Title: Dwarfism and gigantism drive human-mediated extinctions on islands

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Abstract: Islands have long been recognized as unique evolutionary arenas leading to morphologically distinct species, such as dwarfs and giants. We assessed how body size evolution in island mammals may have exacerbated their vulnerability, and how human arrival has contributed to their past and ongoing extinctions, by integrating data on 1,231 extant and 350 extinct species from islands and paleo-islands worldwide spanning the past 23 million years. We found that the likelihood of extinction and of endangerment are highest in the most extreme island dwarfs and giants. Extinction risk of insular mammals was compounded by the arrival of modern humans, which accelerated extinction rates more than 10-fold, resulting in an almost complete demise of these iconic marvels of island evolution.

One-Sentence Summary: Insular dwarfs and giants are disproportionately susceptible to extinction, especially following human arrival.

Main Text:

For over two centuries, scientists have considered islands as laboratories for the study of processes influencing biodiversity, including colonization, extinction and evolution (*1*–*3*). Although islands cover less than 7% of the Earth's land area, they are hotspots for biodiversity, containing 15 to 20% of all terrestrial species on the planet (*3*, *4*). Islands are also hotspots for species extinctions, with around 75% of documented extinctions since 1500 CE (Common Era) and 50% of today's IUCN (International Union for Conservation of Nature) threatened species (*4*). The extinction of island species recorded throughout the late Quaternary (i.e., the last 129,000 years) is indicative of the ongoing human-induced extinctions in continental biotas (*4*–*7*).

Many organisms undergo evolutionary change in response to the unique characteristics of island environments (*3*, *4*), including reduced dispersal capacity, loss of defenses against natural enemies, and modifications of body size (i.e., gigantism or dwarfism) (*8*–*13*). Evolution towards these peculiar features, referred to as "island syndrome(s)" (*3*, *4*, *14*, *15*), frequently confers ecological naiveté (*14*, *16*) and increased susceptibility to anthropogenic extinctions (*3*, *4*, *17*, *18*). As a result, anthropogenic impacts on insular ecosystems have been severe (*17*, *19*–*21*), with human-mediated extinctions documented on islands since at least the end-Pleistocene (*4*, *5*, *22*, *23*). Shifts in body size on islands result from a combination of factors, including release from competition and predation, as well as resource limitation (*8*, *9*, *11*, *13*, *14*). These body size shifts in turn influence a multitude of characteristics including those associated with dispersal, ecological interactions and resource requirements (*4*, *9*, *11*). While body mass is a well-known predictor of extinction risk in both extant and recently extinct faunas (*24*–*28*), and size selectivity is a signature of human-mediated extinctions (*6*, *29*, *30*), the relationship between the magnitude of body size evolution and susceptibility to extinction remains unclear.

Here, we integrate data on extinct and extant island mammals to quantify how evolution towards dwarfism and gigantism may have affected their risk and rate of extinction, both before and after human arrival. We compiled data on extinction risk, body mass and body size change of 1,231 extant species (1,539 populations, since some species live on multiple islands) and 350 extinct species of insular mammals (fig. S1). To examine the paleontological record, we assembled a dataset of >7,800 fossil occurrences from over 1,400 sources representing 182 islands and paleo-islands (formerly isolated landmasses that are now part of mainland areas) worldwide spanning 23.03 Ma (fig. S2). We defined two binary extinction risk variables by classifying species as extant or extinct, and living species as non-threatened or threatened using data from the IUCN Red List (*31*). Body size change was estimated based on island-mainland comparisons of populations of the same species or, in the case of endemic insular species, of sister species. For each island–mainland comparison, we defined dwarfism as a relative decrease in body mass, and gigantism as a relative increase in body mass (*32*). Species or populations were considered giants or dwarfs if the log size ratio was >0 or <0, respectively, compared to mainland counterparts. Body mass values were obtained from the literature or calculated from published allometric relationships (*32*). Using a series of generalized linear mixed-effects models (GLMMs) and phylogenetic logistic regression models, we determined whether there was a significant association between the magnitude of body size change and extinction risk. Importantly, we tested whether the magnitude of body size change is a better predictor of extinction risk than body mass per se. Next, we evaluated how the relationship between body mass and extinction risk differs between insular and mainland mammals. Finally, we applied Bayesian models to the fossil record to estimate how extinction rates of insular mammals have changed over the late Cenozoic (since 23.03 Ma), and whether these rates were related to body size change, body mass, island endemism (hereafter endemism), island type, and hominin and modern human (= *Homo sapiens*) arrival on each island.

Body size change as a predisposing factor for island extinctions

We found that insular species with more extreme body size shifts and larger body mass are characterized by higher extinction risk (Figs. 1 and 2). In particular, species that decreased or increased by more than four and ten times in mass (magnitude of body size change ~0.6 and ~1.0) are associated with probabilities of being threatened or extinct >0.75, respectively (Fig. 1). These dwarfs and giants include critically endangered and endangered species such as the dwarfed tamaraw of Mindoro (*Bubalus mindorensis*) and the giant Jamaican hutia (*Geocapromys brownii*), and extinct evolutionary marvels such as dwarf mammoths and hippos that shrunk to less than one-tenth the mass of their mainland ancestors, and rodents and gymnures that increased in mass by over 100-fold (Fig. 1, B and D). Moreover, the degree of dwarfism and gigantism is significantly and positively associated with vulnerability to extinction in insular mammals. Relationships between the magnitude of body size change and the probability of being threatened ($p < 0.001$; $R^2_{\text{conditional}} = 0.26$; Fig. 1A, fig. S3, and tables S1 and S2) or extinct ($p < 0.001$; $R^2_{\text{conditional}} = 0.63$; Fig. 1C, fig. S4, and table S3) at the species-level are positive. These results are robust and hold at the population-level (but see differences between populations of endemic and non-endemic insular species; fig. S5, C and D, and tables S4 and S5), at the species-level when including only extinctions since 1500 CE (fig. S5A and table S6) (*32*), and when explicitly accounting for phylogenetic dependence (fig. S6 and tables S9 to S12). The disproportionate vulnerability of insular dwarfs and giants is evident across most of the body mass classes in our dataset, with higher mean values of body size change magnitude in threatened and extinct species (Fig. 1, B and D). We also found that insular giant species have a slightly higher extinction risk than insular dwarfs, although the effect of the direction of body size change is only significant when extinct species are included ($p = 0.002$; Odds ratio = 3.16; Fig. 1, A and C, and tables S1 to S3), in agreement with results of our time-and-trait-dependent extinction analysis (Fig. 3G). The association between body size change and current, historic and prehistoric extinction risk which emerged from our analysis highlights the importance of morphological adaptations associated with the island syndrome in predisposing island biotas to extinction.

Our results also indicate that endemism, island type (oceanic vs continental vs continental + oceanic) and body size change had the greatest effects on extinction rates (log Bayes factor greater than 10 and 6, indicating very strong and strong statistical support), followed by body mass (Fig. 3D and fig. S10). In accordance with patterns observed in island biotas today (*4*), we found strong evidence that island endemics, particularly those on oceanic islands, were especially susceptible to extinctions in the past (Fig.3, E and F, and fig. S10). Similarly, species larger than 100 kg and species undergoing insular gigantism were disproportionately prone to extinction (Fig. 3, G and H, and fig. S10). Our sensitivity analyses at different temporal resolutions suggest little change in extinction selectivity over time, at least before 1500 CE (fig. S10). In fact, while phyletic giants might have been intrinsically more vulnerable to extinction, they also provided bigger reward for hunting and, therefore, might have been selectively targeted after human colonization (*4*). Since the European expansion around the globe, however, extinctions have similarly affected dwarfed and giant insular mammals, as shown by our analyses of current and historic extinction risk ($p_{Direction} > 0.05$; tables S1, S2, and S6). This is in agreement with a general effect of ecological naiveté, and likely reflects the impact of more intense and multifaceted human pressures, including not only direct overexploitation but also accelerated habitat loss and introductions of novel diseases and invasive predators (*33*).

Size selectivity of mammal extinctions on islands and mainland

Large terrestrial mammals on both mainland and islands are known to be at a higher risk of extinction, especially due to anthropogenic threats (*21*, *23*, *25*, *26*, *30*, *34*) (Fig. 2, fig. S6B, D, F, H, J, L and tables S1 to S6, and S9 to S12). Here, we also show that the relationship between body mass and extinction risk differs between insular and mainland species when all extinct, late Quaternary or historically extinct species are included (Fig. 2B and table S7). Indeed, the probability of becoming extinct is similar for large-sized mammals on both continents and islands, but small-sized and intermediate-sized mammals (body mass between ~0.001 and ~100 kg) have higher extinction probabilities on islands than on continents (slope $\log_{10}$ body mass * Island or mainland = 2.05, $p < 0.0001$; Fig. 2B, tables S7 and S8). In contrast, the odds of mammals being threatened are 150% higher on islands than on continents, regardless of their body mass (Odds $\text{ratio}_{\text{mainland}} = 0.4$; Fig. 2A and table S7). Insular ecosystems are also characterized by markedly higher proportions of threatened and extinct species of small and intermediate body mass in comparison to mainland ecosystems (Fig. 2, C and D). Small species (between 10 g and 1 kg) are particularly more vulnerable on islands than on the mainland, exhibiting approximately 17.2 times higher incidence of extinctions, 6.8 times higher incidence of historic extinctions since 1500 CE and 2.7 times higher incidence of threat today (= 140 extinct, 40 historically extinct and 303 threatened insular mammals; Fig. 2, C and D, and fig. S5B). The proportions of extinct, historically extinct and threatened large-bodied species (between 100 kg and 10,000 kg) are, instead, only moderately higher on islands (approximately 1.6, 2.5 and 1.4 times), indicating that insular and mainland megafauna were, and still are, similarly vulnerable to extinctions (Fig. 2, C and D, and fig. S5B).

We also found evidence for downsizing of mammal communities over time, as shown by the disproportionate extinction of large-bodied species (*23*, *24*, *30*, *35*) (146 insular and 178 mainland species > 10 kg). Anthropogenic downsizing appears to be ratchetting down to smaller body mass classes, with impacts shifting from the now-extinct megafauna to smaller body mass classes over time [the proportion and number of currently threatened species under 10 kg exceed those for extinct species; Fig. 2, C vs D; see also (*6*, *29*, *30*)]. However, this also reflects the intrinsic vulnerability of small and medium-sized taxa on islands, which include the majority of phyletic giants (albeit still 'small') and dwarfs (now medium-sized mammals) (Fig. 1, B and D), and reinforces our call for the protection of surviving species in the face of ongoing anthropogenic threats, such as introductions of invasive predators and competitors (*33*, *36*).

Interestingly, body size change is a better predictor of extinction risk than body mass per se in all our analyses at the species-level (lower Akaike information criterion scores and higher R^2 in single-predictor models; fig. S6 and tables S1 to S3, S6, S9, S10 and S12), and had a stronger effect on past extinction rates in our time-and-trait-dependent extinction models (Fig. 3D and fig. S10). The reason might be that this trait more accurately reflects the evolution of species in isolation and therefore, ultimately, is a better proxy for their ecological naiveté. Furthermore, dwarfism and gigantism, especially when extreme, are generally accompanied by other peculiar evolutionary innovations that exacerbate the vulnerability of mammals in disturbed island environments (e.g., bone fusions, relaxation of defensive behavior) (*4*, *8*, *14*). Metrics of evolutionary history are already being included in conservation prioritization (*37*, *38*), but we suggest that prioritization of insular species for conservation should also take into account metrics of morphological divergence compared with mainland faunas, to better protect the remaining island species.

Human impacts and the demise of the evolutionary marvels of island life

Our time-and-trait-dependent extinction models revealed a strong temporal association between island extinctions at a global level and the arrival of modern humans [Probability of Direction (*pd*) = 99.9%; *pd* > 97.5% ~ $p < 0.05$ (*32*); Fig. 3I]. Specifically, we found that temporal overlap of insular mammals with *H. sapiens* increased their extinction rates more than 16-fold relative to background rates before modern humans arrived (median: 16.70-fold; 95% credible interval: 5.99 to 43.31-fold; Fig. 3I). This anthropogenic increase in extinction rates was evident even after we accounted for discrepancies between early and late modern human dispersal models, for different temporal resolutions and background rates, and for the occurrence of endemic species that evolved by anagenesis (the latter possibly affecting estimates of extinction rates and their changes) (*32*) (fig. S10). In order to determine whether hominins that colonized islands before modern humans (= pre-*sapiens*) were detrimental to insular mammals, we also evaluated the effect of temporal overlap with Pleistocene hominins on their extinction rates. We found evidence for only a weak impact of early hominins on the extinction of island mammals (*pd* = 92.5%; Fig. 3I), being detected as a two-fold increase in extinction rates (median: 2.05-fold; 95% credible interval: 0.66 to 4.77-fold; Fig. 3I) (*32*). Taken together, these results highlight a critical shift in extinction regime from pre-*sapiens* to *sapiens*-dominated island ecosystems.

To further evaluate whether the positive relationship between body size change and extinction on islands is driven by human impacts, we analyzed the late Cenozoic global fossil record of mammals on islands. Our broader analysis highlights their vulnerability to geologically recent anthropogenic pressures, with the latest increase in their extinction rates being the strongest during at least the past 2.58 Ma (Fig. 3A and figs. S8A and S9B). When we analyzed this at finer temporal resolution, we found that this shift consisted of a series of extinction pulses starting at the end of the Middle Pleistocene (around 200 ka BP; Fig. 3B and figs. S8B and S9C), with the best supported increases in extinction rates occurring approximately 100 ka BP, 16 ka BP, and 2000 years BP (Fig. 3, B and C, and figs. S8, B and C, and S9A, C, D). The first of these Late Pleistocene and Holocene shifts resulted in a 17-fold increase in extinction rate, and occurred between the last appearance of *Homo erectus* (*39*) and the initial colonization of *H. sapiens* in insular Southeast and East Asia (Fig. 3B and fig. S8B). This shift marks the onset of a more acute extinction regime, corroborating the results of our time-and-trait-dependent extinction models discussed above. Modern human arrival on more remote oceanic islands, along with technological and behavioral changes in human populations in the late Quaternary, is often associated with an acceleration in extinctions (*4*, *5*, *20*, *22*). In line with these findings, we recorded further increases in extinction rates beginning in the terminal Pleistocene and continuing in the Late Holocene (Fig. 3C and figs. S8C and S9, A and D). The latest shift (at ~2000 years BP) was the most extreme and characterized by rates more than 88 times higher than those at the beginning of the Late Pleistocene.

Our findings suggest that ongoing biodiversity loss on islands is part of a protracted extinction event that began more than 100,000 years ago. As modern humans spread across islands worldwide during the Late Pleistocene and Holocene, pristine island ecosystems were destabilized by extinction pulses which are apparent in the mammal fossil record. These extinctions have disproportionately impacted the morphologically most divergent species, thereby accelerating their demise and causing dramatic losses in global functional diversity.

Looking toward the future, we recommend that conservation agendas give special priority to protecting insular giants and dwarfs - the surviving evolutionary marvels of island life.

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Author contributions: R.R., M.V.L., J.M.C. and S.K.L designed the study. R.R. compiled the data, conducted the analyses, produced the figures and wrote the first draft. M.V.L., J.M.C., S.K.L., S.T.T., D.S., A.A.E.v.d.G., A.B.-L., J.A.A. and A.Z. contributed substantially to the writing. J.M.C. supported funding acquisition. M.V.L., A.A.E.v.d.G., P.B., S.T.T., J.A.A., C.-H.T., M.F., M.O.K, J.O., M.E.S. compiled the data. A.B.-L. and J.A.A. helped design supporting analyses. D.S. developed the time-and-trait-dependent extinction model and advised on PyRate analyses. A.B.-L. contributed to the preparation of maps. A.Z. helped harmonize the data. All authors provided comments on the draft.

Competing interests: The authors declare no competing interests.

Data and materials availability: All data are available at: https://figshare.com/s/ca942cdae6177e57b703 (main datasets); https://figshare.com/s/d62e378f506610aa5140 (input data to run PyRate analyses); https://figshare.com/s/a4953c285d1e1e7341ae (input data to run time-and-trait-dependent extinction analyses); https://figshare.com/s/96eb03929afb9dbcbd78 (trees generated by TACT and DNA-only trees). A DOI will be provided upon publication. The computer code used for this study is available at https://github.com/RobRozzi/Island_mammals.

