Supporting Information

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SI Methods

Database. We compiled a global dataset of 4,420 species of mammals, excluding cetaceans and species listed under criterion B of the IUCN Red List (see later discussion for more details). The dataset includes taxonomy and a number of ecological and intrinsic characteristics of each species, including body mass ($\log_{10}$ g), mass-specific production rate (1, 2), habitat mode (aquatic, arboreal, fossorial, marine, marine births on land, terrestrial, or volant), trophic category (carnivore, herbivore, or omnivore), activity period (nocturnal, diurnal, or both), geographic range size ($\log_{10}$ km^2), home range size ($\log_{10}$ km^2), population density ($\log_{10}$ number of individuals/km^2), sociality (social or not), average group size ($\log_{10}$ number of individuals), and type of landmass (range limited to islands, found on both island and continent, or continental). Note that geographic range was based on the historic range, because the true current range is not known for most species (3, 4). These ecological characteristics were chosen using existing knowledge from other extinction risk studies (5–9) and on the basis of data availability. The IUCN Red List status also was recorded for each species. We used the IUCN 2007 Red List and updated it with the data currently made available for the IUCN 2008 Red List, using "Table 7: Species changing IUCN Red List status" (10).

The IUCN lists threatened (vulnerable or higher) mammal species under 4 criteria (11): (*i*) Criterion A: species listed because of recent population declines; (*ii*) Criterion B: species listed simply because of limited geographic occurrence, regardless of population status; (*iii*) Criterion C: species listed because of low abundance ($<$ 2500 individuals) resulting from ongoing population declines; and (*iv*) Criterion D: species listed because of extremely low abundance ($<$ 250 individuals). To avoid potential circularity in models evaluating extinction risk, similar studies have restricted their analysis of threatened species to those listed only under criterion A, because these species reflect recent population declines (7, 9, 11); others have adopted a less restrictive approach, excluding only the species listed under criterion B because of their restricted geographic ranges (12). In this paper, we follow the latter approach and exclude only the 362 species listed under criterion B to avoid potential circularity when using geographic range as a predictor. We included species listed under criteria C and D because our data are historic estimates of geographic range and population density (the 2 key components of species abundance) and thus are not circular with the IUCN listing criteria. We necessarily excluded 341 IUCN data-deficient species from the main dataset but predicted their threat status later using our model.

Sources. Data were compiled from the following sources:

(*a*) Smith FA, et al. MOM (2003) *Ecology* 84:3402. (MOM v.6, an updated version of Smith, et al. 2003).

(*b*) Kelt DA, Van Vuren DH (2001) The ecology and macroecology of mammalian home range area. *Am Nat* 157:637–645. (Dataset was not made publicly available and was kindly provided by the authors.)

(*c*) Damuth MJ (1981) Population density and body size in mammals. *Nature* 290:699–700. (Dataset was not made publicly available and was kindly provided by the author.)

(*d*) Ceballos G, Ehrlich PR (2002) Mammal population losses and the extinction crisis. *Science* 296:904–907.

(e) Ceballos G, Ehrlich PR, Soberon J, Salazar I, Fay JP (2005) Global mammal conservation: What must we manage? *Science* 309:603–607.

(*f*) Pantheria. www.pantheria.org Accessed May 13, 2008.

(*g*) Ernest SKM (2003) Life history characteristics of placental nonvolant mammals. *Ecology* 84:3402–3402.

(*h*) Jones KE, Purvis A, Gittleman JL (2003) Biological correlates of extinction risk in bats. *Am Nat* 161:601–614.

(*i*) Nowak RM (1991) *Walker's Mammals of the World* (The John Hopkin's Univ Press, Baltimore), 6th Ed.

(*j*) Dickman C, Woodford Ganf R (2007) *A Fragile Balance: The Extraordinary Story of Australian Marsupials* (Univ of Chicago Press, Chicago).

