

# Expected time-invariant effects of biological traits on mammal species duration

Peter D. Smits<sup>1</sup>

Committee on Evolutionary Biology, University of Chicago, Chicago, IL 60637

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**Determining which biological traits influence differences in extinction risk is vital for understanding the differential diversification of life and for making predictions about species' vulnerability to anthropogenic impacts.** Here I present a hierarchical Bayesian survival model of North American Cenozoic mammal species durations in relation to species-level ecological factors, time of origination, and phylogenetic relationships. I find support for the survival of the unspecialized as a time-invariant generalization of trait-based extinction risk. Furthermore, I find that phylogenetic and temporal effects are both substantial factors associated with differences in species durations. Finally, I find that the estimated effects of these factors are partially incongruous with how these factors are correlated with extinction risk of the extant species. These findings parallel previous observations that background extinction is a poor predictor of mass extinction events and suggest that attention should be focused on mass extinctions to gain insight into modern species loss.

macroevolution | macroecology | extinction | paleobiology | Bayesian

Why extinction risk varies among species remains one of the most fundamental questions in paleobiology and conservation biology (1–5). To address this issue, I test for similarities in associations between extinction risk and multiple species-level traits during times of background extinction and in the modern world; which traits have time-invariant effects on species duration; and whether extinction is age independent. I approach these questions together by using a model of species duration whose parameter estimates act as direct tests of these questions. Cenozoic mammals are an ideal focus for this study because their fossil record is well sampled and well resolved both temporally and spatially and because individual species ecology and taxonomic position are generally understood (1, 4, 6–10).

Time-invariant factors are those that have a constant directional effect even if their magnitude varies. Because change in the magnitude of extinction risk is not necessarily the best indicator of a shift from background to mass extinction (11), it is better to look for changes in either the direction of selection, the loss of a selective pressure, or the appearance of novel selective pressures (12).

The species-level traits studied here are bioprovince occupancy, body mass, and dietary and locomotor categories. These traits are related to aspects of a species' adaptive zone such as population density, expected range size, potential prey, and dispersal ability (8, 13) and are a combination of aggregate and emergent traits (14). It is expected that species with larger geographic ranges have lower extinction rates than species with smaller geographic ranges (12, 15); however, how traits more directly related to species–environment interactions may affect species extinction risk is more nebulous.

Body size is a complex trait related to many life history characteristics. There are three general hypotheses of how body size may effect extinction risk: (i) positive effect where an increase in body size causes an increase in extinction risk, potentially due to associated decrease in reproductive rate or other similar life history traits (7, 16); (ii) negative effect where an increase in body size causes a decrease in extinction risk because of an expected positive

relationship between body size and geographic range; and (iii) no effect of body size on extinction risk (9).

The strongest expectation for the effects of dietary category on extinction risk is that omnivores will have the lowest extinction risk of all species. This expectation is based on the long standing “survival of the unspecialized” hypothesis where more generalist species (e.g., omnivores) have greater survival than specialist species (e.g., carnivores/herbivores) (1, 17). It has also been observed that both carnivores and herbivores have greater diversification rates than omnivores, with herbivores diversifying faster than carnivores (18). How this result translates into differences in extinction risk is currently unknown (19). In modern taxa, higher trophic levels (e.g., carnivores vs. herbivores) have been associated with greater extinction risk, most likely because of human extermination of top predators (16, 20).

Similarly, there are few expectations of how locomotor category may effect extinction risk. During the Cenozoic, there was a shift at the Paleogene/Neogene boundary from predominately closed to predominately open environments (21, 22). Based on this observation, a prediction is that arboreal taxa will have the greatest extinction risk of all, with both scansorial and ground dwelling taxa having lower extinction risks.

I use a hierarchical Bayesian survival model of species duration as predicted by the covariates of interest along with species' temporal and phylogenetic context. Species duration, in 2-My bins, was modeled as realizations from either an exponential or Weibull distribution-based hierarchical model (23). The exponential distribution corresponds to the Law of Constant Extinction, which states that extinction is age independent (2). Note that the exponential is a special case of the Weibull when its shape parameter,  $\alpha$ , is 1. The Weibull distribution allows for extinction to be

## Significance

**Determining which biological traits influence differences in extinction risk is vital for understanding differential diversification of life and for making predictions about species' vulnerability to human impacts. The durations of fossil species are a rich source of information for estimating systematic differences in extinction risk. I analyzed Cenozoic North American fossil mammal species durations and their relationship with multiple ecological traits, their time of origination, and their shared evolutionary histories. I find support for generalists having a lower extinction risk than specialists as a general statement. When these results are compared with risk factors associated with living mammals, I find some incongruities that may indicate that the current biodiversity crisis is akin to the great mass extinctions in Earth's history.**

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<sup>1</sup>Email: psmits@uchicago.edu.

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taxon age dependent, where values of  $\alpha$  greater than 1 corresponds to increasing risk with age and values less than 1 corresponds to decreasing risk with age. Origination cohort and phylogenetic position were modeled as independent effects. Phylogenetic effect was modeled assuming species duration may have evolved via a Brownian motion-like process (24, 25). The results from the Weibull model are detailed here because this model has a better fit to the data the exponential [Weibull widely applicable information criterion (WAIC), 6,140.37; exponential WAIC, 16,697.35; Fig. 1 and *SI Appendix*, Figs. S1 and S2].

## Results

A summary of the posterior distributions for the most relevant parameter estimates is presented in Table 1. All posterior inference is based on these estimates. For the results from the posterior predictive checks and discussion of the estimation of  $\alpha$ , please see *SI Appendix*. Additionally, see *SI Appendix* for discussion surrounding use of Paleobiology Database and accompanying data quality concerns.

Species with greater bioprovince occupancy are found to be associated with lower extinction risk than taxa with smaller bioprovince occupancy ( $\beta_{\text{occupancy}}$  mean = -0.53, SD = 0.08). This is consistent with previous findings. Body size has nearly zero association with expected duration ( $\beta_{\text{size}}$  mean = -0.05, SD = 0.05), a similar result to some previous studies (9). However, previous studies were performed at the generic level and were unable to determine how body size may effect species-level extinction, as the effect of either extinction or speciation cannot be distinguished (7, 9).

Some clear patterns emerge from the pairwise differences in effect of each dietary category on expected duration (Fig. 2). Consistent with expectations from the “survival of the unspecialized” hypothesis (1, 17), omnivory appears to be associated with the lowest expected extinction risk. Carnivory is associated with a greater expected duration than either herbivory or insectivory, but a greater expected extinction risk than omnivory.

Finally, herbivory and insectivory have approximately equal effects on expected duration. Given previous results, these results imply that carnivores have a greater origination rate than omnivores (18). These results also imply that herbivores, which have the greatest extinction risk, must also have a very high origination rate to have the greatest diversification rate among these three categories (18).

For locomotor category, both scansoriality and ground-dwelling life habitat are associated with a greater expected duration than arboreality (Fig. 2). Scansorial and ground-dwelling life habits also have approximately equal expected effects on extinction risk. This result is consistent with the expectation that arboreality will confer greater extinction risk due to the loss of associated environment with the shift from open to closed habitat at the Paleogene/Neogene boundary (21). However, there are two possible processes that could lead to the observed pattern: arboreality confers an intrinsic difference in extinction risk or it might not be that arboreal taxa have an intrinsically higher risk but were instead “hit harder” by the environmental shift than other taxa. This analysis cannot distinguish between these two processes. Note that, although this is a study of North American Cenozoic mammals, for European Cenozoic mammals this transitional period corresponds to the Vallesian, which was a sudden shift in species demography away from arboreality (26, 27).

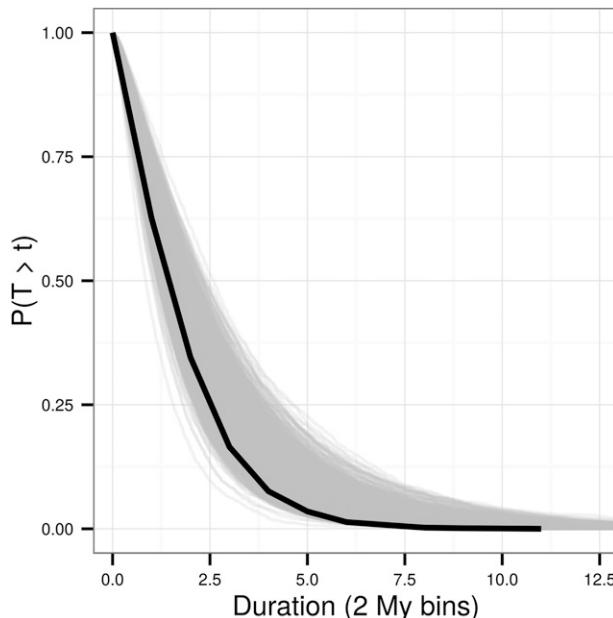
Of the three sources of variance present in the model, individual species variance accounts for ~80% of the observed unmodeled variance (see Fig. 4). Note that the individual variance was approximated using a simulation approach (28) because the Weibull distribution does not have a variance term. Both cohort and phylogenetic effects account for the other 20% of the observed variance. This result means that extinction risk has both temporal and phylogenetic aspects, as both contribute greater than 0% of the observed variability in the data (25).

The estimates for the individual cohort effects show a weak pattern of greater extinction risk in older Cenozoic cohorts compared with younger cohorts (Fig. 3). This potential slowdown in extinction risk is consistent with previous analyses of marine invertebrates (29, 30) and mammals (31, 32). There are two prevailing hypotheses as to the cause of this slowdown: (i) extinction risk is constant within, but varies between, clades so over time clades with low extinction rates increases in proportion of total diversity, thus bringing down expected extinction risk; or (ii) over time taxa increase in mean fitness and thus decrease in expected extinction risk (29). The observed decrease in extinction risk with age, along with the variance partitioning results (Fig. 4), are consistent with both of these hypotheses with neither being more important than the other.

Interestingly, the shift from older cohorts with a higher extinction risk to younger cohorts with lower extinction risk is approximately at the Paleogene–Neogene boundary. Given the association with arboreality and increased extinction risk (Fig. 2), the decrease in expected extinction risk over time might relate to the preferential loss of arboreal taxa over the Cenozoic. However, because the model used here does not allow for time-varying effects, I cannot identify whether this boundary is associated with a shift in the direction or magnitude of the expected effect of arboreality on extinction risk.

## Discussion

My results indicate that Cenozoic North American mammal generalists are expected to have a lower extinction risk than specialists, which implies that the diversification of specialized taxa would have required either a driven trend away from generality (33) or an increase in speciation rate relative to extinction rate (34). For specialist traits to increase in frequency, they would have to be associated with factors that may increase in speciation rate, such as increased niche partitioning among descendant taxa or increasing habitat heterogeneity leading to an increase in both



**Fig. 1.** Weibull-based model estimates (gray) from 1,000 posterior predictive datasets of the empirical survival function (black). The survival function is the probability that a species with duration  $t$  will not have gone extinct. Simulated datasets were generated by drawing parameter values randomly from their estimated posteriors and using the observed covariate information to estimate durations for all of the observed species.

**Table 1.** Marginal posterior estimates for the parameters of interest

Parameter	Effect	Mean	SD	2.5%	25%	50%	75%	97.5%	$\hat{R}$
$\alpha$	"Age"	1.29	0.03	1.23	1.27	1.29	1.31	1.36	1.00
$\beta_0$	Arboreal/carnivore	-0.78	0.14	-1.05	-0.87	-0.78	-0.68	-0.51	1.00
$\beta_{occ}$	Occupancy	-0.53	0.08	-0.69	-0.59	-0.53	-0.48	-0.38	1.00
$\beta_{size}$	Body size	-0.05	0.05	-0.14	-0.08	-0.05	-0.01	0.05	1.00
$\beta_g$	Ground dwelling	-0.28	0.10	-0.47	-0.34	-0.28	-0.21	-0.09	1.00
$\beta_s$	Scansorial	-0.22	0.11	-0.43	-0.29	-0.22	-0.14	-0.00	1.00
$\beta_h$	Herbivore	0.09	0.09	-0.09	0.03	0.09	0.14	0.27	1.00
$\beta_i$	Insectivore	0.10	0.11	-0.11	0.03	0.10	0.17	0.31	1.00
$\beta_o$	Omnivore	-0.12	0.11	-0.33	-0.19	-0.12	-0.05	0.09	1.00
$\sigma_c$	SD cohort	0.33	0.06	0.23	0.29	0.33	0.37	0.48	1.00
$\sigma_p$	SD phylogeny	0.11	0.05	0.03	0.07	0.10	0.14	0.23	1.03

The intercept  $\beta_0$  can also be interpreted as the estimate for the mean observed species. The remaining  $\beta$  values can be interpreted as the effect of a trait on the expected species duration as expressed as deviation from the mean. The categorical variables are binary index variables where an observation is of that category or not. See Eq. 6 for an explanation of the effect of  $\alpha$  on extinction risk.  $\hat{R}$  values of less than 1.1 indicate approximate chain convergence for the posterior samples. Values are based on 1,000 posterior samples.

speciation and extinction. For example, descendant species of omnivores many divide available prey items more finely or arboreal taxa may increase in both extinction and speciation rates via increases in habitat heterogeneity. Possible evidence to support this hypothesis would be to demonstrate differences in speciation rate associated with those traits analyzed here or other similar traits.

When these results are compared with factors contributing to increased extinction risk in extant mammals, there are some incongruities. As expected, large range size is consistently associated with lower extinction risk in the modern world (16, 20, 35, 36). Although my analysis found body size to have almost no time-invariant effect on extinction risk, in extant mammals this is not necessarily the case as increased body size is associated with increased extinction risk (16, 20). However, this pattern is partially clade dependent (35). As stated earlier, higher trophic levels have been found to be associated with greater extinction risk in extant mammals (16, 20). In contrast, I found that omnivores and carnivores have a lower expected extinction risk than either insectivores or herbivores (Fig. 2). Finally, phylogeny has been found to be a good predictor of differences in extinction risk in extant mammals as certain clades are at much higher risks than others (36). This effect seems much greater in the Recent than for the whole Cenozoic, implying that current extinction risk is more phylogenetically concentrated than during times of background extinction levels during the Cenozoic.

Whether these incongruities are within the standard range of time-variant effects is unknown, although my comparisons do imply that current processes are different from those studied here. However, this is not a model of what makes taxa vulnerable during mass extinctions and that may account for these incongruities, assuming mass extinctions are qualitatively different from background extinction (12). These results would also be inapplicable if the current biodiversity crisis is qualitatively different from either background or mass extinction as preserved in the fossil record.

By modeling how different ecologies and historical factors effect a species' expected extinction risk, it is possible to better understand what processes may have driven the resulting pattern of selection (i.e., diversity) while also providing a baseline for evaluating the current biodiversity crisis. This analysis finds support for the survival of the unspecialized hypothesis (1, 17) as a time-invariant generalization about extinction risk. I also find that there are substantial effects of both cohort and phylogeny on extinction risk, which supports the idea that the decrease in extinction risk (29) over time has both temporal and phylogenetic components. Additionally, I found evidence of increasing ex-

tinction risk with species age, the cause of which is unknown. These results show that, like prior mass extinction events in the fossil record, the current biodiversity crisis is qualitatively different from the previous period of background extinction in the fossil record (12).

## Materials and Methods

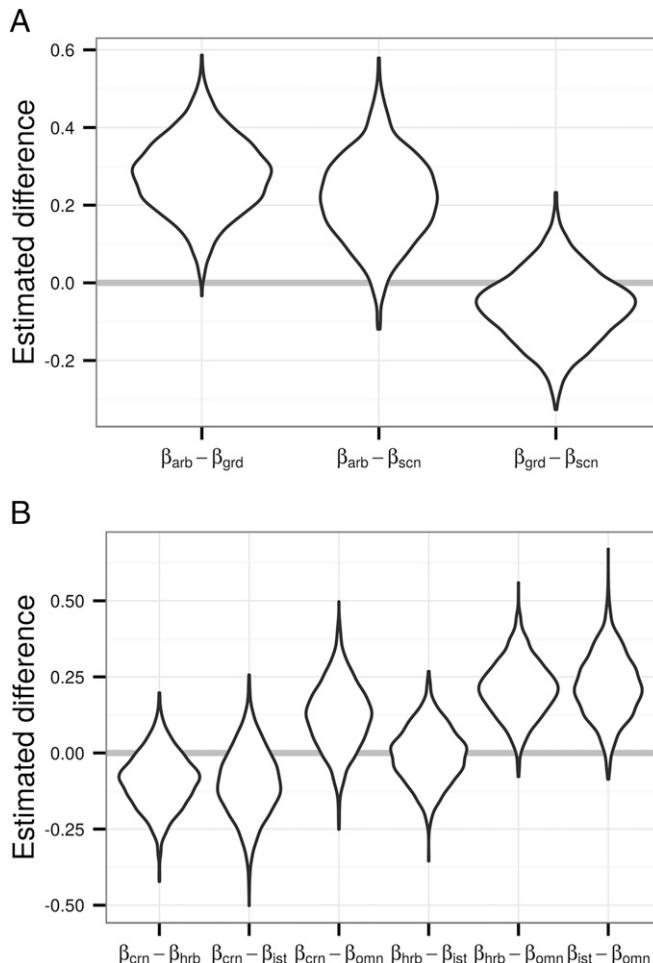
**Species Occurrence and Covariate Information.** Fossil occurrence information was downloaded from the Paleobiology Database (PBDB; <https://paleobiodb.org/#/>). Occurrence, taxonomic, stratigraphic, and biological information was downloaded for all North American mammals. This dataset was filtered so that only occurrences were identified to the species level, excluding all "sp."s. All aquatic and volant taxa were also excluded. Additionally, all occurrences without latitude and longitude information were excluded from the sample.

Species dietary and locomotor category assignments were done using the assignments in the PBDB, which were reassigned into coarser categories (*SI Appendix, Table S1*) in order to improve interpretability, increase sample size per category, and make results comparable to previous studies (13, 18).

All individual fossil occurrences were assigned to 2-My bins ranging through the entire Cenozoic. Taxon duration was measured as the number of 2-My bins from the first occurrence to the last occurrence, inclusive. This bin size was chosen because it approximately reflects the resolution of the North American Cenozoic mammal fossil record (6, 10, 32). Species originating in the youngest cohort, 0–2 My, were excluded from analysis because every species duration would be both left and right censored, which is illogical.

Species body size estimates in grams were sourced from a large selection of primary literature and database compilations. Databases used include the PBDB, PanTHERIA (37), and the Neogene Old World Mammal database (NOW; [www.helsinki.fi/science/now/](http://www.helsinki.fi/science/now/)). Major sources of additional compiled body size estimates include refs. 9 and 38–42, which were then supplemented with an additional literature search to try and fill in the remaining gaps. In many cases, species body mass was estimated using various published regression equations based on tooth or skull measurements (*SI Appendix, Table S2*). If multiple specimens were measured, I used the mean of specimen measures as the species mean. See *Dataset S1* for a complete list of mass estimates and sources.

**Biogeographic Network.** Species geographic extent was measured as the mean of the relative number of bioprovinces occupied by a species for each 2-My bin in which the species was present. Bioprovinces were identified using a network-theoretic approach that has previously been applied to paleontological data (43, 44). This approach relies on defining a biogeographic bipartite network of taxa and localities. In this study, taxa were defined as species and localities were grid cells from a regular lattice on a global equal-area cylinder map projection. The regular lattice was defined as a  $70 \times 34$  global grid, where each cell corresponds to  $\sim 250,000 \text{ km}^2$ . An advantage of this approach is that this approach reduces to occupancy when all localities are independent and to a single bioprovince when all localities are identical.



**Fig. 2.** Pairwise differences in effect of the locomotor (*A*) and dietary categories (*B*) on expected duration from 1,000 samples from the posterior distribution. Comparisons of locomotor categories, from top to bottom (*A*) are as follows: arboreal ( $\beta_{arb} = \beta_0$ ) vs. ground dwelling ( $\beta_{grd} = \beta_0 + \beta_g$ ), arboreal vs. scansorial ( $\beta_{scn} = \beta_0 + \beta_s$ ), and ground dwelling vs. scansorial. For dietary category, from top to bottom (*B*): carnivore ( $\beta_{cnn} = \beta_0$ ) vs. herbivore ( $\beta_{hrb} = \beta_0 + \beta_h$ ), carnivore vs. insectivore ( $\beta_{ist} = \beta_0 + \beta_i$ ), carnivore vs. omnivore ( $\beta_{omn} = \beta_0 + \beta_o$ ), herbivore vs. insectivore, herbivore vs. omnivore, and insectivore vs. omnivore. Negative values indicate that the first category is expected to have a greater duration than the second, whereas positive values indicate that the first category is expected to have a shorter duration.

A biogeographic network was constructed for each of the 2-My bins used in this study. Emergent bioprovinces were then identified using the map Eq (45, 46), as has been done before (43, 44, 47). These bioprovinces correspond to taxa and localities that are more interconnected with each other than with other nodes.

The map projection and regular lattice were made using shape files from [www.naturalearthdata.com/](http://www.naturalearthdata.com/) and the raster package for R (48). Bioprovince identification was done using the map equation as implemented in the igraph package for R (49).

**Supertree.** As there is no single, combined formal phylogenetic hypothesis of all Cenozoic fossils mammals from North America, it was necessary to construct a semiformal supertree. This tree was formed by combining taxonomic information for all of the observed species and a few published phylogenies using matrix representation parsimony (50). For further explanation of the methodology used to construct this supertree, please see *SI Appendix*.

**Survival Model.** Presented here is the model development process used to formulate the two survival models used in this study. First, define  $y$  as a vector of length  $n$  where the  $i$ th element is the duration of species  $i$ , where  $i = 1, \dots, n$ .

The simplest survival model where durations are assumed to follow an exponential distribution with a single rate or inverse-scale parameter  $\lambda$  (51). This is written as

$$\begin{aligned} p(y|\lambda) &= \lambda \exp(-\lambda y) \\ y &\sim \text{Exp}(\lambda). \end{aligned} \quad [1]$$

The exponential distribution corresponds to situations where extinction risk is independent of age. To understand this, we need to define two functions: the survival function  $S(t)$  and the hazard function  $h(t)$ .  $S(t)$  is the probability that a species having existed for  $t$  2-My bins will not have gone extinct, whereas  $h(t)$  corresponds to the instantaneous extinction rate for some taxon age  $t$  (51). For an exponential model,  $S(t)$  is

$$S(t) = \exp(-\lambda t), \quad [2]$$

and  $h(t)$  is defined

$$h(t) = \lambda. \quad [3]$$

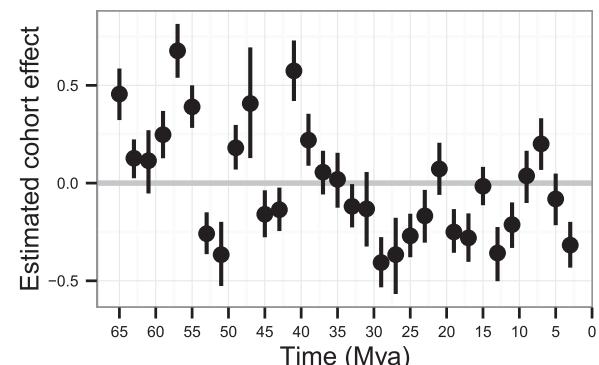
The choice of the exponential distribution corresponds directly to the Law of Constant Extinction (2), because the right side of Eq. 3 does not depend on species age  $t$ .