Supplementary Materials

Materials and Methods

Figs. S1 to S11

Tables S1 to S13

References (*42*–*1994*)

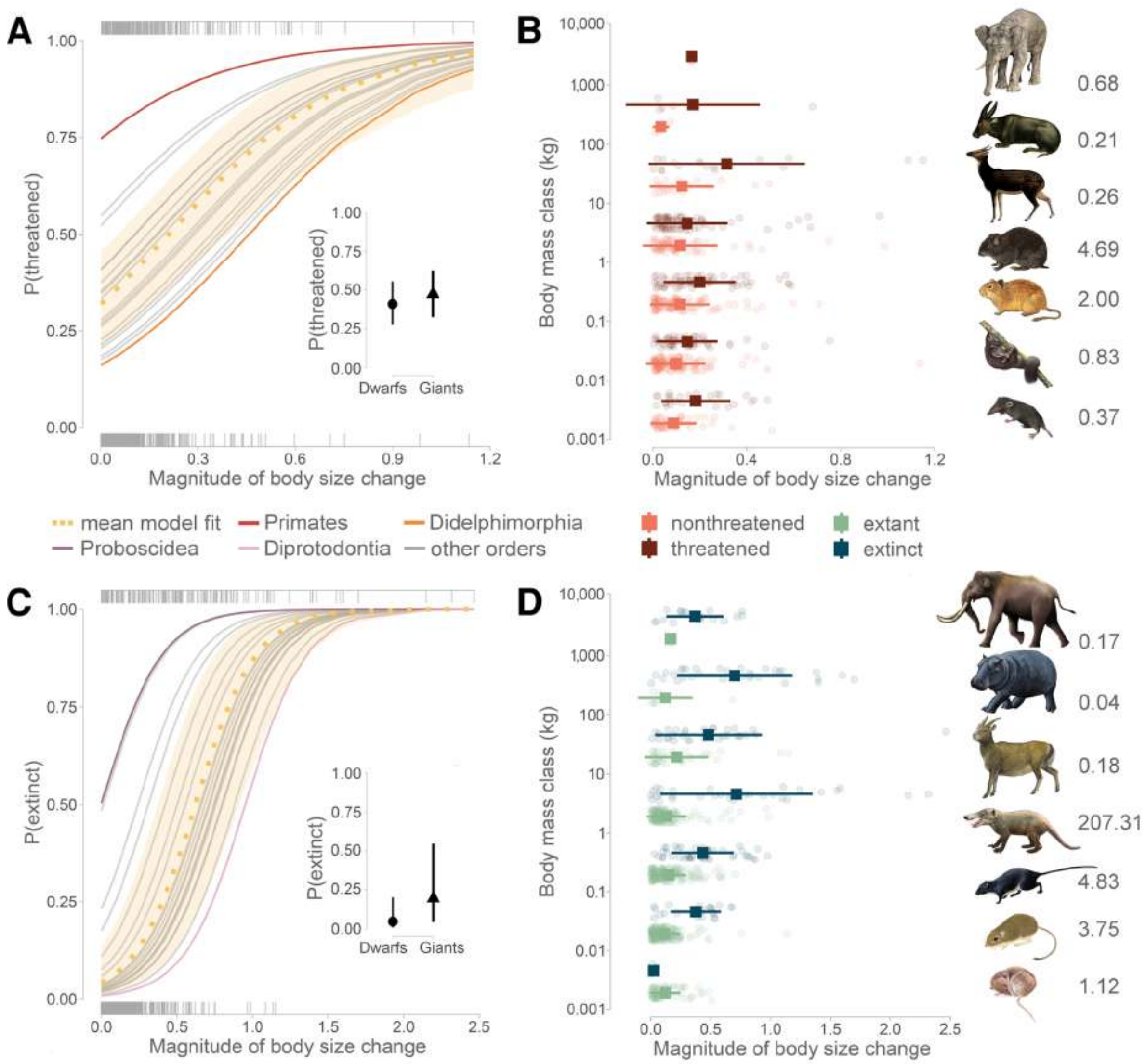

Fig. 1. The effect of body size change on extinction risk of mammals on islands worldwide. Relationships between magnitude and direction of body size change and probability of being threatened (**A**) and extinct (**C**) (see figs. S3 and S4, and tables S1 to S3 for details). The magnitude of body size change was calculated as the absolute value of the log ratio between the mean body mass of individuals from an insular population or species and that of its mainland relative (*9*). Also shown are raw values of the magnitude of size change for each body mass class and extinction risk level (**B**, **D**). Mean and standard deviation values are represented by squares and lines. Extant mammals from top to bottom: Borneo elephant, tamaraw, Visayan spotted deer, Jamaican hutia, Mocha Island degu, Biak glider, Christmas Island shrew. Extinct mammals from top to bottom: Channel Islands mammoth, Cyprus dwarf hippopotamus, Balearian mouse-goat, Gargano giant erinaceid, Martinique rice rat, lava mouse, Pleistocene Sicilian shrew. Non-logged, mean values of the magnitude of size change for each dwarf (below 1) and giant (above 1) taxon are reported behind the silhouettes. Illustrations adapted with permission from Owen Bell, Nils Braun, Roger Hall, George Lyras, Francisco Olea, George Papageorgiou, Peter

Schouten, Egidio Viola and Roman Yevseyev, and adapted from (*40*, *41*) and https://eol.org/media/8766251 (credit photo: 2013 Simon J. Tonge, license: CC-BY-3.0).

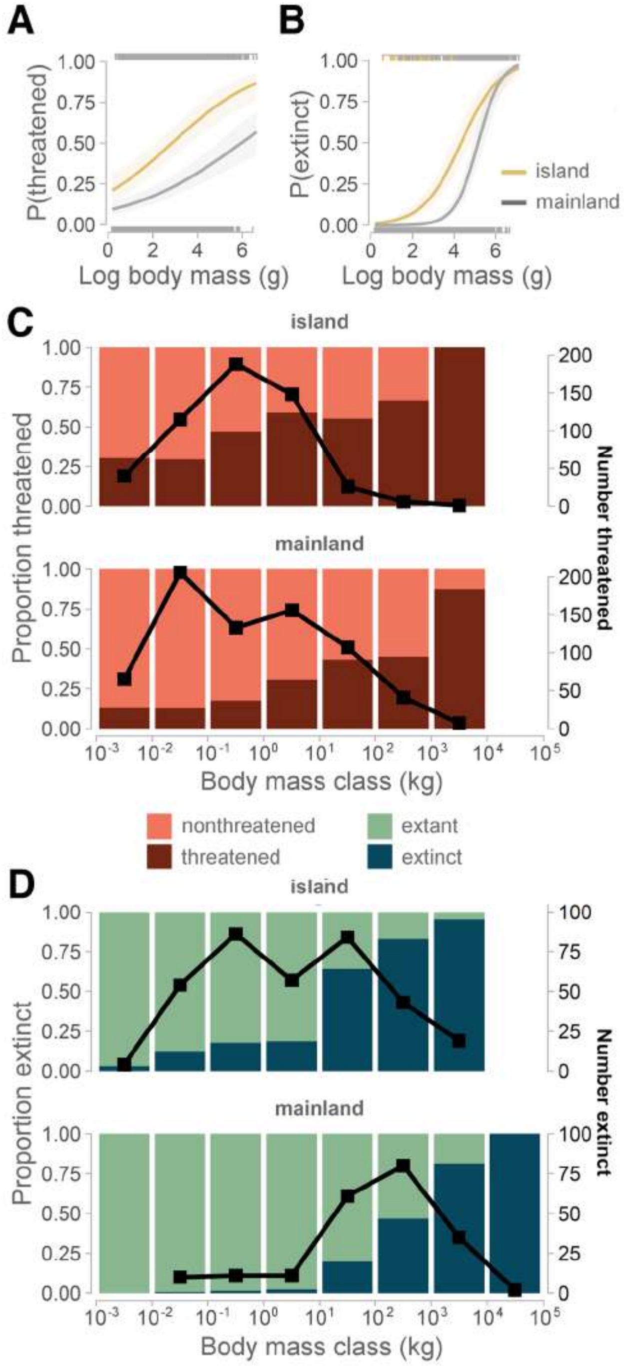

Fig. 2. Differences in size selectivity of mammal extinctions between islands and mainland. Relationships between body mass and probability of being threatened (**A**) and extinct (**B**) on islands and on the mainland (see table S7 for details). Proportion (shaded bars) and number (black boxes) of threatened (**C**) and extinct (**D**) species within each body mass class on islands and on the mainland. Insular ecosystems are characterized by higher proportions of threatened and extinct mammals in all body mass classes, with the artifactual exception of large megafauna which did not inhabit (or dwarfed to a smaller body mass class on) islands.

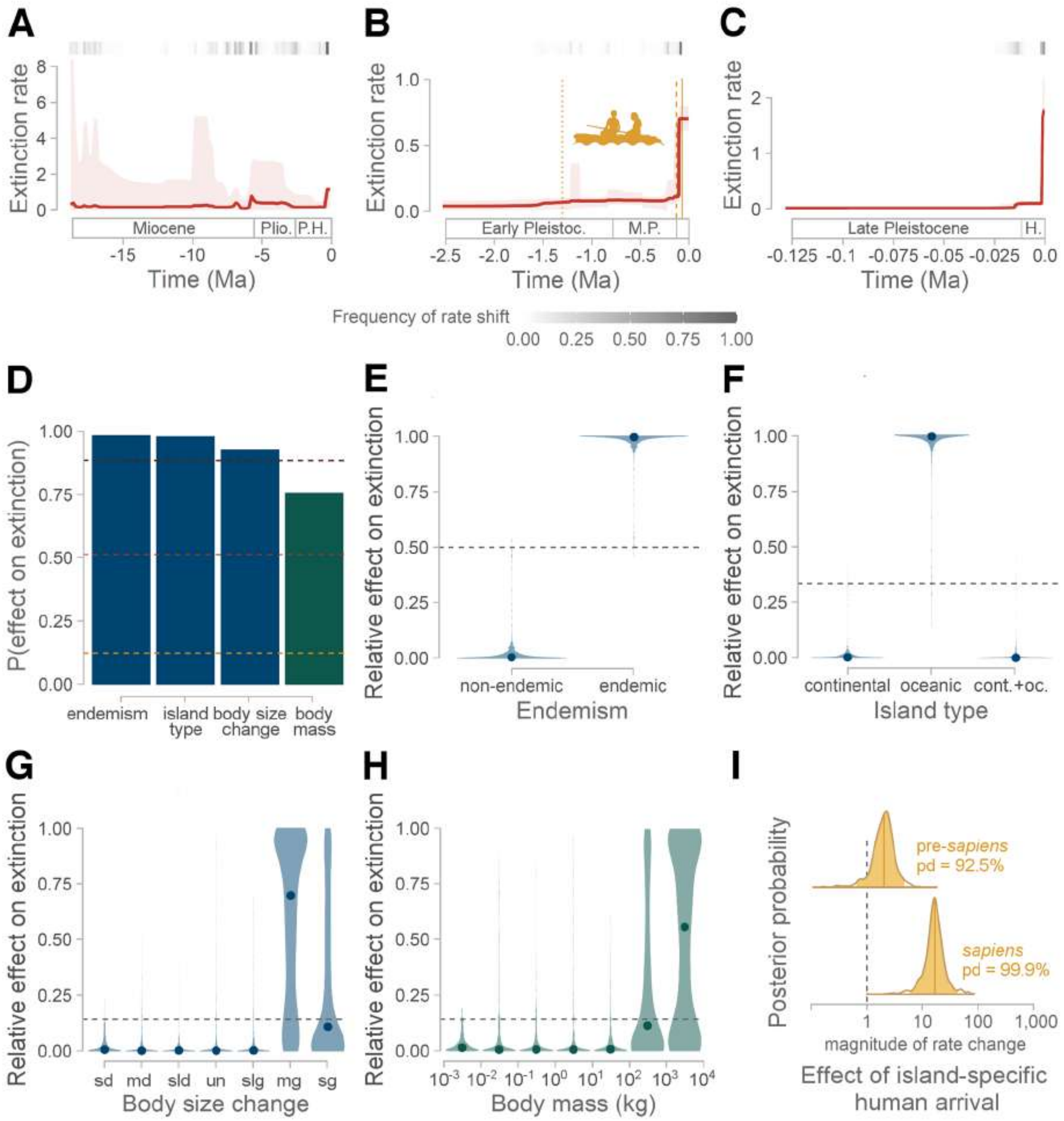

Fig. 3. Body size change and human arrival drove extinctions of mammals on islands. Extinction rates (red lines) and inferred times of rate shifts (gray tiles) of insular mammals since the Miocene (**A**), Pleistocene (**B**) and Late Pleistocene (**C**). Sampling frequencies of rate shifts in the posterior samples show timing and statistical significance of the shifts (see figs. S8 and S9 for details). Yellow vertical lines indicate the first arrival of pre-*sapiens* hominins (dotted line) and *H. sapiens* on islands globally according to early (dashed line) and late (solid line) dispersal models (note, however, that our multi-trait-dependent extinction model is based on recorded dates of arrival of modern humans on each island). All variables have high probabilities of having an effect on extinctions across the analysis interval (**D**). Colored dashed lines indicate the thresholds corresponding to log Bayes factor values of 2 (yellow), 6 (orange), and 10 (red). The

relative effect of endemism (**E**), island type (**F**), body size change (**G**) and body mass (**H**) on extinction rates of insular mammals. Each dashed line represents the expected value of Dirichlet-distributed multipliers under a null model where the trait has no effect on extinction. Body size change was categorized as follows: strongly dwarfed or giant (sd, sg), moderately dwarfed or giant (ms, mg), slightly dwarfed or giant (sld, slg), unchanged (un) species. See table S13 for details and categorization of the other variables. Posterior distributions of the effect size (a multiplier of the background rate) of anthropogenic effects on extinction (**I**). These parameters quantify the rate increase that has occurred across lineages since the arrival of pre-*sapiens* and modern humans, while accounting for the trait-dependent effects (D). This analysis is based on modern human early dispersal models (see Fig. S10 for sensitivity analyses). Posterior medians and 95% credible intervals are shown as vertical lines and shaded areas under the posterior density curves. Plio., Pliocene; P.H., Pleistocene + Holocene; Early Pleistoc., Early Pleistocene; M.P., Middle Pleistocene; H., Holocene.

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Supplementary Materials for

Dwarfism and gigantism drive human-mediated extinctions on islands

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Materials and Methods

Database

We assembled a population-level dataset comprising 1,539 extant native populations of insular terrestrial mammals (390 species from 18 orders; fig. S1) by compiling data from assessments of the island rule (*9*, *11*, *12*, *42*) (172 original data sources) (*43–214*) and other recent studies (*215–222*). To be able to combine data obtained from extant and fossil species in our analyses of extinction risk, we also compiled a species-level dataset, which encompasses 1,231 extant and 350 extinct species of insular terrestrial mammals from 19 orders (fig. S1). Extant species names were standardized based on the Mammal Diversity Database (v1.7) (*223*). To overcome potential issues associated with the use of subspecies in paleontology (*224*, *225*), extinct subspecies and extirpated populations of extant taxa - e.g., *Bison priscus siciliae* from the late Middle Pleistocene-early Late Pleistocene of Sicily (*226*) - were coded as separate species and included in the species-level dataset.

Our population-level and species-level datasets include body masses of insular and mainland or ancestral populations and species, and estimations of body size change. For each island–mainland comparison, we calculated the magnitude of body size change as the absolute value of the common logarithm of the ratio between the mean body mass of individuals from an insular population or species and that of closest known mainland relatives (*9*, *11*, *51–53*). To be able to evaluate the effect of the magnitude of body size change on extinction risk independently of its direction, we coded the direction of body size change as a distinct, categorical variable: dwarfism, gigantism, no substantial change (log size ratio = 0). Different categories of body size change were used in the analysis of extinction rates (see below). Our species-level dataset includes median values of body mass and magnitude of body size change derived from the population-level dataset (382) and data from additional insular endemic species (849 extant), for which population-level information was not available. We obtained body masses of extant and extinct species from the Phylogenetic Atlas of Mammal Macroecology (PHYLACINE v1.2.1) (*227*) and other scientific literature (*11*, *23*, *24*, *42*, *61*, *226*, *228–290*). We complemented these values with mean estimates obtained by using published allometric equations and morphometric data extracted from 22 studies (*54*, *291–311*). We selected the closest mainland species by performing species-specific searches in the Web of Science Core Collection and Google Scholar (*23*, *31*, *166*, *226*, *232–234*, *237*, *239*, *240*, *244–251*, *254–257*, *259*, *262*, *265*, *267*, *272*, *273*, *278*, *279*, *282*, *284–286*, *301*, *312–433*). To overcome potential issues associated with data imputation (*434*, *435*), we excluded from our assessment of the relationship between body size change and extinction risk island-mainland comparisons that were not supported by phylogenetic or taxonomic evidence; however, we included those insular species with uncertain or unknown ancestral taxa in our investigation of the relationship between body mass and extinction risk.

We combined the data on body mass and body size change with information on endemism and extinction risk. We classified insular mammals into two groups: endemic taxa (species endemic to islands or archipelagos and populations of those species); non-endemic taxa (species that also occur or occurred on the mainland and populations of those species). We collated information on species-level and infra-specific extinction risk from the IUCN Red List (v2021.2) (*31*). In particular, in case of populations that were assessed separately by the IUCN (e.g., Zanzibar Small-eared Galago, Golden-bellied Crowned Monkey), subspecies-level information was used in the population-level dataset. In most cases, however, we had to use species-level extinction risk information to complete our population-level dataset, because neither global nor regional Red List assessments included infra-specific information for non-endemic focal taxa.

We took this into account in our analyses at the population-level, by discussing results obtained for endemic and non-endemic taxa separately (see below). For our analyses, we excluded species classified as Data Deficient (DD) and species not yet assessed, such as the Hon Khoai squirrel and Sir David Attenborough's myotis. We focused on taxa listed as Least Concern (LC), Near Threatened (NT), Vulnerable (VU), Endangered (EN), Critically Endangered (CR), and Extinct (EX). Besides historic extinctions (EX), we included an additional, unofficial status, "extinct in prehistory" (EP) (*436–438*), to classify 295 taxa in our database that became extinct before 1500 CE.