(*k*) Wilson DE, Reeder DM (2005), *Mammal Species of the World. A Taxonomic and Geographic Reference* (The Johns Hopkins Univ Press, Baltimore 2005) 3rd Ed. (Available at: http://www.bucknell.edu/msw3/).

(*l*) Primates. (Available at: http://pin.primate.wisc.edu/). Accessed May 13, 2008.

(*m*) Australian wildlife. (Available at: http://www.australian-wildlife.org/). Accessed May 13, 2008.

(*n*) Lioncrusher's Domain. (Available at: http://www.lioncrusher.com/animalinfo.asp). Accessed May 13, 2008.

(*o*) North American Mammals. (Available at: http://www.mnh.si.edu/mna/search_name.cfm.)

(*p*) Seal Conservation. (Available at: http://www.pinnipeds.org/main.htm).

(*q*) Bat Conservation International. (Available at: http://www.batcon.org). Accessed May 13, 2008.

(*r*) Afrotheria Specialist Group. (Available at: http://research.calacademy.org/research/bmammals/afrotheria/ASG.html). Accessed May 13, 2008.

(*s*) MacDonald D, ed (2006) *Encyclopedia of Mammals* (Oxford University Press, Oxford).

(*t*) Mammalian Species. (Available at: http://www.science.smith.edu/departments/Biology/VHAYSSEN/msi/default.html.)

(*u*) Animal Diversity Web. (Available at: http://animaldiversity.ummz.umich.edu/site/index.html.)

(*v*) AnAge Database. (Available at: http://genomics.senescence.info/species/).

(*w*) Wikipedia. (Available at: http://en.wikipedia.org).

(*x*) The Ultimate Ungulate. (Available at: http://www.ultimateungulate.com/).

(*y*) MarineBio. (Available at: www.MarineBio.org.)

(*z*) The Beaked Whale Resource. (Available at: http://www.beakedwhaleresource.com/).

(*aa*) International Union for the Conservation of Nature 2007 Red List of Threatened Species (IUCN/SSC Red List Program, Geneva, Switzerland).

(*bb*) IUCN 2008 Red List of Threatened Species, summary statistics for globally threatened species, Table 7, Species changing IUCN Red List status. (Available at: http://www.iucnredlist.org/documents/2008RL_stats_table_7_v1223294385.pdf).

(*cc*) Cardillo M, et al. (2004) Human population density and extinction risk in the world's carnivores. *PLoS Biol* 2, 10.1371/journal.pbio.0020197.

(*dd*) Leonard WR, Robertson ML (1998) Comparative primate energetics and hominid evolution. *Am J Phys Anthropol* 102:265–281.

Decision-Tree Modeling. Recently, decision trees have emerged as powerful tools for analyzing complex ecological datasets because they offer a useful alternative to traditional statistical techniques when modeling nonlinear data containing multiple interacting variables (13, 14). In studies in which predictive accuracy is the goal, including conservation planning (15, 16), modeling species distributions (17), and global change forecasting (18, 19), decision trees often exhibit greater power for explaining and predicting ecological patterns (20, 21).

A decision tree is a logical model represented as a binary tree that shows how the value of a response variable (here, extinction risk) can be predicted using the values of a set of predictor variables. A decision-tree model predicting a continuous response variable is known as a regression tree; a model predicting a categorical response is a classification tree. Here we used a dichotomous response variable: for our purposes, species listed as vulnerable or higher [vulnerable (VU), endangered (EN), critically endangered (CR), extinct in the wild (EW), extinct (EX)] by the IUCN were considered "threatened," and species of lower risk [least concern (LC), near threatened (NT)] were considered "nonthreatened," producing a classification tree. We chose this split for several reasons. (*i*) We did not treat the IUCN categories as continuous (9), because the differences between adjacent risk levels probably are not equivalent across the IUCN scale. (*ii*) We were less interested in predicting specific IUCN categories than in a generalized analysis of threat.

