asia. However, given that most sister-species pairs show similar niches, it is conceivable that the species outside of Asia also belong to similar biomes as their sister species in Asia. Thus, the diversifications rates estimated by our method should be an accurate representation of the true trends, while the estimates themselves may have some inaccuracies.

Table 1: Table showing the strength of the relationship between PD and SR regressions for all mammals and across different orders.
| Taxa             | R2   | p value |
|------------------|------|---------|
| All mammals      | 0.985| < 0.05  |
| Rodents          | 0.963| < 0.05  |
| Carnivora        | 0.973| < 0.05  |
| Artiodactyla     | 0.935| < 0.05  |
| Chiroptera       | 0.985| < 0.05  |
| Soricomorpha     | 0.947| < 0.05  |
| Lagomorpha       | 0.949| < 0.05  |
| Primates         | 0.97  | < 0.05  |

Table 2: The estimates of shift times for the Kuhn-tree

| Clade              | Number of significant shifts | Shift Time, Mya |
|--------------------|-------------------------------|-----------------|
| Rodentia           | 1                             | 40              |
| Artiodactyla       | 1                             | 30              |
| Chiroptera         | 1                             | 25              |
| Soricomorpha       | 1                             | 5               |
| Lagomorpha         | 2                             | 15, 40          |
| Erinaceomorpha     | 1                             | 5               |
| Scandentia         | 1                             | 25              |
| Carnivora          | 0                             | -               |
| Perrisodactyla     | 0                             | -               |
| Pholidota          | 0                             | -               |
| Primate            | 0                             | -               |
Table 3: The 16 scenarios considered in this study for the GeoSSE models

| Constraints | Interpretation | Constraint on speciation, extinction and dispersal rates | Speciation by biome divergence |
|-------------|----------------|------------------------------------------------------|-------------------------------|
| Full model  | No constraints, all parameters can vary | No constraints | No constraints |
| sAB $\neq 0$ | All vary, except speciation by biome divergence is constrained to be not zero | Speciation, extinction and dispersal can vary | Not zero, ranges can split |
| sAB = 0     | All vary, except speciation in the biomes is equal and speciation by biome divergence is zero | Extinction and dispersal rates can vary | Zero |
| sA = sB, sAB = 0 | All vary, except speciation by biome divergence is not zero and extinction in both biomes is equal | Speciation and extinction rates can vary | Not zero, ranges can split |
| sAB $\neq 0$, xA = xB | All vary, speciation by biome divergence is not zero and dispersal across biomes is equal | Speciation and extinction rates can vary | Not zero, ranges can split |
| sAB $\neq 0$, dA = dB | All vary, speciation by biome divergence is zero and extinction across the regions is equal | Speciation and dispersal rates can vary | Zero |
| sA = sB, sAB $\neq 0$, 0, dA = dB | All vary, speciation and dispersal across the both regions is equal and speciation by biome divergence is not zero | Extinction rates can vary | Not zero, ranges can split |
| sA = sB, sAB = 0, dA = dB | All vary, speciation by biome divergence is zero and dispersal across the biomes is equal | Speciation and extinction rates can vary | Zero |
| sA = 0, xA = xB, dA = dB | All vary, speciation and dispersal are equal across the regions | Speciation rates can vary | Zero |
| sA = sB, sAB = 0, dA = dB | All vary, speciation and dispersal across regions is equal, speciation by biome divergence is zero | Extinction rates can vary | Zero |
| sA = sB, sAB = 0, xA = xB | All vary, speciation and extinction across the regions is equal, speciation by biome divergence is zero | Dispersal rates can vary | Zero |
| sA = sB, sAB $\neq 0$, 0, xA = xB, dA = dB | All vary, speciation, extinction and dispersal across both regions is equal, speciation by biome divergence is not zero | All constrained | Not zero, ranges can split |
| sA = sB, sAB = 0, xA = xB, dA = dB | Speciation, extinction and dispersal across the regions is equal and the speciation by | All constrained | Zero |
Table 4: Estimates of speciation, extinction and dispersal based on GeoSSE for all global mammals (global-tree). The likelihood estimates are presented here.