To delve into the paleontological record of mammals on islands we assembled a dataset of 7,867 fossil occurrences at the species-level from 1,461 sources (*24*, *131*, *226*, *238*, *241*, *244*, *248–254*, *259*, *260*, *263–267*, *269–275*, *278–280*, *282–289*, *292*, *295–297*, *301*, *304*, *308–312*, *314*, *391*, *396*, *430–433*, *439–1843*), including scientific articles, books, collection databases and reports of excavations. Our dataset represents 182 islands and paleo-islands spanning 23.03 Ma (fig. S2). Because our main goal was to investigate the extinction of dwarfs and giants, we included all islands on which at least one extinct, endemic taxon occurred. We excluded the fossil records of the 'island continent' Australia and of Malta, which lacks adequate geochronological data and a robust biochronological scheme (*8*, *1497*). However, we included paleo-islands that are currently part of mainland Europe, but that were isolated from neighboring mainland areas for long periods of time, such as those belonging to the late Miocene Tusco-Sardinian and Apulo-Abruzzi paleobioprovinces (*288*, *439*, *440*, *1844*). We classified islands into two groups, based on their connection to continental landmasses during the time period covered by our dataset (*22*, *251*, *267*, *272*, *277*, *282*, *285*, *288*, *292*, *312*, *341*, *441–448*, *802*, *863*, *1166*, *1610*, *1824*, *1830*, *1839*, *1844–1874*): oceanic islands (islands that have never been connected to continental landmasses since the Miocene or since their formation); continental islands (islands that were connected to continents at least once since the Miocene or since their formation). We compiled occurrences from all paleontological and archeological sites in which fossil remains of at least one extinct (either globally or locally) mammal taxon were found. Our dataset encompasses occurrences also based on fossil remains of native extant species and selected prehistoric introductions which are known to have become established as wild populations (e.g., *Isolobodon portoricensis* from Hispaniola) (*24*, *941*, *1671*). To minimize the risk of species misidentification, we excluded occurrences based on ichnofossils, such as coprolites or footprints. We also excluded occurrences based on genus- or family-level identifications (sp., indet., incertae sedis), except for those likely representing new, undescribed taxa in the literature or the only occurrence of a genus on a given island. However, we included species affines and confer and coded them as separate species or synonyms, respectively. Finally, if a species list of a given site included a taxon identified as "species A or species B", we retained both species in our dataset. To aggregate the best available occurrence data for each island and to address issues associated with 'big data' quantitative approaches to extinction studies (*1875*), we applied a rigorous protocol (fig. S2A). To define the maximum and minimum age of each fossil occurrence, we gave priority to direct absolute dates or, if not available, associated, indirect dates based on remains of other vertebrates, invertebrates or plants. We disregarded indirect dates whose association with the focal species was questionable (e.g., different stratigraphic provenience or other reasons explicitly stated in the original studies). In the case of radiocarbon dates, we used calibrated 2σ age ranges, either obtained from the original studies or, if not available, estimated by calibrating raw dates using the CALIB REV8.2 software (*1876*, *1877*) and relevant calibration curves (IntCal20 (*1878*), MARINE20 (*1879*), SHCal20 (*1880*)). Calibrated ages were expressed in years BP (Before Present, 0 cal BP = 1950 CE). In the absence of dated remains, we used other geochronological data (e.g., tephrochronology, paleomagnetism, radiometric dating of flowstones and stalagmites) and/or stratigraphic evidence to constrain the age of each fossil occurrence. Finally, we relied on biochronological evidence or chronological seriation if no geochronological data were available for a given site. For some localities, we used a combination of these criteria to establish the age of local faunal assemblages as in the original studies. In the case of Madagascar, it was not possible to apply our criteria strictly, as most of the occurrences lack a precise stratigraphic context and no biochronological schemes are available (*690*, *721*, *1719*, *1794*). However, we used dated remains of extant and extinct species from each subfossil locality to constrain the age of co-occurring undated extinct and extant species, respectively. We are aware that, in the absence of stratigraphic information, the accuracy of indirect dates should be viewed with caution (*22*, *1665*, *1881*), so we repeated our analyses by including only direct dates of Madagascan mammals, and this did not change our results substantially (fig. S9A).

To examine how extinction rates of insular mammals have changed over time as a function of their body size evolution and human colonization patterns, we recorded dates of arrival of pre-*sapiens* hominins and *Homo sapiens* on each island, based on the earliest archeological evidence and 86 sources (*22*, *24*, *266*, *287*, *442–444*, *525*, *541*, *610*, *637*, *646*, *714*, *827*, *904*, *910*, *933*, *951*, *1081*, *1235*, *1240*, *1292*, *1409*, *1511*, *1525*, *1569*, *1572*, *1581*, *1624*, *1628*, *1671*, *1697*, *1824*, *1834*, *1840*, *1858*, *1882–1931*). In case of marked discrepancies between different modern human dispersal models - e.g., early and late dispersal models for Madagascar and several islands in Southeast Asia - we provided ranges of human arrival times.

<u>Extinction risk</u>

Input data. To investigate the relationships between extinction risk and body size evolution, we defined two binary response variables: we treated living species as nonthreatened (LC/NT) or threatened (VU/EN/CR) and all species in our database as extant (LC/NT/VU/EN/CR) or extinct (EX/EP). We complemented data on body masses and extinction risk of insular species with data on 3,953 mainland species extracted from PHYLACINE (*227*), including 210 late Quaternary extinct species.

Generalized linear mixed effects models (GLMMs). We ran binomial generalized linear mixed effects models for extant insular mammals and all insular mammals together. We included taxonomic order as a random intercept in all models to account for taxonomic relatedness (*25*, *1932*). We scaled body mass with a Z-transformation and performed model diagnostics by inspecting residual plots created with the DHARMa package (*1933*). To summarize the amount of variance in the data explained by each model, we calculated marginal and conditional R^2 values (*1934*). We tested for predictor collinearity using variance inflation factors (<5 for all predictors) (*1935*).

At the species level, we evaluated the relationship between extinction risk (probability of being threatened or probability of being extinct) and the magnitude of body size change and body mass (Fig. 1, figs. S3 and S4, and tables S1 to S3). We also tested whether the relationship between extinction risk and magnitude of body size change was dependent on body mass and on the direction of body size change, by including the interactions magnitude x body mass and magnitude x direction (Fig. 1 and tables S1 to S3). To explore whether our results were robust to a more restrictive definition of extinction risk, we repeated our analysis by excluding prehistoric extinctions and by coding the remaining species as extant or historically extinct (EX) (fig. S5A and table S6).

We also assessed whether the probability of being threatened is correlated with the magnitude of body size change at the population-level (fig. S5, C and D, and tables S4 and S5). In this analysis, we included both the direction of body size change (interaction) and endemism (interaction) as fixed effects to account for the fact that our population-level dataset encompasses not only populations of island endemics, but also several populations of taxa with a wider geographic range (which occur both on the mainland and on one or multiple islands). In our dataset, the latter populations were often assigned to different threat categories based on species-level extinction risk information, potentially leading to an over-representation of non-threatened populations of non-endemic species which might be, in fact, locally endangered on islands. This might have affected the results of our assessment of the relationship between extinction risk and body size change for populations of non-endemic species and might explain the gentler slopes - and even a negative slope for populations of non-endemic giants - that we recorded (fig. S5D and tables S4 and S5).

To avoid rank deficiency in fixed-effect matrices of multiple predictor models, we excluded the few insular species (6 extant, 8 extinct) and populations (16) which have not experienced any change in body size from our analyses of extinction risk. Nevertheless, we reported models including those taxa in tables S2 and S5 to show that, despite their inclusion, the simple relationship between the probability of being threatened and the magnitude of body size change remains significant and positive. Fossil taxa that are assumed not to have undergone any size change (n=8) were excluded because in most cases their body size change was assessed qualitatively [e.g., *Cervus elaphus rossii* from Corsica (*246*), *Oryzomys antillarum* from Jamaica (*240*)].

Moreover, we investigated the relationship between body mass and extinction risk and whether it is significantly different between mainland and insular species (additive and interaction effects) (Fig. 2, A and B, and tables S7 and S8). Because our dataset does not include mainland species that went extinct before the Late Pleistocene, we repeated the analysis by excluding older insular species and prehistoric extinctions and obtained similar results (table S7). We also explored raw data by plotting the proportion and number of threatened, extinct, and historically extinct species within each body mass class on islands and on the mainland (Fig. 2, C and D, and fig. S5B).

Finally, in addition to testing the effect of each predictor separately, we also fitted more complex models with different combinations of all predictors (magnitude and direction of body size change, body mass), and a null model (intercept-only). We used Akaike information criterion scores corrected for small sample size (AICc) (*1936–1938*) to rank our models and to assess whether the magnitude of body size change is a better predictor of extinction risk for insular mammals than body mass per se.

Phylogenetic logistic regressions. As a sensitivity analysis and to further control for phylogenetic dependence we fitted phylogenetic logistic regressions (*1939*, *1940*) (fig. S6 and tables S9 to S12). We assessed the effect of the magnitude of body size change and body mass separately and reported AICc scores to rank our models. We also computed a coefficient of determination based on the likelihood of fitted models, R^2_{lik} (*1941*). This score is suitable for models with correlated errors, such as phylogenetic logistic regressions, and it reflects the amount of information that the models contain (*1941*). Each phylogenetic logistic model also includes an estimated parameter (alpha) that controls the strength of the phylogenetic signal in the dependent variable (i.e., extinction risk) (*1939*, *1940*). This parameter is scaled so that smaller values of alpha, closer to zero, indicate greater phylogenetic signal.

To be able to include all extant and extinct taxa with trait information in these analyses, we generated a pseudo-posterior distribution of completely sampled phylogenies by using a stochastic polytomy resolver - Taxonomic Addition for Complete Trees (TACT) (*1942*). First, we selected 100 randomly drawn node-dated backbone trees from the most recent mammal phylogenies currently available at the species-level (*417*). We then compiled a taxonomic list which included all taxonomic ranks (e.g., genus, family, order) for both sampled and unsampled taxa – that is, extant and extinct taxa not included in the backbone trees, but for which we had trait data. For the extant species names included in the taxonomic list, trait database, and backbone trees, we followed Upham et al (*417*). We used TACT to convert the taxonomic list into a topology and, finally, to add our unsampled species to each of the 100 backbone trees indicated above. All in all, we obtained 100 pseudo-posterior, complete trees, that we used to run phylogenetic logistic regressions.

We used the package sensiPhy (*1943*) to estimate the impact of different types of uncertainty on our phylogenetic analyses. We ran phylogenetic logistic regressions across our 100 complete trees obtained by TACT to account for phylogenetic uncertainty (i.e., variation in tree topologies and node ages) (fig. S6 and tables S9 to S12) (*417*, *1943*). We also used 100 DNA-only trees in our analyses across extant insular species and populations, because taxonomically imputed species move around at random within the taxonomic constraints (*417*, *1944*). Despite this and other potential uncertainties associated with the expansion of phylogenies (e.g., our complete trees include taxonomically imputed extinct species that are thought to be part of anagenetic lineages), our combined approach of phylogenetic logistic regressions and GLMMs further ensures that our results are robust. In addition, we used our population-level dataset to investigate the relationship between the probability of being threatened and our traits while evaluating not only phylogenetic uncertainty, but also data uncertainty (i.e., intraspecific variability in explanatory variables) (fig. S6 and table S11). SensiPhy accounts for intraspecific variation by simulating trait values for each species derived from the intraspecific standard deviation of the mean, which we calculated from our population-level dataset, and assuming a normal distribution (*1943*). Because different types of uncertainty can interact and potentially further reduce the robustness of results, we also accounted for the interaction between data and phylogenetic uncertainty (*1943*). For each analysis and estimated parameter, we reported standard deviation, maximum, minimum, mean values and 95% confidence intervals.

<u>Phylogenetic signal of body size change</u>

To assess the robustness of our approach in analyzing extinction risk, we tested for phylogenetic signal in the magnitude of body size change using Blomberg's K (*1945*) and Pagel's λ (*1946*) and in the direction of body size change using the D-statistic (*1947*). We performed the estimates of phylogenetic signal across our 100 complete trees to incorporate the uncertainty in tree topology (fig. S7B). Finally, we synthesized the evolution of insular dwarfs and giants by plotting the direction of body size change, as defined in our extinction risk analysis, on the mammal tree of life (fig. S7A). The phylogeny in fig. S7A includes only insular species (N = 827). We found no phylogenetic signal in the magnitude of body size change using Blomberg's K (mean K across replicates = 0.01, $p > 0.05$ for all replicates) and values of Pagel's λ (mean λ across replicates = 0.80, $p < 0.001$ for all replicates) indicate that this trait has not evolved according to a pure Brownian motion model (fig. S7B). Furthermore, we found that closely related island mammals were not necessarily more similar in their direction of body size change than distantly related species (fig. S7B, mean D across replicates = 0.59). These results further support our decision to not impute missing values for the magnitude and direction of body size change (see above). In fact, the accuracy of phylogenetic imputations decreases in the absence of a strong phylogenetic signal in the focal traits (*434*, *1948*).

Extinction rates in the fossil record

We analyzed the fossil record of mammals on islands using the Bayesian framework implemented in the program PyRate (*1949–1951*). We estimated extinction and preservation rates through time and speciation and extinction times of each species, while accounting for dating uncertainties and incomplete sampling due to preservation processes. To account for potential discrepancies between rates calculated at different temporal scales – i.e., different temporal resolution and extent (*7*, *1952*), we adopted a nuanced approach and ran three separate analyses. First, we ran a broad analysis through the complete temporal interval (last 23.03 Ma) to detect times of significant extinction rate change. To quantify the magnitude and extent of the latest rate shift, we then ran two analyses over the last 2.58 Ma (Quaternary) and 0.129 Ma (Late Pleistocene + Holocene) at progressively finer temporal resolutions (setting the time units in the analyses to 100 kyr and 10 kyr, respectively).

We determined the best-fitting preservation model for our dataset of fossil occurrences using maximum likelihood and implemented a time-variable Poisson process in each analysis (*1949–1951*). This model of preservation assumes constant preservation rates within predefined time frames, but it allows them to vary across time frames (in our case, geological stages). We used reversible-jump Markov Chain Monte Carlo (RJMCMC) to estimate the number and temporal placement of extinction rate shifts. For each analysis, we ran PyRate for 100 million RJMCMC iterations and sampled every 10,000 iterations to obtain the posterior estimates of all parameters (origination and extinction times of all species, preservation rates, extinction rates). We used the program Tracer (*1953*) to ensure that the analyses reached convergence. Shifts in extinction rates were allowed to take place every time unit in the first two analyses (250 ka and 100 ka, respectively) and every 0.1 time units (= 1000 years) in the analysis starting from the Late Pleistocene (using the argument -min_dt 0.1). To incorporate dating uncertainties, we ran 10 parallel PyRate runs after randomly resampling the ages of the fossil occurrences from their stratigraphic ranges and combined their results in joint posterior samples. In total, we obtained 3 joint posterior samples and, after discarding the first 200 samples (equivalent to the first 2 million iterations) as burnin, we used them to calculate the sampling frequencies of birth-death models with different number of extinction rate shifts (fig. S11) and to plot extinction rates through time and inferred times of rate shifts (Fig. 3, A to C, and fig. S8). We used the command -grid_plot 0.05 to increase the resolution of the plots. This command allows to define shorter temporal bins (0.05 time units) utilized to calculate marginal rates and times of rate shift. From the estimated extinction rates, we also calculated the relative magnitudes of rate change for each analysis by dividing the extinction rate at a given time point by the extinction rate at the beginning of each time frame (23.03 Ma, 2.58 Ma and 0.129 Ma; fig. S8). Finally, we combined times of extinction inferred from our broader analysis and from the literature (*31*, *417*, *1805*) to map extinctions of 226 insular dwarfs and giants through time (fig. S7C).

Our dataset includes fossil occurrences of species that are part of endemic anagenetic lineages, and this might affect the temporal placement and magnitude of estimated extinction rate shifts. Accordingly, we repeated our PyRate analyses by excluding basal and intermediate members of anagenetic lineages (N = 51; fig. S9). Results of these sensitivity analyses were not substantially different than those obtained for the complete dataset, as they confirmed the temporal placement and magnitude of the best supported extinction rate shifts, especially over the last 2.58 Ma and 0.129 Ma (fig. S9).

Time-and-trait-dependent extinctions

To explore how extinction rates changed across lineages as a function of our traits (body mass, body size change, endemism and island type), we implemented a novel multi-trait-dependent extinction model included in the software PyRate (*1954*). The multi-trait-dependent extinction model fits an extinction process with lineage-specific extinction rates, which depend on the states of one or multiple categorical traits. Specifically, the extinction rate of a lineage is defined as the product between an estimated average rate (shared by all lineages) and Dirichlet-distributed multipliers associated to each state of the categorical traits. In the presence of multiple traits, extinction rates are modulated by multipliers associated with each trait. To control for over-parameterization and assess the significance of each trait-dependent effect, the trait multipliers are coupled with trait-specific indicators, $I \in \{0, 1\}$, that can turn off the effect of a trait on extinction rate when $I = 0$. Comparing the prior and posterior probabilities of $I = 1$, we can compute the statistical support for a trait-specific effect through Bayes factors (*1954*). Here, we further expanded the multi-trait-dependent extinction model to incorporate the potential effect of time-dependent and lineage-specific traits, namely the overlap with pre-*sapiens* and with modern humans on the same island. To achieve this we quantified, for each lineage, the time after which the species co-existed with pre-*sapiens* and the time after which the species co-existed with humans, based on its geographic distribution and estimated dates of human arrival on the island(s). We note that for species that went extinct before human arrival on their island the amount of time of coexistence with humans is set to 0. We then considered the trait-dependent lineage-specific extinction rates as background rates and multiplied them by a factor h_p after the time of pre-*sapiens* arrival and by a factor h_s after the time of arrival of modern humans. Thus $h > 1$ indicates a rate increase associated with human arrival, while $h < 1$ indicates a rate decrease. The parameters h_p and h_s were treated as independent parameters shared among all lineages (while having an effect at different times and only on lineages with overlap with humans) and sampled jointly with the mean extinction rate and trait-dependent multipliers through MCMC. We assigned a log-normal prior on h_p and h_s centered in 1 (i.e., no effect) such that $\log_{10}(h) \sim N(0, 1)$. We termed this model that adds time-dependent effects to the trait-dependent extinction model as time-and-trait-dependent extinction model.