Classification Tree. We used the *rpart* package in R to build a classification tree model for global mammal threat status (22, 23). Missing data points were interpolated automatically based on the correlation matrix between predictor variables. The tree was built by repeatedly partitioning the dataset into a nested series of mutually exclusive groups, each group as homogenous as possible with respect to the response variable. Homogeneity (or node impurity) was measured by the Gini index (24). Branches or split points in the tree were determined by considering all possible splits of all predictor variables and selecting the split that resulted in the most homogenous subgroups for the data. The branching process continued until further subdivision no longer reduced the Gini index. Lower branches were pruned by 10-fold cross-validation to produce an optimal tree, balancing complexity (i.e., number of nodes) versus prediction accuracy (25). The smallest tree (11 terminal nodes) with an error rate within 1 standard error of the minimum-error tree was taken as the optimal tree (supporting information (SI) Fig. S2; 13). However, we also examined a larger tree (20 terminal nodes) within 1 standard error of the minimum-error tree to visualize interactions between predictors not included in the optimal tree. To ensure that all splits included in the expanded tree were meaningful, we performed standard χ^2 tests at each node following Duda et al. (26). The χ^2 test compared the number of species of each category (threatened or nonthreatened) placed in each daughter node versus a random split of the data at that node. All splits in the optimal and extended trees were significantly different from random ($P \leq 0.001$).

Random Forest. Under certain conditions, decision trees can be unstable, when small changes in the data can lead to significant changes in the variables used in the splits and the overall tree shape (21). To ensure the robustness of our results, we used a random forest, a modeling technique that combines the predictions of many independent decision-tree models to produce a more accurate classification (20). However, the random forest is a "black box" classification method (14) and does not produce a final tree for graphical interpretation of the model. Using a random forest of 500 trees (package *randomForest* in R; ref 27), we produced predictions of mammal threat status and determined the relative importance of the predictor variables. Predictor importance was measured by the decrease in classification accuracy resulting from the removal of the focal variable from the model (27). Pair-wise z-tests on the mean importance of each predictor across all 500 trees were used to identify significant differences between predictors.

Model Accuracy. Decision trees do not provide probability levels or confidence intervals associated with splits or predictions. However, we quantified overall model accuracy using the percentage of species correctly classified (PCC), specificity (percentage of nonthreatened species correctly classified), and sensitivity (percentage of threatened species correctly classified). We also used Cohen's kappa statistic (function *kappa2* in R package *irr*; ref 28) to measure the agreement between predicted and actual categorizations while correcting for agreement caused by chance (14). Both the classification tree and the random forest were highly accurate (PCC $\geq$ 80%) and statistically significant (Cohen's kappa, $P < 0.001$; Table S1) predictive models of threat status. We used the random forest for all subsequent predictions of threat status caused by the additional predictive power gained from the bootstrap procedure. Together, classification trees and random forests represent a promising approach to the study and prediction of extinction that is especially well suited to conservation problems (15, 16, 20, 21).

Misclassification Costs. Because wrongly classifying a species as unthreatened when it actually is threatened (false negatives) should be penalized in a conservation-oriented model, we repeated the analyses assigning different relative costs to the 2 types of misclassification (false positives and false negatives). However, the model was robust to the effect of increasing misclassification costs, even when the cost of a false negative was increased to 8 times the cost of a false positive; therefore only results from the equal costs model are shown.

Phylogenetic Relationships. Although extinction risk often is not phylogenetically random, and species traits are the product of shared evolutionary history, decision-tree models identify the observed relationships between predictors and extinction risk and are not designed to test evolutionary hypotheses. Because the decision-tree model does not rely on the assumption of independence between data points, there is no need to "correct" for phylogenetic relationships between species (15, 29).

Threat Predictions. An important outcome of the random forest model is the prediction of threat for each species. These predictions were used to identify species that share many of the characteristics of threatened species but currently were not considered threatened by the IUCN (false positives, yellow in Figs. 3 and 4). The model also identified some species (false negatives, cyan in Figs. 3 and 4) as not threatened because their ecologies were not generally associated with high extinction risk. For these species, extinction risk must be related to factors other than the ecological predictors in the model. Finally, using the species-level predictive power of the random forest model, we predicted the threat status for 341 data-deficient species. We also were able to revise our predictions for 67 false-negative species after updating their geographic range data from historical (before 1900) to current estimates of geographic range. This exercise improved our understanding of how reduction in geographic range impacts species' extinction risk.