The current sampling statement (Eq. 1) assumes that all species share the same rate parameter with no variation. To allow for variation in  $\lambda$  associated with relevant covariate information like species body size,  $\lambda$  is reparameterized as  $\lambda_i = \exp(\sum \beta^T X_i)$ , where  $i$  is indexing a given observation and its covariates,  $\beta$  is a vector of regression coefficients, and  $X$  is a matrix of covariates. Using a standard regression approach, one column of  $X$  is all 1's and its corresponding  $\beta$  coefficient is the intercept.

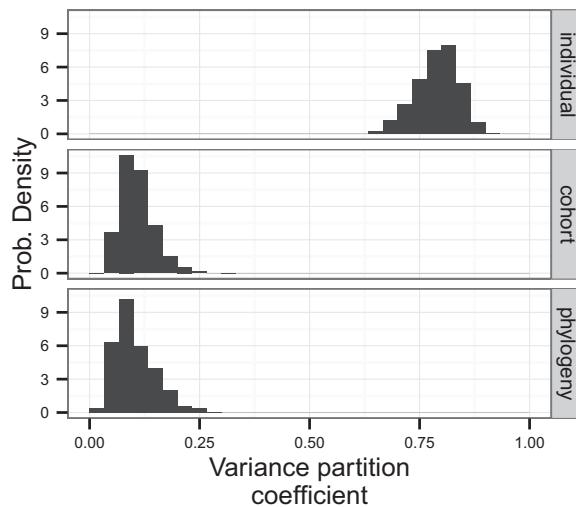
$X$  is an  $n \times K$  matrix of species-level covariates. Three of the covariates of interest are the logit of mean relative occupancy, and the logarithm of body size (grams). The discrete covariate index variables of dietary and locomotor category were transformed into  $n \times (k - 1)$  matrices where each column is an indicator variable (0/1) for that species' category, with  $k$  being the number of categories of the index variable (3 and 4, respectively). Only  $k - 1$  indicator variables are necessary as the intercept takes on the remaining value. For example, the difference in effect of arboreality vs. scansoriality on extinction risk, given that arboreality is the reference category, is the coefficient for the scansorial indicator variable as that is the difference between the effect of arboreality (the intercept  $\beta_0$ ) and scansoriality (the intercept + scansorial effect  $\beta_s$ ) (Fig. 2). Finally, a vector of 1's was included in the matrix  $X$  whose corresponding  $\beta$  coefficient is the intercept, making  $K$  equal 8.

$\beta$  is the vector of regression coefficients. The intercept term was given a weak normal prior,  $\beta_0 \sim \mathcal{N}(0, 10)$ , whereas all of these other coefficients were slightly more informative priors, e.g.,  $\beta_{mass} \sim \mathcal{N}(0, 0.5)$ . These priors were chosen because it is expected that the effect size of each variable on duration will be small, as is generally the case with binary covariates (52).

Regression coefficients are not directly comparable without first standardizing the input variables to have equal SDs. Standardization was accomplished by subtracting the mean of the covariate from all values and



**Fig. 3.** Summaries of posterior estimates of individual cohort effect depicted as medians and 80% credible intervals. High values correspond to shorter species durations, whereas lower values correspond to greater species durations compared with the mean duration. Lines are placed at the middle of the 2-My origination cohorts.



**Fig. 4.** Estimates of the variance partitioning coefficients for the three different sources of variance: species, cohort, and phylogeny. Higher values correspond to greater contribution to total observed variance. Each of the estimates is a distribution of 1,000 approximating simulations due to the model's nonnormally distributed errors.

then dividing by the SD, resulting in a variable with mean of 0 and an SD of 1. This linear transform greatly improves the interpretability of the coefficients as expected change in mean duration given a difference of 1 SD in the covariate (53). Additionally, this makes the intercept directly interpretable as the estimate of mean (transformed)  $\sigma$  (Eq. 7). However, because the expected SD for a random binary variable is 0.5, to make comparisons between the binary and continuous variables, the continuous inputs were divided by twice their SD (54).

The origination cohort is defined as the group of species that all originated during the same 2-My temporal bin. Because the most recent temporal bin, 0–2 My, was excluded, there are 32 total cohorts. The effect of origination cohort  $j$  was modeled with each group being a sample from a common cohort effect,  $\eta_j$ , which was considered normally distributed with mean of 0 and SD of  $\sigma_c$ . The value of  $\sigma_c$  was then estimated from the data itself, corresponding to the amount of pooling in the individual estimates of  $\eta_j$ . This approach is a conceptual and statistical unification between dynamic and cohort survival analysis in paleontology (55–59), with  $\sigma_c$  acting as a measure of compromise between these two end members. The choice of the half-Cauchy prior for  $\sigma_c$  follows (60)

$$\eta_j \sim \mathcal{N}(0, \sigma_c),$$

$$\sigma_c \sim C^+(0, 2.5).$$

The impact of shared evolutionary history, or phylogeny, was modeling as an individual effect where each observation,  $i$ , is modeled as a multivariate normal,  $h$ , where the covariance matrix  $\Sigma$  is known up to a constant,  $\sigma_p^2$  (24, 25). This is written

$$h \sim MVN(0, \Sigma)$$

$$\Sigma = \sigma_p^2 V_{phy}$$

$$\sigma_p \sim C^+(0, 2.5).$$

$V_{phy}$  is the phylogenetic covariance matrix defined as an  $n \times n$  matrix where the diagonal elements are the distance from root to tip, in branch length, for each observation, and the off-diagonal elements are the amount of shared history, measured in branch length, between observations  $i$  and  $j$ .  $\sigma_p$  was given a weakly informative half-Cauchy hyperprior. Note that because the phylogeny used here is primarily based on taxonomy, estimates of  $\sigma_p$  represent minimum estimates (24, 25). Improved phylogenetic estimates of all fossil Cenozoic mammals would greatly improve this estimate.

To relax the assumption of age-independent extinction of the Law of Constant Extinction, the Weibull distribution is substituted for the exponential (51). The Weibull distribution has a shape parameter  $\alpha$  and scale parameter  $\sigma$ . Conceptually,  $\sigma$  is the inverse of  $\lambda$ .  $\alpha$  modifies the impact of taxon age on extinction risk. When  $\alpha > 1$ , then  $h(t)$  is a monotonically increasing function, but

when  $\alpha < 1$ , then  $h(t)$  is a monotonically decreasing function. When  $\alpha = 1$ , then the Weibull distribution is equivalent to the exponential.

The Weibull distribution and sampling statement were defined as

$$p(y|\alpha, \sigma) = \frac{\alpha}{\sigma} \left(\frac{y}{\sigma}\right)^{\alpha-1} \exp\left[-\left(\frac{y}{\sigma}\right)^\alpha\right] \quad [4]$$

$$y \sim \text{Weibull}(\alpha, \sigma).$$

The corresponding  $S(t)$  and  $h(t)$  functions are defined as

$$S(t) = \exp\left[-\left(\frac{t}{\sigma}\right)^\alpha\right], \quad [5]$$

$$h(t) = \frac{\alpha}{\sigma} \left(\frac{t}{\sigma}\right)^{\alpha-1}. \quad [6]$$

To allow for  $\sigma$  to vary with a given observation's covariate information, it is reparameterized in a similar fashion to  $\lambda$  with a few key differences. Because  $\sigma = 1/\lambda$  to preserve the interpretation of  $\beta$ , while taking  $\alpha$  into account,  $\sigma$  is reparameterized as

$$\sigma_i = \exp\left(\frac{-\beta}{\alpha}\right). \quad [7]$$

Given the above, the survival model was then fit in a Bayesian context using both exponential and Weibull distributions. The Weibull's  $\alpha$  parameter was assumed constant across species, which is standard practice in survival analysis (51).  $\alpha$  was given a weakly informative half-Cauchy ( $C^+$ ) prior.  $\sigma$  was reparameterized as an exponentiated regression model (Eq. 7). Eq. 8 was further expanded to allow for two hierarchical factors as discussed above. This is written

$$\sigma_i = \exp\left[\frac{-(h_i + \eta_{j[i]} + \sum \beta^T \mathbf{X}_i)}{\alpha}\right] \quad [8]$$

where an equivalent statement for the exponential distribution is defined as

$$\lambda_i = \exp(h_i + \eta_{j[i]} + \sum \beta^T \mathbf{X}_i). \quad [9]$$

An important part of survival analysis is the inclusion of censored observations where the failure time has not been observed (51, 61). The most common censored observation is right censored, where the point of extinction had not yet been observed in the period of study, such as taxa that are still present in the most recent time bin (0–2 My). Left censored observations, on the other hand, correspond to observations that went extinct any time between 0 and some known point. To account for this uncertainty, the probability of a left censored observation is found by integrating over all possible durations between the 0 and 1 time bins. For an explanation of how censored observations are included in the sampling statement, please see *SI Appendix*.

**Estimation.** Parameter posteriors were approximated using a Markov-chain Monte Carlo (MCMC) routine implemented in the Stan programming language (62). Stan implements a version of Hamiltonian Monte Carlo called the No-U-Turn sampler (63). Posterior approximation was done using four parallel MCMC chains run for 30,000 steps, thinned to every 30th sample, split evenly between warmup and sampling. Convergence was evaluated using the scale reduction factor,  $\hat{R}$ . Values of  $\hat{R}$  close to 1, or less than or equal to 1.1, indicate approximate convergence. Convergence means that the chains are approximately stationary and the samples are well mixed (23).

**Posterior Evaluation.** The most basic assessment of model fit is that simulated data generated given the model should be similar to the observed; this is the idea behind posterior predictive checks. Using the covariates from each of the observed durations, and randomly drawn parameter estimates from their marginal posteriors, a simulated data set  $y^{rep}$  was generated. This process was repeated 1,000 times, and the distribution of  $y^{rep}$  was compared with the observed (23). For results from the posterior predictive tests used in this study, please see *SI Appendix*.

The exponential and Weibull models were compared for out-of-sample predictive accuracy using the WAIC (64). Because the Weibull model reduces to the exponential model when  $\alpha = 0$ , our interest is not in choosing between these models. Instead comparison of WAIC values is useful for better understanding the effect of model complexity on out-of-sample predictive

accuracy. An explanation of how WAIC is calculated is presented in *SI Appendix* following the recommended WAIC 2 formulation (23).

There are three different variance components in this model: sample component, cohort  $\sigma_c^2$ , and phylogenetic  $\sigma_p^2$ . Partitioning the variance between these sources allows the relative amount of unexplained variance of the sample to be compared. The sample component is similar to the residual variance from a normal linear regression. However, the Weibull-based model used here (Eq. 4) does not include an estimate of the variance similar to the squared scale term of a normal distribution. Instead, the sample component was approximated via a simulation approach modified from ref. 28. For explanation of this method, please see *SI Appendix*.

I used variance partitioning coefficients (VPCs) to estimate the relative importance of the different variance components (52). Phylogenetic heritability,  $h_p^2$

- (24, 25), is identical to the VPC of the phylogenetic effect. Phylogenetic heritability is a measure of how shared evolutionary history impacts differences in individual species trait values (e.g., duration), a broad sense definition of "heritability" as it combines both genetic inheritance and other, nongenetic shared history factors. Importantly, because phylogenetic effect was estimated using a principally taxonomy-based tree, the estimates derived here can be considered minimum estimates of the phylogenetic effect.
- ACKNOWLEDGMENTS.** I thank M. Foote, K. Angielczyk, R. Ree, and P. D. Polly for discussion; N. Pierrehumbert, E. Sander, and L. Southcott for draft comments; and J. Alroy and the Fossilworks/Paleobiology Database for data accumulation, management, and availability. This is Paleobiology Database publication number 239.
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# Supplemental information for “Death and taxa”

Peter D Smits

## 1 Supertree inference

As there is no single, combined formal phylogenetic hypothesis of all Cenozoic fossils mammals from North America, it was necessary to construct a semi-formal supertree. This was done by combining taxonomic information for all the observed species and a few published phylogenies.

The initial taxonomic classification of the observed species was based on the associated taxonomic information from the PBDB. This information was then updated using the Encyclopedia of Life (<http://eol.org/>) which collects and collates taxonomic information in a single database. This was done programatically using the `taxize` package for R [1]. Finally, this taxonomic information was further updated using a published taxonomy of fossil mammals [2, 3].

This taxonomy serves as an initial phylogenetic hypothesis which was then combined with a selection of species-level phylogenies [4, 5] in order to better constrain a minimum estimate of the actual phylogenetic relationships of the species. The supertree was inferred via matrix representation parsimony implemented in the `phytools` package for R [6]. Of the two most parsimonious trees found, I used only one for analysis.

Polytomies were resolved in order of species first appearance in order to minimize stratigraphic gaps. The resulting tree was then time scaled using the `paleotree` package via the “minimum branch length” approach with a minimum length of 0.1 My [7]. The minimum length is necessary to avoid zero-length branches which cause the phylogenetic covariance matrix not to be positive definite, which is important for computation (see below). While other time scaling approaches are possible [8, 9] this method was chosen for its simplicity and not requiring additional information about diversification rates which are the interest of this study.

## 2 Modeling censored observations

Censored data are modeled using the survival function of the distribution,  $S(t)$ , defined earlier for the Weibull distribution (Eq. 5, 6) with  $\sigma$  defined as above (Eq. 8, 9).  $S(t)$  is the probability that an observation will survive longer than a given time  $t$ .

The likelihood of uncensored observations is evaluated as normal using equation 4 while right censored observations are evaluated at  $S(t)$  and left

censored observations are evaluated at  $1 - S(t)$ . Note,  $1 - S(t)$  is equivalent to the cumulative distribution function and  $S(t)$  is equivalent to the complementary cumulative distribution function [10].

The final sampling statement/likelihood for both uncensored and both right and left censored observations is then written

$$L \propto \prod_{i \in C} \text{Weibull}(y_i | \alpha, \sigma) \prod_{j \in R} S(y_j | \alpha, \sigma) \prod_{k \in L} (1 - S(y_k | \alpha, \sigma)),$$

where  $C$  is the set of uncensored observations,  $R$  is the set of right censored observations, and  $L$  is the set of left censored observations.

### 3 Deviance residuals

In standard linear regression, residuals are defined as  $r_i = y_i - y_i^{est}$ . For the model used here, this definition is inadequate. The equivalent values for survival analysis are deviance residuals. To define how deviance residuals are calculated, we first define the cumulative hazard function [11]. Given  $S(t)$ , we define the cumulative hazard function as

$$\Lambda(t) = -\log(S(t)).$$

Next, we define martingale residuals  $m$  as

$$m_i = I_i - \Lambda(t_i).$$

$I$  is the inclusion vector of length  $n$ , where  $I_i = 1$  means the observation is completely observed and  $I_i = 0$  means the observation is censored. Martingale residuals have a mean of 0, range between 1 and  $-\infty$ , and can be viewed as the difference between the observed number of deaths between 0 and  $t_i$  and the expected number of deaths based on the model. However, martingale residuals are asymmetrically distributed, and can not be interpreted in the same manner as standard residuals.

The solution to this is to use the deviance residuals,  $D$ . This is defined as a function of martingale residuals and takes the form

$$D_i = \text{sign}(m_i) \sqrt{-2[m_i + I_i \log(I_i - m_i)]}.$$

Deviance residuals have a mean of 0 and a standard deviation of 1 by definition.

### 4 Variance partitioning

I calculated VPC using a resampling approach based on [12]. The procedure is as follows:

1. Simulate  $w$  (50,000) values of  $\eta$ ;  $\eta \sim \mathcal{N}(0, \sigma_c)$ .

2. For a given value of  $\beta^T \mathbf{X}$ , calculate  $\sigma^{c*}$  (Eq. 7) for all  $w$  simulations, holding  $h$  constant at 0.
3. Calculate  $v_c$ , the Weibull variance (Eq. 1) of each element of  $\sigma^{c*}$  with  $\alpha$  drawn from the posterior estimate.
4. Simulate  $w$  values of  $h$ ;  $h \sim \mathcal{N}(0, \sigma_p)$ .
5. For a given value of  $\beta^T \mathbf{X}$ , calculate  $\sigma^{p*}$  (Eq. 7) for all  $w$  simulations, holding  $\eta$  constant at 0.
6. Calculate  $v_p$ , the Weibull variance (Eq. 1) of each element of  $\sigma^{p*}$  with  $\alpha$  drawn from the posterior estimate.
7.  $\sigma_{y*}^2 = \frac{1}{2} \left( \left( \frac{1}{w} \sum_i^w v_{pi} \right) + \left( \frac{1}{w} \sum_j^w v_{cj} \right) \right)$ .
8.  $\sigma_{c*}^2 = var(v_c)$  and  $\sigma_{p*}^2 = var(v_p)$ .

The simulated values of  $h$  were drawn from a univariate normal distribution because each simulated value is in isolation, so there is no concern of phylogenetic autocorrelation. The chosen value for  $\beta^T \mathbf{X}$  was a draw from the posterior estimate of the intercept. Because input variables were standardized prior to model fitting, the intercept corresponds to the estimated effect on survival of the sample mean.

Weibull variance is calculated as

$$var(x) = \sigma^2 \left( \Gamma \left( 1 + \frac{2}{\alpha} \right) - \left( \Gamma \left( 1 + \frac{1}{\alpha} \right) \right)^2 \right), \quad (1)$$

where  $\Gamma$  is the gamma function.

The variance partitioning coefficients are then calculated, for example, as  $VPC_{phylo} = \frac{\sigma_{p*}^2}{\sigma_{y*}^2 + \sigma_{c*}^2 + \sigma_{p*}^2}$  and similarly for the other components.

## 5 Widely applicable information criterion

WAIC can be considered fully Bayesian alternative to the Akaike information criterion, where WAIC acts as an approximation of leave-one-out cross-validation which acts as a measure of out-of-sample predictive accuracy [10]. The following explanation uses the “WAIC 2” formulation recommended by [10].

WAIC is calculated starting with the log pointwise posterior predictive density calculated as

$$lppd = \sum_{i=1}^n \log \left( \frac{1}{S} \sum_{s=1}^S p(y_i | \Theta^S) \right), \quad (2)$$

where  $n$  is sample size,  $S$  is the number posterior simulation draws, and  $\Theta$  represents all of the estimated parameters of the model. This is similar to calculating the likelihood of each observation given the entire posterior.

A correction for the effective number of parameters is then added to lppd to adjust for overfitting. The effective number of parameters is calculated, following derivation and recommendations of [10], as

$$p_{\text{WAIC}} = \sum_{i=1}^n V_{s=1}^S (\log p(y_i | \Theta^S)). \quad (3)$$

where  $V$  is the sample posterior variance of the log predictive density for each data point.

Given both equations 2 and 3, WAIC is then calculated

$$\text{WAIC} = \text{lppd} - p_{\text{WAIC}}. \quad (4)$$

When comparing two or more models, lower WAIC values indicate better out-of-sample predictive accuracy. Importantly, WAIC is just one way of comparing models. When combined with posterior predictive checks it is possible to get a more complete understanding of model fit.

## 6 Results from posterior predictive checks

With all marginal posterior estimates having converged ( $\hat{R} < 1.1$ ) it is possible to examine the quality of model fit (Table 1). If the model is an adequate descriptor of the observed data, then relatively confident inference can be made [10].

Visual examination of the deviance residuals from twelve different sets of posterior predictive simulations indicates a systematic weakness estimating durations greater than 3 2-My bins (Fig. S1). However, the comparison of posterior predictive estimates of the 25th, 50th, and 75th quantiles to the observed indicate adequate fit. (Fig. S2). Importantly, this indicates that the model has approximate fit for 50+% of the data. Because, the inferred model can be inferred to be approximately adequate at capturing the observed variation.

The Weibull model (6140.37) also had a much lower WAIC score than the Exponential model (16697.35). This large a difference indicates that the Weibull model probably has the lower out-of-sample predictive accuracy of the two.

## 7 Data quality concerns

A concern with using the PBDB as a primary data source, though this concerns are general to most paleontological data, is that the results are an artifact of taxonomy or the database itself [13]. However, to obtain the results obtained in this analysis there would need to be a systematic error in assignments of all of diet, locomotor, and taxonomic categories for a large portion of the close to 2000 sampled species. It is important to note that species included have to have body size information, much of which is found from other sources (see Supplementary Dataset 1). this means that, for many taxa, that species name has to appear in occur in more than one place. this is a strong filter for misspellings and

potentially invalid taxa. Additionally, given that most mammal fossils are teeth which allows for relatively accurate dietary category assignement.

A possible concern, however, is that omnivorous taxa have feature poor morphology and thus longer durations may reflect a single anagenetic lineage as opposed to a single “species.” However it is possible to consider that, from a population genetic perspective, it can be argued that a single unbranching lineage is still a single biological “unit.”

## 8 Concerns surrounding estimates of $\alpha$

The estimate of the Weibull shape parameter,  $\alpha$ , is greater than 1 meaning that extinction risk is expected to increase with taxon age (Table 1). As the value of  $\alpha$  is between 1 and 1.5, extinction risk for a given species only gradually increases with age (Fig. S3). There are three possible explanations for this result: 1) older taxa being out competed by younger taxa [14]; or 2) this is an artifact of the minimum resolution of the fossil record [15].

An additional concern is that there may be an upward bias in estimates of  $\alpha$  at this sample size, similar to that for scale parameters [10]. The plausibility of third possibility in this example can be explored in simulation. I simulated from 10, 100, 1000, and 10000 samples from a Weibull( $\alpha = 1.3$ ,  $\sigma = 1$ ) 100 times each. For each of these simulated datasets, I then estimated the values of  $\alpha$  and  $\sigma$  in a simple maximum likelihood context in order to just get the model estimate. The modal estimates of both parameters for the simulated datasets were then compared to the known values (Fig. S4). The results from these simulations demonstrate that the estimates of  $\alpha$  in the above analyses (Table 1) should not be particularly biased based on my sample size of approximately 2000 species.

The model used in this analysis, however, is unable to distinguish between the remaining two hypotheses [15, 14]. Further work on how to better constrain estimates  $\alpha$  is necessary. A possibly is somehow incorporating these hypotheses as prior information.