We classified species in seven body mass categories and seven categories of body size change (table S13). Furthermore, we coded endemism and island type as two (endemic, non-endemic) and three (continental, oceanic, continental + oceanic) categories, respectively (table S13). Unraveling the contributions of anthropogenic and environmental drivers on pre-Holocene local extinctions of mammals on each island or archipelago is challenging (*5*, *22*, *23*). Accordingly, we restricted our assessment of human impacts to evaluating how the time overlap of insular mammals with humans affected global extinction rates on islands. We used times of origination and extinction inferred from the joint posterior samples obtained from our PyRate analyses over the last 23.03 Ma, 2.58 Ma, and 0.129 Ma (see above) to implement the time-and-trait-dependent extinction model for extant and extinct insular mammals with trait data (N = 374, 355, and 285). We ran analyses based on early and late modern human dispersal models and including or excluding basal and intermediate members of anagenetic lineages (Fig. 3 and fig. S10). We used the Probability of Direction to evaluate the strength of empirical evidence in favor of a positive or negative effect of overlap with pre-*sapiens* and with modern humans on extinction rates. The Probability of Direction indicates the certainty associated with the most probable direction (positive or negative) of the effect and it is strongly correlated with the frequentist *p*-value (Probability of Direction > 97.5% ~ $p < 0.05$) (*1955*). We found that extinction rates during phases of temporal overlap of insular mammals with *H. sapiens* were significantly higher than before modern human arrival (Probability of Direction = 98.2% to 99.9% and 99.4% to 99.9%

for the early and late dispersal scenarios, respectively). Most of our time-and-trait-dependent extinction analyses show that co-occurrence with modern humans has increased extinction rates of over 10 times relative to pre-*sapiens*, background rates (Fig. 3I and fig. S10). In particular, the significant, positive effect of temporal overlap with modern humans is estimated at 7.50 to 24.33-fold depending on the baseline extinction rate used, on whether basal and intermediate members of anagenetic lineages were included or excluded, and on different modern human dispersal models (fig. S10). In contrast, we found that the effect of temporal overlap of insular mammals with pre-*sapiens* humans on their extinction rates, albeit positive (~2-fold), was weakly significant (Probability of Direction = 87.1% to 92.5% and 88.5% to 92.6% for the early and late dispersal scenarios, respectively; Fig. 3I and fig. S10). We also found that endemism and island type have the highest probabilities of having an effect on extinction rates ($P\mu$), with very strong statistical support ($P\mu > 0.887$, which is equivalent to a Bayes factor of 10 given the default prior (*1954*); Fig. 3D and fig. S10). Moreover, in all analyses body size change has a higher $P\mu$ than body mass per se and higher extinction rates are associated with moderately to strongly giant and large to very large species (Fig. 3, G and H, and fig. S10).

Software used

We conducted analyses of fossil occurrences and generated our complete phylogenies in Python 3 (*1956*), using the program PyRate (*1949–1951*) and the stochastic polytomy resolver TACT (*1942*). We performed all other analyses in R version 4.1.2 (*1957*), using the packages ape v5.6-2 (*1958*), bayesplot v1.9.0 (*1959*, *1960*), Cairo v1.5-15 (*1961*), caper v1.0.1 (*1962*), car v3.0-12 (*1963*), carData v3.0-5 (*1964*), DHARMa v0.4.5 (*1933*), dplyr v1.0.8 (*1965*), extrafont v0.17 (*1966*), forcats v0.5.1 (*1967*), ggeffects v1.1.1 (*1968*), ggplot2 v3.3.5 (*1969*), ggpubr v0.4.0 (*1970*), ggtree v3.2.0 (*1971–1973*), gridExtra v2.3 (*1974*), gt v0.4.0 (*1975*), IUCNpalette v0.1.0 (*1976*), lme4 v1.1-29 (*1977*), maps v3.4.0 (*1978*), MASS v7.3-54 (*1979*), Matrix v1.3-4 (*1980*), mvtnorm v1.1-3 (*1981*, *1982*), phylolm v2.6.2 (*1983*), phytools v1.0-3 (*1984*), RColorBrewer v1.1-3 (*1985*), rnaturalearth v0.1.0 (*1986*), rnaturalearthdata v0.1.0 (*1987*), rr2 v1.0.2 (*1941*, *1988*), sensiPhy v0.8.5 (*1943*), sf v1.0-7 (*1989*), sjPlot v2.8.10 (*1990*), tidyr v1.2.0 (*1991*) and visreg v2.7.0 (*1992*).

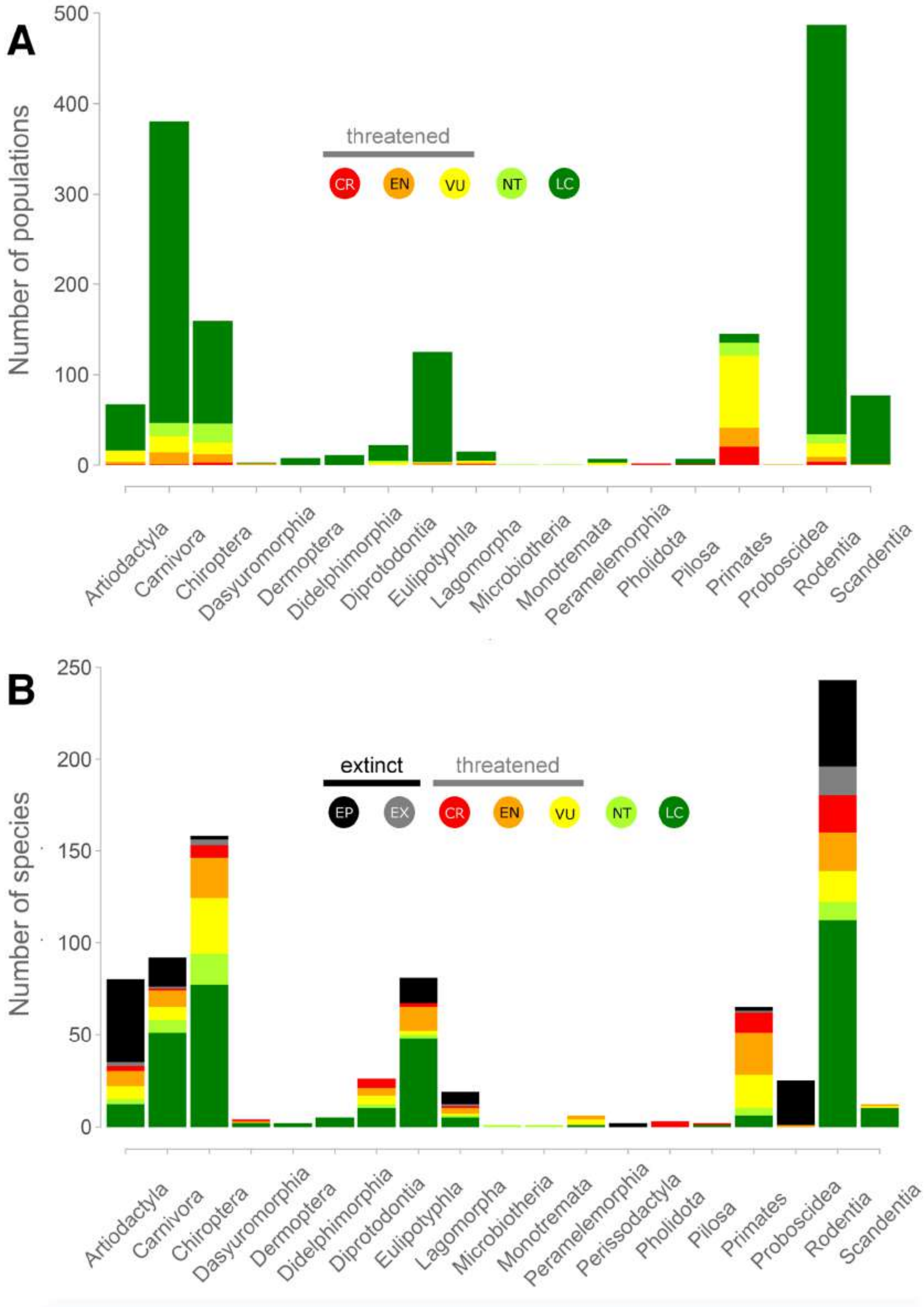

Fig. S1.

Number of populations (A) and species (B) of insular mammals by order and global conservation status included in our analysis of extinction risk.

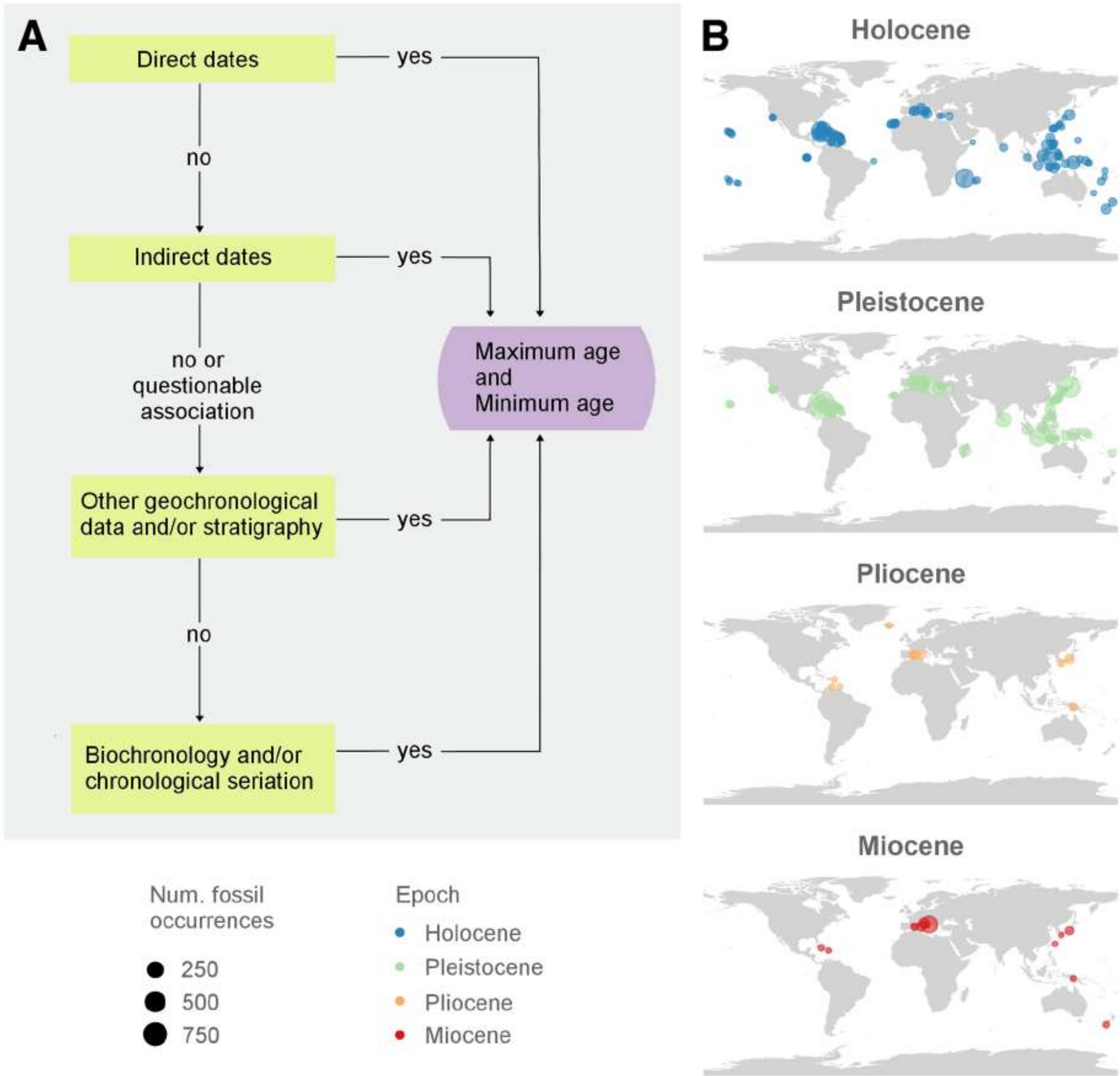

Fig. S2.
Flowchart outlining the protocol used to define the maximum and minimum age of each fossil occurrence in our global dataset (A). Priority was given to direct absolute dates, followed in this order by associated indirect dates, other geochronological data, stratigraphy, biochronology and chronological seriation. Location of fossil occurrences of insular mammals by geological epoch included in our extinction rate analysis (B). Fossil occurrences from Miocene (N = 455), Pliocene (N = 105), Pleistocene (N = 4603) and Holocene (N = 2704) local faunal assemblages are shown in orange, red, green and blue, respectively. The size of each point indicates the number of occurrences on each island or paleo-island (N = 182).

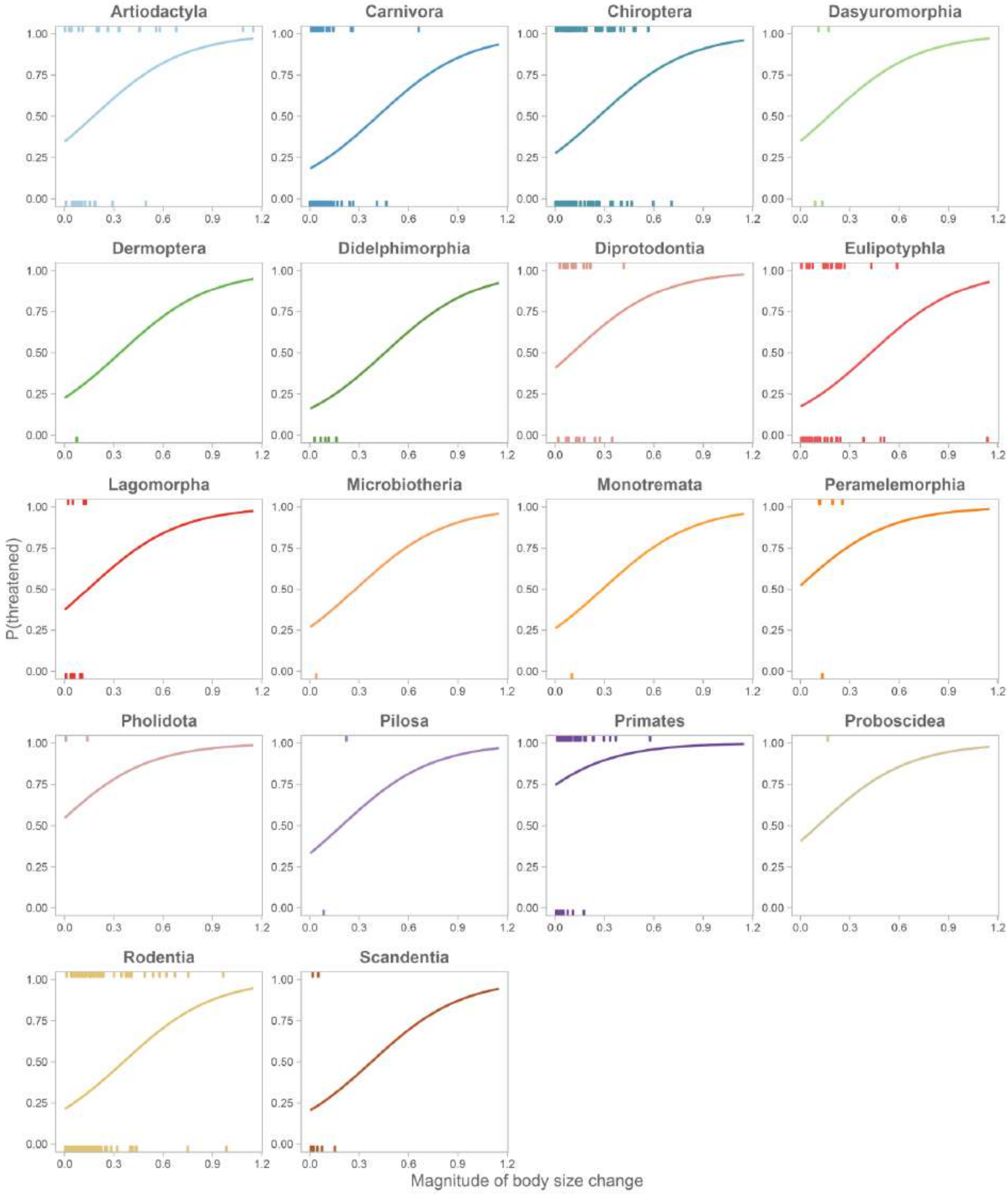

Fig. S3.
The effect of body size change on the probability of being threatened for insular mammals across 18 orders. Relationships between magnitude of body size change and probability of being threatened at the species level based on logistic GLMMs (see table S1 for details). Taxonomic order was used as a random effect on the intercept (reflected with colored lines).