| Model | Constrains | sA     | sB     | sAB    | xA     | xB     | dA     | dB     | AIC  |
|-------|-------------|--------|--------|--------|--------|--------|--------|--------|------|
| fitp  | Full model  | 1.58E-01 | 4.46E-02 | 1.69E-07 | 7.72E-02 | 5.27E-01 | 2.61E+00 | 4.47E-03 | 331  |
| fit1c | sAB =! 0    | 1.59E-01 | 1.45E-05 | 1.00E+00 | 1.08E-01 | 4.46E+00 | 1.76E+01 | 1.34E-01 | 341  |
| fit2c | sA = sB, sAB =! 0 | 1.23E-01 | 1.23E-01 | 1.00E+00 | 1.23E-01 | 5.07E+00 | 1.94E+01 | 4.17E-01 | 342  |
| fit3c | sAB = 0     | 1.58E-01 | 4.13E-02 | 0.00E+00 | 7.64E-02 | 5.10E-01 | 2.37E+00 | 1.52E-03 | 331  |
| fit4c | sA = sB, sAB = 0 | 1.34E-01 | 1.34E-01 | 0.00E+00 | 5.04E-02 | 6.71E-01 | 2.75E+00 | 3.51E-04 | 333  |
| fit5c | sAB =! 0, xA = xB | 9.76E-09 | 9.76E-03 | 1.00E+00 | 1.27E+00 | 1.27E+00 | 4.14E+00 | 5.79E+00 | 352  |
| fit6c | sAB =! 0, dA = dB | 1.84E-07 | 1.06E-02 | 1.00E+00 | 8.91E-01 | 2.05E+00 | 5.48E+00 | 5.48E+00 | 352  |
| fit7c | sAB =! 0, xA = xB, dA = dB | 6.43E-03 | 3.34E-06 | 1.00E+00 | 1.36E+00 | 1.36E+00 | 5.44E+00 | 5.44E+00 | 352  |
| fit8c | sAB = 0, xA = xB | 0.209727 | 0.017196 | 0.009459 | 0.356199 | 0.356199 | 1.870885 | 1.352968 | 331  |
| fit9c | sA = sB, sAB =! 0, dA = dB | 0.002962 | 0.002962 | 0.942030 | 942 | 1.993341 | 146 | 5.616598 | 5.616598 | 352  |
| fit10c | sAB = 0, dA = dB | 0.014847 | 0.217096 | 0.221097 | 0.388700 | 1.288284 | 1.288284 | 331  |
| fit11c | sA = 0, xA = xB, dA = dB | 0.207046 | 0.009459 | 0.347930 | 0.347930 | 1.702022 | 1.702022 | 352  |
Table 5: Estimates of speciation, extinction and dispersal based on GeoSSE for all mammals in Asia (Asia-tree). The likelihood estimates are presented here.

| Likelihood models | Constraints | sA       | sB       | sAB      | xA       | xB       | dA       | dB       | AIC  |
|-------------------|-------------|----------|----------|----------|----------|----------|----------|----------|------|
| likp, fitp        |             | 1.30E-01 | 6.22E-02 | 2.87E-06 | 1.16E-05 | 3.90E-02 | 2.10E-01 | 1.27E-02 | 14341|
| lik2, fitp2       |             | 1.78E-01 | 1.78E-01 | 1.00E+00 | 1.25E-01 | 2.18E+00 | 3.77E+00 | 1.01E-02 | 15182|
| lik3, fitp3       |             | 1.30E-01 | 6.22E-02 | 0.00E+00 | 1.16E-05 | 3.90E-02 | 2.10E-01 | 1.27E-02 | 14339|
| lik4, fitp4       |             | 1.13E-01 | 1.13E-01 | 0.00E+00 | 5.14E-05 | 1.14E-01 | 2.67E-01 | 6.85E-03 | 14415|
| lik5, fitp5       |             | 1.81E-03 | 1.16E-01 | 1.00E+00 | 6.15E-01 | 6.15E-01 | 9.39E-01 | 1.74E+00 | 15262|
| lik6, fitp6       |             | 2.77E-06 | 1.53E-01 | 1.00E+00 | 4.38E-01 | 1.01E+00 | 1.44E+00 | 1.44E+00 | 15246|
| lik7, fitp7       |             | 0.11723  | 0.01332  | 0.00E+00 | 0.63676  | 0.63676  | 1.29685  | 1.29685  | 15284|
| lik8, fitp8       |             | 1.34E-01 | 4.75E-02 | 0.00E+00 | 3.25E-08 | 3.25E-08 | 3.25E-08 | 1.64E-01 | 1.93E+02 | 14390|
| lik9, fitp9       |             | 5.51E-02 | 5.51E-02 | 1.00E+00 | 4.98E-01 | 8.76E-01 | 1.44E+00 | 1.44E+00 | 15261|
| lik10, fitp10     |             | 0.15994  | 0.06240  | 0.00E+00 | 0.13923  | 0.09077  | 0.21011  | 0.21011  | 15261|