## 9 Supplementary figures

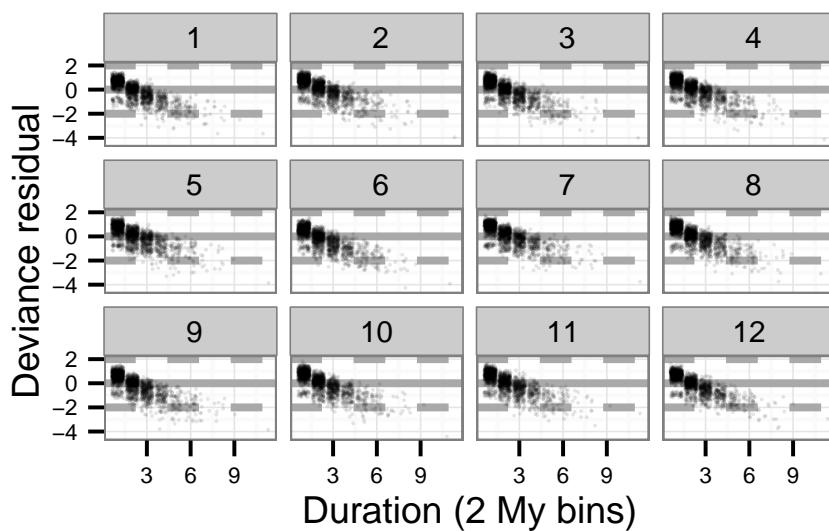


Figure S1: Deviance residuals from the fitted survival model compared to observed durations. Each graph depicts the residuals from single draws from the posterior distributions of all estimated parameters. Positive values indicate an underestimate of the observed duration, while negative values indicate an overestimate of the observed duration. A small amount of noise is added to each point to increase clarity. Twelve different examples are provided here to indicate consistency across multiple realizations.

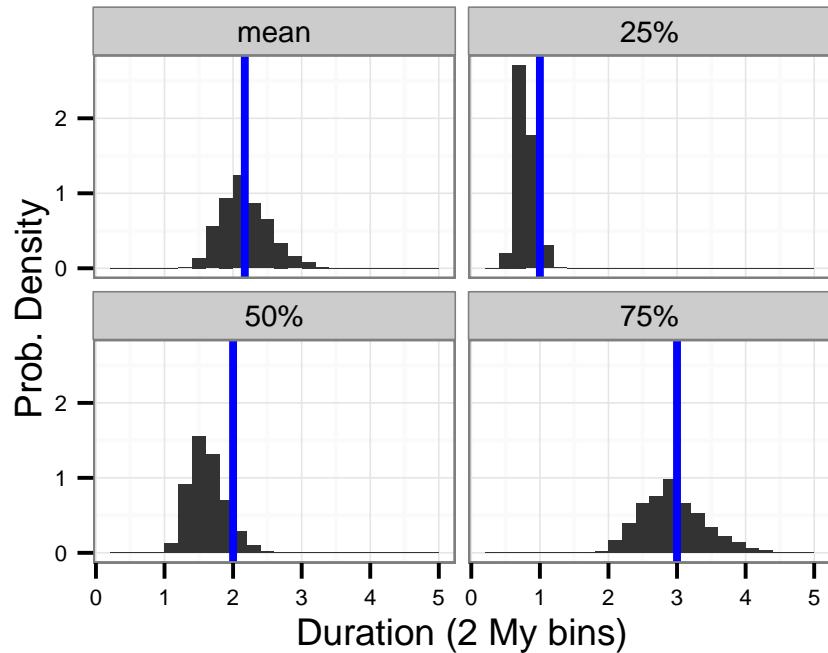


Figure S2: The results of additional posterior predictive checks for four summaries of the observed durations, as labeled. Blue vertical lines indicate the observed value. None of the observed values are significantly different from the posterior predictive distributions.

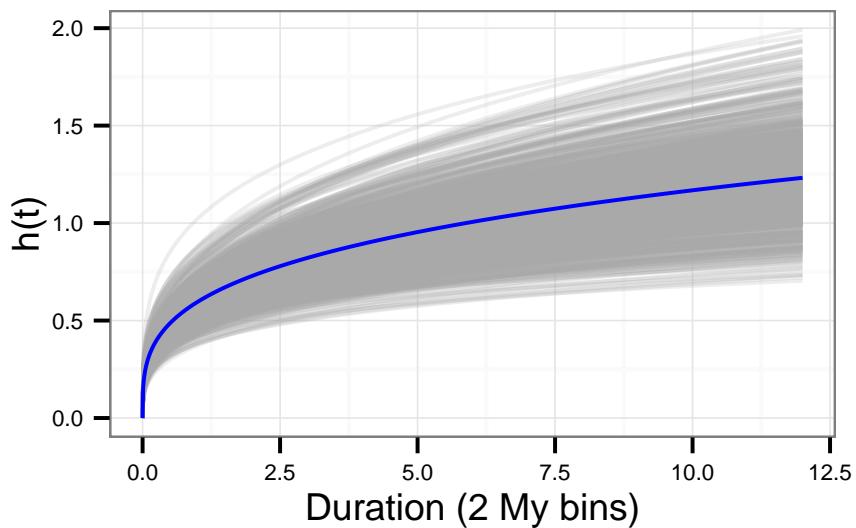


Figure S3: 1000 estimates of the hazard function ( $h(t)$ ) for the observed species mean (grey), along with the median estimated hazard function (blue).  $h(t)$  is an estimate of the rate at which a species of age  $t$  is expected to go extinct. Hazard functions were estimated from random draws from the estimated posterior distributions and evaluated with all covariate information set to 0, which corresponds to the expected duration of the mean species.

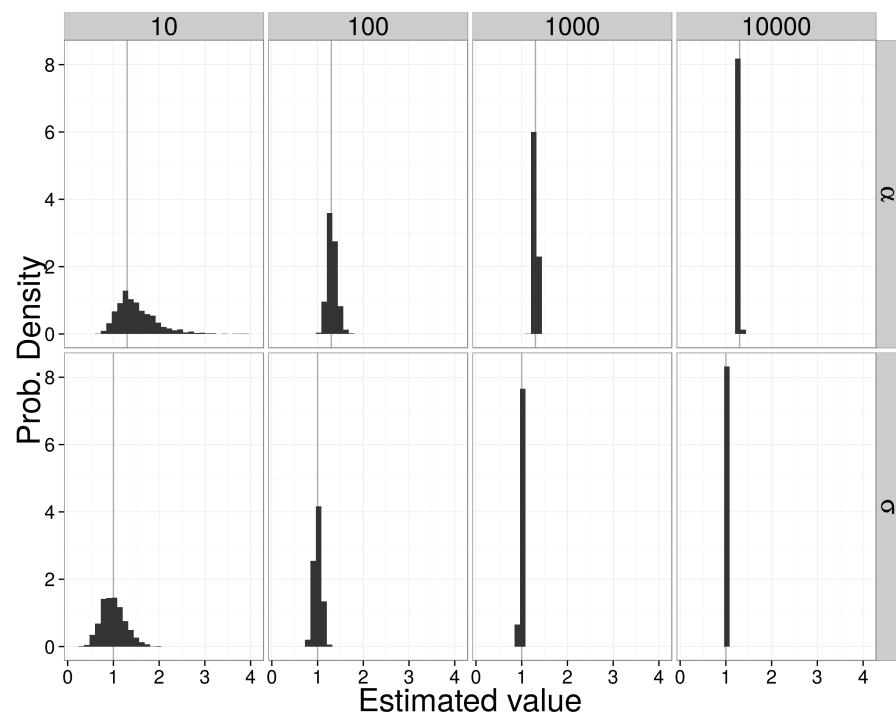


Figure S4: Comparison of maximum likelihood estimates of shape ( $\alpha$ ) and scale ( $\sigma$ ) parameters from 1000 simulated data sets from 4 different sample sizes. Vertical lines are the actual parameter value used to generate the data. When sample size is approximately 100 or greater, estimates are not overly biased.

## 10 Supplementary tables

Table S1: Species trait assignments in this study are a coarser version of the information available in the PBDB. Information was coarsened to improve per category sample size and uniformity and followed this table.

This study		PBDB categories
Diet	Carnivore	Carnivore
	Herbivore	Browser, folivore, granivore, grazer, herbivore.
	Insectivore	Insectivore.
	Omnivore	Frugivore, omnivore.
Locomotor	Arboreal	Arboreal.
	Ground dwelling	Fossorial, ground dwelling, semifossorial, saltatorial.
	Scansorial	Scansorial.

Table S2: Regression equations used in this study for estimating body size. Equations are presented with reference to taxonomic grouping, part name, and reference.

Group	Equation	log(Measurement)	Source
General	$\log(m) = 1.827x + 1.81$	lower m1 area	[16]
General	$\log(m) = 2.9677x - 5.6712$	mandible length	[17]
General	$\log(m) = 3.68x - 3.83$	skull length	[18]
Carnivores	$\log(m) = 2.97x + 1.681$	lower m1 length	[19]
Insectivores	$\log(m) = 1.628x + 1.726$	lower m1 area	[20]
Insectivores	$\log(m) = 1.714x + 0.886$	upper M1 area	[20]
Lagomorph	$\log(m) = 2.671x - 2.671$	lower toothrow area	[21]
Lagomorph	$\log(m) = 4.468x - 3.002$	lower m1 length	[21]
Marsupials	$\log(m) = 3.284x + 1.83$	upper M1 length	[22]
Marsupials	$\log(m) = 1.733x + 1.571$	upper M1 area	[22]
Rodentia	$\log(m) = 1.767x + 2.172$	lower m1 area	[16]
Ungulates	$\log(m) = 1.516x + 3.757$	lower m1 area	[23]
Ungulates	$\log(m) = 3.076x + 2.366$	lower m2 length	[23]
Ungulates	$\log(m) = 1.518x + 2.792$	lower m2 area	[23]
Ungulates	$\log(m) = 3.113x - 1.374$	lower toothrow length	[23]

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Dataset S1: Body mass estimates in grams for all mammal species included in this study. Also included is the source of this measurement. PBDB = Paleobiology Database, NOW = Neogene Old World Database, EOL = Encyclopedia of Life, ADW = Animal Diversity Web. PBDB + regression indicates that body mass was estimated from a measurement on the PBDB using one of the many regression equations listed in Table S3.