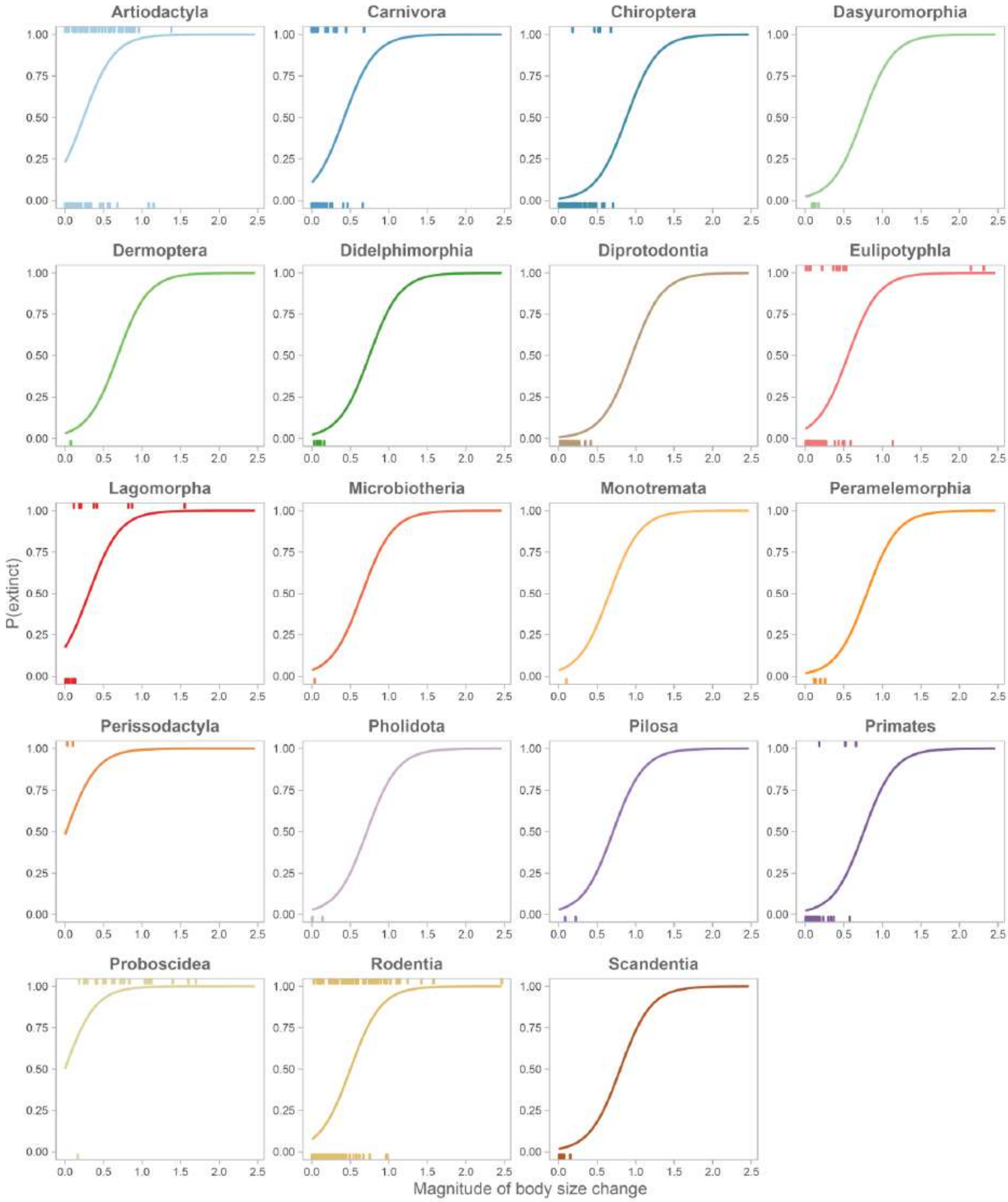

Fig. S4.
The effect of body size change on the probability of being extinct for insular mammals across 19 orders. Relationships between magnitude of body size change and probability of being extinct at the species level based on logistic GLMMs (see table S3 for details). Taxonomic order was used as a random effect on the intercept (reflected with colored lines).

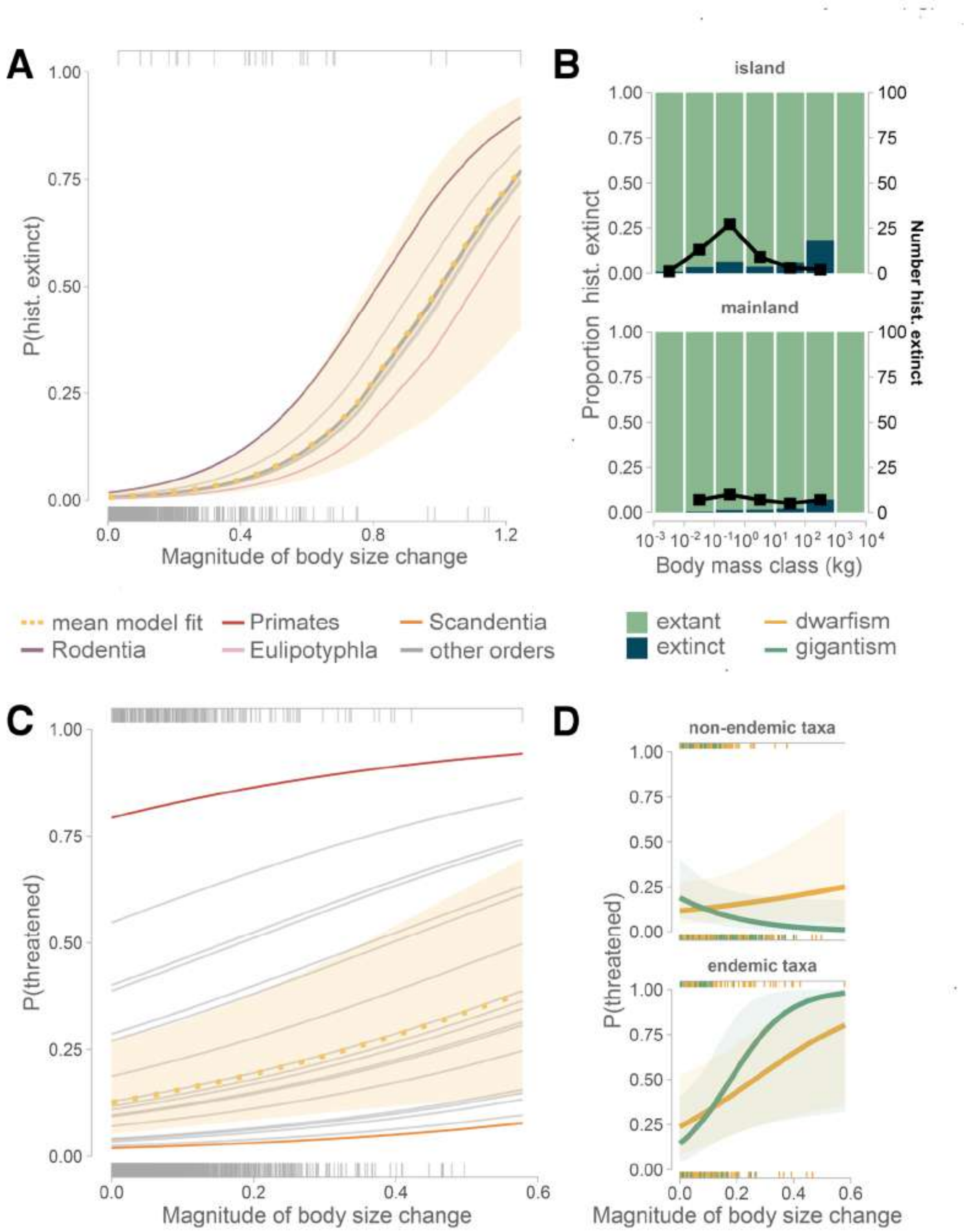

Fig. S5.
Relationship between magnitude of body size change and probability of being extinct at the species-level, based on historic extinctions since 1500 CE only (A) (see table S6 for details). Proportion and number of historically extinct species within each body mass class on islands (B). Relationship between magnitude of body size change and probability of being threatened for populations of insular mammals (C). Relationship between magnitude and direction of body size change and probability of being threatened for insular populations of endemic and non-endemic species (D) (see table S4 for details). Lines in the graphs indicate the predicted probabilities of being historically extinct and threatened (and 95% confidence intervals) based on logistic GLMMs with taxonomic random effects.

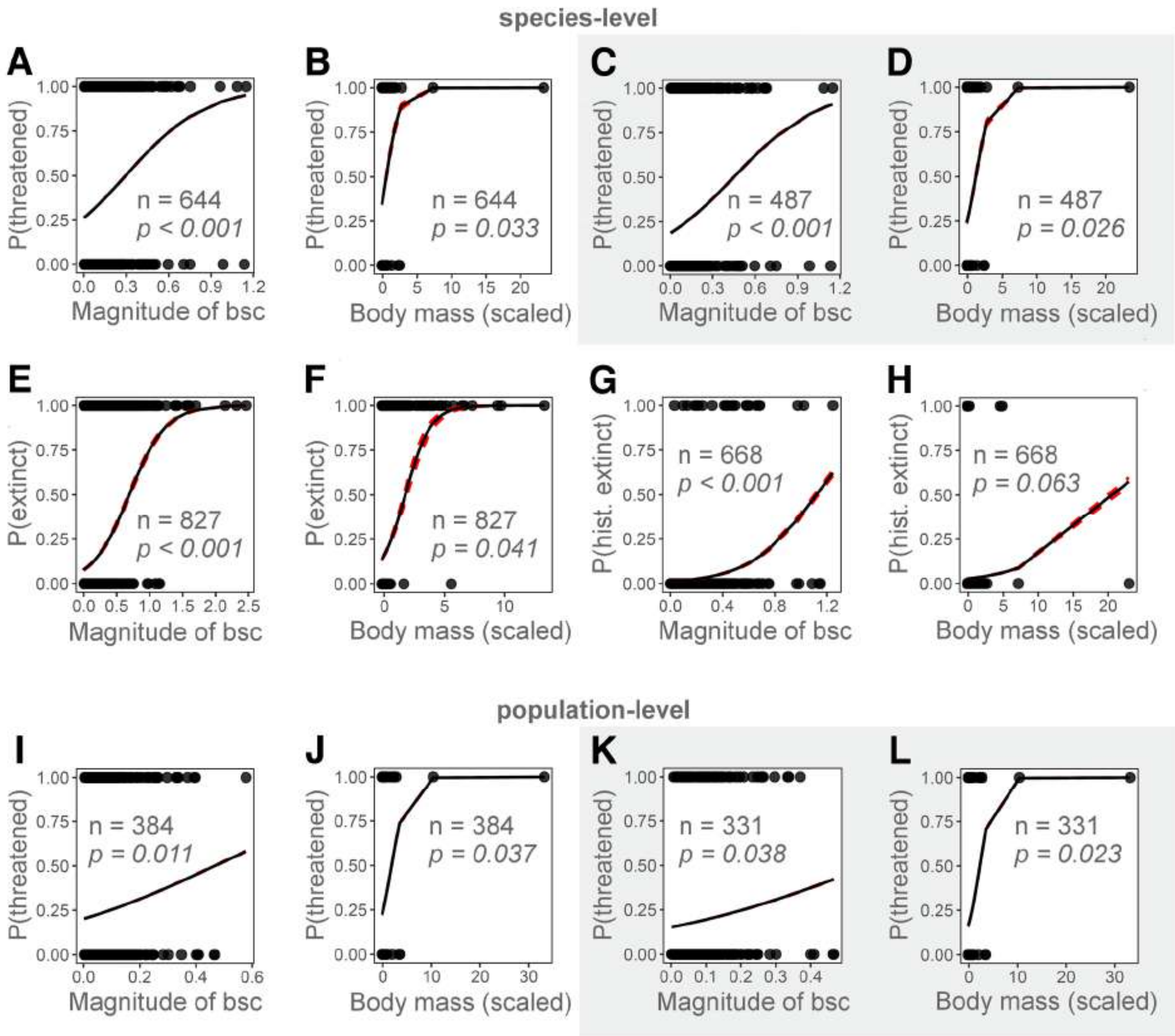

Fig. S6.
Relationships between magnitude of body size change (A, C, E, G, I, K), body mass (B, D, F, G, J, L), and extinction risk based on phylogenetic logistic regressions. Lines in the graphs indicate the predicted probabilities of being threatened, extinct and historically extinct (and 95% confidence intervals) as a function of magnitude of body size change and body mass (see tables S9 to S12 for details). We ran these models across 100 complete trees (white background) and 100 DNA-only trees (gray background) to account for uncertainties in trees topologies. Results at the species level (A-H). Results at the population level, also accounting for intraspecific variability in explanatory variables (I-L).

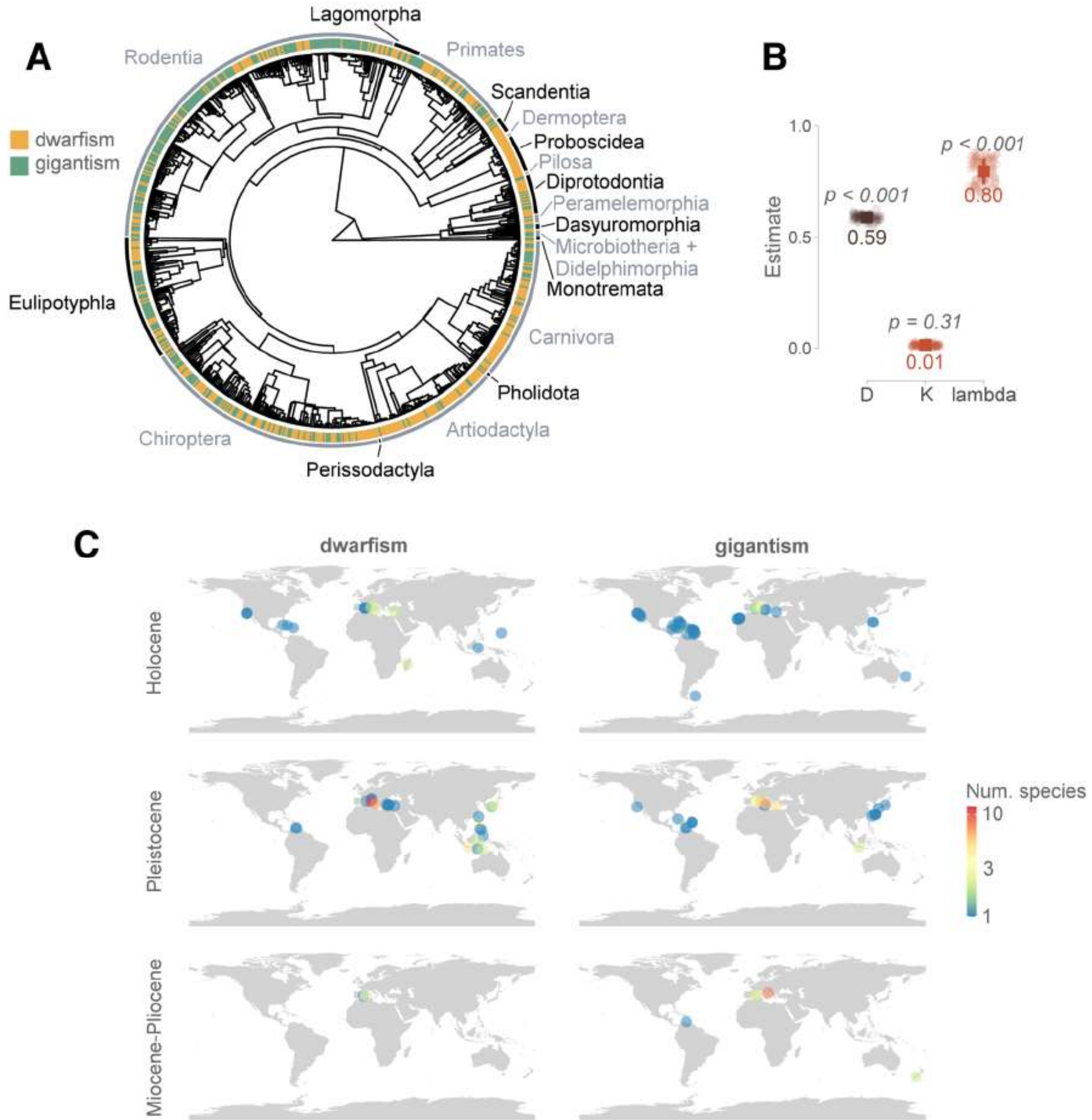

Fig. S7.
Phylogenetic distribution of dwarfs and giants and their extinctions through space and time. Dwarfism and gigantism (i.e., the direction of body size change) across the mammal tree of life (A). The phylogeny includes only insular species (N = 827). Phylogenetic signal in the magnitude of body size change based on Blomberg's K and Pagel's λ and in the direction of body size change based on the D-statistic (B). Extinctions of 226 insular dwarfs (N = 94) and giants (N = 132) through space and time (C). Examples of dwarfism and gigantism in insular mammals are known since the Mesozoic (*1993*, *1994*), but the effects of body size change in these taxa are much better documented starting from the Miocene.