| Order                      | Model  | Phylogenetic tree | sA   | sB   | sAB   | xA     | xB   | dA    | dB    |
|----------------------------|--------|-------------------|------|------|-------|--------|------|-------|-------|
| All Global Mammals         | Rolland| 1.58E-01          | 4.13E-02 | 0.00E+00 | 7.64E-02 | 5.10E-01 | 2.37E+00 | 0.00E+00 | 1.52E-03 |
|                            | Kuhn   | 1.44E-01          | 3.44E-02 | 0.00E+00 | 6.74E-02 | 4.27E-01 | 2.08E+00 | 0.00E+00 | 1.96E-06 |
| All Asian Mammals          | Rolland| 1.30E-01          | 6.22E-02 | 0.00E+00 | 1.16E-05 | 3.90E-02 | 2.10E-01 | 1.20E-02 |
|                            | Kuhn   | 1.20E-01          | 6.19E-02 | 0.00E+00 | 1.36E-09 | 4.58E-02 | 2.11E-01 | 1.04E-02 |
| Rodents                    | Rolland| 1.53E-01          | 9.19E-02 | 0.00E+00 | 4.72E-09 | 4.01E-02 | 1.72E-01 | 9.14E-03 |
|                            | Kuhn   | 1.29E-01          | 8.73E-02 | 0.00E+00 | 7.81E-09 | 4.86E-02 | 1.58E-01 | 6.96E-03 |
| Soricomorpha               | Rolland| 1.39E-01          | 6.26E-02 | 4.12E-03 | 7.43E-09 | 5.23E-09 | 1.22E-01 | 1.89E-02 |
|                            | Kuhn   | 1.35E-01          | 6.55E-02 | 9.52E-04 | 1.95E-07 | 1.30E-02 | 1.40E-01 | 1.64E-02 |
| Chiroptera                 | Rolland| 1.64E-01          | 4.61E-02 | 0.00E+00 | 7.62E-02 | 4.49E-01 | 9.80E-01 | 2.23E-07 |
|                            | Kuhn   | 1.64E-01          | 3.73E-02 | 0.00E+00 | 8.28E-02 | 4.45E-01 | 9.96E-01 | 4.49E-07 |

Table 6: Global and Asia: Summary of best models for each order based on analyses from trees from two trees - Rolland et al and Kuhn et al trees. Additionally also for Nyakatura tree for Carnivores.
| Genus   | Carnivora | Artiodactyla |
|---------|-----------|--------------|
| Ursus   | 1         | 3            |
| Rangifer| 2         | 4            |
| Dicrostonyx | 3    | 5            |
| Canis   | 4         | 6            |
| Mustela | 5         | 7            |

Table 7: List of Asian genera

| Sl No | Genus   |
|-------|---------|
| 1     | Ursus   |
| 2     | Rangifer|
| 3     | Dicrostonyx|
| 4     | Canis   |
| 5     | Mustela |
|   | Species   |
|---|-----------|
| 6 | Lepus     |
| 7 | Lemmus    |
| 8 | Gulo      |
| 9 | Microtus  |
|10 | Ochotona  |
|11 | Sorex     |
|12 | Vulpes    |
|13 | Rattus    |
|14 | Sciurus   |
|15 | Alces     |
|16 | Myodes    |
|17 | Mus       |
|18 | Muscardinus |
|19 | Musonycteris |
|20 | Alticola  |
|21 | Pteromyscus |
|22 | Pteromys  |
|23 | Lynx      |
|24 | Myopus    |
|25 | Marmota   |
|26 | Ovis      |
|27 | Arvicola  |
|28 | Martes    |
|29 | Ovibos    |
|30 | Talpa     |
|31 | Tamias    |
|32 | Tamiasciurus |
|33 | Spermophilus |
|34 | Moschus   |
|35 | Apodemus  |
|36 | Sicista   |
|37 | Meles     |
|38 | Micromys  |
|   | Species   |
|---|-----------|
| 39| Eptesicus |
| 40| Capreolus |
| 41| Myotis    |
| 42| Lutra     |
| 43| Plecotus  |
| 44| Neomys    |
| 45| Erinaceus |
| 46| Vespertilio |
| 47| Castor    |
| 48| Cricetus  |
| 49| Crocidura |