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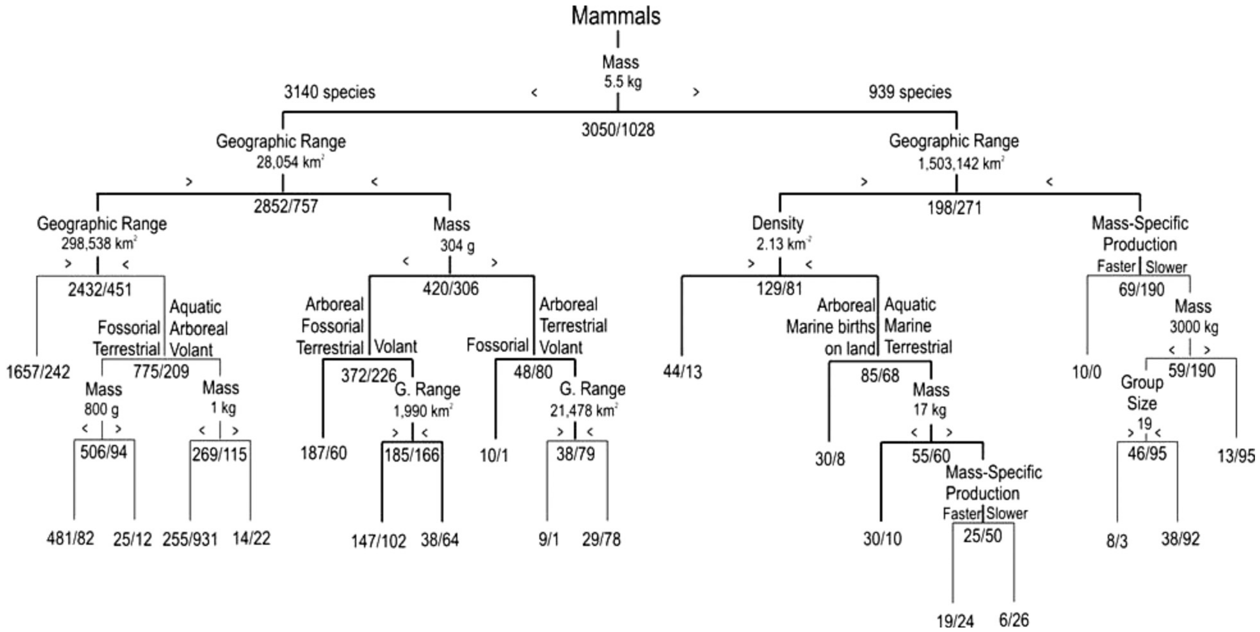

Fig. S1. Decision tree from Fig. 2 showing the number of nonthreatened and threatened species at each node (nonthreatened/threatened).