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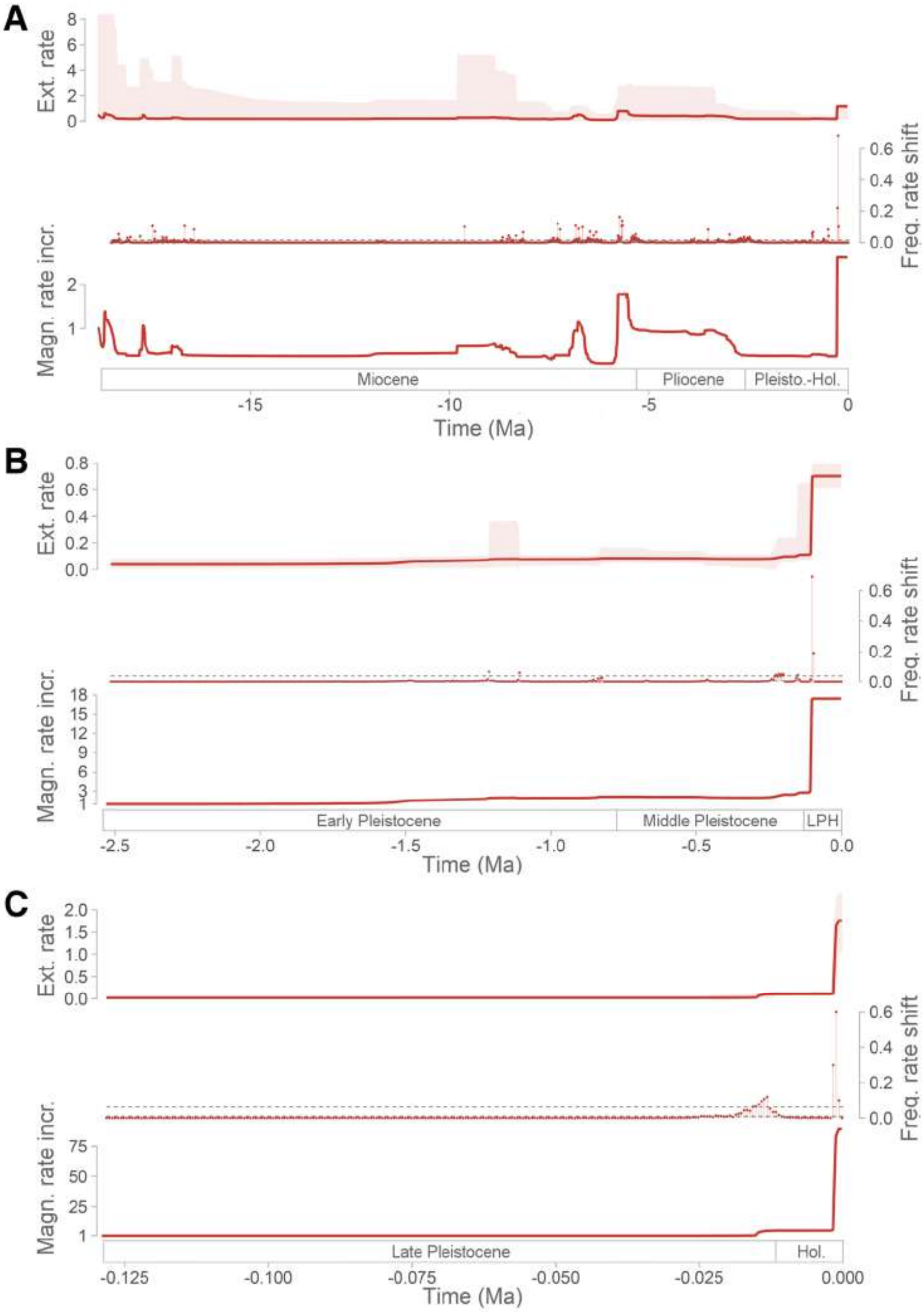

Fig. S8.
Extinction rates (μ) through time estimated by PyRate. Analysis over the last 23.03 Ma (A), 2.58 Ma (B) and 0.129 Ma (C). The solid lines and shaded areas represent the mean posterior rates and 95% credible intervals, respectively. Also shown are timing and statistical significance of extinction rate shifts. The dashed lines indicate threshold levels corresponding to a log Bayes factor = 2 (bottom line; positive evidence of a rate shift) and log Bayes factor = 6 (top line; strong evidence of a rate shift). We also report the magnitude of extinction rate changes relative to the starting rate (red lines, mean values) through time. Pleisto.-Hol., Pleistocene + Holocene; LPH, Late Pleistocene + Holocene; Hol., Holocene.

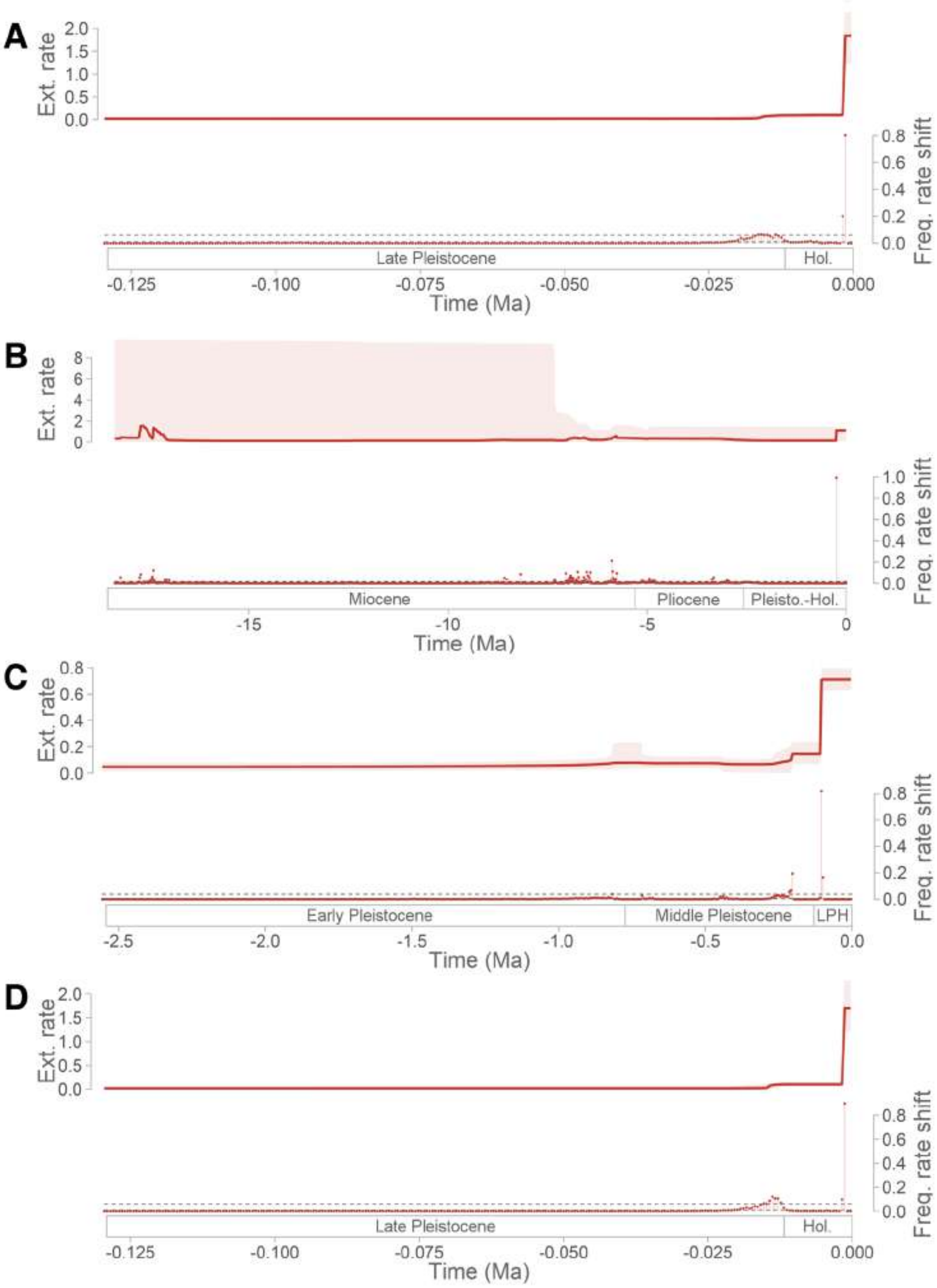

Fig. S9.
Extinction rates (μ) through time estimated by PyRate. Analysis over the last 0.129 Ma including only direct dates of Madagascan mammals (A). Analyses over the last 23.03 Ma, 2.58 Ma and 0.129 Ma excluding basal and intermediate members of anagenetic lineages (B-D). The solid lines and shaded areas represent the mean posterior rates and 95% credible intervals, respectively. Also shown are timing and statistical significance of extinction rate shifts. The dashed lines indicate threshold levels corresponding to a log Bayes factor = 2 (bottom line; positive evidence of a rate shift) and log Bayes factor = 6 (top line; strong evidence of a rate shift). Pleisto.-Hol., Pleistocene + Holocene; LPH, Late Pleistocene + Holocene; Hol., Holocene.

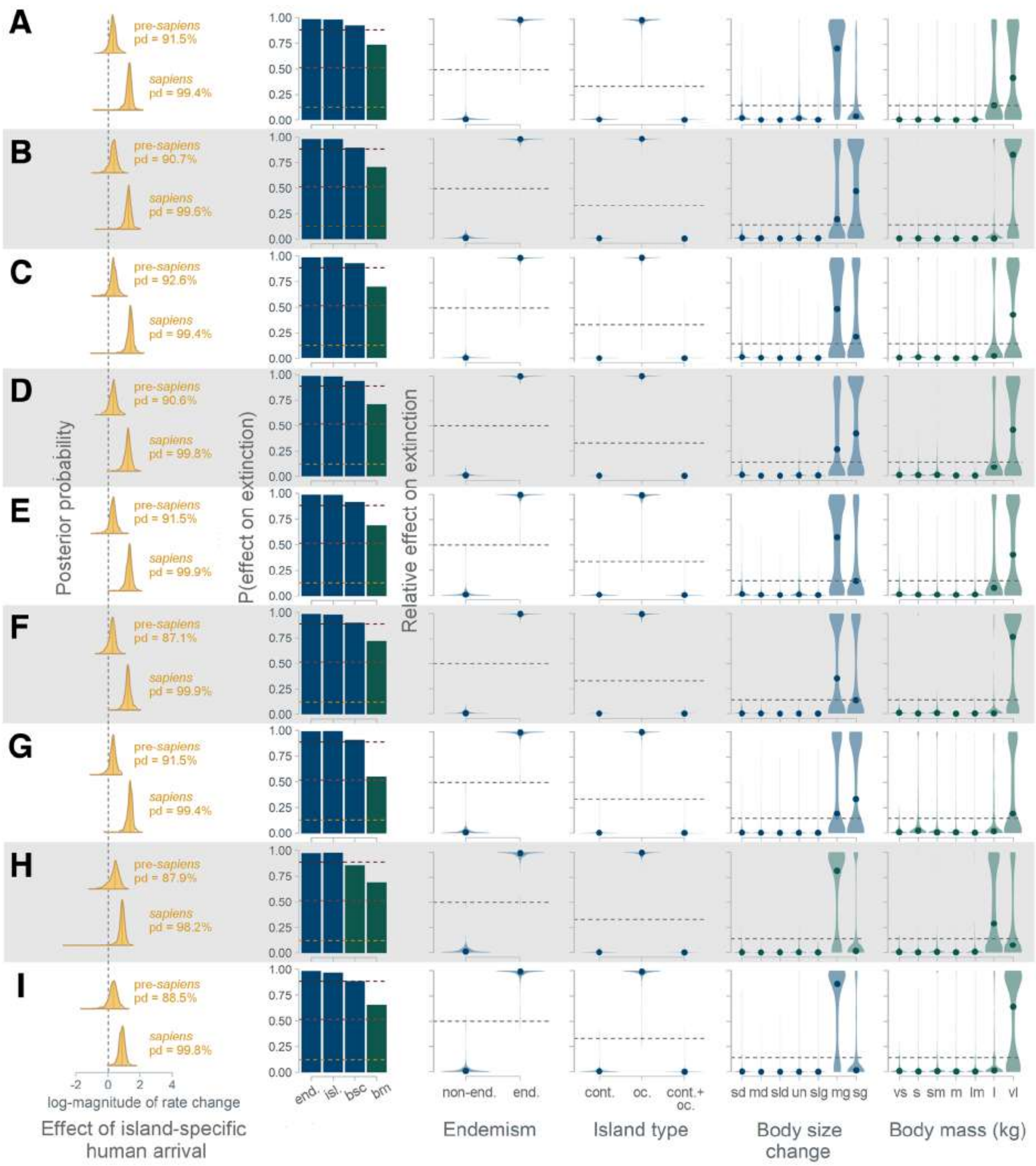

Fig. S10.
Sensitivity of time-and-trait-dependent extinction analyses on islands globally to modern human dispersal models, different temporal resolutions and baseline extinction rates, and anagenetic lineages. Positive effect of temporal overlap of insular mammals with humans on their extinction rates based on late (white background) and early (gray background) *H. sapiens* dispersal models. Posterior medians and 95% credible intervals are shown as vertical lines and shaded areas under the posterior density curves. All variables have high probabilities of having an effect on extinctions, with island type and endemism having the strongest statistical support. Colored

dashed lines indicate the thresholds corresponding to log Bayes factor values of 2 (yellow, positive support), 6 (orange, strong support), and 10 (red, very strong support). Also shown the relative effect of endemism, island type, body size change and body mass on extinction rates of insular mammals. Each dashed line represents the expected value of Dirichlet-distributed multipliers under a null model where the trait has no effect on extinction. Extinction analyses over the last 23.03 Ma and including (A) or excluding (B, C) basal and intermediate members of anagenetic lineages. Extinction analyses over the last 2.58 Ma and including (D, E) or excluding (F, G) basal and intermediate members of anagenetic lineages. Extinction analyses over the last 0.129 Ma and including basal and intermediate members of anagenetic lineages (H, I).

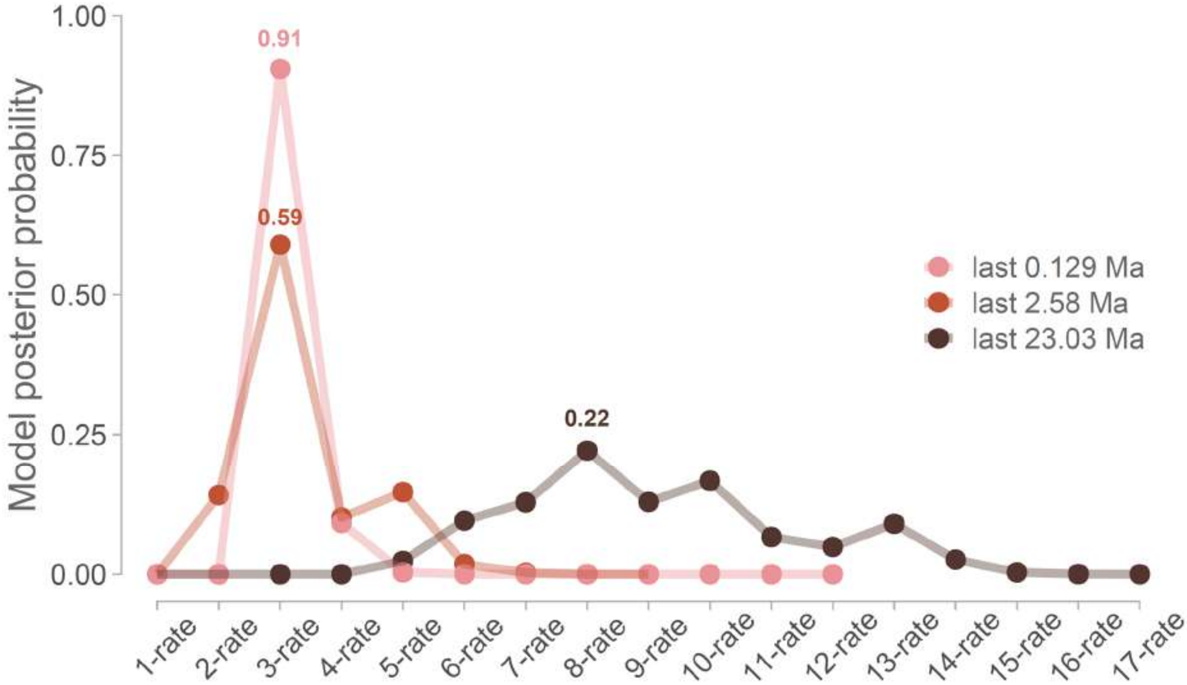

Fig. S11.
Sampling frequencies of birth-death models with different numbers of extinction rate shifts calculated through the focal temporal intervals: last 23.03 Ma, 2.58 Ma and 0.129 Ma. Models with 8, 3 and 3 rate shifts, respectively, are the best supported (i.e., they are characterized by higher relative probabilities).

Table S1.

Comparison of GLMMs for the probability of being threatened at the species-level. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient; * = best model.

	P(threatened)			P(threatened)			P(threatened)			P(threatened)		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.73	0.42 – 1.29	0.281	0.47	0.26 – 0.84	**0.011**	0.71	0.40 – 1.25	0.236	0.45	0.25 – 0.82	**0.008**
Magnitude				37.88	10.45 – 137.29	**<0.001**				39.19	10.66 – 144.08	**<0.001**
Body mass							2.10	0.93 – 4.71	0.073	2.07	0.91 – 4.73	0.083
Random Effects												
σ^2	3.29			3.29			3.29			3.29		
τ_{00}	0.87 $_{Order}$			0.85 $_{Order}$			0.83 $_{Order}$			0.86 $_{Order}$		
ICC	0.21			0.21			0.20			0.21		
N	18 $_{Order}$			18 $_{Order}$			18 $_{Order}$			18 $_{Order}$		
Observations	644			644			644			644		
Marginal R^2 / Conditional R^2	0.000 / 0.209			0.072 / 0.262			0.117 / 0.296			0.176 / 0.346		
AICc	812.328			777.311			808.126			773.302*		

	P(threatened)			P(threatened)			P(threatened)		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.45	0.25 – 0.82	**0.008**	0.44	0.24 – 0.82	**0.010**	0.42	0.22 – 0.79	**0.007**
Magnitude	39.79	10.59 – 149.46	**<0.001**	30.10	5.62 – 161.13	**<0.001**	32.87	5.92 – 182.58	**<0.001**
Body mass	2.01	0.82 – 4.91	0.126				2.12	0.92 – 4.85	0.077
Magnitude * Body mass	1.60	0.01 – 327.88	0.862						
Direction [gigantism]				1.17	0.71 – 1.92	0.545	1.21	0.74 – 2.00	0.448
Magnitude * Direction [gigantism]				2.06	0.15 – 29.08	0.593	1.83	0.13 – 26.48	0.657
Random Effects									
σ^2	3.29			3.29			3.29		
τ_{00}	0.86 $_{Order}$			0.86 $_{Order}$			0.85 $_{Order}$		
ICC	0.21			0.21			0.21		
N	18 $_{Order}$			18 $_{Order}$			18 $_{Order}$		
Observations	644			644			644		
Marginal R^2 / Conditional R^2	0.190 / 0.357			0.075 / 0.267			0.182 / 0.350		
AICc	775.299			779.401			775.138		

Table S2.