| 50| Cervus    |
| 51| Murina    |
| 52| Desmana   |
| 53| Lagurus   |
| 54| Sus       |
| 55| Myospalax |
| 56| Meriones  |
| 57| Allactaga |
| 58| Ellobius  |
| 59| Phodopus  |
| 60| Cricetulus|
| 61| Mesechinus|
| 62| Cuon      |
| 63| Eliomys   |
| 64| Allocricetulus |
| 65| Hemiechinus |
| 66| Nyctalus  |
| 67| Enhydra   |
| 68| Panthera  |
| 69| Nyctereutes |
| 70| Vormela   |
| 71| Capra     |
|   | Common Name     |
|---|----------------|
| 72| Pipistrellus   |
| 73| Stylodipus     |
| 74| Dipus          |
| 75| Tscherskia     |
| 76| Pygeretmus     |
| 77| Saiga          |
| 78| Cardiocranius  |
| 79| Lasiopodomys   |
| 80| Diplomesodon   |
| 81| Spalax         |
| 82| Dryomys        |
| 83| Eolagurus      |
| 84| Gazella        |
| 85| Procapra       |
| 86| Prionailurus   |
| 87| Rhombomys      |
| 88| Salpingotus    |
| 89| Mogera         |
| 90| Allactodipus   |
| 91| Selevinia      |
| 92| Felis          |
| 93| Equus          |
| 94| Naemorhedus    |
| 95| Eremodipus     |
| 96| Spermophilopsis|
| 97| Arctonyx       |
| 98| Scaptochirus   |
| 99| Caracal        |
|100| Euchoreutes    |
|101| Camelus        |
|102| Niviventer     |
|103| Miniopterus    |
|104| Nesokia        |
|   | Species  |
|---|----------|
| 105 | Barbastella |
| 106 | Rhinolophus |
| 107 | Prometheomys |
| 108 | Chionomys |
| 109 | Glis |
| 110 | Glischropus |
| 111 | Rupicapra |
| 112 | Otonycteris |
| 113 | Hystrix |
| 114 | Paradipus |
| 115 | Tadarida |
| 116 | Brachiones |
| 117 | Eospalax |
| 118 | Mesocricetus |
| 119 | Jaculus |
| 120 | Suncus |
| 121 | Hyaena |
| 122 | Paraechinus |
| 123 | Mellivora |
| 124 | Sciurotamias |
| 125 | Blanfordimys |
| 126 | Neodon |
| 127 | Pseudois |
| 128 | Paguma |
| 129 | Trogopterus |
| 130 | Capricornis |
| 131 | Dymecodon |
| 132 | Macaca |
| 133 | Petaurista |
| 134 | Euroscaptor |
| 135 | Chimarroga |
| 136 | Glirulus |
| 137 | Urotrichus |
| Page | Taxon               |
|------|--------------------|
| 138  | Herpestes          |
| 139  | Myomimus           |
| 140  | Calomyscus         |
| 141  | Phaiomys           |
| 142  | Przewalskium       |
| 143  | Taphozous          |
| 144  | Tamiops            |
| 145  | Chodsigoa          |
| 146  | Aeretes            |
| 147  | Hydropotes         |
| 148  | Bos                |
| 149  | Boselaphus         |
| 150  | Eozapus            |
| 151  | Caryomys           |
| 152  | Elaphurus          |
| 153  | Damaliscus         |
| 154  | Dama               |
| 155  | Rousettus          |
| 156  | Gerbillus          |
| 157  | Tatera             |
| 158  | Asellia            |
| 159  | Acinonyx           |
| 160  | Eupetaurus         |
| 161  | Pantholops         |
| 162  | Cansumys           |
| 163  | Scapanulus         |
| 164  | Acomys             |
| 165  | Psammomomys        |
| 166  | Rhinopoma          |
| 167  | Semnopithecus       |
| 168  | Eoglaucomys        |
| 169  | Hyperacrius        |
| 170  | Pteropus           |
|   | Species           |
|---|------------------|
|171| Blarinella       |
|172| Eothenomys       |
|173| Rhizomys         |