Species	Mass (g)	Source
<i>Aaptoryctes ivyi</i>	9.40	PBDB + regression
<i>Absarokius abbotti</i>	6.30	PBDB + regression
<i>Absarokius metoecus</i>	6.10	PBDB + regression
<i>Acarictis ryani</i>	8.30	PBDB + regression
<i>Achaenodon robustus</i>	484.90	PBDB + regression
<i>Achlyoscapter longirostris</i>	11.94	(1)
<i>Acmeodon secans</i>	12.10	PBDB + regression
<i>Acritohippus isonesus</i>	135944.23	(1)
<i>Acritohippus quinni</i>	178082.11	(1)
<i>Akritoparamys atwateri</i>	5.70	PBDB + regression
<i>Akritoparamys francesi</i>	4.50	PBDB + regression
<i>Akritoparamys pattersoni</i>	9.07	PBDB
<i>Akritoparamys wyomingensis</i>	7.02	PBDB
<i>Adelobilarina berklandi</i>	12.68	(1)
<i>Adelphailurus kansensis</i>	33189.87	(1)
<i>Adilophontes brachykolos</i>	119372.01	(1)
<i>Adjidaumo burkei</i>	0.72	PBDB
<i>Adjidaumo craigi</i>	0.90	PBDB + regression
<i>Adjidaumo intermedius</i>	1.10	PBDB + regression
<i>Adjidaumo maximus</i>	1.60	PBDB + regression
<i>Adjidaumo minimus</i>	0.90	PBDB + regression
<i>Adjidaumo minutus</i>	1.40	PBDB + regression
<i>Adunator ladae</i>	2.00	PBDB + regression
<i>Aelurodon asthenostylus</i>	22026.47	(1)
<i>Aelurodon ferox</i>	26370.47	(1)
<i>Aelurodon mcgrewi</i>	22247.84	(1)
<i>Aelurodon montanensis</i>	27722.51	(1)
<i>Aelurodon stirtoni</i>	20537.34	(1)
<i>Aelurodon taxoides</i>	29436.77	(1)
<i>Aepinacodon americanus</i>	809.20	(2)
<i>Aepycamelus bradyi</i>	922.04	(3)
<i>Aepycamelus giraffinus</i>	901.44	PBDB
<i>Aepycamelus robustus</i>	420836.64	(1)
<i>Aepycamelus stocki</i>	348014.70	(1)
<i>Aethomylos simplicidens</i>	2.80	PBDB + regression
<i>Ageitodendron matthewi</i>	8.90	PBDB + regression
<i>Agriochoerus antiquus</i>	56387.34	(1)
<i>Agriochoerus guyotianus</i>	59000.00	(4)
<i>Agriotherium schneideri</i>	355045.06	(1)
<i>Alagomys russelli</i>	0.70	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
Aletodon conardae	17.20	PBDB + regression
Aletodon gunnelli	17.90	PBDB + regression
Aletodon quadravus	13.00	PBDB + regression
Aletomeryx gracilis	27173.57	(1)
Alforjas taylori	408399.03	(1)
Alilepus vagus	7.20	PBDB + regression
Alilepus wilsoni	4.90	PBDB + regression
Allomys cristabrevis	6.50	PBDB + regression
Allomys simplicidens	122.00	(4)
Allomys storeri	3.80	PBDB + regression
Alluvisorex arcadentes	5.70	(1)
Alphagaulus pristinus	521.00	(4)
Alphagaulus vetus	523.22	(1)
Alticonus gazini	17.50	PBDB + regression
Alveojunctus minutus	2.20	PBDB + regression
Alveugena carbonensis	21.27	PBDB
Alwoodia harkseni	7.30	PBDB + regression
Alwoodia magna	226.00	(4)
Amebelodon floridanus	8243.20	PBDB + regression
Amelotabes simpsoni	3.40	PBDB + regression
Ammospermophilus hanfordi	58.00	(4)
Ammospermophilus junturensis	53.52	(1)
Amphechinus horncloudi	175.91	(1)
Amphicaenopus platycephalus	2397650.84	(1)
Amphicyon frendens	245241.81	(1)
Amphicyon galushai	138690.48	(1)
Amphicyon ingens	600000.00	(5)
Amphicyon longiramus	113550.16	(1)
Amphicyon riggsi	443.30	PBDB
Amphimachairodus coloradensis	31.90	PBDB + regression
Ampliconus antoni	29.20	PBDB + regression
Amynodon advenus	1197.30	PBDB + regression
Amynodon reedi	994.15	PBDB
Amynodontopsis bodei	548.30	PBDB + regression
Anaptomorphus aemulus	4.50	PBDB + regression
Anaptomorphus westi	6.50	PBDB + regression
Anasazia williamsoni	6.49	(6)
Anchitherium clarencei	230960.04	(1)
Anconodon cochranei	57.00	(7)
Anemorhysis natronensis	2.50	PBDB + regression
Anemorhysis pattersoni	3.40	PBDB + regression
Anemorhysis pearcei	2.48	(8)
Anemorhysis wortmani	2.90	PBDB + regression
Angustidens vireti	18.17	(1)
Anisonchus oligistus	9.70	PBDB + regression
Anisonchus onostus	12.50	PBDB + regression
Anisonchus sectorius	21.20	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
Ankalagon saurognathus	17.90	PBDB + regression
Ankyloodon annectens	30.27	(1)
Anomoeomys lewisi	5.99	(9)
Ansomys hepburnensis	44.70	(1)
Ansomys nevadensis	51.94	(1)
Ansomys nexodens	3.80	PBDB + regression
Antecalomys phthanus	22.87	(1)
Antecalomys valensis	13.60	(1)
Antecalomys vasquezi	10.70	PBDB
Antiacodon pygmaeus	10.70	PBDB + regression
Antiacodon venustus	24.80	PBDB + regression
Apataelurus kayi	60.00	PBDB + regression
Apatemys bellulus	2.00	PBDB + regression
Apatemys bellus	2.30	PBDB + regression
Apatemys chardini	1.80	PBDB + regression
Apatemys downsi	4.50	PBDB + regression
Apatemys hendryi	1.60	PBDB + regression
Apatemys uintensis	2.70	PBDB + regression
Apatosciuravus bifax	2.20	PBDB + regression
Apatosciuravus jacobsi	2.00	PBDB + regression
Apheliscus chydaeus	3.70	PBDB + regression
Apheliscus insidiosus	4.30	PBDB + regression
Apheliscus nitidus	5.00	PBDB + regression
Apheliscus wapitiensis	2.60	PBDB + regression
Aphelops malacorhinus	3541284.24	(1)
Aphelops megalodus	1689595.99	(1)
Aphelops mutilus	4325334.34	(1)
Aphronorus fraudator	6.30	PBDB + regression
Aphronorus orieli	14.30	PBDB + regression
Aphronorus ratatoski	8.30	PBDB + regression
Apletotomeus crassus	1.00	PBDB + regression
Apternodus gregoryi	5.50	PBDB + regression
Apternodus iliffensis	5.40	PBDB + regression
Arapahovius advena	2.90	PBDB + regression
Archaeocyon falkenbachi	88.00	(10)
Archaeocyon leptodus	3533.34	(1)
Archaeocyon pavidus	2275.60	(1)
Archaeohippus blackbergi	33189.87	(1)
Archaeohippus mannulus	104.00	PBDB + regression
Archaeohippus mourningi	54176.36	(1)
Archaeohippus penultimus	71682.36	(1)
Archaeohippus stenolophus	123.76	PBDB
Archaeolagus acariculus	578.25	(1)
Archaeolagus emeraldensis	2344.90	(1)
Archaeolagus ennisianus	1064.22	(1)
Archaeolagus macrocephalus	1826.21	(1)
Archaeolagus primigenius	1540.71	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Archaeotherium lemleyi</i>	932.90	PBDB + regression
<i>Archaeotherium mortoni</i>	297.60	PBDB + regression
<i>Archaeotherium trippensis</i>	1691.00	PBDB + regression
<i>Arctocyon montanensis</i>	71.10	PBDB + regression
<i>Arctocyon mumak</i>	149.00	PBDB
<i>Arctodontomys nuptus</i>	8.70	PBDB + regression
<i>Arctodontomys simplicidens</i>	7.10	PBDB + regression
<i>Arctodontomys wilsoni</i>	7.40	PBDB + regression
<i>Arctodus pristinus</i>	239.13	(11)
<i>Arctonasua eurybates</i>	15994.50	(1)
<i>Arctonasua gracilis</i>	8866.19	(1)
<i>Arctonasua minimus</i>	7044.48	(1)
<i>Arctostylops steini</i>	11.30	PBDB + regression
<i>Ardynomys occidentalis</i>	5.90	PBDB + regression
<i>Arfia junnei</i>	17.90	PBDB + regression
<i>Arfia opisthotoma</i>	61.70	PBDB + regression
<i>Arfia shoshoniensis</i>	56.00	PBDB + regression
<i>Arfia zele</i>	25.30	PBDB + regression
<i>Arretotherium acridens</i>	179871.86	(1)
<i>Arretotherium fricki</i>	138690.48	(1)
<i>Arretotherium leptodus</i>	575.99	PBDB
<i>Artimonius australis</i>	5.40	PBDB + regression
<i>Artimonius nocerai</i>	3.70	PBDB + regression
<i>Artimonius witteri</i>	4.40	PBDB + regression
<i>Astrohippus stockii</i>	203.04	PBDB
<i>Aulolithomys bounites</i>	3.20	PBDB + regression
<i>Aulolithomys vexilliames</i>	1.50	PBDB + regression
<i>Australocamelus orarius</i>	100709.96	(1)
<i>Auxontodon pattersoni</i>	26.80	PBDB + regression
<i>Avunculus didelphodonti</i>	4.30	PBDB + regression
<i>Aycrossia lovei</i>	5.20	PBDB + regression
<i>Aztlanolagus agilis</i>	27.14	(11)
<i>Azygonyx ancylion</i>	74.20	PBDB + regression
<i>Azygonyx grangeri</i>	94.00	PBDB + regression
<i>Azygonyx xenicus</i>	48.40	PBDB + regression
<i>Baiocodon denverensis</i>	35.70	PBDB + regression
<i>Baiocodon nordicus</i>	21.60	PBDB + regression
<i>Baiomys rexroadi</i>	0.90	PBDB + regression
<i>Baiotomeus douglassi</i>	6.60	PBDB + regression
<i>Baiotomeus rhothonion</i>	1.50	PBDB + regression
<i>Barbourofelis fricki</i>	255250.32	(1)
<i>Barbourofelis loveorum</i>	32.10	PBDB + regression
<i>Barbourofelis morrisi</i>	90219.42	(1)
<i>Barbourofelis osborni</i>	264.00	(12)
<i>Barbourofelis whitfordi</i>	77652.58	(1)
<i>Barbouromyx trigonocorneus</i>	33860.35	(1)
<i>Barylambda faberi</i>	726.70	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Barylambda jackwilsoni</i>	246.20	PBDB + regression
<i>Basirepomys pliocenicus</i>	3.30	PBDB + regression
<i>Basirepomys robertsi</i>	2.80	PBDB + regression
<i>Bassariscus antiquus</i>	1881.83	(1)
<i>Bassariscus casei</i>	1652.43	(1)
<i>Bassariscus minimus</i>	6.15	(13)
<i>Bassariscus ogallalae</i>	21.94	(14)
<i>Bassariscus parvus</i>	1685.81	(1)
<i>Bathygenys alpha</i>	26.50	PBDB + regression
<i>Bathygenys reevesi</i>	24.00	PBDB + regression
<i>Batodonoides powayensis</i>	0.70	PBDB + regression
<i>Batodonoides vanhouteni</i>	0.40	PBDB + regression
<i>Beckiasorex hibbardi</i>	1.10	PBDB + regression
<i>Bensonomys arizonae</i>	1.73	PBDB
<i>Bensonomys baskini</i>	1.89	PBDB
<i>Bensonomys elachys</i>	1.00	(15)
<i>Bensonomys gidleyi</i>	1.30	PBDB
<i>Bensonomys lindsayi</i>	1.00	PBDB + regression
<i>Bensonomys meadensis</i>	1.55	PBDB
<i>Bensonomys winklerorum</i>	1.02	PBDB
<i>Bensonomys yazhi</i>	1.08	(16)
<i>Bettonia tsosia</i>	3.84	(17)
<i>Bisonalveus browni</i>	5.50	PBDB + regression
<i>Bisonalveus holtzmanii</i>	7.40	PBDB + regression
<i>Blacktops latidens</i>	18.02	PBDB
<i>Blacktops longinaires</i>	15.14	PBDB
<i>Blarina brevicauda</i>	16.40	PBDB
<i>Blarina carolinensis</i>	3.10	(11)
<i>Blastomeryx gemmifer</i>	10938.02	(1)
<i>Blastomeryx pristinus</i>	168.00	PBDB
<i>Blickomylus galushai</i>	16983.54	(1)
<i>Boreameryx braskerudi</i>	56.30	PBDB + regression
<i>Borophagus diversidens</i>	34891.55	(1)
<i>Borophagus dudleyi</i>	247.00	(18)
<i>Borophagus hilli</i>	29143.87	(1)
<i>Borophagus littoralis</i>	23388.51	(1)
<i>Borophagus orc</i>	16814.55	(1)
<i>Borophagus parvus</i>	19341.34	(1)
<i>Borophagus pugnator</i>	24100.79	(1)
<i>Borophagus secundus</i>	24100.79	(1)
<i>Bothriodon rostratus</i>	451.00	(19)
<i>Bouromeryx americanus</i>	68186.37	(1)
<i>Bouromeryx submilleri</i>	50011.09	(1)
<i>Brachycrus buwaldi</i>	250196.03	(1)
<i>Brachycrus laticeps</i>	387.96	PBDB
<i>Brachycrus rusticus</i>	185.22	PBDB
<i>Brachycrus siouense</i>	145801.30	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Brachyerix hibbardi</i>	5.04	(20)
<i>Brachyerix incertis</i>	79.84	(1)
<i>Brachyerix macrotis</i>	131.63	(1)
<i>Brachyerix richi</i>	340.36	(1)
<i>Brachyhyops viensis</i>	298.00	PBDB + regression
<i>Brachyhyops wyomingensis</i>	199.30	PBDB + regression
<i>Brachypsalis modicus</i>	512.86	(1)
<i>Brachypsalis obliquidens</i>	157.50	PBDB
<i>Brachypsalis pachycephalus</i>	487.85	(1)
<i>Brachyrhynchocyon dodgei</i>	14.10	PBDB + regression
<i>Brachyrhynchocyon montanus</i>	11.40	PBDB + regression
<i>Brontops tyleri</i>	571500.00	PBDB
<i>Buisnictis breviramus</i>	5.50	PBDB + regression
<i>Buisnictis burrowsi</i>	14.58	PBDB
<i>Buisnictis schoffi</i>	22.42	(1)
<i>Bunomeryx montanus</i>	17.20	PBDB + regression
<i>Bunophorus etsagicus</i>	44.10	PBDB + regression
<i>Bunophorus grangeri</i>	45.50	PBDB + regression
<i>Bunophorus macropternus</i>	37.40	PBDB + regression
<i>Bunophorus pattersoni</i>	27.00	(21)
<i>Bunophorus robustus</i>	23.60	PBDB + regression
<i>Bunophorus sinclairi</i>	50.40	PBDB + regression
<i>Caenolambda jepseni</i>	235.70	PBDB + regression
<i>Calippus cerasinus</i>	81633.91	(1)
<i>Calippus elachistus</i>	43044.94	(1)
<i>Calippus hondurensis</i>	71682.36	(1)
<i>Calippus martini</i>	119372.01	(1)
<i>Calippus placidus</i>	79221.26	(1)
<i>Calippus proplacidus</i>	64860.88	(1)
<i>Calippus regulus</i>	45251.90	(1)
<i>Camelops hesternus</i>	420.31	(11)
<i>Camelops traviswhitei</i>	774.70	PBDB + regression
<i>Campestrallomys annectens</i>	3.50	PBDB + regression
<i>Campestrallomys dawsonae</i>	298.87	(1)
<i>Campestrallomys siouxensis</i>	159.17	(1)
<i>Canis armbrusteri</i>	30333.26	(1)
<i>Canis edwardii</i>	25.40	PBDB + regression
<i>Canis latrans</i>	11765.00	PBDB
<i>Canis lepophagus</i>	14617.87	(1)
<i>Canis rufus</i>	15566.00	PBDB
<i>Cantius abditus</i>	28.60	PBDB + regression
<i>Cantius angulatus</i>	10.10	PBDB + regression
<i>Cantius frugivorus</i>	15.50	PBDB + regression
<i>Cantius mckennai</i>	15.40	PBDB + regression
<i>Cantius nunienus</i>	18.10	PBDB + regression
<i>Cantius ralstoni</i>	13.80	PBDB + regression
<i>Cantius simonsi</i>	34.10	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Cantius torresi</i>	10.00	PBDB + regression
<i>Cantius trigonodus</i>	2000.00	(22)
<i>Capricamelus gettyi</i>	389.10	PBDB + regression
<i>Capromeryx tauntonensis</i>	15835.35	(1)
<i>Cardiolophus radinskyi</i>	79.10	PBDB + regression
<i>Cardiolophus semihians</i>	80.80	PBDB + regression
<i>Carpocristes cygneus</i>	2.20	PBDB + regression
<i>Carpocristes hobackensis</i>	33.00	(22)
<i>Carpocyon compressus</i>	15214.44	(1)
<i>Carpocyon robustus</i>	19341.34	(1)
<i>Carpocyon webbi</i>	20537.34	(1)
<i>Carpodaptes hazelae</i>	3.20	PBDB + regression
<i>Carpodaptes stonleyi</i>	2.50	PBDB + regression
<i>Carpolestes nigridens</i>	87.00	(23)
<i>Carpolestes simpsoni</i>	2.30	PBDB + regression
<i>Carpomegodon jepseni</i>	6.10	PBDB + regression
<i>Catopsalis alexanderi</i>	31.90	PBDB + regression
<i>Catopsalis calgariensis</i>	90.20	PBDB + regression
<i>Catopsalis foliatus</i>	48.60	PBDB + regression
<i>Catopsalis joyneri</i>	2435.00	(7)
<i>Cedromus wardi</i>	6.60	PBDB + regression
<i>Centetodon aztecus</i>	2.00	PBDB + regression
<i>Centetodon bembicophagus</i>	1.50	PBDB + regression
<i>Centetodon chadronensis</i>	2.40	PBDB + regression
<i>Centetodon divaricatus</i>	30.57	(1)
<i>Centetodon hendryi</i>	2.00	PBDB + regression
<i>Centetodon kuenzii</i>	2.60	PBDB + regression
<i>Centetodon magnus</i>	33.45	(1)
<i>Centetodon neashami</i>	4.00	PBDB + regression
<i>Centetodon pulcher</i>	2.80	PBDB + regression
<i>Centimomys major</i>	6.50	PBDB + regression
<i>Ceratogaulus hatcheri</i>	80.00	(19)
<i>Cernictis hesperus</i>	177.68	(1)
<i>Cernictis repenningi</i>	53.55	(24)
<i>Chacomylus sladei</i>	5.80	PBDB + regression
<i>Chadrolagus emryi</i>	3.60	PBDB + regression
<i>Chalicomomys willwoodensis</i>	0.80	PBDB + regression
<i>Chasmaporthetes ossifragus</i>	28.10	PBDB + regression
<i>Chipetaia lamporea</i>	10.10	PBDB + regression
<i>Chiromyoides caesor</i>	7.10	PBDB + regression
<i>Chiromyoides minor</i>	3.80	PBDB + regression
<i>Chiromyoides potior</i>	6.80	PBDB + regression
<i>Chriacus badgleyi</i>	18.00	PBDB + regression
<i>Chriacus baldwini</i>	20.70	PBDB + regression
<i>Chriacus gallinae</i>	20.10	PBDB + regression
<i>Chriacus pelvidens</i>	39.50	PBDB + regression
<i>Chumashius balchi</i>	4.90	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Churcheria baroni</i>	2.70	PBDB + regression
<i>Cimexomys minor</i>	2.30	PBDB + regression
<i>Cimolestes incisus</i>	9.10	PBDB + regression
<i>Colodon cingulatus</i>	282.74	PBDB
<i>Colodon kayi</i>	104.20	PBDB + regression
<i>Colodon occidentalis</i>	178.10	PBDB + regression
<i>Colodon stovalli</i>	115.70	PBDB + regression
<i>Colodon woodi</i>	150.60	PBDB + regression
<i>Conacodon cophater</i>	7.40	PBDB + regression
<i>Conacodon delphae</i>	31.40	PBDB + regression
<i>Conacodon entoconus</i>	25.50	PBDB + regression
<i>Conacodon kohlbergeri</i>	12.20	PBDB + regression
<i>Conoryctes comma</i>	76.10	PBDB + regression
<i>Copecion brachypternus</i>	37.10	PBDB + regression
<i>Copecion davisi</i>	28.60	PBDB + regression
<i>Copedelphys innominata</i>	2.10	PBDB + regression
<i>Copedelphys titanelix</i>	1.00	PBDB + regression
<i>Copelemur australotutus</i>	21.30	PBDB + regression
<i>Copelemur tutus</i>	22.90	PBDB + regression
<i>Copemys barstowensis</i>	32.14	(1)
<i>Copemys esmeraldensis</i>	27.94	(1)
<i>Copemys lindsayi</i>	14.88	(1)
<i>Copemys longidens</i>	26.84	(1)
<i>Copemys loxodon</i>	28.79	(1)
<i>Copemys mariae</i>	31.50	(1)
<i>Copemys pagei</i>	15.18	(1)
<i>Copemys russelli</i>	24.29	(1)
<i>Copemys shotwelli</i>	1.10	PBDB + regression
<i>Copemys tenuis</i>	23.34	(1)
<i>Coriphagus encinensis</i>	10.40	PBDB + regression
<i>Coriphagus montanus</i>	6.90	PBDB + regression
<i>Cormocyon copei</i>	4817.45	(1)
<i>Cormocyon haydeni</i>	4359.01	(1)
<i>Coryphodon armatus</i>	882.70	PBDB + regression
<i>Coryphodon eocaenius</i>	659.70	PBDB + regression
<i>Coryphodon lobatus</i>	1189.40	PBDB + regression
<i>Coryphodon proterus</i>	1068.80	PBDB + regression
<i>Coryphodon radians</i>	864.30	PBDB + regression
<i>Cosoryx cerroensis</i>	16814.55	(1)
<i>Cosoryx furcatus</i>	44.87	PBDB
<i>Cranioceras clarendonensis</i>	18.90	PBDB + regression
<i>Cranioceras teres</i>	96761.07	(1)
<i>Cranioceras unicornis</i>	134591.56	(1)
<i>Cratogeomys sansimoniensis</i>	4.80	PBDB + regression
<i>Crucimys milleri</i>	36.60	(1)
<i>Crypholestes vaughni</i>	2.09	PBDB
<i>Cryptotis adamsi</i>	13.33	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Cryptotis kansasensis</i>	3.00	PBDB + regression
<i>Cryptotis parva</i>	4.10	PBDB
<i>Cupidinimus avawatzensis</i>	20.09	(1)
<i>Cupidinimus bidahochiensis</i>	27.39	(1)
<i>Cupidinimus boronensis</i>	14.59	(1)
<i>Cupidinimus eurekensis</i>	0.54	PBDB
<i>Cupidinimus halli</i>	1.10	PBDB + regression
<i>Cupidinimus lindsayi</i>	7.61	(1)
<i>Cupidinimus madisonensis</i>	1.11	PBDB
<i>Cupidinimus magnus</i>	1.70	PBDB + regression
<i>Cupidinimus nebraskensis</i>	9.30	(1)
<i>Cupidinimus prattensis</i>	21.33	(1)
<i>Cupidinimus tertius</i>	16.44	(1)
<i>Cupidinimus whitlocki</i>	16.78	(1)
<i>Cuvieronioides tropicus</i>	10934.90	PBDB + regression
<i>Cuyamalagus dawsoni</i>	639.06	(1)
<i>Cylindrodon fontis</i>	3.70	PBDB + regression
<i>Cylindrodon nebraskensis</i>	5.30	PBDB + regression
<i>Cynarctoides acridens</i>	2921.93	(1)
<i>Cynarctoides gawnae</i>	2643.87	(1)
<i>Cynarctoides harlowi</i>	1863.11	(1)
<i>Cynarctoides lemur</i>	2321.57	(1)
<i>Cynarctoides luskensis</i>	2392.27	(1)
<i>Cynarctoides roii</i>	1826.21	(1)
<i>Cynarctus crucidens</i>	4964.16	(1)
<i>Cynarctus galushai</i>	9228.02	(1)
<i>Cynarctus saxatilis</i>	10097.06	(1)
<i>Cynelos caroniavorus</i>	16647.24	(1)
<i>Cynelos idoneus</i>	105873.47	(1)
<i>Cynelos sinapius</i>	213202.99	(1)
<i>Cynodesmus martini</i>	14185.85	(1)
<i>Cynodesmus thoooides</i>	9228.02	(1)
<i>Cynorca occidentale</i>	20537.34	(1)
<i>Cynorca sociale</i>	82.80	PBDB + regression
<i>Cyriacotherium psamminum</i>	70.30	PBDB
<i>Dakotallomys lillegraveni</i>	5.81	PBDB
<i>Dakotallomys pelycomyoides</i>	6.57	(25)
<i>Daphoenodon falkenbachi</i>	137310.49	(1)
<i>Daphoenodon notionastes</i>	43477.55	(1)
<i>Daphoenodon superbis</i>	77652.58	(1)
<i>Daphoenus hartshornianus</i>	13.90	PBDB + regression
<i>Daphoenus lambei</i>	11.40	PBDB + regression
<i>Daphoenus ruber</i>	13.70	PBDB + regression
<i>Daphoenus socialis</i>	13000.00	(4)
<i>Daphoenus vetus</i>	19535.72	(1)
<i>Dartonius jepseni</i>	1.47	(26)
<i>Dasypus bellus</i>	104.90	(11)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Delahomeryx browni</i>	38948.67	(1)
<i>Desmatippus avus</i>	179871.86	(1)
<i>Desmatippus texanus</i>	169.36	PBDB
<i>Desmatochoerus hesperus</i>	296.24	(27)
<i>Desmatochoerus megalodon</i>	335100.00	(4)
<i>Desmatoclaenus hermaeus</i>	61.70	PBDB + regression
<i>Desmatolagus schizopetrus</i>	6.72	PBDB
<i>Desmocyon matthewi</i>	8103.08	(1)
<i>Desmocyon thomsoni</i>	6974.39	(1)
<i>Diacocherus meizon</i>	2.10	PBDB + regression
<i>Diacocherus minutus</i>	3.00	PBDB + regression
<i>Diacodexis gracilis</i>	14.30	PBDB + regression
<i>Diacodexis kelleyi</i>	20.70	PBDB + regression
<i>Diacodexis metsiacus</i>	17.80	PBDB + regression
<i>Diacodexis minutus</i>	11.80	PBDB + regression
<i>Diacodexis primus</i>	19.50	PBDB + regression
<i>Diacodexis secans</i>	24.60	PBDB + regression
<i>Diacodon alticuspis</i>	8.80	PBDB + regression
<i>Diceratherium annectens</i>	864580.76	(1)
<i>Diceratherium armatum</i>	3541284.24	(1)
<i>Diceratherium gregorii</i>	734.10	PBDB + regression
<i>Diceratherium niobrarense</i>	2105366.25	(1)
<i>Diceratherium tridactylum</i>	965112.54	(1)
<i>Didelphodus absarokae</i>	12.90	PBDB + regression
<i>Didelphodus altidens</i>	10.20	PBDB + regression
<i>Didelphodus rheos</i>	7.20	PBDB + regression
<i>Didelphodus serus</i>	7.00	PBDB + regression
<i>Didymictis altidens</i>	105.86	PBDB
<i>Didymictis leptomylus</i>	8.61	PBDB + regression
<i>Didymictis protenus</i>	11.30	PBDB + regression
<i>Didymictis proteus</i>	8.95	PBDB + regression
<i>Didymictis vancleveae</i>	160.55	(28)
<i>Dikkomys matthewi</i>	47.47	(1)
<i>Dillerlemur pagei</i>	5.40	PBDB + regression
<i>Dilophodon destitutus</i>	29.93	(29)
<i>Dilophodon minusculus</i>	70.40	PBDB + regression
<i>Dinaelurus crassus</i>	37320.00	(4)
<i>Dinofelis palaeoonca</i>	24.30	PBDB + regression
<i>Dinohippus interpolatus</i>	257815.63	(1)
<i>Dinohippus leardi</i>	392385.48	(1)
<i>Dinohippus leidyanus</i>	229900.00	(30)
<i>Dinohippus mexicanus</i>	609259.77	(1)
<i>Dinohippus spectans</i>	536500.00	(4)
<i>Dinohyus hollandi</i>	1215.50	PBDB + regression
<i>Diplobunops matthewi</i>	167.50	PBDB + regression
<i>Dipodomys compactus</i>	5.43	(11)
<i>Dipodomys gidleyi</i>	1.50	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Dipodomys hibbardi</i>	17.81	(1)
<i>Diprionomys agrarius</i>	2.00	PBDB + regression
<i>Diprionomys parvus</i>	11.00	(4)
<i>Dipsalidictis aequidens</i>	126.40	PBDB + regression
<i>Dipsalidictis platypus</i>	54.00	PBDB + regression
<i>Dipsalidictis transiens</i>	89.10	PBDB + regression
<i>Dipsalodon churchillorum</i>	98.20	PBDB + regression
<i>Dipsalodon matthewi</i>	162.00	PBDB + regression
<i>Dissacus navajoivius</i>	10.80	PBDB + regression
<i>Dissacus praenuntius</i>	14.40	PBDB + regression
<i>Domnina dakotensis</i>	28.50	(1)
<i>Domnina gradata</i>	36.60	(1)
<i>Domnina greeni</i>	33.78	(1)
<i>Domnina thompsoni</i>	2.20	PBDB + regression
<i>Domninoides hessei</i>	149.90	(1)
<i>Domninoides knoxjonesi</i>	2.88	PBDB
<i>Domninoides mimicus</i>	135.64	(1)
<i>Domninoides riparensis</i>	56.83	(1)
<i>Dorraletes diminutivus</i>	3.20	PBDB + regression
<i>Douglassciurus jeffersoni</i>	8.19	(25)
<i>Downsimus chadwicki</i>	56.26	(1)
<i>Drepanomeryx falciformis</i>	90219.42	(1)
<i>Dromomeryx borealis</i>	144350.55	(1)
<i>Dryomomys dulcifer</i>	0.85	(31)
<i>Dryomomys szalayi</i>	1.00	(31)
<i>Duchesneodus uintensis</i>	1358.50	PBDB + regression
<i>Dyseohyus fricki</i>	21807.30	(1)
<i>Dyseolemur pacificus</i>	3.80	PBDB + regression
<i>Ectocion cedrus</i>	38.60	PBDB + regression
<i>Ectocion collinus</i>	42.90	PBDB + regression
<i>Ectocion major</i>	64.70	PBDB + regression
<i>Ectocion mediotuber</i>	41.20	PBDB + regression
<i>Ectocion osbornianus</i>	46.50	PBDB + regression
<i>Ectocion parvus</i>	30.30	PBDB + regression
<i>Ectocion superstes</i>	68.50	PBDB + regression
<i>Ectoconus ditrigonus</i>	89.20	PBDB + regression
<i>Ectoganus gliriformes</i>	140.40	(31)
<i>Ectoganus gliriformis</i>	140.40	PBDB + regression
<i>Ectopocynus antiquus</i>	8266.78	(1)
<i>Ectopocynus intermedius</i>	12456.53	(1)
<i>Ectypodus aphronorus</i>	18.00	(7)
<i>Ectypodus childei</i>	1.60	PBDB + regression
<i>Ectypodus lovei</i>	1.60	PBDB + regression
<i>Ectypodus musculus</i>	2.40	PBDB + regression
<i>Ectypodus powelli</i>	1.90	PBDB + regression
<i>Ectypodus szalayi</i>	1.80	PBDB + regression
<i>Ectypodus tardus</i>	1.70	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Edwirthia lerbekmoi</i>	2.10	PBDB + regression
<i>Ekgmowechashala philotau</i>	2079.74	(1)
<i>Elomeryx armatus</i>	157944.66	(1)
<i>Elphidotarsius florencae</i>	1.80	PBDB + regression
<i>Elphidotarsius russelli</i>	2.10	PBDB + regression
<i>Elphidotarsius wightoni</i>	2.30	PBDB + regression
<i>Elpidophorus elegans</i>	14.70	PBDB + regression
<i>Elpidophorus minor</i>	5.80	PBDB + regression
<i>Elwynella oreas</i>	4.60	PBDB + regression
<i>Elymus complexus</i>	0.80	PBDB + regression
<i>Enhydritherium terraenovae</i>	16.50	PBDB + regression
<i>Enhydrocyon basilatus</i>	20332.99	(1)
<i>Enhydrocyon crassidens</i>	18582.95	(1)
<i>Enhydrocyon pahinsintewakpa</i>	14764.78	(1)
<i>Enhydrocyon stenocephalus</i>	14044.69	(1)
<i>Entoptychus grandiplanus</i>	59.74	(1)
<i>Entoptychus individens</i>	84.00	(4)
<i>Entoptychus planifrons</i>	134.29	(1)
<i>Entoptychus sheppardi</i>	94.63	(1)
<i>Entoptychus wheelerensis</i>	84.00	(4)
<i>Eoconodon gaudrianus</i>	8.50	(32)
<i>Eoconodon hutchisoni</i>	55.68	PBDB
<i>Eoconodon nidhoggi</i>	6.90	PBDB + regression
<i>Eohaplomys matutinus</i>	18.60	PBDB + regression
<i>Eohaplomys serus</i>	14.20	PBDB + regression
<i>Eohaplomys tradux</i>	12.60	PBDB + regression
<i>Eomoropus amarorum</i>	128.80	PBDB + regression
<i>Eoryctes melanus</i>	4.00	PBDB + regression
<i>Eotitanops borealis</i>	297.00	PBDB + regression
<i>Eotitanops minimus</i>	14.90	PBDB + regression
<i>Eotitanotherium osborni</i>	988.00	PBDB
<i>Eotylopus reedi</i>	88.90	PBDB + regression
<i>Epeiromys spanius</i>	4.00	PBDB + regression
<i>Epicyon haydeni</i>	41772.77	(1)
<i>Epicyon saevus</i>	27722.51	(1)
<i>Epihippus gracilis</i>	54.50	PBDB + regression
<i>Epihippus intermedius</i>	61.09	PBDB
<i>Epitriplopus uintensis</i>	32600.00	(30)
<i>Eporeodon occidentalis</i>	118300.00	(4)
<i>Equus complicatus</i>	270.97	(11)
<i>Equus conversidens</i>	241.29	(11)
<i>Equus cumminsii</i>	354.80	PBDB + regression
<i>Equus francisci</i>	278.00	PBDB + regression
<i>Equus fromanius</i>	172311.00	(4)
<i>Equus giganteus</i>	270.97	(11)
<i>Equus idahoensis</i>	560.70	PBDB + regression
<i>Equus leidyi</i>	337.30	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Equus occidentalis</i>	317.03	(11)
<i>Equus scotti</i>	312.31	(11)
<i>Equus simplicidens</i>	296558.57	(1)
<i>Eremotherium eomigrans</i>	2584400.00	(33)
<i>Eremotherium laurillardi</i>	366.13	(11)
<i>Erethizon bathygnathum</i>	51.10	PBDB + regression
<i>Erethizon kleini</i>	31.30	PBDB + regression
<i>Escavadodon zygus</i>	5.50	PBDB + regression
<i>Esthonyx acutidens</i>	80.80	PBDB + regression
<i>Esthonyx bisulcatus</i>	48.00	PBDB + regression
<i>Esthonyx spatularius</i>	60.80	PBDB + regression
<i>Eucyon davisii</i>	10509.13	(1)
<i>Eudaemonema cuspidata</i>	11.50	PBDB + regression
<i>Eumys brachyodus</i>	126.47	(1)
<i>Eumys elegans</i>	4.10	PBDB + regression
<i>Euoploctyon brachygnathus</i>	11271.13	(1)
<i>Euoploctyon spissidens</i>	9798.65	(1)
<i>Eusmilus cerebralis</i>	804.32	(1)
<i>Eusmilus sicarius</i>	19.20	PBDB + regression
<i>Eutypomys acares</i>	3.60	PBDB + regression
<i>Eutypomys hibernodus</i>	12.20	PBDB + regression