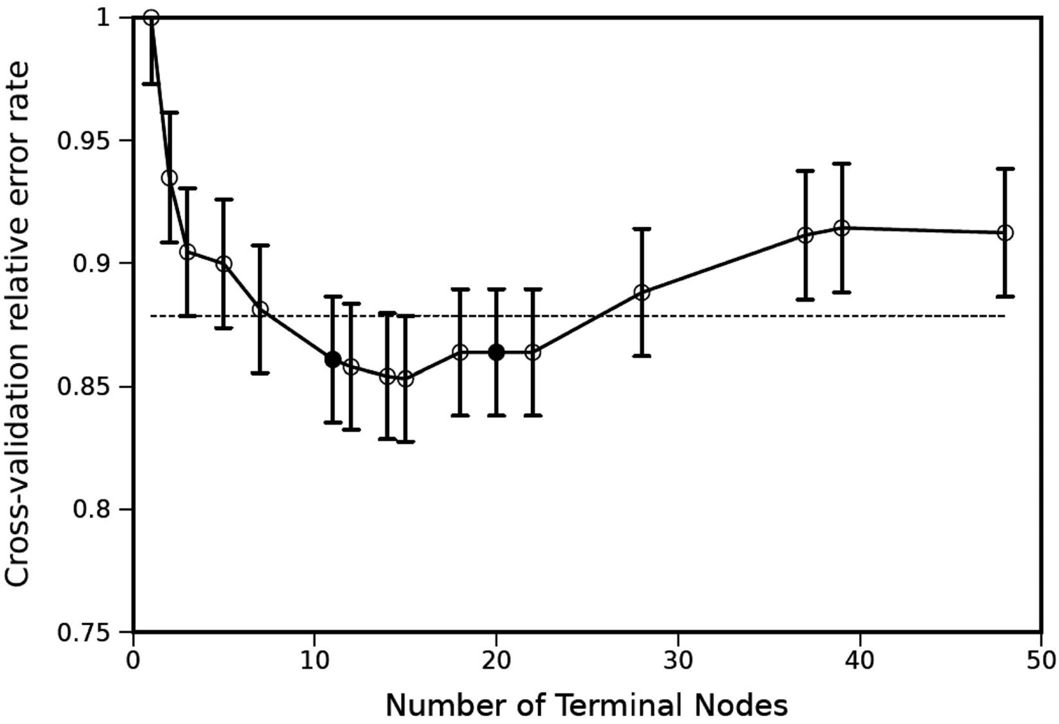

Fig. S2. Relative error for the fitted classification tree determined by 10-fold cross-validation. The dashed line represents ± 1 SE of the error for the minimum-error tree. Optimal (n = 11) and expanded (n = 20) trees are indicated by filled circles.

Table S1. Accuracy measures for predictions of threat status in mammal species (n = 4078).

Accuracy Metric	Classification Model		
	Random Forest	Classification Tree: expanded (n = 20)	Classification Tree: optimal (n = 11)
PCC	81.8%	80.9%	80.0%
Specificity	93.3%	94.9%	94.4%
Sensitivity	47.7%	39.5%	37.3%
Error rate (null error = 25.2%)	18.2%	19.1%	20.0%
Kappa (P-value)	0.44 ($<$ 0.001)	0.40 ($<$ 0.001)	0.37 ($<$ 0.001)

For classification tree models, n is the number of terminal nodes in the tree. PCC denotes percentage correctly classified. Specificity is the percentage of nonthreatened species correctly classified, and sensitivity is the percentage of threatened species correctly classified. Null error rate refers to error expected if all species were predicted in the more common category (nonthreatened). Cohen's kappa is a measure of the agreement between predictions and actual values, corrected for agreement resulting from chance alone; kappa for all models was highly significant, indicating a very low probability that agreement can be attributed to chance.

Table S2. Correlation matrix of all continuous predictor variables

Predictor Variables	Log_{10} Mass (g)	Log_{10} Geographic Range (km^2)	Log_{10} Home Range (km^2)	Log_{10} Density (km^{-2})	Log_{10} Group Size
Log_{10} geographic range (km^2)	0.044	–	–	–	–
	0.000				
Log_{10} home range (km^2)	0.775	0.214	–	–	–
	0.000	0.000			
Log_{10} density km^{-2})	−0.780	0.211	−0.864	–	–
	0.000	0.000	0.000		
Log_{10} group size	0.008	0.059	0.349	−0.204	–
	0.167	0.015	0.000	0.000	
Mass-specific production (g)	−0.503	0.130	−0.403	0.471	0.052
	0.000	0.025	0.000	0.000	0.358

Upper values are correlation coefficients. Lower values are *P* values. All correlations are significant at the 95% confidence level, apart from the correlation of log mass and log group size, and log group size and mass-specific production.