|174| Myocastor        |
|175| Procavia         |
|176| Megaderma        |
|177| Scotophilus      |
|178| Kerivoula        |
|179| Bandicota        |
|180| Pardofelis       |
|181| Muntiacus        |
|182| Rhinopithecus    |
|183| Proedromys       |
|184| Vernaya          |
|185| Ia               |
|186| Nectogale        |
|187| Callosciurus     |
|188| Belomys          |
|189| Nycteris         |
|190| Hipposideros     |
|191| Funambulus       |
|192| Golunda          |
|193| Manis            |
|194| Hemitragus       |
|195| Rusa             |
|196| Viverra          |
|197| Anourosorex      |
|198| Leopoldamys      |
|199| Scaptonyx        |
|200| Ailurus          |
|201| Budorcas         |
|202| Elaphodus        |
|203| Viverricula      |
|   |   |
|---|---|
| 204 | Melogale |
| 205 | Uropsilus |
| 206 | Dremomys |
| 207 | Ailuropoda |
| 208 | Typhlomys |
| 209 | Cynopterus |
| 210 | Scotoecus |
| 211 | Scotozous |
| 212 | Millardia |
| 213 | Paradoxurus |
| 214 | Neofelis |
| 215 | Volemys |
| 216 | Chaetocauda |
| 217 | Oryx |
| 218 | Lutrogale |
| 219 | Axis |
| 220 | Vandeleuria |
| 221 | Prionodon |
| 222 | Neotetracus |
| 223 | Hylopetes |
| 224 | Scotomanes |
| 225 | Sekeetamys |
| 226 | Melursus |
| 227 | Aonyx |
| 228 | Sphaerias |
| 229 | Falsistrellus |
| 230 | Soriculus |
| 231 | Episoriculus |
| 232 | Parascaptor |
| 233 | Tylonycteris |
| 234 | Atherurus |
| 235 | Coelops |
| 236 | Berylmys |
| 237 | Triaenops |
| 238 | Salpingotulus |
| 239 | Tetracerus |
| 240 | Rucervus |
| 241 | Elephas |
| 242 | Eonycteris |
| 243 | Tupaia |
| 244 | Trachypithecus |
| 245 | Cremnomys |
| 246 | Antilope |
| 247 | Moschiola |
| 248 | Caprolagus |
| 249 | Rhinoceros |
| 250 | Megaerops |
| 251 | Arctictis |
| 252 | Ratufa |
| 253 | Helarctos |
| 254 | Aselliscus |
| 255 | Hesperoptenus |
| 256 | Philetor |
| 257 | Dacnomys |
| 258 | Arielulus |
| 259 | Cannomys |
| 260 | Macroglossus |
| 261 | Harpiocephalus |
| 262 | Nycticebus |
| 263 | Arctogalidia |
| 264 | Bubalus |
| 265 | Biswamoyopterus |
| 266 | Chiropodomys |
| 267 | Tokudaia |
| 268 | Pentalagus |
| 269 | Diplothrix |
|   | Species         |
|---|----------------|
| 270 | Diomys        |
| 271 | Petinomys     |
| 272 | Ichneumia     |
| 273 | Saccolaaimus  |
| 274 | Otomops       |
| 275 | Hadromys      |
| 276 | Hylomyscusc   |
| 277 | Hylomys       |
| 278 | Nomascus      |
| 279 | Hapalomys     |
| 280 | Anathana      |
| 281 | Madromys      |
| 282 | Menetes       |
| 283 | Genetta       |
| 284 | Hylobates     |
| 285 | Chiromyscus   |
| 286 | Chrotogale    |
| 287 | Maxomys       |
| 288 | Tragulus      |
| 289 | Eudiscopus    |
| 290 | Phoniscus     |
| 291 | Dendrogale    |
| 292 | Galeopterus   |
| 293 | Eidolon       |
| 294 | Myomyscus     |
| 295 | Pygathrix     |
| 296 | Nesolagus     |
| 297 | Paracoelops   |
| 298 | Neohylomys    |
| 299 | Acerodon      |
| 300 | Emballonura   |
| 301 | Otopteropus   |
| 302 | Ptenochirus   |
|   |   |
|---|---|
| 303 | Haplonycteris |
| 304 | Cheiromeles |
| 305 | Dyacopterus |
| 306 | Phloeomys |
| 307 | Apomys |
| 308 | Bullimus |