<i>Eutypomys inexpectatus</i>	12.00	PBDB + regression
<i>Eutypomys montanensis</i>	943.88	(1)
<i>Eutypomys obliquidens</i>	5.90	PBDB + regression
<i>Eutypomys parvus</i>	7.00	PBDB + regression
<i>Eutypomys thomsoni</i>	10.70	PBDB + regression
<i>Fanimus clasoni</i>	3.67	PBDB
<i>Fanimus ultimus</i>	164.02	(1)
<i>Felis rexroadensis</i>	30333.26	(1)
<i>Ferinestrix vorax</i>	103.50	PBDB
<i>Florentiamys agnewi</i>	84.77	(1)
<i>Florentiamys kinseyi</i>	157.59	(1)
<i>Florentiamys loomisi</i>	151.41	(1)
<i>Florentiamys tiptoni</i>	117.92	(1)
<i>Floridachoerus olsenii</i>	35596.41	(1)
<i>Floridameryx floridanus</i>	8184.52	(1)
<i>Floridatragulus dolichanthereus</i>	43477.55	(1)
<i>Floridatragulus texanus</i>	61083.68	(1)
<i>Fouchia elvensis</i>	36.80	PBDB + regression
<i>Galbreathia bettae</i>	165.67	(1)
<i>Galbreathia novellus</i>	6.97	PBDB
<i>Galecyon mordax</i>	23.70	PBDB + regression
<i>Gazinius amplus</i>	875.00	(22)
<i>Gazinocyon vulpeculus</i>	39.60	PBDB + regression
<i>Gelastops joni</i>	8.50	PBDB + regression
<i>Gelastops parcus</i>	7.50	PBDB + regression
<i>Geomys carrranzai</i>	2.00	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Geringia gloveri</i>	26.84	(1)
<i>Geringia mcgregori</i>	41.26	(1)
<i>Gigantocamelus spatulus</i>	1435.10	PBDB + regression
<i>Glossotherium chapadmalense</i>	310540.00	(33)
<i>Glyptotherium arizonae</i>	789680.00	(33)
<i>Gomphotherium obscurum</i>	10056.96	PBDB
<i>Gomphotherium osborni</i>	117.00	(34)
<i>Goniodontomys disjunctus</i>	44.26	(1)
<i>Gracilicyon winkleri</i>	13.30	PBDB + regression
<i>Grangeria anarsius</i>	126.00	PBDB + regression
<i>Gregorymys curtus</i>	106.70	(1)
<i>Gregorymys formosus</i>	77.48	(1)
<i>Gregorymys riograndensis</i>	43.82	(1)
<i>Gripholagomys lavocati</i>	507.76	(1)
<i>Griphomys alecer</i>	1.40	PBDB + regression
<i>Griphomys toltecus</i>	1.83	(25)
<i>Guanajuatomys hibbardi</i>	5.30	PBDB + regression
<i>Guildayomys hibbardi</i>	82.27	(1)
<i>Hapalodectes anthracinus</i>	4.09	PBDB + regression
<i>Hapalodectes leptognathus</i>	4.94	PBDB + regression
<i>Haplaletes disceptatrix</i>	5.30	PBDB + regression
<i>Haplaletes pelicatus</i>	6.90	PBDB + regression
<i>Haploconus angustus</i>	18.00	PBDB + regression
<i>Haplohippus texanus</i>	63.70	PBDB + regression
<i>Haplolambda quinni</i>	276.64	PBDB
<i>Haplolambda simpsoni</i>	595.34	(35)
<i>Haplomylus bozemanensis</i>	5.40	PBDB + regression
<i>Haplomylus palustris</i>	4.80	PBDB + regression
<i>Haplomylus scottianus</i>	6.40	PBDB + regression
<i>Haplomylus simpsoni</i>	7.90	PBDB + regression
<i>Haplomylus sperianus</i>	5.80	PBDB + regression
<i>Haplomys galbreathi</i>	2.30	PBDB + regression
<i>Haplomys liophorus</i>	39.00	(4)
<i>Harpagolestes leotensis</i>	30.60	PBDB + regression
<i>Harpagolestes uintensis</i>	28.00	PBDB + regression
<i>Harrymys irvini</i>	83.93	(1)
<i>Harrymys magnus</i>	50.40	(1)
<i>Harrymys woodi</i>	2.48	(15)
<i>Heliscomys hatcheri</i>	0.89	(7)
<i>Heliscomys ostranderi</i>	0.60	PBDB + regression
<i>Heliscomys senex</i>	0.70	PBDB + regression
<i>Heliscomys vetus</i>	0.70	PBDB + regression
<i>Heliscomys woodi</i>	1.10	PBDB + regression
<i>Hemiacodon engardae</i>	11.60	PBDB + regression
<i>Hemiacodon gracilis</i>	11.90	PBDB + regression
<i>Hemiauchenia gracilis</i>	225.00	PBDB + regression
<i>Hemiauchenia macrocephala</i>	154.62	(11)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Hemiauchenia minima</i>	85819.37	(1)
<i>Hemiauchenia vera</i>	299.50	PBDB + regression
<i>Hemipsalodon grandis</i>	453.84	(36)
<i>Hemithlaeus harbourae</i>	18.67	(37)
<i>Hendryomeryx defordi</i>	25.31	PBDB
<i>Hendryomeryx esulcatus</i>	27.80	PBDB + regression
<i>Hendryomeryx wilsoni</i>	16.50	PBDB + regression
<i>Heptacodon pellionis</i>	153.70	PBDB + regression
<i>Heptodon calciculus</i>	69.50	PBDB + regression
<i>Herpetotherium fugax</i>	1.90	PBDB + regression
<i>Herpetotherium knighti</i>	3.20	PBDB + regression
<i>Herpetotherium merriami</i>	2.20	PBDB + regression
<i>Herpetotherium valens</i>	3.40	PBDB + regression
<i>Herpetotherium youngi</i>	2.80	PBDB + regression
<i>Hesperhys pinensis</i>	68186.37	(1)
<i>Hesperhys vagrans</i>	73865.41	(1)
<i>Hesperocyon gregarius</i>	3533.34	(1)
<i>Hesperolagomys fluviatilis</i>	169.02	(1)
<i>Hesperolagomys galbreathi</i>	149.90	(1)
<i>Hesperoscalops mcgrewi</i>	8.60	PBDB + regression
<i>Heteraletes leotanus</i>	45.60	PBDB + regression
<i>Heteromeryx dispar</i>	107.00	PBDB + regression
<i>Heteropliohippus hulberti</i>	302549.45	(1)
<i>Hexacodus pelodes</i>	12.60	PBDB + regression
<i>Hexameryx simpsoni</i>	30638.11	(1)
<i>Hexobelomeryx fricki</i>	118.50	PBDB + regression
<i>Hibbarderix obfuscatus</i>	3.00	PBDB + regression
<i>Hibbardomys fayae</i>	3.00	PBDB + regression
<i>Hibbardomys marthae</i>	3.60	PBDB + regression
<i>Hibbardomys skinneri</i>	3.00	PBDB + regression
<i>Hibbardomys voorhiesi</i>	3.00	PBDB + regression
<i>Hipparrison forcei</i>	194852.86	(1)
<i>Hipparrison tehonense</i>	100709.96	(1)
<i>Hippotherium emsliei</i>	264.70	PBDB + regression
<i>Hippotherium ingenuum</i>	176.70	PBDB + regression
<i>Hippotherium plicatile</i>	232.00	PBDB + regression
<i>Hippotherium quinni</i>	431.00	PBDB + regression
<i>Hitonkala macdonaldtau</i>	24.53	(1)
<i>Holmesina floridanus</i>	164.90	PBDB + regression
<i>Homacodon vagans</i>	28.00	PBDB + regression
<i>Homogalax protapirinus</i>	57.30	PBDB + regression
<i>Homotherium crusafonti</i>	322.50	PBDB
<i>Homotherium idahoensis</i>	257900.00	(4)
<i>Homotherium johnstoni</i>	29.50	PBDB + regression
<i>Hoplophoneus mentalis</i>	206.00	PBDB + regression
<i>Hoplophoneus primaevus</i>	16.00	PBDB + regression
<i>Huerfanodon polecatensis</i>	104.30	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Huerfanodon torrejonius</i>	85.80	PBDB + regression
<i>Hyaenodon brevirostrus</i>	118.10	PBDB + regression
<i>Hyaenodon crucians</i>	71.10	PBDB + regression
<i>Hyaenodon horridus</i>	193.20	PBDB + regression
<i>Hyaenodon montanus</i>	101.60	PBDB + regression
<i>Hyaenodon mustelinus</i>	51.10	PBDB + regression
<i>Hyaenodon raineyi</i>	17.10	PBDB + regression
<i>Hyaenodon venturae</i>	27.20	PBDB + regression
<i>Hyaenodon vetus</i>	111.00	PBDB + regression
<i>Hylomeryx quadricuspis</i>	23.00	PBDB + regression
<i>Hyopsodus fastigatus</i>	23.10	PBDB + regression
<i>Hyopsodus lepidus</i>	12.60	PBDB + regression
<i>Hyopsodus loomisi</i>	11.00	PBDB + regression
<i>Hyopsodus lysitensis</i>	15.60	PBDB + regression
<i>Hyopsodus mentalis</i>	20.20	PBDB + regression
<i>Hyopsodus minor</i>	10.40	PBDB + regression
<i>Hyopsodus minusculus</i>	10.40	PBDB + regression
<i>Hyopsodus paulus</i>	14.10	PBDB + regression
<i>Hyopsodus pauxillus</i>	6.40	PBDB + regression
<i>Hyopsodus powellianus</i>	19.70	PBDB + regression
<i>Hyopsodus simplex</i>	13.70	PBDB + regression
<i>Hyopsodus tonksi</i>	10.70	PBDB + regression
<i>Hyopsodus uintensis</i>	20.30	PBDB + regression
<i>Hyopsodus walcottianus</i>	44.10	PBDB + regression
<i>Hyopsodus wortmani</i>	14.40	PBDB + regression
<i>Hypertragulus calcaratus</i>	8880.00	(4)
<i>Hypertragulus hesperius</i>	4572.00	(4)
<i>Hypohippus affinis</i>	442413.39	(1)
<i>Hypohippus equinus</i>	271034.12	(1)
<i>Hypohippus osborni</i>	299539.03	(1)
<i>Hypolagus edensis</i>	665.14	(1)
<i>Hypolagus fontinalis</i>	1211.97	(1)
<i>Hypolagus furlongi</i>	678.58	(1)
<i>Hypolagus gidleyi</i>	1998.20	(1)
<i>Hypolagus oregonensis</i>	2344.90	(1)
<i>Hypolagus parviplicatus</i>	1702.75	(1)
<i>Hypolagus ringoldensis</i>	319.00	(4)
<i>Hypolagus vetus</i>	2892.86	(1)
<i>Hypolagus voorhiesi</i>	319.00	(4)
<i>Hypsiops bannackensis</i>	214.80	(38)
<i>Hypsiops breviceps</i>	156373.08	(1)
<i>Hyrachyus affinis</i>	178.70	PBDB + regression
<i>Hyrachyus eximius</i>	262.00	PBDB + regression
<i>Hyrachyus modestus</i>	278.50	PBDB + regression
<i>Hyracodon leidyanus</i>	455.80	PBDB + regression
<i>Hyracodon mediis</i>	169.40	PBDB + regression
<i>Hyracodon nebraskensis</i>	211081.59	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Hyracodon petersoni</i>	354.50	PBDB + regression
<i>Hyracodon priscidens</i>	381.90	PBDB + regression
<i>Hyracotherium cristatum</i>	64.84	PBDB
<i>Hyracotherium vasacciense</i>	24900.00	(30)
<i>Ictidopappus mustelinus</i>	4.10	PBDB + regression
<i>Ignacius fremontensis</i>	1.90	PBDB + regression
<i>Ignacius frugivorus</i>	3.90	PBDB + regression
<i>Ignacius graybullianus</i>	5.30	PBDB + regression
<i>Indarctos nevadensis</i>	42.80	PBDB + regression
<i>Indarctos oregonensis</i>	302549.45	(1)
<i>Ischyrocyon gidleyi</i>	282095.23	(1)
<i>Ischyromys typus</i>	12.50	PBDB + regression
<i>Ischyromys veterior</i>	9.60	PBDB + regression
<i>Jacobsonomys verdensis</i>	50.91	(1)
<i>Janimus dawsonae</i>	1.50	PBDB + regression
<i>Jaywilsonomys ojinagaensis</i>	13.70	PBDB + regression
<i>Jemezius szalayi</i>	4.50	PBDB + regression
<i>Jepsenella praepropera</i>	2.10	PBDB + regression
<i>Jimomys labaughii</i>	69.41	(1)
<i>Jimomys lulli</i>	28.00	(4)
<i>Kansasimys dubius</i>	135.64	(1)
<i>Kansasimys wilsoni</i>	6.33	(39)
<i>Kimbethia mziae</i>	72.00	(7)
<i>Knightomys cremneus</i>	1.90	PBDB + regression
<i>Knightomys cuspidatus</i>	2.62	PBDB
<i>Knightomys depressus</i>	3.10	PBDB + regression
<i>Knightomys huerfanensis</i>	4.70	PBDB + regression
<i>Knightomys minor</i>	1.90	PBDB + regression
<i>Knightomys reginensis</i>	1.10	PBDB + regression
<i>Knightomys senior</i>	2.50	PBDB + regression
<i>Kolponomos clallamensis</i>	253.10	(40)
<i>Kolponomos newportensis</i>	664.45	(41)
<i>Kyptoceras amatorum</i>	369534.73	(1)
<i>Labidolemur kayi</i>	3.00	PBDB + regression
<i>Labidolemur serus</i>	4.60	PBDB + regression
<i>Labidolemur soricoides</i>	1.80	PBDB + regression
<i>Lambdotherium popoagicum</i>	74.70	PBDB + regression
<i>Lambertocyon eximus</i>	43.60	PBDB + regression
<i>Lambertocyon ischyrus</i>	23.90	PBDB + regression
<i>Lanthanotherium sawini</i>	5.50	PBDB + regression
<i>Laredochoerus edwardsi</i>	41.50	PBDB + regression
<i>Laredomys riograndensis</i>	0.80	PBDB + regression
<i>Leidymys cerasus</i>	41.68	(1)
<i>Leidymys korthii</i>	2.20	PBDB + regression
<i>Leipsanolestes siegfriedti</i>	2.60	PBDB + regression
<i>Lemoynea biradicularis</i>	45.60	(1)
<i>Lepoides lepoidei</i>	3640.95	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Leptacodon munusculum</i>	1.10	PBDB + regression
<i>Leptacodon packi</i>	1.80	PBDB + regression
<i>Leptacodon tener</i>	1.30	PBDB + regression
<i>Leptarctus mummorum</i>	129.10	PBDB + regression
<i>Leptarctus oregonensis</i>	2580.00	(4)
<i>Leptarctus primus</i>	149.90	(1)
<i>Leptarctus supremus</i>	125.10	PBDB
<i>Leptauchenia decora</i>	20130.67	(1)
<i>Leptauchenia major</i>	30946.03	(1)
<i>Leptictis dakotensis</i>	63.70	PBDB + regression
<i>Leptochoerus elegans</i>	33.10	PBDB + regression
<i>Leptochoerus spectabilis</i>	34.10	PBDB + regression
<i>Leptochoerus supremus</i>	56.50	PBDB + regression
<i>Leptocyon mollis</i>	3300.00	(4)
<i>Leptocyon vafer</i>	5377.61	(1)
<i>Leptodontomys douglassi</i>	0.70	PBDB + regression
<i>Leptodontomys stirtoni</i>	0.90	(42)
<i>Leptolambda schmidti</i>	383.51	(43)
<i>Leptomeryx blacki</i>	21.80	PBDB + regression
<i>Leptomeryx elissae</i>	27.50	PBDB + regression
<i>Leptomeryx evansi</i>	35.10	PBDB + regression
<i>Leptomeryx mammifer</i>	55.40	PBDB + regression
<i>Leptomeryx speciosus</i>	34.60	PBDB + regression
<i>Leptomeryx yoderi</i>	38.20	PBDB + regression
<i>Leptoreodon edwardsi</i>	44.00	PBDB + regression
<i>Leptoreodon leptolophus</i>	34.60	PBDB + regression
<i>Leptoreodon major</i>	79.60	PBDB + regression
<i>Leptoreodon marshi</i>	58.90	PBDB + regression
<i>Leptoreodon pusillus</i>	19.80	PBDB + regression
<i>Leptoreodon stocki</i>	59.50	PBDB + regression
<i>Leptromys wilsoni</i>	4.20	PBDB + regression
<i>Leptotomus caryophilus</i>	13.50	PBDB + regression
<i>Leptotomus leptodus</i>	26.40	PBDB + regression
<i>Leptotomus parvus</i>	14.10	PBDB + regression
<i>Leptotragulus clarki</i>	24.20	PBDB + regression
<i>Leptotragulus medius</i>	44.10	PBDB + regression
<i>Leptotragulus proavus</i>	40.70	PBDB + regression
<i>Lepus californicus</i>	2288.00	PBDB
<i>Lignimus austridakotensis</i>	14.88	(1)
<i>Lignimus montis</i>	2.30	PBDB + regression
<i>Limaconyssus habrus</i>	2.10	PBDB + regression
<i>Limnoecus niobrarensis</i>	7.17	(1)
<i>Limnoecus tricuspis</i>	5.10	(1)
<i>Liodontia alexandrae</i>	198.34	(1)
<i>Litaletes disjunctus</i>	13.20	PBDB + regression
<i>Litocherus lacunatus</i>	5.30	PBDB + regression
<i>Litocherus notissimus</i>	3.20	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Litocherus zygeus</i>	4.10	PBDB + regression
<i>Litolagus molidens</i>	4.70	PBDB + regression
<i>Litolestes ignotus</i>	2.10	PBDB + regression
<i>Litomylus dissentaneus</i>	6.70	PBDB + regression
<i>Litomylus orthronepius</i>	6.40	PBDB + regression
<i>Litoyoderimys auogoleus</i>	2.60	PBDB + regression
<i>Longirostromeryx clarendonensis</i>	13226.80	(1)
<i>Longirostromeryx wellsi</i>	17500.77	(1)
<i>Lophiparamys debequensis</i>	2.00	PBDB + regression
<i>Lophiparamys murinus</i>	3.70	PBDB + regression
<i>Loveina minuta</i>	3.00	PBDB + regression
<i>Loveina zephyri</i>	3.70	PBDB + regression
<i>Loxolophus criswelli</i>	24.70	PBDB + regression
<i>Loxolophus hyattianus</i>	23.70	PBDB + regression
<i>Loxolophus pentacus</i>	71.30	PBDB + regression
<i>Loxolophus priscus</i>	34.30	PBDB + regression
<i>Loxolophus schizophrenus</i>	15.20	PBDB + regression
<i>Loxolophus spiekeri</i>	80.00	PBDB + regression
<i>Lutravus halli</i>	454.86	(1)
<i>Lycophocyon hutchisoni</i>	9.90	PBDB + regression
<i>Lynx proterolyncis</i>	15677.78	(1)
<i>Lynx rufus</i>	10482.00	PBDB
<i>Machaeromeryx gilchristensis</i>	4536.90	(1)
<i>Machaeromeryx tragulus</i>	4536.90	(1)
<i>Macrocranion junnei</i>	1.90	PBDB + regression
<i>Macrocranion nitens</i>	3.00	PBDB + regression
<i>Macrogenis crassigenis</i>	174.00	PBDB
<i>Macrognathomys gemmacolis</i>	0.80	PBDB + regression
<i>Macrognathomys nanus</i>	5.16	(1)
<i>Macrotarsius montanus</i>	17.60	PBDB + regression
<i>Macrotarsius roederi</i>	1640.00	(22)
<i>Macrotarsius siegerti</i>	17.90	PBDB + regression
<i>Mahgarita stevensi</i>	9.29	(44)
<i>Malaquiferus tourteloti</i>	47.30	PBDB + regression
<i>Mammacyon obtusidens</i>	70262.96	(1)
<i>Mammut americanum</i>	777.43	(11)
<i>Mammut cosoensis</i>	7029.00	(45)
<i>Mammut furlongi</i>	7102.00	PBDB + regression
<i>Mammuthus columbi</i>	995.26	(11)
<i>Mammut raki</i>	8929.90	PBDB + regression
<i>Marmota korthi</i>	2038.56	(1)
<i>Marmota vetus</i>	658.52	(1)
<i>Martes gazini</i>	1767.00	(4)
<i>Martes parviloba</i>	42.75	(46)
<i>Martinogale alveodens</i>	17.99	(1)
<i>Mattimys kalicola</i>	2.10	PBDB + regression
<i>Megacamelus merriami</i>	1905014.16	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Megadelphus lundeliusi</i>	32.90	PBDB + regression
<i>Megahippus matthewi</i>	882046.45	(1)
<i>Megalagus abaconis</i>	1118.79	(1)
<i>Megalagus brachyodon</i>	9.50	PBDB + regression
<i>Megalagus primitivus</i>	3165.29	(1)
<i>Megalagus turgidus</i>	3071.74	(1)
<i>Megalesthonyx hopsoni</i>	132.29	(47)
<i>Megalictis ferox</i>	1587.63	(1)
<i>Megalictis frazieri</i>	111.47	PBDB
<i>Megalonyx curvidens</i>	185050.00	(33)
<i>Megalonyx leptostomus</i>	355.40	PBDB + regression
<i>Megalonyx wheatleyi</i>	336.20	PBDB + regression
<i>Megantereon hesperus</i>	67507.91	(1)
<i>Megapeomys bobwilsoni</i>	411.58	(1)
<i>Megasmithus tiheni</i>	55.70	(1)
<i>Megatylopus cochrani</i>	702.00	PBDB + regression
<i>Megatylopus matthewi</i>	1383324.20	(1)
<i>Megatylopus primaevus</i>	701.90	PBDB + regression
<i>Meniscomys hippodus</i>	69.41	(1)
<i>Meniscomys uhtoffi</i>	70.00	(4)
<i>Meniscotherium chamense</i>	77.80	PBDB + regression
<i>Meniscotherium tapiacitum</i>	22.90	PBDB + regression
<i>Menoceras arikarense</i>	597195.61	(1)
<i>Menoceras barbouri</i>	1251683.50	(1)
<i>Menops bakeri</i>	1897.40	PBDB
<i>Mentoclaenodon acrogenius</i>	118.30	PBDB + regression
<i>Mephitis mephitis</i>	2055.00	PBDB
<i>Merriamoceros coronatus</i>	15214.44	(1)
<i>Merychippus brevidontus</i>	124243.67	(1)
<i>Merychippus calamarius</i>	196811.17	(1)
<i>Merychippus californicus</i>	86681.87	(1)
<i>Merychippus goorisi</i>	282.80	PBDB + regression
<i>Merychippus gunteri</i>	92041.97	(1)
<i>Merychippus insignis</i>	125492.34	(1)
<i>Merychippus primus</i>	95798.28	(1)
<i>Merychippus relictus</i>	60471.00	(4)
<i>Merychippus sejunctus</i>	75357.60	(1)
<i>Merychys arenarium</i>	109.50	PBDB + regression
<i>Merychys crabilli</i>	117.00	(48)
<i>Merychys elegans</i>	45706.69	(1)
<i>Merychys medius</i>	108012.26	(1)
<i>Merychys minimus</i>	74.70	PBDB + regression
<i>Merychys relictus</i>	164.00	PBDB
<i>Merychys smithi</i>	203.50	PBDB + regression
<i>Merycochoerus carrikeri</i>	354.04	(49)
<i>Merycochoerus chelydra</i>	336.00	PBDB
<i>Merycochoerus magnus</i>	331041.82	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Merycochoerus matthewi</i>	275.00	PBDB + regression
<i>Merycochoerus proprius</i>	265667.29	(1)
<i>Merycochoerus superbus</i>	438400.00	(4)
<i>Merycodus prodromus</i>	9.00	(50)
<i>Merycodus sabulonis</i>	10509.13	(1)
<i>Merycodus warreni</i>	42.50	(51)
<i>Merycoides harrisonensis</i>	90219.42	(1)
<i>Merycoides longiceps</i>	215.00	(52)
<i>Merycoides pariogonus</i>	77000.00	(4)
<i>Merycidodon bullatus</i>	109500.00	(4)
<i>Merycidodon culbertsoni</i>	184.60	PBDB + regression
<i>Merycidodon major</i>	62200.00	(4)
<i>Mesalerolemur horneri</i>	6.62	(53)
<i>Mesocyon brachyops</i>	7942.63	(1)
<i>Mesocyon coryphaeus</i>	10198.54	(1)
<i>Mesocyon temnodon</i>	7186.79	(1)
<i>Mesodma ambigua</i>	5.00	PBDB + regression
<i>Mesodma formosa</i>	2.50	PBDB + regression
<i>Mesodma garfieldensis</i>	2.70	PBDB + regression
<i>Mesodma pygmaea</i>	1.20	PBDB + regression
<i>Mesodma thompsoni</i>	3.30	PBDB + regression
<i>Mesogaulus paniensis</i>	13.97	PBDB
<i>Mesohippus bairdi</i>	89.90	PBDB + regression
<i>Mesohippus exoletus</i>	102.10	PBDB + regression
<i>Mesohippus texanus</i>	84.40	PBDB + regression
<i>Mesohippus westoni</i>	90.10	PBDB + regression
<i>Mesonyx obtusidens</i>	279.00	PBDB
<i>Mesoreodon chelonyx</i>	201.25	(54)
<i>Mesoreodon floridensis</i>	104820.01	(1)
<i>Mesoreodon minor</i>	159700.00	(4)
<i>Mesoscalops montanensis</i>	85.63	(1)
<i>Mesoscalops scopelotemos</i>	95.58	(1)
<i>Metadjidaumo hendryi</i>	10.38	(1)
<i>Metaliomys sevierensis</i>	1.40	PBDB + regression
<i>Metanoiamys agorus</i>	1.20	PBDB + regression
<i>Metanoiamys fantasma</i>	1.60	PBDB + regression
<i>Metanoiamys korthi</i>	1.30	PBDB + regression
<i>Metanoiamys lacus</i>	1.10	PBDB + regression
<i>Metanoiamys marinus</i>	1.00	PBDB + regression
<i>Metarhinus pater</i>	810.00	PBDB
<i>Metatomarctus canavus</i>	10938.02	(1)
<i>Metechinus amplior</i>	24.12	(35)
<i>Miacis deutschi</i>	16.00	PBDB + regression
<i>Miacis exiguum</i>	22.30	PBDB + regression
<i>Miacis hookwayi</i>	26.00	(55)
<i>Miacis latidens</i>	25.30	PBDB + regression
<i>Miacis parvivorus</i>	26.20	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Miacis petilus</i>	21.00	PBDB + regression
<i>Michenia agatensis</i>	99707.88	(1)
<i>Michenia exilis</i>	65512.75	(1)
<i>Microcosmodon conus</i>	1.70	PBDB + regression
<i>Microcosmodon rosei</i>	2.30	PBDB + regression
<i>Microeutypomys karenae</i>	1.20	PBDB + regression
<i>Microeutypomys tilliei</i>	1.70	PBDB + regression
<i>Micromomys antelucanus</i>	0.90	PBDB
<i>Microparamys cheradius</i>	2.90	PBDB + regression
<i>Microparamys dubius</i>	1.60	PBDB + regression
<i>Microparamys hunterae</i>	1.32	PBDB
<i>Microparamys minutus</i>	1.80	PBDB + regression
<i>Microparamys nimius</i>	2.00	PBDB + regression
<i>Microparamys sambucus</i>	2.40	PBDB + regression
<i>Microparamys tricus</i>	2.90	PBDB + regression
<i>Microparamys woodi</i>	2.10	PBDB + regression
<i>Micropternodus borealis</i>	3.40	PBDB + regression
<i>Micropternodus montrosensis</i>	6.00	PBDB + regression
<i>Micropternodus morgani</i>	72.24	(1)
<i>Microsus cuspidatus</i>	15.00	PBDB + regression
<i>Microsyops angustidens</i>	9.20	PBDB + regression
<i>Microsyops annectens</i>	20.50	PBDB + regression
<i>Microsyops cardiores</i>	6.50	PBDB + regression
<i>Microsyops elegans</i>	13.80	PBDB + regression
<i>Microsyops knightensis</i>	11.40	PBDB + regression
<i>Microsyops kratos</i>	20.00	PBDB + regression
<i>Microsyops latidens</i>	10.80	PBDB + regression
<i>Microsyops scottianus</i>	12.70	PBDB + regression
<i>Microtomarctus conferta</i>	8866.19	(1)
<i>Mictomys vetus</i>	3.40	PBDB + regression
<i>Mimatuta morgoth</i>	11.30	PBDB + regression
<i>Mimetodon silberlingi</i>	2.00	PBDB + regression
<i>Mimomys mcknighti</i>	110.70	PBDB
<i>Mimomys panacaensis</i>	3.60	PBDB + regression
<i>Mimomys parvus</i>	99.10	PBDB
<i>Mimomys primus</i>	163.60	PBDB
<i>Mimomys taylori</i>	80.90	PBDB
<i>Mimoperadectes labrus</i>	8.20	PBDB + regression
<i>Mimotricentes fremontensis</i>	27.90	PBDB + regression
<i>Mimotricentes subtrigonus</i>	23.70	PBDB + regression
<i>Miniochoerus affinis</i>	84.70	PBDB
<i>Miniochoerus gracilis</i>	48.60	PBDB
<i>Minippus index</i>	22.55	PBDB
<i>Mioclaenus turgidus</i>	36.70	PBDB + regression
<i>Miocyon scotti</i>	125.60	PBDB + regression
<i>Miocyon vallisrubrae</i>	69.70	PBDB + regression
<i>Mioheteromys amplissimus</i>	41.26	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Miohippus anceps</i>	41650.00	(4)
<i>Miohippus assiniboiensis</i>	142.10	PBDB + regression
<i>Miohippus equiceps</i>	41650.00	(4)
<i>Miohippus equinanus</i>	35954.16	(1)
<i>Miohippus gidleyi</i>	197.80	PBDB + regression
<i>Miohippus grandis</i>	139.38	PBDB
<i>Miohippus intermedius</i>	82454.34	(1)
<i>Miohippus obliquidens</i>	52575.21	(1)
<i>Miolabis fricki</i>	240385.70	(1)
<i>Miomustela madisonae</i>	13.46	(1)
<i>Mionictis elegans</i>	11.00	PBDB
<i>Mionictis incertus</i>	12.30	PBDB
<i>Mionictis letifer</i>	134.29	(1)
<i>Mionictis pristinus</i>	18.70	PBDB + regression
<i>Miosciurus ballovianus</i>	36.60	(1)
<i>Miosicista angulus</i>	0.96	PBDB
<i>Miospermophilus lavertyi</i>	106.70	(1)
<i>Miospermophilus wyomingensis</i>	83.10	(1)
<i>Miotapirus harrisonensis</i>	325.20	PBDB + regression
<i>Miotylopus gibbi</i>	48050.12	(1)
<i>Miotylopus leonardi</i>	43044.94	(1)
<i>Miotylopus taylori</i>	73865.41	(1)
<i>Miracinonyx inexpectatus</i>	20.40	PBDB + regression
<i>Miracinonyx studeri</i>	17.30	PBDB + regression
<i>Mithrandir gillianus</i>	12.80	PBDB + regression
<i>Mixodectes malaris</i>	11.60	PBDB + regression
<i>Mixodectes pungens</i>	20.80	PBDB + regression
<i>Mojavemys galushai</i>	28.22	(1)
<i>Mojavemys lophatus</i>	1.36	PBDB
<i>Mojavemys magnumarcus</i>	56.26	(1)
<i>Montanatylopus matthewi</i>	242.70	PBDB + regression
<i>Mookomys altifluminis</i>	13.07	(1)
<i>Mookomys formicarum</i>	1.19	PBDB
<i>Mookomys thrinax</i>	11.94	(1)
<i>Moropus elatus</i>	707858.86	(1)
<i>Moropus merriami</i>	173767.00	(4)
<i>Moropus oregonensis</i>	189094.09	(1)
<i>Mustela frenata</i>	8.73	(11)
<i>Mustela meltoni</i>	5.60	PBDB + regression
<i>Mustela rexroadensis</i>	9.58	(1)
<i>Mylanodon rosei</i>	2.30	PBDB + regression
<i>Mylohyus elmorei</i>	235.60	PBDB + regression
<i>Myrmecoboides montanensis</i>	3.60	PBDB + regression
<i>Myrmecophaga tridactyla</i>	32544.00	PBDB
<i>Mysops parvus</i>	2.80	PBDB + regression
<i>Mystipterus martini</i>	29.37	(1)
<i>Mystipterus pacificus</i>	14.88	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Mytonolagus petersoni</i>	7.00	PBDB + regression
<i>Mytonolagus wyomingensis</i>	4.20	PBDB + regression
<i>Mytonomeryx scotti</i>	24.50	PBDB + regression
<i>Mytonomys burkei</i>	25.90	PBDB + regression
<i>Mytonomys mytonensis</i>	16.00	PBDB + regression
<i>Mytonomys robustus</i>	26.10	PBDB + regression
<i>Namatomys lloydii</i>	1.80	PBDB + regression
<i>Nannippus aztecus</i>	173.50	PBDB + regression
<i>Nannippus beckensis</i>	205.70	PBDB + regression
<i>Nannippus peninsulae</i>	68871.66	(1)
<i>Nannippus westoni</i>	62317.65	(1)
<i>Nannodectes gidleyi</i>	11.40	PBDB + regression
<i>Nannodectes intermedius</i>	5.40	PBDB + regression
<i>Nannodectes simpsoni</i>	9.90	PBDB + regression
<i>Nanodelphys huntii</i>	1.10	PBDB + regression
<i>Nanotragulus loomisi</i>	2724.39	(1)
<i>Nanotragulus ordinatus</i>	5541.39	(1)
<i>Nanotragulus planiceps</i>	3678.00	(4)
<i>Navajovius kohlhaasae</i>	1.50	PBDB + regression
<i>Nebraskomys mcgregori</i>	46.06	(1)
<i>Nebraskomys rexroadensis</i>	2.60	PBDB + regression
<i>Nekrolagus progressus</i>	1510.20	(1)
<i>Neohipparion affine</i>	167711.41	(1)
<i>Neohipparion eurystyle</i>	133252.35	(1)
<i>Neohipparion leptodea</i>	233281.23	(1)
<i>Neohipparion trampasense</i>	120571.71	(1)
<i>Neoliotomus conventus</i>	23.10	PBDB + regression
<i>Neoliotomus ultimus</i>	25.40	PBDB + regression
<i>Neoplagiaulax donaldorum</i>	52.00	(7)
<i>Neoplagiaulax grangeri</i>	93.00	(7)
<i>Neoplagiaulax hazeni</i>	4.50	PBDB + regression
<i>Neoplagiaulax hunteri</i>	2.90	PBDB + regression
<i>Neoplagiaulax macrotomeus</i>	1.60	PBDB + regression
<i>Neoplagiaulax mckennai</i>	3.50	PBDB + regression
<i>Neotoma cinerea</i>	11.89	(11)
<i>Neotoma fossilis</i>	5.20	PBDB + regression
<i>Neotoma leucopetrica</i>	8.56	(56)
<i>Neotoma quadriplicata</i>	9.60	PBDB + regression
<i>Neotoma sawrockensis</i>	99.48	(1)
<i>Neotoma taylori</i>	5.70	PBDB + regression
<i>Neotoma vaughani</i>	5.70	PBDB + regression
<i>Nerterogeomys anzensis</i>	36.20	PBDB
<i>Nerterogeomys garbanii</i>	43.40	PBDB
<i>Nerterogeomys minor</i>	2.30	PBDB + regression
<i>Nerterogeomys persimilis</i>	2.67	(56)
<i>Nexuotapirus marslandensis</i>	144350.55	(1)
<i>Nexuotapirus robustus</i>	302549.45	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Niglarodon koernerri</i>	68.03	(1)
<i>Nimravides galiani</i>	159532.03	(1)
<i>Nimravides thinobates</i>	2460.50	PBDB
<i>Nimravus brachyops</i>	3789.54	(1)
<i>Nimravus sectator</i>	28.50	PBDB + regression
<i>Niptomomys doreenae</i>	1.80	PBDB + regression
<i>Niptomomys thelmae</i>	1.90	PBDB + regression
<i>Nonomys gutzleri</i>	1.60	PBDB + regression
<i>Nonomys simplicidens</i>	1.40	PBDB + regression
<i>Notharctus pugnax</i>	29.90	PBDB + regression
<i>Notharctus robinsoni</i>	31.40	PBDB + regression
<i>Notharctus robustior</i>	6900.00	(22)