Table S3. IUCN data-deficient species predicted to be at risk

Order	Family	Genus	Species
Artiodactyla	Cervidae	*Elaphodus*	*cephalophus*
Artiodactyla	Cervidae	*Muntiacus*	*feae*
Artiodactyla	Cervidae	*Muntiacus*	*gongshanensis*
Artiodactyla	Cervidae	*Muntiacus*	*vuquangensis*
Artiodactyla	Cervidae	*Hippocamelus*	*antisensis*
Artiodactyla	Cervidae	*Mazama*	*nana*
Carnivora	Viverridae	*Osbornictis*	*piscivora*
Carnivora	Canidae	*Vulpes*	*rueppelli*
Carnivora	Mustelidae	*Lutra*	*sumatrana*
Chiroptera	Hipposideridae	*Hipposideros*	*schistaceus*
Chiroptera	Vespertilionidae	*Hypsugo*	*lophurus*
Chiroptera	Vespertilionidae	*Murina*	*ryukyuana*
Chiroptera	Vespertilionidae	*Pipistrellus*	*minahassae*
Chiroptera	Pteropodidae	*Pteropus*	*argentatus*
Chiroptera	Vespertilionidae	*Myotis*	*yambarensis*
Dasyuromorphia	Dasyuridae	*Antechinus*	*wilhelmina*
Dasyuromorphia	Dasyuridae	*Phascolosorex*	*doriae*
Diprotodontia	Phalangeridae	*Ailurops*	*ursinus*
Diprotodontia	Macropodidae	*Dendrolagus*	*inustus*
Diprotodontia	Macropodidae	*Dendrolagus*	*spadix*
Diprotodontia	Macropodidae	*Dendrolagus*	*ursinus*
Diprotodontia	Pseudocheiridae	*Pseudochirulus*	*caroli*
Diprotodontia	Pseudocheiridae	*Pseudochirulus*	*schlegeli*
Diprotodontia	Phalangeridae	*Strigocuscus*	*celebensis*
Peramelidae	Peroryctidae	*Echymipera*	*clara*
Peramelidae	Peroryctidae	*Echymipera*	*davidi*
Peramelidae	Peroryctidae	*Echymipera*	*echinista*
Peramelidae	Peroryctidae	*Microperoryctes*	*murina*

Table S4. Species not currently recognized as threatened by the IUCN (i.e., LR or LC) but predicted to be at risk by our model.