Comparison of GLMMs for the probability of being threatened at the species-level, including 6 species that have not experienced any change in body size. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient; * = best model.

	P(threatened)			**P(threatened)**			**P(threatened)**			**P(threatened)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.73	0.41 – 1.29	0.277	0.46	0.26 – 0.83	**0.010**	0.71	0.40 – 1.25	0.231	0.45	0.25 – 0.81	**0.008**
Magnitude				38.53	10.67 – 139.18	**<0.001**				39.83	10.87 – 145.94	**<0.001**
Body mass							2.11	0.94 – 4.75	0.069	2.09	0.92 – 4.75	0.080
Random Effects												
σ^2	3.29			3.29			3.29			3.29		
τ_{00}	0.88 Order			0.86 Order			0.85 Order			0.86 Order		
ICC	0.21			0.21			0.20			0.21		
N	18 Order			18 Order			18 Order			18 Order		
Observations	650			650			650			650		
Marginal R^2 / Conditional R^2	0.000 / 0.211			0.072 / 0.264			0.119 / 0.299			0.178 / 0.349		
AICc	817.873			782.306			813.572			778.223*		

	P(threatened)			**P(threatened)**			**P(threatened)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.45	0.25 – 0.81	**0.008**	0.44	0.23 – 0.82	**0.010**	0.42	0.22 – 0.79	**0.007**
Magnitude	40.42	10.81 – 151.20	**<0.001**	29.78	5.57 – 159.27	**<0.001**	32.53	5.86 – 180.60	**<0.001**
Body mass	2.02	0.83 – 4.94	0.121				2.12	0.93 – 4.86	0.075
Magnitude * Body mass	1.57	0.01 – 315.52	0.867						
Direction [gigantism]				1.16	0.71 – 1.91	0.549	1.21	0.73 – 2.00	0.452
Direction [no change]				0.74	0.08 – 6.59	0.788	0.78	0.09 – 6.99	0.826
Magnitude * Direction [gigantism]				2.10	0.15 – 29.67	0.583	1.87	0.13 – 26.98	0.646
Random Effects									
σ^2	3.29			3.29			3.29		
τ_{00}	0.86 Order			0.87 Order			0.86 Order		
ICC	0.21			0.21			0.21		
N	18 Order			18 Order			18 Order		
Observations	650			650			650		
Marginal R^2 / Conditional R^2	0.191 / 0.359			0.076 / 0.269			0.183 / 0.352		
AICc	780.222			786.283			781.974		

Table S3.

Comparison of GLMMs for the probability of being extinct at the species-level. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient; * = best model.

	P(extinct)			P(extinct)			P(extinct)			P(extinct)		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.08	0.02 – 0.44	**0.004**	0.04	0.01 – 0.15	**<0.001**	0.12	0.04 – 0.36	**<0.001**	0.05	0.02 – 0.10	**<0.001**
Magnitude				152.59	53.52 – 435.10	**<0.001**				188.25	66.72 – 531.14	**<0.001**
Body mass							3.02	1.45 – 6.27	**0.003**	3.43	1.92 – 6.15	**<0.001**
Random Effects												
σ^2	3.29			3.29			3.29			3.29		
τ_{00}	6.46 $_{Order}$			3.52 $_{Order}$			2.40 $_{Order}$			1.07 $_{Order}$		
ICC	0.66			0.52			0.42			0.25		
N	19 $_{Order}$			19 $_{Order}$			19 $_{Order}$			19 $_{Order}$		
Observations	827			827			827			827		
Marginal R^2 / Conditional R^2	0.000 / 0.663			0.241 / 0.633			0.177 / 0.524			0.502 / 0.624		
AICc	709.773			570.371			697.523			542.777		

	P(extinct)			P(extinct)			P(extinct)		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.05	0.02 – 0.10	**<0.001**	0.02	0.00 – 0.11	**<0.001**	0.02	0.01 – 0.06	**<0.001**
Magnitude	189.87	65.70 – 548.66	**<0.001**	50.17	10.64 – 236.62	**<0.001**	110.82	23.81 – 515.71	**<0.001**
Body mass	3.36	1.58 – 7.18	**0.002**				3.91	2.11 – 7.23	**<0.001**
Magnitude * Body mass	1.11	0.09 – 14.04	0.938						
Direction [gigantism]				3.16	1.52 – 6.54	**0.002**	3.85	1.82 – 8.13	**<0.001**
Magnitude * Direction [gigantism]				7.85	0.91 – 67.83	0.061	3.31	0.39 – 27.99	0.271
Random Effects									
σ^2	3.29			3.29			3.29		
τ_{00}	1.08 $_{Order}$			5.96 $_{Order}$			1.29 $_{Order}$		
ICC	0.25			0.64			0.28		
N	19 $_{Order}$			19 $_{Order}$			19 $_{Order}$		
Observations	827			827			827		
Marginal R^2 / Conditional R^2	0.505 / 0.627			0.243 / 0.731			0.534 / 0.665		
AICc	544.795			537.291			511.100*		

Table S4.

Comparison of GLMMs for the probability of being threatened at the population-level. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient; * = best model.

	P(threatened)			**P(threatened)**			**P(threatened)**			**P(threatened)**			**P(threatened)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.19	0.07 – 0.48	**<0.001**	0.14	0.06 – 0.37	**<0.001**	0.17	0.06 – 0.42	**<0.001**	0.13	0.05 – 0.32	**<0.001**	0.13	0.05 – 0.32	**<0.001**
Magnitude				12.52	1.74 – 89.79	**0.012**				15.71	2.14 – 115.47	**0.007**	15.48	2.12 – 113.11	**0.007**
Body mass							1.66	1.25 – 2.21	**<0.001**	1.71	1.28 – 2.28	**<0.001**	1.95	1.33 – 2.87	**0.001**
Magnitude * Body mass													0.10	0.00 – 9.16	0.314
Random Effects															
σ^2	3.29			3.29			3.29			3.29			3.29		
τ_{00}	3.04 $_{Order}$			2.90 $_{Order}$			2.90 $_{Order}$			2.77 $_{Order}$			2.77 $_{Order}$		
ICC	0.48			0.47			0.47			0.46			0.46		
N	18 $_{Order}$			18 $_{Order}$			18 $_{Order}$			18 $_{Order}$			18 $_{Order}$		
Observations	1518			1518			1518			1518			1518		
Marginal R^2 / Conditional R^2	0.000 / 0.481			0.007 / 0.472			0.040 / 0.490			0.053 / 0.486			0.030 / 0.473		
AICc	907.970			904.064			894.356			889.524			890.554		

	P(threatened)			**P(threatened)**			**P(threatened)**			**P(threatened)**			**P(threatened)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.13	0.05 – 0.33	**<0.001**	0.10	0.04 – 0.27	**<0.001**	0.17	0.06 – 0.45	**<0.001**	0.12	0.04 – 0.32	**<0.001**	0.13	0.05 – 0.38	**<0.001**
Magnitude	50.36	5.25 – 482.56	**0.001**	25.78	2.34 – 283.47	**0.008**	0.54	0.03 – 9.30	0.670	18.40	1.73 – 196.19	**0.016**	5.04	0.19 – 133.14	0.333
Body mass				1.77	1.32 – 2.38	**<0.001**									
Magnitude * Body mass															
Direction [gigantism]	1.63	0.95 – 2.80	0.077	1.57	0.90 – 2.75	0.112				1.51	0.87 – 2.62	0.143	1.79	0.96 – 3.33	0.066
Magnitude * Direction [gigantism]	0.00	0.00 – 0.35	**0.018**	0.00	0.00 – 0.61	**0.032**				0.01	0.00 – 0.93	**0.047**	0.00	0.00 – 0.56	**0.032**
Endemism [yes]				2.94	1.83 – 4.75	**<0.001**	1.58	0.80 – 3.10	0.186	2.86	1.79 – 4.59	**<0.001**	2.38	0.96 – 5.92	0.062
Magnitude * Endemism [yes]							408.36	4.33 – 38534.11	**0.010**				16.89	0.10 – 2924.16	0.282
Direction [gigantism] * Endemism [yes]													0.30	0.07 – 1.25	0.100
(Magnitude * Direction [gigantism]) * Endemism [yes]													246963.57	1.89 – 32226657324.69	**0.039**
Random Effects															
σ^2	3.29			3.29			3.29			3.29			3.29		
τ_{00}	2.92 $_{Order}$			2.97 $_{Order}$			3.28 $_{Order}$			3.14 $_{Order}$			3.32 $_{Order}$		
ICC	0.47			0.47			0.50			0.49			0.50		
N	18 $_{Order}$			18 $_{Order}$			18 $_{Order}$			18 $_{Order}$			18 $_{Order}$		
Observations	1518			1518			1518			1518			1518		
Marginal R^2 / Conditional R^2	0.012 / 0.476			0.081 / 0.517			0.030 / 0.514			0.033 / 0.505			0.040 / 0.523		
AICc	902.150			870.043*			881.299			886.155			883.235		

Table S5.

Comparison of GLMMs for the probability of being threatened at the population-level, including 16 populations that have not experienced any change in body size. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient; * = best model.

	P(threatened)			**P(threatened)**			**P(threatened)**			**P(threatened)**			**P(threatened)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.18	0.07 – 0.47	**<0.001**	0.14	0.06 – 0.37	**<0.001**	0.16	0.06 – 0.42	**<0.001**	0.13	0.05 – 0.32	**<0.001**	0.13	0.05 – 0.32	**<0.001**
Magnitude				11.74	1.66 – 83.14	**0.014**				14.72	2.03 – 106.59	**0.008**	14.53	2.02 – 104.71	**0.008**
Body mass							1.62	1.23 – 2.14	**0.001**	1.67	1.26 – 2.21	**<0.001**	1.86	1.28 – 2.69	**0.001**
Magnitude * Body mass													0.14	0.00 – 12.34	0.390
Random Effects															
σ^2	3.29			3.29			3.29			3.29			3.29		
τ_{00}	3.05 $_{\text{Order}}$			2.90 $_{\text{Order}}$			2.90 $_{\text{Order}}$			2.77 $_{\text{Order}}$			2.77 $_{\text{Order}}$		
ICC	0.48			0.47			0.47			0.46			0.46		
N	18 $_{\text{Order}}$			18 $_{\text{Order}}$			18 $_{\text{Order}}$			18 $_{\text{Order}}$			18 $_{\text{Order}}$		
Observations	1534			1534			1534			1534			1534		
Marginal R^2 / Conditional R^2	0.000 / 0.481			0.006 / 0.472			0.036 / 0.488			0.048 / 0.484			0.029 / 0.473		
AICc	919.559			915.868			906.613			902.000			903.289		

	P(threatened)			**P(threatened)**			**P(threatened)**			**P(threatened)**			**P(threatened)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.12	0.05 – 0.33	**<0.001**	0.10	0.04 – 0.27	**<0.001**	0.16	0.06 – 0.44	**<0.001**	0.12	0.04 – 0.32	**<0.001**	0.13	0.05 – 0.37	**<0.001**
Magnitude	49.65	5.19 – 474.77	**0.001**	24.12	2.20 – 264.59	**0.009**	0.57	0.03 – 9.55	0.694	17.72	1.66 – 188.77	**0.017**	5.06	0.19 – 132.75	0.331
Body mass				1.72	1.29 – 2.29	**<0.001**									
Magnitude * Body mass															
Direction [gigantism]	1.63	0.95 – 2.79	0.078	1.56	0.89 – 2.73	0.117				1.50	0.87 – 2.61	0.147	1.79	0.96 – 3.32	0.066
Direction [no change]	1.97	0.41 – 9.54	0.400	1.63	0.33 – 8.14	0.552				1.83	0.37 – 8.98	0.459	1.13	0.13 – 9.58	0.909
Magnitude * Direction [gigantism]	0.00	0.00 – 0.39	**0.020**	0.00	0.00 – 0.70	**0.036**				0.01	0.00 – 1.05	0.052	0.00	0.00 – 0.59	**0.034**
Endemism [yes]				3.02	1.88 – 4.84	**<0.001**	1.70	0.87 – 3.30	0.118	2.93	1.83 – 4.67	**<0.001**	2.39	0.96 – 5.93	0.061
Magnitude * Endemism [yes]							275.72	3.09 – 24594.27	**0.014**				16.32	0.10 – 2797.71	0.287
Direction [gigantism] * Endemism [yes]													0.30	0.07 – 1.25	0.098
Direction [no change] * Endemism [yes]													4.82	0.13 – 178.19	0.393
(Magnitude * Direction [gigantism]) * Endemism [yes]													251162.32	1.94 – 32515484547.09	**0.038**
Random Effects															
σ^2	3.29			3.29			3.29			3.29			3.29		
τ_{00}	2.92 $_{\text{Order}}$			2.98 $_{\text{Order}}$			3.29 $_{\text{Order}}$			3.15 $_{\text{Order}}$			3.32 $_{\text{Order}}$		
ICC	0.47			0.48			0.50			0.49			0.50		
N	18 $_{\text{Order}}$			18 $_{\text{Order}}$			18 $_{\text{Order}}$			18 $_{\text{Order}}$			18 $_{\text{Order}}$		
Observations	1534			1534			1534			1534			1534		
Marginal R^2 / Conditional R^2	0.012 / 0.477			0.077 / 0.516			0.030 / 0.515			0.033 / 0.506			0.041 / 0.523		
AICc	915.762			883.324*			892.623			898.613			897.175		

Table S6.

Comparison of GLMMs for the probability of being extinct at the species-level based on historic extinctions since 1500 CE only. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient; * = best model.

	P(hist. extinct)			P(hist. extinct)			P(hist. extinct)			P(hist. extinct)		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.02	0.01 – 0.05	**<0.001**	0.01	0.00 – 0.02	**<0.001**	0.02	0.01 – 0.05	**<0.001**	0.01	0.00 – 0.02	**<0.001**
Magnitude				141.65	30.15 – 665.45	**<0.001**				141.52	29.75 – 673.22	**<0.001**
Body mass							1.15	0.94 – 1.41	0.168	1.14	0.93 – 1.42	0.214
Random Effects												
σ^2	3.29			3.29			3.29			3.29		
τ_{00}	0.62 $_{Order}$			0.44 $_{Order}$			0.65 $_{Order}$			0.50 $_{Order}$		
ICC	0.16			0.12			0.17			0.13		
N	18 $_{Order}$			18 $_{Order}$			18 $_{Order}$			18 $_{Order}$		
Observations	668			668			668			668		
Marginal R^2 / Conditional R^2	0.000 / 0.159			0.168 / 0.266			0.005 / 0.169			0.171 / 0.280		
AICc	203.459			163.580			204.100			164.568		

	P(hist. extinct)			P(hist. extinct)			P(hist. extinct)		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.00	0.00 – 0.02	**<0.001**	0.00	0.00 – 0.02	**<0.001**	0.00	0.00 – 0.02	**<0.001**
Magnitude	134.78	24.23 – 749.70	**<0.001**	70.40	5.58 – 888.05	**0.001**	69.60	5.34 – 906.86	**0.001**
Body mass	0.79	0.43 – 1.46	0.455				1.19	0.99 – 1.43	0.068
Magnitude * Body mass	6.59	0.49 – 89.33	0.156						
Direction [gigantism]				3.66	0.74 – 18.11	0.111	4.18	0.79 – 22.10	0.092
Magnitude * Direction [gigantism]				3.71	0.15 – 92.12	0.424	3.75	0.15 – 95.66	0.424
Random Effects									
σ^2	3.29			3.29			3.29		
τ_{00}	1.29 $_{Order}$			0.00 $_{Order}$			0.00 $_{Order}$		
ICC	0.28								
N	18 $_{Order}$			18 $_{Order}$			18 $_{Order}$		
Observations	668			668			668		
Marginal R^2 / Conditional R^2	0.165 / 0.400			0.284 / NA			0.303 / NA		
AICc	163.362			157.452*			157.618		

Table S7.

Comparison of GLMMs for the probability of being threatened or extinct (all extinctions, late Quaternary extinctions, historic extinctions since 1500 CE) at the species-level between island and mainland mammal communities. CI = 95% confidence intervals; AICc = Akaike Information Criterion with small-sample correction; ICC = Intraclass Correlation Coefficient.