<i>Notharctus tenebrosus</i>	36.30	PBDB + regression
<i>Notharctus venticulus</i>	28.00	PBDB + regression
<i>Nothokemas floridanus</i>	100709.96	(1)
<i>Nothokemas waldropi</i>	22925.38	(1)
<i>Nothotylopus campognathus</i>	334368.85	(1)
<i>Nothrotheriops shastensis</i>	613762.01	(57)
<i>Nothrotheriops texanus</i>	228.60	PBDB + regression
<i>Notiosorex jacksoni</i>	1.52	(58)
<i>Notiosorex repenningi</i>	1.98	(59)
<i>Notiotitanops mississippiensis</i>	2039.60	PBDB + regression
<i>Notolagus lepusculus</i>	372.41	(1)
<i>Nototamias hulberti</i>	17.12	(1)
<i>Nototamias quadratus</i>	35.87	(1)
<i>Nyctitherium serotinum</i>	1.60	PBDB + regression
<i>Nyctitherium velox</i>	2.50	PBDB + regression
<i>Ochotona spanglei</i>	188.67	(1)
<i>Odocoileus virginianus</i>	52607.00	PBDB
<i>Ogmodontomys poaphagus</i>	131.63	(1)
<i>Ogmodontomys sawrockensis</i>	140.40	PBDB
<i>Oklahomalagus whisenhunti</i>	387.61	(1)
<i>Oligobunis floridanus</i>	17.00	PBDB + regression
<i>Oligoryctes cameronensis</i>	0.90	PBDB + regression
<i>Oligoscalops galbreathi</i>	2.90	PBDB + regression
<i>Oligospermophilus douglassi</i>	4.30	PBDB + regression
<i>Omomys carteri</i>	6.20	PBDB + regression
<i>Omomys lloydii</i>	3.70	PBDB + regression
<i>Onychomys hollisteri</i>	1.60	PBDB + regression
<i>Onychomys martini</i>	18.36	(1)
<i>Onychomys pedroensis</i>	36.23	(1)
<i>Oregonomys magnus</i>	1.60	PBDB + regression
<i>Oregonomys pebblespringsensis</i>	26.58	(1)
<i>Oregonomys sargentii</i>	26.05	(1)
<i>Oreodontoides oregonensis</i>	25336.47	(1)
<i>Oreolagus colteri</i>	3.10	PBDB + regression
<i>Oreolagus nebrascensis</i>	336.97	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Oreolagus nevadensis</i>	78.00	(4)
<i>Oreolagus wallacei</i>	354.25	(1)
<i>Oreotalpa florissantensis</i>	1.50	PBDB + regression
<i>Orohippus pumilus</i>	39.20	PBDB + regression
<i>Orohippus sylvaticus</i>	37.00	PBDB + regression
<i>Oromeryx plicatus</i>	32.90	PBDB + regression
<i>Oropyctis pediasius</i>	5.20	PBDB + regression
<i>Osbornoceros osborni</i>	17326.63	(1)
<i>Osbornodon brachypus</i>	141.90	(60)
<i>Osbornodon fricki</i>	25848.30	(1)
<i>Osbornodon iamonensis</i>	13904.95	(1)
<i>Osbornodon renjiei</i>	12.33	PBDB + regression
<i>Osbornodon scitulus</i>	11849.01	(1)
<i>Osbornodon sesnoni</i>	8349.86	(1)
<i>Otarocyon cooki</i>	1826.21	(1)
<i>Otarocyon macdonaldi</i>	6.30	PBDB + regression
<i>Ottoceros peacevalleyensis</i>	13493.99	(1)
<i>Ourayia hopsoni</i>	12.20	PBDB + regression
<i>Ourayia uintensis</i>	14.00	PBDB + regression
<i>Oxetocyon cuspidatus</i>	2440.60	(1)
<i>Oxyacodon agapetillus</i>	9.20	PBDB + regression
<i>Oxyacodon apiculatus</i>	17.30	PBDB + regression
<i>Oxyacodon ferronensis</i>	12.50	PBDB + regression
<i>Oxyacodon priscilla</i>	14.50	PBDB + regression
<i>Oxyaena forcipata</i>	137.50	PBDB + regression
<i>Oxyaena gulo</i>	126.30	PBDB + regression
<i>Oxyaena intermedia</i>	130.30	PBDB + regression
<i>Oxyclaenus cuspidatus</i>	5.30	PBDB + regression
<i>Oxyclaenus pugnax</i>	7.10	PBDB + regression
<i>Oxyclaenus simplex</i>	4.80	PBDB + regression
<i>Oxydactylus longipes</i>	112420.32	(1)
<i>Oxydactylus lulli</i>	275.00	PBDB
<i>Oxyprimus erikseni</i>	5.40	PBDB + regression
<i>Pachyaena gigantea</i>	24.50	PBDB + regression
<i>Pachyaena gracilis</i>	19.80	PBDB + regression
<i>Pachyaena ossifraga</i>	380.00	PBDB
<i>Pachyarmatherium leiseyi</i>	15420.00	(33)
<i>Paciculus montanus</i>	3.20	PBDB + regression
<i>Paciculus nebraskensis</i>	80.64	(1)
<i>Paciculus woodi</i>	2.10	(61)
<i>Paenemarmota barbouri</i>	10301.04	(1)
<i>Paenemarmota mexicana</i>	56.60	PBDB + regression
<i>Paenemarmota nevadensis</i>	7644.00	(4)
<i>Paenemarmota sawrockensis</i>	5943.18	(1)
<i>Palaechthon alticuspis</i>	3.20	PBDB + regression
<i>Palaechthon woodi</i>	2.30	PBDB + regression
<i>Palaeictops bicuspis</i>	7.31	(9)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Palaeictops bridgeri</i>	7.20	PBDB + regression
<i>Palaeictops multicuspis</i>	7.50	PBDB + regression
<i>Palaeogale dorothiae</i>	607.89	(1)
<i>Palaeogale minuta</i>	400.00	NOW
<i>Palaeogale sectoria</i>	13.57	PBDB
<i>Palaeolagus burkei</i>	307.97	(1)
<i>Palaeolagus hemirhizis</i>	5.30	PBDB + regression
<i>Palaeolagus hypsodus</i>	678.58	(1)
<i>Palaeolagus philoi</i>	1211.97	(1)
<i>Palaeolagus primus</i>	5.10	PBDB + regression
<i>Palaeolagus temnodon</i>	6.20	PBDB + regression
<i>Palaeonictis occidentalis</i>	117.30	PBDB + regression
<i>Palaeonictis peloria</i>	154.40	PBDB + regression
<i>Palaeoryctes cruaris</i>	4.40	PBDB + regression
<i>Palaeoryctes puerensis</i>	2.50	PBDB + regression
<i>Palaeosyops laevidens</i>	787.30	PBDB + regression
<i>Palaeosyops paludosus</i>	945.00	PBDB + regression
<i>Palaeosyops robustus</i>	1046.40	PBDB + regression
<i>Palenochtha minor</i>	1.30	PBDB + regression
<i>Palenochtha weissae</i>	1.30	PBDB + regression
<i>Paleotomus junior</i>	6.20	PBDB + regression
<i>Paleotomus radagasti</i>	19.20	PBDB
<i>Panthera onca</i>	100000.00	PBDB
<i>Pantolambda bathmodon</i>	308.05	PBDB
<i>Pantolambda cavirictus</i>	214.50	PBDB + regression
<i>Pantolambda intermedius</i>	147.80	PBDB + regression
<i>Parablastomyx galushi</i>	56.40	PBDB + regression
<i>Paracosoryx furlongi</i>	13493.99	(1)
<i>Paracosoryx wilsoni</i>	10.67	PBDB
<i>Paracryptotis gidleyi</i>	28.22	(1)
<i>Paracryptotis rex</i>	42.10	(1)
<i>Paracynnarctus kelloggi</i>	8349.86	(1)
<i>Paracynnarctus sinclairi</i>	8022.46	(1)
<i>Paradaphoenus cuspigerus</i>	4023.87	(1)
<i>Paradaphoenus minimus</i>	8.70	PBDB + regression
<i>Paradaphoenus tooheyi</i>	3498.19	(1)
<i>Paradjidaumo alberti</i>	1.40	PBDB + regression
<i>Paradjidaumo hypsodus</i>	2.00	PBDB + regression
<i>Paradjidaumo reynoldsi</i>	1.60	PBDB + regression
<i>Paradjidaumo spokanensis</i>	2.80	PBDB + regression
<i>Paradjidaumo trilophus</i>	2.10	PBDB + regression
<i>Paradjidaumo validus</i>	3.00	PBDB + regression
<i>Paradomnina relictus</i>	23.81	(1)
<i>Paraenhydrocyon josephi</i>	7942.63	(1)
<i>Paraenhydrocyon wallovianus</i>	14185.85	(1)
<i>Parahippus leonensis</i>	94845.07	(1)
<i>Parahippus pawniensis</i>	99707.88	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Parahippus tyleri</i>	173.20	PBDB + regression
<i>Parahippus wyomingensis</i>	98400.00	(30)
<i>Parahyus vagus</i>	250.90	PBDB + regression
<i>Paralabis cedrensis</i>	138.80	PBDB + regression
<i>Parallomys americanus</i>	162.39	(1)
<i>Paramiolabis taylori</i>	131926.47	(1)
<i>Paramylodon harlani</i>	491.20	PBDB + regression
<i>Paramys adamus</i>	2.70	PBDB + regression
<i>Paramys atavus</i>	2.60	PBDB + regression
<i>Paramys compressidens</i>	20.00	PBDB + regression
<i>Paramys copei</i>	10.30	PBDB + regression
<i>Paramys delicatior</i>	12.00	PBDB + regression
<i>Paramys delicatus</i>	20.30	PBDB + regression
<i>Paramys excavatus</i>	6.80	PBDB + regression
<i>Paramys taurus</i>	7.60	PBDB + regression
<i>Paranamatomys storeri</i>	0.92	PBDB
<i>Parapliohippus carrizoensis</i>	80821.64	(1)
<i>Parapliosacomys oregonensis</i>	24.29	(1)
<i>Parapliosacomys transversus</i>	2.54	PBDB
<i>Parapotos tedfordi</i>	3533.34	(1)
<i>Pararyctes pattersoni</i>	2.00	PBDB + regression
<i>Paratomarctus euthos</i>	14472.42	(1)
<i>Paratomarctus temerarius</i>	11498.82	(1)
<i>Paratylopus labiatus</i>	101.80	PBDB + regression
<i>Paratylopus primaevus</i>	13.20	PBDB + regression
<i>Parectypodus clemensi</i>	2.10	PBDB + regression
<i>Parectypodus corystes</i>	2.80	PBDB + regression
<i>Parectypodus laytoni</i>	1.40	PBDB + regression
<i>Parectypodus lunatus</i>	2.00	PBDB + regression
<i>Parectypodus simpsoni</i>	2.70	PBDB + regression
<i>Parectypodus sinclairi</i>	19.00	(7)
<i>Parectypodus sylviae</i>	1.50	PBDB + regression
<i>Parectypodus trovessartianus</i>	4.30	PBDB + regression
<i>Pareumys boskeyi</i>	3.70	PBDB + regression
<i>Pareumys grangeri</i>	2.90	PBDB + regression
<i>Pareumys guensburgi</i>	4.80	PBDB + regression
<i>Pareumys milleri</i>	3.40	PBDB + regression
<i>Parictis parvus</i>	6.80	PBDB + regression
<i>Parictis personi</i>	7.60	PBDB + regression
<i>Paromomys depressidens</i>	3.40	PBDB + regression
<i>Paromomys maturus</i>	6.70	PBDB + regression
<i>Paronychomys alticuspis</i>	17.12	(1)
<i>Paronychomys lemredfieldi</i>	20.09	(1)
<i>Paronychomys tuttlei</i>	38.86	(1)
<i>Paroreodon parvus</i>	51150.00	(4)
<i>Parvericius montanus</i>	41.26	(1)
<i>Parvericius voorhiesi</i>	28.79	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Patriofelis ferox</i>	22418.00	(4)
<i>Patriofelis ulta</i>	136.00	PBDB + regression
<i>Patriolestes novaceki</i>	10.20	PBDB + regression
<i>Pauromys exallos</i>	1.50	PBDB + regression
<i>Pauromys lillegravemi</i>	1.20	PBDB + regression
<i>Pauromys simplex</i>	1.30	PBDB + regression
<i>Pauromys texensis</i>	1.50	PBDB + regression
<i>Pediomeryx hemphillensis</i>	167711.41	(1)
<i>Pelycodus jarrovii</i>	30.90	PBDB + regression
<i>Pelycomys brulanus</i>	6.10	PBDB + regression
<i>Pelycomys rugosus</i>	7.80	PBDB + regression
<i>Penetrigonias hudsoni</i>	544.50	PBDB
<i>Pentacemylus leotensis</i>	24.90	PBDB + regression
<i>Pentacemylus progressus</i>	29.20	PBDB + regression
<i>Pentacodon inversus</i>	17.70	PBDB + regression
<i>Pentacodon occultus</i>	31.70	PBDB + regression
<i>Peraceras hessei</i>	936589.16	(1)
<i>Peraceras profectum</i>	2326789.55	(1)
<i>Peraceras superciliosum</i>	1639660.88	(1)
<i>Peradectes californicus</i>	1.00	PBDB + regression
<i>Peradectes chesteri</i>	0.90	PBDB + regression
<i>Peradectes elegans</i>	1.40	PBDB + regression
<i>Peradectes minor</i>	1.40	(62)
<i>Peradectes protinnominatus</i>	1.50	PBDB + regression
<i>Peratherium comstocki</i>	4.30	PBDB + regression
<i>Peratherium marsupium</i>	4.40	PBDB + regression
<i>Perchoerus probus</i>	94.00	PBDB + regression
<i>Peridiomys halis</i>	63.43	(1)
<i>Peridiomys oregonensis</i>	2.20	PBDB + regression
<i>Peridiomys rusticus</i>	69.41	(1)
<i>Peritychus carinidens</i>	106.00	PBDB + regression
<i>Peritychus coarctatus</i>	90.00	PBDB + regression
<i>Perognathus ancenensis</i>	11.47	(1)
<i>Perognathus coquorum</i>	2.20	PBDB + regression
<i>Perognathus dunklei</i>	7.92	(1)
<i>Perognathus furlongi</i>	9.68	(1)
<i>Perognathus gidleyi</i>	11.82	(1)
<i>Perognathus maldei</i>	1.10	PBDB + regression
<i>Perognathus mclaughlini</i>	8.33	(1)
<i>Perognathus minutus</i>	5.93	(1)
<i>Perognathus pearlettensis</i>	6.89	(1)
<i>Perognathus rexroadensis</i>	1.50	PBDB + regression
<i>Perognathus tectoioansrum</i>	3.63	(1)
<i>Peromyscus antiquus</i>	26.84	(1)
<i>Peromyscus brachygynathus</i>	1.10	PBDB + regression
<i>Peromyscus complexus</i>	1.83	PBDB
<i>Peromyscus cragini</i>	15.49	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Peromyscus dentalis</i>	1.20	PBDB + regression
<i>Peromyscus hagermanensis</i>	19.89	(1)
<i>Peromyscus minimus</i>	0.70	PBDB + regression
<i>Peromyscus nosher</i>	1.40	PBDB + regression
<i>Peromyscus polionotus</i>	14.30	PBDB
<i>Peromyscus sarmocophinus</i>	1.50	PBDB + regression
<i>Petauristodon jamesi</i>	307.97	(1)
<i>Petauristodon mathewsi</i>	214.86	(1)
<i>Petauristodon pattersoni</i>	336.97	(1)
<i>Pewelagus dawsonae</i>	57.70	(63)
<i>Pewelagus mexicanus</i>	6.50	PBDB + regression
<i>Phelosaccomys annae</i>	26.31	(1)
<i>Phelosaccomys hibbardi</i>	46.53	(1)
<i>Phelosaccomys neomexicanus</i>	19.89	(1)
<i>Phelosaccomys shotwelli</i>	20.49	(1)
<i>Phenacocoelus typus</i>	52052.08	(1)
<i>Phenacodaptes sabulosus</i>	6.20	PBDB + regression
<i>Phenacodus bisonensis</i>	76.90	PBDB + regression
<i>Phenacodus grangeri</i>	101.90	PBDB + regression
<i>Phenacodus intermedius</i>	131.50	PBDB + regression
<i>Phenacodus magnus</i>	169.80	PBDB + regression
<i>Phenacodus matthewi</i>	41.18	(64)
<i>Phenacodus trilobatus</i>	159.30	PBDB + regression
<i>Phenacodus vortmani</i>	59.40	PBDB + regression
<i>Phenacolemur fortior</i>	6.50	(65)
<i>Phenacolemur mcgrewi</i>	3.60	PBDB + regression
<i>Phenacolemur praecox</i>	5.80	PBDB + regression
<i>Phenacolemur simonsi</i>	2.80	PBDB + regression
<i>Phenacomys gryci</i>	228.00	(4)
<i>Philotrox condoni</i>	11968.10	(1)
<i>Phlaocyon achoros</i>	2951.30	(1)
<i>Phlaocyon annexens</i>	3498.19	(1)
<i>Phlaocyon latidens</i>	2779.43	(1)
<i>Phlaocyon leucosteus</i>	3827.63	(1)
<i>Phlaocyon minor</i>	3498.19	(1)
<i>Phlaocyon taylori</i>	1939.14	(1)
<i>Phlaocyon yatkolai</i>	9604.62	(1)
<i>Phoberocyon johnhenryi</i>	179871.86	(1)
<i>Picrodus calgariensis</i>	1.50	PBDB + regression
<i>Picrodus canpaci</i>	3.10	PBDB + regression
<i>Picrodus silberlingi</i>	3.10	PBDB + regression
<i>Pipistoneomys bisulcatus</i>	2.60	PBDB + regression
<i>Plagioctenodon krausae</i>	0.90	PBDB + regression
<i>Plagioctenodon rosei</i>	1.50	PBDB + regression
<i>Plagiomene accola</i>	9.30	PBDB + regression
<i>Plagiomene multicuspis</i>	14.90	PBDB + regression
<i>Planisorex dixonensis</i>	1.60	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Platygonus bicalcaratus</i>	182.50	PBDB + regression
<i>Platygonus oregonensis</i>	40134.84	(1)
<i>Platygonus pearcei</i>	55826.28	(1)
<i>Platygonus vetus</i>	65463.62	(57)
<i>Plesiadapis anceps</i>	8.30	PBDB + regression
<i>Plesiadapis churchilli</i>	15.10	PBDB + regression
<i>Plesiadapis cookei</i>	36.80	PBDB + regression
<i>Plesiadapis dubius</i>	10.10	PBDB + regression
<i>Plesiadapis fodinatus</i>	13.50	PBDB + regression
<i>Plesiadapis gingerichi</i>	28.20	PBDB + regression
<i>Plesiadapis praecursor</i>	6.60	PBDB + regression
<i>Plesiadapis rex</i>	13.30	PBDB + regression
<i>Plesiocolopirus hancocki</i>	94.70	PBDB + regression
<i>Plesiogulo lindsayi</i>	4628.55	(1)
<i>Plesiogulo marshalli</i>	3133.79	(1)
<i>Plesiolestes nacimenti</i>	233.00	(22)
<i>Plesiolestes problematicus</i>	5.00	PBDB + regression
<i>Plesiolestes wilsoni</i>	9.40	PBDB + regression
<i>Plesiosminthus clivosus</i>	9.30	(1)
<i>Plesiosorex coloradensis</i>	192.48	(1)
<i>Plesiosorex donroosai</i>	685.40	(1)
<i>Pleurolicus dakotensis</i>	60.95	(1)
<i>Pleurolicus exiguum</i>	1.80	PBDB + regression
<i>Pleurolicus sellardsi</i>	2.77	(66)
<i>Pleurolicus sulcifrons</i>	83.93	(1)
<i>Pliocyon medius</i>	172818.99	(1)
<i>Pliocyon robustus</i>	176310.16	(1)
<i>Pliogale furlongi</i>	10.60	(65)
<i>Pliogale manka</i>	8.40	PBDB + regression
<i>Pliogeomys parvus</i>	10.28	(1)
<i>Pliogeomys russelli</i>	15.18	(1)
<i>Pliohippus fossilatus</i>	257815.63	(1)
<i>Pliohippus pernix</i>	198789.15	(1)
<i>Pliohippus tehonensis</i>	231.80	PBDB + regression
<i>Pliometanastes galushai</i>	53.00	PBDB
<i>Pliometanastes protistus</i>	189.00	PBDB + regression
<i>Plionarctos edensis</i>	56954.05	(1)
<i>Plionarctos harroldorum</i>	21.30	PBDB + regression
<i>Plionictis ogygia</i>	36.97	(1)
<i>Pliophenacomys dixonensis</i>	2.70	PBDB + regression
<i>Pliophenacomys finneyi</i>	3.10	PBDB + regression
<i>Pliophenacomys meadensis</i>	2.80	PBDB + regression
<i>Pliophenacomys osborni</i>	86.49	(1)
<i>Pliophenacomys primaevus</i>	61.56	(1)
<i>Pliosaccommys dubius</i>	27.66	(1)
<i>Pliosaccommys higginsensis</i>	18.17	(1)
<i>Pliotaxidea garberi</i>	9.60	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Pliotaxidea nevadensis</i>	130.32	(1)
<i>Pliotomodon primitivus</i>	107.77	(1)
<i>Pliozapus solus</i>	18.73	(1)
<i>Plithocyon ursinus</i>	189094.09	(1)
<i>Poabromylus golzi</i>	40.90	PBDB + regression
<i>Poabromylus kayi</i>	64.10	PBDB + regression
<i>Poebrotherium eximium</i>	106.10	PBDB + regression
<i>Poebrotherium wilsoni</i>	119.80	PBDB + regression
<i>Pogonodon eileenae</i>	242.00	(67)
<i>Pratifelis martini</i>	215345.72	(1)
<i>Pratilepus kansasensis</i>	972.63	(1)
<i>Premnoides douglassi</i>	2.80	PBDB + regression
<i>Presbymys lophatus</i>	3.30	PBDB + regression
<i>Presbytherium rhodorugatus</i>	46.40	PBDB + regression
<i>Princetonia yalensis</i>	21.80	PBDB + regression
<i>Probassariscus matthewi</i>	7.80	PBDB + regression
<i>Probathyopsis harrisorum</i>	162.70	PBDB + regression
<i>Probathyopsis praecursor</i>	187.80	PBDB + regression
<i>Problastomyx primus</i>	14913.17	(1)
<i>Procamelus grandis</i>	400312.19	(1)
<i>Procamelus occidentalis</i>	189094.09	(1)
<i>Procerberus formicarum</i>	4.60	PBDB + regression
<i>Prochetodon cavus</i>	7.00	PBDB + regression
<i>Prochetodon foxi</i>	6.80	PBDB + regression
<i>Prochetodon speirsae</i>	10.10	PBDB
<i>Prochetodon taxus</i>	10.90	PBDB + regression
<i>Procranioceras skinneri</i>	169396.94	(1)
<i>Procynodictis progressus</i>	9.00	PBDB + regression
<i>Procyon lotor</i>	5814.00	PBDB
<i>Procyon rexroadensis</i>	12.46	PBDB + regression
<i>Prodiacodon concordiaricensis</i>	3.50	PBDB + regression
<i>Prodiacodon crustulum</i>	10.01	(68)
<i>Prodiacodon furor</i>	4.58	(36)
<i>Prodiacodon puercensis</i>	9.66	(69)
<i>Prodiacodon tauricinerei</i>	5.20	PBDB + regression
<i>Prodipodomys centralis</i>	1.65	(70)
<i>Prodipodomys idahoensis</i>	22.42	(1)
<i>Prodipodomys kansensis</i>	12.81	(1)
<i>Prodipodomys timoteoensis</i>	1.60	PBDB + regression
<i>Prohesperocyon wilsoni</i>	9.10	PBDB + regression
<i>Proheteromys fediti</i>	1.50	PBDB + regression
<i>Proheteromys floridanus</i>	5.37	(1)
<i>Proheteromys gremmelsi</i>	1.93	(70)
<i>Proheteromys ironcloudi</i>	10.59	(1)
<i>Proheteromys maximus</i>	87.36	(1)
<i>Proheteromys nebraskensis</i>	1.66	PBDB
<i>Proheteromys sulculus</i>	1.40	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Proheteromys toledoensis</i>	59.15	(1)
<i>Prolapsus junctionis</i>	3.30	PBDB + regression
<i>Prolapsus sibilatoris</i>	5.50	PBDB + regression
<i>Prolimnocyon antiquus</i>	19.90	PBDB + regression
<i>Prolimnocyon atavus</i>	26.70	PBDB + regression
<i>Prolimnocyon haematus</i>	16.80	PBDB + regression
<i>Promartes darbyi</i>	97.00	(71)
<i>Promartes gemmarosae</i>	86.00	(71)
<i>Promartes lepidus</i>	46.41	(72)
<i>Promioclænus acolytus</i>	10.00	PBDB + regression
<i>Promioclænus pipiringosi</i>	13.90	PBDB + regression
<i>Promioclænus thnetus</i>	7.80	(73)
<i>Promylagaulus riggsi</i>	85.63	(1)
<i>Pronodens silberlingi</i>	22247.84	(1)
<i>Pronothodectes gaoi</i>	7.70	PBDB + regression
<i>Pronothodectes jepi</i>	7.50	PBDB + regression
<i>Pronothodectes matthewi</i>	5.60	PBDB + regression
<i>Pronotolagus apachensis</i>	445.86	(1)
<i>Pronotolagus nevadensis</i>	60.34	(1)
<i>Pronotolagus whitei</i>	1436.55	(1)
<i>Proscalops miocaenus</i>	2.70	PBDB + regression
<i>Proscalops secundus</i>	72.97	(1)
<i>Proscalops tertius</i>	96.54	(1)
<i>Prosciurus magnus</i>	4.10	PBDB + regression
<i>Prosciurus parvus</i>	3.20	PBDB + regression
<i>Prosciurus relictus</i>	3.10	PBDB + regression
<i>Prosigmodon chihuahuensis</i>	3.30	PBDB + regression
<i>Prosigmodon ferrusquiae</i>	2.63	PBDB
<i>Prosigmodon holocuspis</i>	113.30	(1)
<i>Prosigmodon oroscoi</i>	1.90	PBDB + regression
<i>Prosomys mimus</i>	2.10	PBDB + regression
<i>Prosthenrops niobrarensis</i>	43044.94	(1)
<i>Prosthenrops serus</i>	53637.30	(1)
<i>Prosthenrops xiphodonticus</i>	23860.99	(1)
<i>Prosynthetoceras francisi</i>	134591.56	(1)
<i>Prosynthetoceras orthrionanus</i>	40134.84	(1)
<i>Protadjidaumo pauli</i>	1.50	PBDB + regression
<i>Protadjidaumo typus</i>	1.20	PBDB + regression
<i>Protapirus obliquidens</i>	440.00	(74)
<i>Protapirus simplex</i>	253.90	PBDB + regression
<i>Protepycyon raki</i>	23623.56	(1)
<i>Proterix bicuspis</i>	46.00	(75)
<i>Proterix loomisi</i>	16.20	PBDB + regression
<i>Proterixoides davisii</i>	10.10	PBDB + regression
<i>Prothryptacodon albertensis</i>	10.70	PBDB + regression
<i>Prothryptacodon furens</i>	19.20	PBDB + regression
<i>Prothryptacodon hilli</i>	23.50	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Protictis haydenianus</i>	7.43	PBDB + regression
<i>Protictis microlestes</i>	13.63	PBDB
<i>Protictis minor</i>	6.30	PBDB + regression
<i>Protictis paralus</i>	4.10	PBDB + regression
<i>Protictis paulus</i>	8.40	PBDB
<i>Protictis simpsoni</i>	8.60	PBDB + regression
<i>Protitanops curryi</i>	142477.00	(4)
<i>Protitanotherium superbum</i>	1522.00	PBDB + regression
<i>Protoceras celer</i>	172.20	PBDB + regression
<i>Protoceras skinneri</i>	272.16	PBDB
<i>Protohippus gidleyi</i>	164390.50	(1)
<i>Protohippus perditus</i>	135944.23	(1)
<i>Protohippus supremus</i>	167711.41	(1)
<i>Protohippus vetus</i>	191.40	PBDB
<i>Protolabis coartatus</i>	110194.25	(1)
<i>Protolabis heterodontus</i>	219695.99	(1)
<i>Protomarcus optatus</i>	11271.13	(1)
<i>Protoreodon pacificus</i>	82.10	PBDB + regression
<i>Protoreodon parvus</i>	80.30	PBDB + regression
<i>Protoreodon pearcei</i>	88.30	PBDB + regression
<i>Protoreodon petersoni</i>	55.40	PBDB + regression
<i>Protoreodon pumilus</i>	108.10	PBDB + regression
<i>Protoreodon walshi</i>	118.90	PBDB + regression
<i>Protorohippus ventriculus</i>	47.20	PBDB + regression
<i>Protosciurus mengi</i>	8.70	PBDB + regression
<i>Protosciurus tecuyensis</i>	478.19	(1)
<i>Protoselene griffithsii</i>	21.20	PBDB + regression
<i>Protoselene opisthacanthus</i>	21.80	PBDB + regression
<i>Protospermophilus kelloggi</i>	202.35	(1)
<i>Protospermophilus malheurensis</i>	103.54	(1)
<i>Protospermophilus oregonensis</i>	450.34	(1)
<i>Protospermophilus quatalensis</i>	273.14	(1)
<i>Protospermophilus vortmanni</i>	230.44	(1)
<i>Prototomus deimos</i>	11.20	PBDB + regression
<i>Prototomus martis</i>	32.70	PBDB + regression
<i>Prototomus phobos</i>	28.00	PBDB + regression
<i>Prototomus robustus</i>	26.50	PBDB + regression
<i>Prototomus secundarius</i>	20.50	PBDB + regression
<i>Protungulatum donnae</i>	11.70	PBDB + regression
<i>Protylopus annectens</i>	47.30	PBDB + regression
<i>Protylopus pearsonensis</i>	88.60	PBDB + regression
<i>Protylopus petersoni</i>	54.70	PBDB + regression
<i>Protylopus robustus</i>	53.10	PBDB + regression
<i>Protylopus stocki</i>	48.60	PBDB + regression
<i>Proviverrroides piercei</i>	48.50	PBDB + regression
<i>Psalidocyon mariana</i>	8777.97	(1)
<i>Pseudaelurus aeluroides</i>	31571.18	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Pseudaelurus intrepidus</i>	40945.61	(1)
<i>Pseudaelurus marshi</i>	33189.87	(1)
<i>Pseudaelurus stouti</i>	5767.53	(1)
<i>Pseudhipparion curtivallum</i>	58104.59	(1)
<i>Pseudhipparion gratum</i>	108012.26	(1)
<i>Pseudhipparion hessei</i>	75357.60	(1)
<i>Pseudhipparion retrusum</i>	86681.87	(1)
<i>Pseudhipparion simpsoni</i>	48050.12	(1)
<i>Pseudhipparion skinneri</i>	54176.36	(1)
<i>Pseudoblastomeryx advena</i>	10097.06	(1)
<i>Pseudoceras skinneri</i>	10938.02	(1)
<i>Pseudocylindrodon lateriviae</i>	4.00	PBDB + regression
<i>Pseudocylindrodon medius</i>	2.50	PBDB + regression
<i>Pseudocylindrodon neglectus</i>	3.70	PBDB + regression
<i>Pseudocylindrodon pintoensis</i>	5.78	MIOMAP
<i>Pseudodiplacodon progressum</i>	888.00	PBDB
<i>Pseudolabis dakotensis</i>	59874.14	(1)
<i>Pseudoparablastomeryx francescita</i>	22.80	PBDB
<i>Pseudoparablastomeryx scotti</i>	5884.05	(1)
<i>Pseudoprotoceras longinaris</i>	83.40	PBDB + regression
<i>Pseudoprotoceras minor</i>	57.60	PBDB + regression
<i>Pseudotheridomys cuyamensis</i>	12.43	(1)
<i>Pseudotheridomys hesperus</i>	14.15	(1)
<i>Pseudotheridomys pagei</i>	8.17	(1)
<i>Pseudotomus californicus</i>	30.40	PBDB + regression
<i>Pseudotomus eugenei</i>	65.90	PBDB + regression
<i>Pseudotomus hians</i>	90.00	PBDB
<i>Pseudotomus horribilis</i>	27.02	(76)
<i>Pseudotomus johanniculi</i>	60.20	PBDB + regression
<i>Pseudotomus littoralis</i>	24.50	PBDB + regression
<i>Pseudotomus petersoni</i>	32.90	(76)
<i>Pseudotomus robustus</i>	32.20	PBDB + regression
<i>Pseudotrimylus mawbyi</i>	7.30	PBDB + regression
<i>Ptilodus fractus</i>	105.00	(7)
<i>Ptilodus gnomus</i>	4.30	PBDB + regression
<i>Ptilodus kummae</i>	6.90	PBDB + regression
<i>Ptilodus mediaevus</i>	8.60	PBDB + regression
<i>Ptilodus montanus</i>	9.50	PBDB + regression
<i>Ptilodus wyomingensis</i>	147.00	(7)
<i>Puercolestes simpsoni</i>	10.60	PBDB + regression
<i>Puma concolor</i>	48009.00	PBDB
<i>Puma lacustris</i>	15.30	PBDB + regression
<i>Pyrocyon dioctetus</i>	22.70	PBDB + regression
<i>Quadratomus grandis</i>	19.00	PBDB + regression
<i>Quadratomus grossus</i>	34.70	PBDB + regression
<i>Quadrodens wilsoni</i>	46.06	(1)
<i>Rakomeryx sinclairi</i>	111301.72	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Rapamys fricki</i>	15.00	PBDB + regression
<i>Raphictis gausion</i>	3.70	PBDB + regression
<i>Reithrodontomys galushai</i>	1.10	PBDB + regression
<i>Reithrodontomys rexroadensis</i>	0.90	PBDB + regression
<i>Reithrodontomys wetmorei</i>	9.03	(1)
<i>Reithroparamys debequensis</i>	5.70	PBDB + regression
<i>Reithroparamys delicatissimus</i>	9.40	PBDB + regression
<i>Reithroparamys huerfanensis</i>	7.90	PBDB + regression
<i>Reithroparamys sciuroides</i>	9.66	(77)
<i>Repomys arizonensis</i>	2.80	PBDB + regression
<i>Repomys gustelyi</i>	81.45	(1)
<i>Repomys maxumi</i>	122.73	(1)
<i>Repomys panacaensis</i>	38.47	(1)
<i>Rhizocyon oregonensis</i>	3361.02	(1)
<i>Rhynchotherium falconeri</i>	10697.20	PBDB + regression
<i>Russellagus vonhofi</i>	214.86	(1)
<i>Sanctimus falkenbachi</i>	151.41	(1)
<i>Sanctimus stouti</i>	120.30	(1)
<i>Sanctimus stuartae</i>	100.48	(1)
<i>Satherium piscinarium</i>	934.49	(1)
<i>Saxonella naylori</i>	3.00	PBDB + regression
<i>Scalopoides isodens</i>	32.14	(1)
<i>Scalopoides ripafodiator</i>	27.39	(1)
<i>Scalopus aquaticus</i>	39.60	PBDB
<i>Scapanoscapter simplicidens</i>	58.56	(1)
<i>Scapanus hagermanensis</i>	7.00	(4)
<i>Scapanus latimanus</i>	55.00	PBDB
<i>Scapanus proceridens</i>	65.37	(1)
<i>Scapanus shultzii</i>	97.00	(4)
<i>Scapanus townsendii</i>	8.59	(11)
<i>Scaphohippus sumani</i>	171.00	PBDB
<i>Scenopagus curtidens</i>	2.60	PBDB + regression
<i>Scenopagus edenensis</i>	4.80	PBDB + regression
<i>Scenopagus priscus</i>	2.00	PBDB + regression
<i>Schaubeamys galbreathi</i>	1.57	(78)
<i>Schaubeamys grangeri</i>	1.60	PBDB + regression
<i>Schaubeamys sabrae</i>	1.48	(39)
<i>Schizodontomys amnicolus</i>	111.05	(1)
<i>Schizodontomys greeni</i>	94.00	(4)
<i>Schizodontomys harkseni</i>	105.64	(1)
<i>Sciuravus bridgeri</i>	2.40	PBDB + regression
<i>Sciuravus nitidus</i>	5.30	PBDB + regression
<i>Sciuravus popi</i>	7.90	PBDB + regression
<i>Sciuravus powayensis</i>	3.70	PBDB + regression
<i>Sciuravus wilsoni</i>	3.60	PBDB + regression
<i>Sciurion campestre</i>	1.90	PBDB + regression
<i>Sciurus carolinensis</i>	518.00	PBDB