| 309 | Rhynchomys |
| 310 | Batomys |
| 311 | Archboldomys |
| 312 | Carpomys |
| 313 | Chrotomys |
| 314 | Crunomys |
| 315 | Papio |
| 316 | Craseonycteris |
| 317 | Tryphomys |
| 318 | Abditomys |
| 319 | Crateromys |
| 320 | Tapirus |
| 321 | Loris |
| 322 | Arvicanthis |
| 323 | Platacanthomys |
| 324 | Hemigalus |
| 325 | Harpyionycteris |
| 326 | Cynogale |
| 327 | Presbytis |
| 328 | Styloctenium |
| 329 | Anonymomys |
| 330 | Exilisciurus |
| 331 | Sundasciurus |
| 332 | Cynocephalus |
| 333 | Tarsius |
| 334 | Feroculus |
| 335 | Sundamys |
| 336   | Echinosorex  |
| 337   | Mydaus      |
| 338   | Haeromys    |
| 339   | Nyctimene   |
| 340   | Dobsonia    |
| 341   | Latidens    |
| 342   | Podogymnura |
| 343   | Urogale     |
| 344   | Rhinosciurus|
| 345   | Lariscus    |
| 346   | Palawanomys |
| 347   | Alionycteris|
| 348   | Tarsomys    |
| 349   | Limnomys    |
| 350   | Srilankamys |
| 351   | Balionycteris|
| 352   | Aeromys     |
| 353   | Chironax    |
| 354   | Solisorex   |
| 355   | Penthetor   |
| 356   | Ptilocercus |
| 357   | Petaurillus |
| 358   | Rheithrosciurus|
| 359   | Trichys     |
| 360   | Aethalops   |
| 361   | Symphalangus|
| 362   | Nannosciurus|
| 363   | Iomys       |
| 364   | Lenothrix   |
| 365   | Pithecheir  |
| 366   | Dicerorhinus|
| 367   | Pongo       |
| 368   | Diplogale   |
|   |   |
|---|---|
| 369 | Glyphotes |
| 370 | Nasalis |
| 371 | Mormopterus |
| 372 | Melomys |
| 373 | Ailurops |
| 374 | Thoopterus |
| 375 | Prosciurillus |
| 376 | Strigocuscus |
| 377 | Phalanger |
| 378 | Mosia |
| 379 | Macrogalidia |
| 380 | Taeromys |
| 381 | Lenomys |
| 382 | Paruromys |
| 383 | Bunomys |
| 384 | Rubrisciurus |
| 385 | Echiothrix |
| 386 | Margaretamys |
| 387 | Petaurus |
| 388 | Syconycteris |
| 389 | Babyrousia |
| 390 | Hyosciurus |
| 391 | Neopteryx |
| 392 | Dendrolagus |
| 393 | Dactylopsila |
| 394 | Echymipera |
| 395 | Spilocuscus |
| 396 | Uromys |
| 397 | Myoictis |
| 398 | Paranyctimene |
| 399 | Paramelomys |
| 400 | Dasyurus |
| 401 | Hydromys |
|   |   |
|---|---|
| 402 | Pseudochirulus |
| 403 | Cercartetus |
| 404 | Xenuromys |
| 405 | Peroryctes |
| 406 | Pseudochirops |
| 407 | Zaglossus |
| 408 | Simias |
| 409 | Melasmothrix |
| 410 | Tateomys |
| 411 | Eropeplus |
| 412 | Dorcopsis |
| 413 | Nyctophilus |
| 414 | Pogonomelomys |
| 415 | Phascolosorex |
| 416 | Distoechurus |
| 417 | Pogonomys |
| 418 | Hyomys |
| 419 | Murexia |
| 420 | Microperoryctes |
| 421 | Parahydromys |
| 422 | Thylogale |
| 423 | Mammelomys |
| 424 | Paraleptomys |
| 425 | Nesoromys |
| 426 | Rhynchomeles |
| 427 | Neophascogale |
| 428 | Anisomys |
| 429 | Mallomys |
| 430 | Dorcopsulus |
| 431 | Microhydromys |
| 432 | Macruromys |
| 433 | Lorentzimys |
| 434 | Pseudohydromys |
Coccymys
Crossomys
Sminthopsis
Aproteles
Abeomelomys
Protochromys
Tachyglossus
Leptomys
Melonycteris
Chiruromys
Scotorepens
Kadarsanomys
Macropus
Chalinolobus
Komodomys
Papagomys
Planigale
Isoodon
Pseudomys
Lagorchestes
Conilurus
Xeromys
Pharotis

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