Order	Family	Genus	Species
Artiodactyla	Antilocapridae	*Antilocapra*	*americana*
Artiodactyla	Bovidae	*Capra*	*sibirica*
Artiodactyla	Bovidae	*Capra*	*pyrenaica*
Artiodactyla	Bovidae	*Cephalophus*	*silvicultor*
Artiodactyla	Bovidae	*Cephalophus*	*maxwellii*
Artiodactyla	Bovidae	*Cephalophus*	*niger*
Artiodactyla	Bovidae	*Cephalophus*	*leucogaster*
Artiodactyla	Bovidae	*Cephalophus*	*callipygus*
Artiodactyla	Bovidae	*Cephalophus*	*ogilbyi*
Artiodactyla	Bovidae	*Connochaetes*	*gnou*
Artiodactyla	Bovidae	*Gazella*	*bennettii*
Artiodactyla	Bovidae	*Naemorhedus*	*goral*
Artiodactyla	Bovidae	*Oreamnos*	*americanus*
Artiodactyla	Bovidae	*Ovis*	*dalli*
Artiodactyla	Bovidae	*Redunca*	*fulvorufula*
Artiodactyla	Bovidae	*Sylvicapra*	*grimmia*
Artiodactyla	Bovidae	*Taurotragus*	*derbianus*
Artiodactyla	Bovidae	*Tragelaphus*	*derbianus*
Artiodactyla	Cervidae	*Alces*	*alces*
Artiodactyla	Cervidae	*Cervus*	*nippon*
Artiodactyla	Cervidae	*Mazama*	*rufina*
Artiodactyla	Cervidae	*Muntiacus*	*atherodes*
Artiodactyla	Cervidae	*Pudu*	*mephistophiles*
Artiodactyla	Giraffidae	*Okapia*	*johnstoni*
Artiodactyla	Moschidae	*Moschus*	*fuscus*
Artiodactyla	Moschidae	*Moschus*	*berezovskii*
Artiodactyla	Suidae	*Phacochoerus*	*africanus*
Artiodactyla	Suidae	*Phacochoerus*	*aethiopicus*
Artiodactyla	Suidae	*Sus*	*heureni*
Artiodactyla	Suidae	*Sus*	*timoriensis*
Carnivora	Canidae	*Canis*	*lupus*
Carnivora	Hyaenidae	*Hyaena*	*hyaena*
Carnivora	Mustelidae	*Aonyx*	*capensis*
Carnivora	Mustelidae	*Melogale*	*orientalis*
Carnivora	Otariidae	*Arctocephalus*	*australis*
Carnivora	Phocidae	*Halichoerus*	*grypus*
Carnivora	Ursidae	*Ursus*	*americanus*
Chiroptera	Emballonuridae	*Emballonura*	*beccarii*
Chiroptera	Hipposideridae	*Hipposideros*	*wollastoni*
Chiroptera	Hipposideridae	*Hipposideros*	*edwardshilli*
Chiroptera	Pteropodidae	*Pteropus*	*seychellensis*
Chiroptera	Pteropodidae	*Pteropus*	*macrotis*
Chiroptera	Pteropodidae	*Pteropus*	*anetianus*
Chiroptera	Pteropodidae	*Rousettus*	*celebensis*
Chiroptera	Rhinolophidae	*Rhinolophus*	*monoceros*
Chiroptera	Vespertilionidae	*Eudiscopus*	*denticulus*
Chiroptera	Vespertilionidae	*Myotis*	*martiniquensis*
Dasyuromorphia	Dasyuridae	*Murexia*	*longicaudata*
Dasyuromorphia	Dasyuridae	*Sarcophilus*	*harrisii*
Diprotodontia	Macropodidae	*Dendrolagus*	*lumholtzi*
Diprotodontia	Macropodidae	*Dendrolagus*	*bennettianus*
Diprotodontia	Macropodidae	*Dorcopsis*	*hageni*
Diprotodontia	Macropodidae	*Dorcopsis*	*muelleri*
Diprotodontia	Macropodidae	*Macropus*	*irma*
Diprotodontia	Macropodidae	*Macropus*	*parryi*
Diprotodontia	Macropodidae	*Macropus*	*bernardus*
Diprotodontia	Macropodidae	*Onychogalea*	*unguifera*
Diprotodontia	Petauridae	*Dactylopsila*	*palpator*
Diprotodontia	Phalangeridae	*Phalanger*	*intercastellanus*
Diprotodontia	Phalangeridae	*Phalanger*	*sericeus*
Diprotodontia	Phalangeridae	*Phalanger*	*carmelitae*
Diprotodontia	Phalangeridae	*Phalanger*	*orientalis*
Diprotodontia	Phalangeridae	*Spilocuscus*	*maculatus*
Diprotodontia	Phalangeridae	*Strigocuscus*	*pelengensis*