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Sciurus olsoni</i>	1.71	PBDB
<i>Scottimus exiguus</i>	3.21	(31)
<i>Scottimus longiquus</i>	111.05	(1)
<i>Scottimus lophatus</i>	4.65	PBDB
<i>Scottimus viduus</i>	2.50	PBDB + regression
<i>Selenaletes scopaeus</i>	32.10	PBDB + regression
<i>Serbelodon barboureensis</i>	910.00	(45)
<i>Sespedectes singularis</i>	2.70	PBDB + regression
<i>Sespedectes stocki</i>	2.40	PBDB + regression
<i>Sespemys thurstoni</i>	290.03	(1)
<i>Sespia californica</i>	3604.72	(1)
<i>Sespia nitida</i>	91.00	(79)
<i>Shoshonius bowni</i>	5.60	PBDB + regression
<i>Shoshonius cooperi</i>	3.40	PBDB + regression
<i>Sifrhippus aemulor</i>	45.36	(80)
<i>Sifrhippus grangeri</i>	40.20	PBDB + regression
<i>Sifrhippus sandrae</i>	38.00	PBDB + regression
<i>Sigmodon curtisi</i>	3.80	PBDB + regression
<i>Sigmodon hudspethensis</i>	3.20	PBDB + regression
<i>Sigmodon minor</i>	52.98	(1)
<i>Simidectes magnus</i>	9.10	PBDB + regression
<i>Simidectes medius</i>	8.30	PBDB + regression
<i>Simidectes merriami</i>	11.10	PBDB + regression
<i>Similisciurus maxwelli</i>	259.82	(1)
<i>Simimeryx hudsoni</i>	20.50	PBDB + regression
<i>Simimeryx minutus</i>	11.50	PBDB + regression
<i>Simimys landeri</i>	2.30	PBDB + regression
<i>Simimys simplex</i>	1.30	PBDB + regression
<i>Simocyon primigenius</i>	70000.00	NOW
<i>Simojovelhyus pocitosense</i>	57.20	(38)
<i>Simpsonictis pegus</i>	3.62	PBDB + regression
<i>Simpsonictis tenuis</i>	2.90	PBDB + regression
<i>Simpsonlemur citatus</i>	171.00	(22)
<i>Simpsonlemur jepseni</i>	121.00	(22)
<i>Simpsonodus chacensis</i>	18.50	PBDB + regression
<i>Sinclairella dakotensis</i>	7.20	PBDB + regression
<i>Sinopa major</i>	49.30	PBDB + regression
<i>Sinopa rapax</i>	31.30	PBDB + regression
<i>Smilodectes gracilis</i>	16.60	PBDB + regression
<i>Smilodectes mcgrewi</i>	18.10	PBDB + regression
<i>Smilodectes sororis</i>	15.70	PBDB + regression
<i>Smilodon gracilis</i>	22.70	PBDB + regression
<i>Sminthosinus bowleri</i>	100.48	(1)
<i>Sorex cinereus</i>	3.80	PBDB
<i>Sorex edwardsi</i>	1.13	PBDB
<i>Sorex hagermanensis</i>	1.20	PBDB + regression
<i>Sorex meltoni</i>	3.46	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Sorex palustris</i>	3.09	(11)
<i>Sorex powersi</i>	7.77	(1)
<i>Sorex rexroadensis</i>	8.00	(4)
<i>Sorex yatkolai</i>	0.92	PBDB
<i>Spermophilus argonautus</i>	131.63	(1)
<i>Spermophilus bensoni</i>	184.93	(1)
<i>Spermophilus boothi</i>	9.83	(45)
<i>Spermophilus cragini</i>	578.25	(1)
<i>Spermophilus dotti</i>	270.43	(1)
<i>Spermophilus fricki</i>	6.38	(9)
<i>Spermophilus gidleyi</i>	700.00	(4)
<i>Spermophilus howelli</i>	139.77	(1)
<i>Spermophilus jerae</i>	87.36	(1)
<i>Spermophilus matachicensis</i>	6.20	PBDB + regression
<i>Spermophilus matthewi</i>	8.68	(81)
<i>Spermophilus meadensis</i>	100.48	(1)
<i>Spermophilus rexroadensis</i>	8.00	PBDB + regression
<i>Spermophilus russelli</i>	166.00	(4)
<i>Spermophilus shotwelli</i>	204.00	(4)
<i>Spermophilus tephirus</i>	89.12	(1)
<i>Spermophilus wellingtonensis</i>	295.89	(1)
<i>Spermophilus wilsoni</i>	247.15	(1)
<i>Sphacorhysis burntforkensis</i>	2.80	PBDB + regression
<i>Sphenophalos nevadanus</i>	63.00	PBDB
<i>Spilogale microdens</i>	6.30	(60)
<i>Spilogale putorius</i>	12.59	(11)
<i>Spilogale rexroadi</i>	5.60	PBDB + regression
<i>Stegomastodon mirificus</i>	7985.90	PBDB + regression
<i>Steinius annectens</i>	397.75	(82)
<i>Steinius vespertinus</i>	5.10	PBDB + regression
<i>Stelocyon arctylus</i>	7.50	PBDB + regression
<i>Stenoechinus tantalus</i>	48.42	(1)
<i>Stenomylus gracilis</i>	44801.64	(1)
<i>Stenomylus hitchcocki</i>	38948.67	(1)
<i>Stenomylus taylori</i>	192.72	PBDB
<i>Sthenictis dolichops</i>	665.14	(1)
<i>Sthenictis junturensis</i>	330.30	(1)
<i>Stibarus montanus</i>	17.60	PBDB + regression
<i>Stibarus obtusilobus</i>	19.70	PBDB + regression
<i>Stibarus quadricuspis</i>	24.40	PBDB + regression
<i>Stockia powayensis</i>	6.00	PBDB + regression
<i>Stratimus strobeli</i>	20.09	(1)
<i>Strigorhysis bridgerensis</i>	4.40	PBDB + regression
<i>Strigorhysis huferfanensis</i>	6.30	PBDB + regression
<i>Stygimys gratus</i>	5.30	PBDB + regression
<i>Stygimys jepseni</i>	84.00	(7)
<i>Stygimys kuszmauli</i>	8.30	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Stylinodon mirus</i>	135.50	PBDB + regression
<i>Subdromomyx antilopinus</i>	59874.14	(1)
<i>Subhyracodon mitis</i>	455.00	(83)
<i>Subhyracodon occidentalis</i>	580.10	PBDB + regression
<i>Sunkahetanka geringensis</i>	11158.98	(1)
<i>Swainodelphys cifellii</i>	2.14	PBDB
<i>Symmetrodontomys simplicidens</i>	26.84	(1)
<i>Syndioceras cooki</i>	73865.41	(1)
<i>Tachylagus gawneae</i>	5.70	PBDB + regression
<i>Taeniolabis taoensis</i>	173.80	PBDB + regression
<i>Talpavoides dartoni</i>	1.20	PBDB + regression
<i>Talpavus conjunctus</i>	3.00	PBDB + regression
<i>Talpavus duplus</i>	1.80	PBDB + regression
<i>Talpavus nitidus</i>	1.40	PBDB + regression
<i>Tamias ateles</i>	2.10	PBDB + regression
<i>Tanymycter brachydontus</i>	102744.44	(1)
<i>Tapiravus validus</i>	64860.88	(1)
<i>Tapirus simpsoni</i>	369534.73	(1)
<i>Tapochoerus egressus</i>	35.70	PBDB + regression
<i>Tapochoerus mcmillini</i>	21.10	PBDB + regression
<i>Tapocyon dawsonae</i>	77.90	PBDB + regression
<i>Tapocyon robustus</i>	87.70	PBDB + regression
<i>Tardontia nevadans</i>	157.59	(1)
<i>Tardontia occidentale</i>	5.60	PBDB + regression
<i>Tarka stylifera</i>	34.10	PBDB + regression
<i>Tatmanius szalayi</i>	3.04	(84)
<i>Taxidea mexicana</i>	12.80	(85)
<i>Taxidea taxus</i>	47.09	(11)
<i>Tayassu protervus</i>	98.60	PBDB
<i>Teilhardina americana</i>	3.70	PBDB + regression
<i>Teilhardina crassidens</i>	3.40	PBDB + regression
<i>Teleoceras meridianum</i>	2022813.66	(1)
<i>Teletaceras mortivallis</i>	155.00	PBDB + regression
<i>Telmatherium altidens</i>	1236.90	PBDB + regression
<i>Telmatherium cultridens</i>	560.00	PBDB + regression
<i>Telmatherium manteoceras</i>	468.00	PBDB + regression
<i>Temnocyon altigenis</i>	32532.67	(1)
<i>Temnocyon percussor</i>	68871.66	(1)
<i>Tenuodomys bodei</i>	43.38	(1)
<i>Tenuodomys macdonaldi</i>	79.84	(1)
<i>Tephrocyon rurestris</i>	13095.19	(1)
<i>Tetonius ambiguus</i>	4.43	PBDB
<i>Tetonius matthewi</i>	4.80	PBDB + regression
<i>Tetonius mckennai</i>	3.40	PBDB + regression
<i>Tetraclaenodon puercensis</i>	55.60	PBDB + regression
<i>Tetrapassalus mckennai</i>	0.90	PBDB
<i>Texomys ritchiei</i>	97.51	(1)