	P(threatened)			**P(extinct)**			**P(extinct_late_Quaternary)**			**P(hist. extinct)**		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
(Intercept)	0.24	0.14 – 0.41	**<0.001**	0.01	0.00 – 0.02	**<0.001**	0.01	0.00 – 0.01	**<0.001**	0.01	0.00 – 0.03	**<0.001**
log_{10} body mass	1.64	1.41 – 1.92	**<0.001**	2.96	2.47 – 3.56	**<0.001**	3.04	2.49 – 3.72	**<0.001**	1.63	1.14 – 2.31	**0.007**
Island or mainland [mainland]	0.40	0.27 – 0.58	**<0.001**	0.01	0.00 – 0.02	**<0.001**	0.01	0.01 – 0.03	**<0.001**	0.07	0.02 – 0.21	**<0.001**
log_{10} body mass * Island or mainland [mainland]	0.90	0.77 – 1.05	0.191	2.05	1.63 – 2.57	**<0.001**	2.06	1.62 – 2.61	**<0.001**	1.49	1.00 – 2.21	**0.050**
Random Effects												
σ^2	3.29			3.29			3.29			3.29		
τ_{00}	0.52 $_{Order}$			0.77 $_{Order}$			0.83 $_{Order}$			0.57 $_{Order}$		
ICC	0.14			0.19			0.20			0.15		
N	28 $_{Order}$			30 $_{Order}$			30 $_{Order}$			28 $_{Order}$		
Observations	4974			5531			5438			5065		
Marginal R^2 / Conditional R^2	0.116 / 0.238			0.626 / 0.697			0.611 / 0.690			0.292 / 0.396		
AICc	4812.897			2217.470			2010.692			822.433		

Table S8.

Predicted values from GLMMs for the probability of being threatened or extinct (all extinctions) at the species-level by body mass and type of mammal community (island or mainland). See table S7 for details on the models.

	P(threatened)		**P(extinct)**	
Body mass (kg)	*island*	*mainland*	*island*	*mainland*
0.001	0.194	0.087	0.009	9.23E-05
0.01	0.284	0.124	0.026	0.001
0.1	0.394	0.174	0.073	0.003
1	0.517	0.238	0.190	0.020
10	0.638	0.317	0.410	0.111
100	0.743	0.407	0.673	0.432
1,000	0.827	0.505	0.859	0.822
10,000	0.889	0.602	0.948	0.966

Table S9.

Comparison of phylogenetic logistic regressions for the probability of being threatened at the species-level. AICc = Akaike Information Criterion with small-sample correction; alpha = strength of the phylogenetic signal in extinction risk; R2_lik = R^2 statistic based on the likelihood of fitted models. To account for phylogenetic uncertainty, we ran phylogenetic logistic regressions across 100 complete TACT trees and 100 DNA-only trees.

	P(threatened)						**P(threatened)**					
	100 complete TACT trees											
Predictors	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*
Intercept	-1.088	-0.971	-1.036	0.018	-1.039	-1.032	-0.585	-0.463	-0.525	0.028	-0.530	-0.519
Se Intercept	0.143	0.157	0.148	0.002	0.148	0.149	0.103	0.117	0.110	0.003	0.109	0.111
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Magnitude	3.345	3.643	3.505	0.060	3.493	3.516						
Se Magnitude	0.598	0.620	0.609	0.004	0.608	0.610						
Pval Magnitude	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**						
Body mass							0.425	1.494	0.989	0.303	0.929	1.049
Se Body mass							0.292	0.530	0.420	0.063	0.407	0.432
Pval Body mass							**0.004**	0.146	**0.033**	**0.034**	**0.026**	**0.040**
Observations	644						644					
Alpha	0.088	0.130	0.108	0.008	0.106	0.109	0.133	0.204	0.163	0.018	0.159	0.166
R2_lik	0.153	0.228	0.188	0.016	0.185	0.192	-0.941	0.161	-0.553	0.340	-0.620	-0.485
AICc	751.073	792.460	773.354	8.908	771.586	775.121	788.389	1209.698	1078.007	132.671	1051.682	1104.332

	P(threatened)						**P(threatened)**					
	100 DNA-only trees											
Predictors	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*
Intercept	-1.514	-1.428	-1.474	0.018	-1.477	-1.470	-1.084	-0.998	-1.042	0.017	-1.045	-1.039
Se Intercept	0.171	0.180	0.177	0.001	0.176	0.177	0.133	0.141	0.137	0.001	0.137	**0.138**
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Magnitude	3.110	3.388	3.290	0.065	3.277	3.303						
Se Magnitude	0.690	0.710	0.702	0.004	0.701	0.703						
Pval Magnitude	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**						
Body mass							0.529	1.186	0.892	0.186	0.855	0.929
Se Body mass							0.308	0.430	0.379	0.032	0.373	0.386
Pval Body mass							**0.006**	0.085	**0.026**	**0.020**	**0.022**	**0.030**
Observations	487						487					
Alpha	0.095	0.135	0.112	0.007	0.111	0.114	0.117	0.162	0.138	0.008	0.136	0.140
R2_lik	0.215	0.239	0.229	0.005	0.228	0.230	-0.474	0.205	-0.013	0.191	-0.050	0.025
AICc	507.922	517.763	512.083	2.155	511.655	512.511	521.628	737.378	597.634	63.061	585.121	610.146

Table S10.

Comparison of phylogenetic logistic regressions for the probability of being extinct at the species-level. AICc = Akaike Information Criterion with small-sample correction; alpha = strength of the phylogenetic signal in extinction risk; R2_lik = R^2 statistic based on the likelihood of fitted models. To account for phylogenetic uncertainty, we ran phylogenetic logistic regressions across 100 complete TACT trees.

	P(extinct)						**P(extinct)**					
	100 complete TACT trees											
Predictors	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*
Intercept	-3.073	-2.165	-2.479	0.173	-2.513	-2.445	-2.027	-0.851	-1.642	0.166	-1.675	-1.609
Se Intercept	0.243	0.339	0.276	0.018	0.272	0.280	0.181	0.278	0.219	0.019	0.215	0.223
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Magnitude	3.131	4.214	3.593	0.209	3.552	3.635						
Se Magnitude	0.374	0.444	0.408	0.014	0.405	0.410						
Pval Magnitude	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**						
Body mass							-0.039	1.943	0.948	0.319	0.885	1.011
Se Body mass							0.021	0.434	0.189	0.056	0.178	0.200
Pval Body mass							**<0.001**	0.999	**0.041**	0.183	**0.005**	0.078
Observations	827						827					
Alpha	0.031	0.056	0.044	0.005	0.043	0.045	0.037	0.070	0.050	0.006	0.049	0.052
R2_lik	0.404	0.580	0.544	0.032	0.538	0.550	-0.008	0.513	0.328	0.169	0.294	0.361
AICc	487.089	627.015	517.166	25.734	512.059	522.272	543.192	884.596	673.528	113.455	651.016	696.040

Table S11.

Comparison of phylogenetic logistic regressions for the probability of being threatened at the population-level. AIC = Akaike Information Criterion; AICc = Akaike Information Criterion with small-sample correction; alpha = strength of the phylogenetic signal in extinction risk; R2_lik = R^2 statistic based on the likelihood of fitted models. To account for phylogenetic uncertainty, we ran phylogenetic logistic regressions across 100 complete TACT trees and 100 DNA-only trees. We also evaluated data uncertainty, that is, intraspecific variability in magnitude of size change and body mass, and the interaction between data and phylogenetic uncertainty.

	P(threatened)																	
	100 complete TACT trees																	
Predictors	*Min all*	*Max all*	*Mean all*	*Sd all*	*CI low all*	*CI high all*	*Min intra*	*Max intra*	*Mean intra*	*Sd intra*	*CI low intra*	*CI high intra*	*Min tree*	*Max tree*	*Mean tree*	*Sd tree*	*CI low tree*	*CI high tree*
Intercept	-1.571	-1.027	-1.377	0.047	-1.379	-1.376	-1.385	-1.372	-1.377	0.003	-1.379	-1.376	-1.447	-1.292	-1.377	0.030	- 1.378	-1.377
Se Intercept	0.194	0.231	0.212	0.005	0.212	0.212	0.212	0.213	**0.212**	<0.001	0.212	0.212	0.204	0.220	0.212	0.003	0.212	0.212
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Magnitude	1.141	4.425	2.974	0.416	2.959	2.989	2.909	3.027	2.974	0.032	2.962	2.986	2.614	3.197	2.974	0.116	2.968	2.980
Se Magnitude	0.974	1.224	1.115	0.037	1.113	1.116	1.108	1.121	1.115	0.003	1.113	1.116	1.087	1.149	1.115	0.012	1.114	1.115
Pval Magnitude	**<0.001**	0.268	**0.011**	**0.013**	**0.011**	**0.012**	**0.009**	**0.015**	**0.011**	**0.001**	**0.011**	**0.012**	**0.006**	**0.041**	**0.011**	**0.004**	**0.011**	**0.012**
Observations	384																	
Alpha	0.065	0.119	0.091	0.009	0.090	0.091	0.089	0.091	0.091	<0.001	0.091	0.091	0.075	0.107	0.091	0.008	0.091	0.091
R2_lik													0.115	0.225	0.177	0.022	0.173	0.181
AIC	398.217	442.141	417.719	7.221	417.461	417.978	417.141	418.128	417.719	0.211	417.641	417.798	403.090	436.203	417.719	6.748	417.678	417.761
AICc													402.013	435.551	417.052	6.819	415.699	418.405

	P(threatened)																	
	100 complete TACT trees																	
Predictors	*Min all*	*Max all*	*Mean all*	*Sd all*	*CI low all*	*CI high all*	*Min intra*	*Max intra*	*Mean intra*	*Sd intra*	*CI low intra*	*CI high intra*	*Min tree*	*Max tree*	*Mean tree*	*Sd tree*	*CI low tree*	*CI high tree*
Intercept	-1.237	-1.002	-1.147	0.026	-1.148	-1.146	-1.149	-1.145	-1.147	0.001	-1.147	-1.146	-1.203	-1.07	-1.147	0.025	-1.147	-1.146
Se Intercept	0.159	0.177	0.167	0.003	0.167	0.167	0.167	0.167	0.167	<0.001	0.167	0.167	0.16	0.174	0.167	0.003	0.167	0.167
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Body mass	0.23	1.011	0.634	0.151	0.629	0.639	0.611	0.656	0.634	0.013	0.629	0.639	0.513	0.801	0.635	0.058	0.633	0.638
Se Body mass	0.147	0.41	0.293	0.043	0.291	0.294	0.287	0.299	0.293	0.004	0.292	0.294	0.263	0.328	0.293	0.013	0.292	0.294
Pval Body mass	**0.006**	0.124	**0.037**	**0.020**	**0.037**	**0.038**	**0.035**	**0.041**	**0.037**	**0.002**	**0.037**	**0.038**	**0.016**	0.059	**0.037**	**0.009**	**0.037**	**0.037**
Observations	384																	
Alpha	0.079	0.129	0.104	0.008	0.104	0.104	0.103	0.104	0.104	<0.001	0.104	0.104	0.086	0.126	0.104	0.008	0.104	0.104
R2_lik													-0.488	0.204	-0.102	0.173	-0.136	-0.068
AIC	399.561	434.677	415.429	6.697	415.189	415.669	414.839	415.819	415.426	0.224	415.342	415.510	402.983	431.075	415.579	6.623	415.534	415.623
AICc													408.655	580.632	491.792	45.041	482.855	500.729

	P(threatened)																	
	100 DNA-only trees																	
Predictors	*Min all*	*Max all*	*Mean all*	*Sd all*	*CI low all*	*CI high all*	*Min intra*	*Max intra*	*Mean intra*	*Sd intra*	*CI low intra*	*CI high intra*	*Min tree*	*Max tree*	*Mean tree*	*Sd tree*	*CI low tree*	*CI high tree*
Intercept	-1.934	-1.528	-1.722	0.049	-1.723	-1.72	-1.733	-1.71	-1.722	0.005	-1.724	-1.72	-1.772	-1.672	-1.722	0.021	-1.723	-1.721

Se Intercept	0.223	0.264	0.242	0.005	0.242	0.242	0.241	0.243	0.242	<0.001	0.242	0.242	0.238	0.247	0.242	0.002	0.242	0.242
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Magnitude	1.778	4.806	3.043	0.469	3.027	3.06	2.907	3.163	3.043	0.059	3.022	3.065	2.824	3.328	3.043	0.093	3.032	3.055
Se Magnitude	1.176	1.539	1.404	0.054	1.402	1.406	1.389	1.413	1.404	0.005	1.402	1.406	1.373	1.438	1.404	0.013	1.403	1.405
Pval Magnitude	**0.001**	0.181	**0.038**	**0.026**	**0.037**	**0.039**	**0.031**	**0.044**	**0.038**	**0.003**	**0.036**	**0.039**	**0.023**	**0.05**	**0.038**	**0.005**	**0.037**	**0.038**
Observations	331																	
Alpha	0.072	0.135	0.105	0.009	0.105	0.105	0.104	0.106	0.105	<0.001	0.105	0.105	0.087	0.123	0.105	0.008	0.105	0.105
R2_lik													0.140	0.182	0.161	0.007	0.160	0.163
AIC	306.464	324.523	315.253	2.661	315.158	315.349	314.650	315.811	315.253	0.250	315.160	315.347	309.650	320.132	315.253	1.852	315.204	315.303
AICc													308.768	318.856	313.760	1.738	313.415	314.105

	P(threatened)																	
	100 DNA-only trees																	
Predictors	*Min all*	*Max all*	*Mean all*	*Sd all*	*CI low all*	*CI high all*	*Min intra*	*Max intra*	*Mean intra*	*Sd intra*	*CI low intra*	*CI high intra*	*Min tree*	*Max tree*	*Mean tree*	*Sd tree*	*CI low tree*	*CI high tree*
Intercept	-1.605	-0.661	-1.540	0.026	-1.541	-1.539	-1.542	-1.528	-1.540	0.002	-1.541	-1.539	-1.577	-1.491	-1.540	0.019	-1.540	-1.539
Se Intercept	0.128	0.198	0.191	0.002	0.191	0.191	0.190	0.191	0.191	<0.001	0.191	0.191	0.186	0.195	0.191	0.002	0.191	0.191
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Body mass	0.341	1.051	0.703	0.132	0.698	0.708	0.678	0.723	0.703	0.013	0.698	0.708	0.626	0.800	0.704	0.033	0.701	0.706
Se Body mass	0.182	0.407	0.302	0.038	0.301	0.304	0.294	0.309	0.302	0.004	0.301	0.304	0.282	0.325	0.303	0.009	0.302	0.303
Pval Body mass	**0.005**	0.073	**0.023**	**0.011**	**0.023**	**0.024**	**0.021**	**0.025**	**0.023**	**0.001**	**0.023**	**0.024**	**0.015**	**0.031**	**0.023**	**0.003**	**0.023**	**0.023**
Observations	331																	
Alpha	0.090	0.299	0.111	0.009	0.110	0.111	0.110	0.113	0.111	<0.001	0.111	0.111	0.094	0.129	0.111	0.008	0.111	0.111
R2_lik													-0.279	0.060	-0.205	0.044	-0.214	-0.196
AIC	299.468	350.770	309.310	2.637	309.216	309.405	309.036	309.624	309.309	0.157	309.251	309.368	302.699	315.279	309.321	2.027	309.290	309.352
AICc													337.116	405.063	391.350	8.668	389.630	393.070

Table S12.

Comparison of phylogenetic logistic regressions for the probability of being extinct at the species-level based on historic extinctions since 1500 CE only. AICc = Akaike Information Criterion with small-sample correction; alpha = strength of the phylogenetic signal in extinction risk; R2_lik = R^2 statistic based on the likelihood of fitted models. To account for phylogenetic uncertainty, we ran phylogenetic logistic regressions across 100 complete TACT trees.

	P(hist. extinct)						**P(hist. extinct)**					
	100 complete TACT trees											
Predictors	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*	*Min*	*Max*	*Mean*	*Sd tree*	*CI low*	*CI high*
Intercept	-4.641	-4.171	-4.393	0.104	-4.413	-4.372	-3.725	-3.387	-3.558	0.073	-3.572	-3.543
Se Intercept	0.461	0.563	0.506	0.023	0.501	0.51	0.372	0.483	0.423	0.022	0.419	0.427
Pval Intercept	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Magnitude	3.484	4.373	3.929	0.185	3.892	3.965						
Se Magnitude	0.788	0.848	0.816	0.014	0.813	0.819						
Pval Magnitude	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**						
Body mass							0.116	0.218	0.168	0.018	0.165	0.172
Se Body mass							0.087	0.105	0.089	0.003	0.088	0.090
Pval Body mass							**0.034**	0.218	0.063	**0.028**	0.058	0.069
Observations	668						668					
Alpha	0.056	0.127	0.078	0.014	0.076	0.081	0.056	0.111	0.075	0.010	0.073	0.077
R2_lik	0.311	0.421	0.361	0.024	0.356	0.366	0.208	0.341	0.265	0.026	0.259	0.270
AICc	133.493	155.181	145.362	4.708	144.428	146.296	149.193	174.727	164.036	4.876	163.068	165.003

Table S13.
Explanation and categorization of traits used in the time-and-trait-dependent extinction analysis.

Ecological traits	
Body mass	***Explanation***
very small (vs)	0.001-0.01 kg
Small (s)	0.01-0.1 kg
small medium (sm)	0.1-1 kg
medium (m)	1-10 kg
large medium (lm)	10-100 kg
large (l)	100-1,000 kg
very large (vl)	>1,000 kg
Body size change	***Explanation***
strongly dwarfed (sd)	between -10 and -1
moderately dwarfed (md)	between -1 and -0.1
slightly dwarfed (sld)	between -0.1 and -0.01
unchanged (un)	between -0.01 and 0.01
slightly giant (slg)	between 0.01 and 0.1
moderately giant (mg)	between 0.1 and 1
strongly giant (sg)	between 1 and 10
Endemism	***Explanation***
non-endemic	taxon occurs or occurred also on the mainland
endemic	taxon occurs or occurred only on islands
Island type	***Explanation***
oceanic	taxon occurs or occurred only on oceanic islands
continental	taxon occurs or occurred only on continental islands
continental + oceanic	taxon occurs or occurred on oceanic and continental islands