Order	Family	Genus	Species
Diprotodontia	Phalangeridae	*Trichosurus*	*caninus*
Diprotodontia	Phalangeridae	*Wyulda*	*squamicaudata*
Diprotodontia	Potoroidae	*Bettongia*	*gaimardi*
Diprotodontia	Pseudocheiridae	*Pseudochirops*	*cupreus*
Diprotodontia	Pseudocheiridae	*Pseudochirulus*	*herbertensis*
Diprotodontia	Pseudocheiridae	*Pseudochirulus*	*cinereus*
Diprotodontia	Pseudocheiridae	*Hemibelideus*	*lemuroides*
Lagomorphia	Leporidae	*Sylvilagus*	*mansuetus*
Perissodactyla	Equidae	*Equus*	*kiang*
Primates	Cebidae	*Alouatta*	*palliata*
Primates	Cebidae	*Alouatta*	*sara*
Primates	Cebidae	*Pithecia*	*albicans*
Primates	Cercopithecidae	*Cercocebus*	*atys*
Primates	Cercopithecidae	*Cercopithecus*	*lhoesti*
Primates	Cercopithecidae	*Cercopithecus*	*hamlyni*
Primates	Cercopithecidae	*Colobus*	*polykomos*
Primates	Cercopithecidae	*Papio*	*anubis*
Primates	Cercopithecidae	*Papio*	*papio*
Primates	Cercopithecidae	*Presbytis*	*rubicunda*
Primates	Cercopithecidae	*Presbytis*	*femoralis*
Primates	Cercopithecidae	*Theropithecus*	*gelada*
Primates	Lemuridae	*Eulemur*	*fulvus*
Primates	Lemuridae	*Hapalemur*	*griseus*
Rodentia	Agoutidae	*Agouti*	*taczanowskii*
Rodentia	Capromyidae	*Capromys*	*pilorides*
Rodentia	Capromyidae	*Mysateles*	*meridionalis*
Rodentia	Dasyproctidae	*Dasyprocta*	*guamara*
Rodentia	Erethizontidae	*Coendou*	*rothschildi*
Rodentia	Hystricidae	*Hystrix*	*africaeaustralis*
Rodentia	Hystricidae	*Hystrix*	*pumila*
Rodentia	Hystricidae	*Hystrix*	*sumatrae*
Rodentia	Hystricidae	*Hystrix*	*crassispinis*
Rodentia	Hystricidae	*Hystrix*	*javanica*
Rodentia	Muridae	*Akodon*	*markhami*
Rodentia	Muridae	*Chiropodomys*	*muroides*
Rodentia	Muridae	*Eliurus*	*tanala*
Rodentia	Muridae	*Eospalax*	*smithii*
Rodentia	Muridae	*Haeromys*	*minahassae*
Rodentia	Muridae	*Hyomys*	*goliath*
Rodentia	Muridae	*Mallomys*	*aroaensis*
Rodentia	Muridae	*Mallomys*	*istapantap*
Rodentia	Muridae	*Melomys*	*leucogaster*
Rodentia	Muridae	*Microhydromys*	*musseri*
Rodentia	Muridae	*Microtus*	*breweri*
Rodentia	Muridae	*Niviventer*	*coxingi*
Rodentia	Muridae	*Niviventer*	*lepturus*
Rodentia	Muridae	*Parahydromys*	*asper*
Rodentia	Muridae	*Peromyscus*	*guardia*
Rodentia	Muridae	*Peromyscus*	*sejugis*
Rodentia	Muridae	*Pogonomys*	*loriae*

Table S5. Species predicted to be at risk on the basis of current geographic range

Order	Family	Genus	Species
Artiodactyla	Bovidae	*Damaliscus*	*lunatus*
Artiodactyla	Bovidae	*Tragelaphus*	*eurycerus*
Artiodactyla	Camelidae	*Lama*	*guanicoe*
Artiodactyla	Cervidae	*Cervus*	*elaphus*
Artiodactyla	Cervidae	*Rangifer*	*tarandus*
Artiodactyla	Tayassuidae	*Tayassu*	*pecari*
Carnivora	Felidae	*Herpailurus*	*yaguarondi*
Carnivora	Felidae	*Leopardus*	*pardalis*
Carnivora	Felidae	*Leopardus*	*wiedii*
Carnivora	Felidae	*Leptailurus*	*serval*
Carnivora	Hyaenidae	*Hyaena*	*brunnea*
Carnivora	Mustelidae	*Conepatus*	*mesoleucus*
Carnivora	Mustelidae	*Conepatus*	*leuconotus*
Cingulata	Dasypodidae	*Chaetophractus*	*vellerosus*
Cingulata	Dasypodidae	*Dasypus*	*hybridus*
Cingulata	Dasypodidae	*Euphractus*	*sexcinctus*
Cingulata	Dasypodidae	*Tolypeutes*	*matacus*