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Thinobadistes segnis</i>	645890.00	(33)
<i>Thinocyon velox</i>	23.30	PBDB + regression
<i>Thinohyus latus</i>	101400.00	(4)
<i>Thisbemys corrugatus</i>	14.30	PBDB + regression
<i>Thisbemys elachistos</i>	4.80	PBDB + regression
<i>Thisbemys perditus</i>	10.80	PBDB + regression
<i>Thisbemys uintensis</i>	20.20	PBDB + regression
<i>Thomomys bottae</i>	7.85	(11)
<i>Thomomys carsonensis</i>	2.00	PBDB + regression
<i>Thomomys gidleyi</i>	37.34	(1)
<i>Thryptacodon antiquus</i>	35.30	PBDB + regression
<i>Thryptacodon australis</i>	28.30	PBDB + regression
<i>Thryptacodon orthogonius</i>	20.60	PBDB + regression
<i>Thryptacodon pseudarctos</i>	43.70	PBDB + regression
<i>Thylacaelurus campester</i>	2.60	PBDB + regression
<i>Thylacaelurus montanus</i>	3.60	PBDB + regression
<i>Thylacodon pusillus</i>	3.10	PBDB + regression
<i>Ticholeptus zygomaticus</i>	106937.52	(1)
<i>Tillodon fodiens</i>	266.10	PBDB + regression
<i>Tillomys senex</i>	3.60	PBDB + regression
<i>Tinimomys graybulliensis</i>	1.40	PBDB + regression
<i>Tinimomys tribos</i>	0.93	(86)
<i>Titanoides gidleyi</i>	260.10	PBDB + regression
<i>Titanoides nanus</i>	223.10	PBDB + regression
<i>Titanoides primaevus</i>	335.40	PBDB + regression
<i>Tomarctus brevirostris</i>	17500.77	(1)
<i>Tomarctus hippophaga</i>	13766.59	(1)
<i>Torrejonia sirokyi</i>	10.40	PBDB + regression
<i>Toxotherium hunteri</i>	157.70	PBDB + regression
<i>Tregosorex holmani</i>	26.84	(1)
<i>Tremarctos floridanus</i>	176.97	(11)
<i>Trigenicus profectus</i>	73.20	PBDB + regression
<i>Trigonias osborni</i>	542.90	PBDB + regression
<i>Trigonias yoderensis</i>	316.90	PBDB + regression
<i>Trigonictis cookii</i>	11.40	PBDB + regression
<i>Trigonictis macrodon</i>	419.89	(1)
<i>Triisodon quivirensis</i>	16.50	PBDB + regression
<i>Trilaccogaulus ovatus</i>	103.54	(1)
<i>Triplopus cubitalis</i>	82.00	PBDB + regression
<i>Triplopus implicatus</i>	124.90	PBDB + regression
<i>Triplopus obliquidens</i>	161.30	PBDB + regression
<i>Triplopus rhinocerinus</i>	154.00	PBDB
<i>Triplopus woodi</i>	131.13	PBDB
<i>Tritemnodon agilis</i>	10780.00	(87)
<i>Tritemnodon strenuus</i>	38.00	PBDB + regression
<i>Trogolemur amplior</i>	3.50	PBDB + regression
<i>Trogolemur myodes</i>	2.50	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
<i>Trogonys rupinimenthae</i>	12.55	(1)
<i>Trogosus castoridens</i>	178.20	PBDB + regression
<i>Trogosus grangeri</i>	242.10	PBDB + regression
<i>Trogosus latidens</i>	373.10	PBDB + regression
<i>Tubulodon atopum</i>	6.50	PBDB + regression
<i>Tubulodon taylori</i>	4.94	PBDB
<i>Tuscalomys medius</i>	3.60	PBDB
<i>Tuscalomys minor</i>	2.50	PBDB
<i>Tylocephalonyx skinneri</i>	2018.54	PBDB
<i>Uintaceras radinskyi</i>	492.30	PBDB + regression
<i>Uintacyon asodes</i>	43.80	PBDB + regression
<i>Uintacyon massetericus</i>	30.80	PBDB + regression
<i>Uintacyon rudis</i>	22.90	PBDB + regression
<i>Uintanius ameghini</i>	3.10	PBDB + regression
<i>Uintanius rutherfordi</i>	3.20	PBDB + regression
<i>Uintasorex montezumicus</i>	0.60	PBDB + regression
<i>Uintasorex parvulus</i>	1.00	PBDB + regression
<i>Uintatherium anceps</i>	33.50	PBDB + regression
<i>Untermannerix copiosus</i>	121.51	(1)
<i>Unuchinia dysmathes</i>	6.37	PBDB
<i>Uriscus californicus</i>	4.60	PBDB + regression
<i>Urocyon cinereoargenteus</i>	3829.00	PBDB
<i>Ursavus brevirhinus</i>	80000.00	NOW
<i>Ursavus pawniensis</i>	61697.58	(1)
<i>Ursavus primaevus</i>	90000.00	NOW
<i>Ursus abstrusus</i>	20.70	PBDB + regression
<i>Ursus americanus</i>	93431.00	PBDB
<i>Utahia carina</i>	1.80	PBDB + regression
<i>Utahia kayi</i>	2.70	PBDB + regression
<i>Valenia wilsoni</i>	8.10	PBDB + regression
<i>Vassacyon promicronodon</i>	41.10	PBDB + regression
<i>Viverravus acutus</i>	4.55	PBDB + regression
<i>Viverravus gracilis</i>	5.50	PBDB + regression
<i>Viverravus laytoni</i>	3.60	PBDB + regression
<i>Viverravus lutosus</i>	4.90	PBDB + regression
<i>Viverravus minutus</i>	4.90	PBDB + regression
<i>Viverravus politus</i>	5.83	PBDB + regression
<i>Viverravus rosei</i>	3.06	PBDB + regression
<i>Viverravus sicarius</i>	6.80	PBDB + regression
<i>Vulpavus australis</i>	22.10	PBDB + regression
<i>Vulpavus palustris</i>	28.80	PBDB + regression
<i>Vulpavus profectus</i>	100.00	(88)
<i>Vulpes stenognathus</i>	7331.97	(1)
<i>Vulpes velox</i>	28.28	(11)
<i>Washakius insignis</i>	4.90	PBDB + regression
<i>Washakius izetti</i>	3.90	PBDB + regression
<i>Washakius woodringi</i>	3.10	PBDB + regression

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**Dataset S1 – continued from previous page**

Species	Mass (g)	Source
Wilsoneumys planidens	51.70	PBDB
Worlandia inusitata	3.90	PBDB + regression
Wyolestes apeles	6.80	PBDB + regression
Wyolestes iglesius	6.33	PBDB + regression
Wyonycteris chalix	1.30	PBDB + regression
Xenicohippus craspedotum	10895.00	(4)
Xenicohippus grangeri	41.80	PBDB + regression
Ysengrinia americana	110194.25	(1)
Yumaceras figginsi	293607.76	(1)
Yumaceras hamiltoni	247706.54	(1)
Yumaceras ruminalis	314896.72	(1)
Zapus burti	21.33	(1)
Zapus rinker	1.90	PBDB + regression
Zapus sandersi	18.92	(1)
Zemiodontomys burkei	4.40	PBDB + regression
Zetamys nebraskensis	60.34	(1)

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