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Supplementary Material for

Defaunation in the Anthropocene

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Materials and Methods

Mammal and Bird Richness Map

We compiled the mammal and bird map by developing a geographic information system including Arc-GIS shapefiles for all land mammal and bird species catalogued as with declining populations by the International Union for Conservation of Nature (*17*). The files contain the known geographic range depicted by a boundary map (i.e. extent of occurrence). Maps for mammals were obtained from our database (see (*82*) for more details). Maps for birds were obtained from Birdlife International. Earth's surface was divided into a 10,000-km^2 grid cell network using the Behrmann equal area projection. Species richness was defined as the total number of mammal and bird species in a single cell.

Population declines of selected mammal species

For six species we were able to locate relatively high quality data on global population size over multiple decades (Fig S1B). Populations of many of these species of mammals had already greatly reduced when these data began. Aggressive conservation efforts have had some successes in slowing declines of some of these species; however in the last two decades there have been major conservation setbacks for most of these species. The reasons for these setbacks vary by species, but include increasing demand for products from these endangered animals, habitat loss and fragmentation, and introduced diseases, resulting in recent collapses of many of these populations. Whenever available we deferred to IUCN data (*17*); additional sources were used to supplement IUCN data when available (*83-91*).

Trends in UK insects based on presence-only biological records

Biological records are observations of species in a known point in space and time. The UK has an unrivalled history of biological recording, with over 90 million species records now available through the Global Biodiversity Information Facility (GBIF; around 12% of the global total). Volunteer recorders make most records in the UK, and the vast majority of records are collected without a specific protocol. The intensity of recording varies in both space and time (*92*), which is a challenge for estimating robust quantitative trends. Fortunately, a range of methods now exist for producing such trends using unstructured biological records data e.g. (*93-95*). In effect, these methods identify long-term changes in species distributions; the term 'frequency of occurrence' is however technically more accurate.

Most methods for trend estimation use the records themselves to get at the data collection process, generally assuming that a record of species A indicates that species B was not observed. Specifically, the number of species recorded at a site on a particular date (the list length) is a commonly used metric of sampling intensity e.g. (*96*). We employ one such method, which seeks to remove the bias inherent in

biological records and identifying the 'well-sampled' set that retains a signal of genuine biological change (*97*).

The input data for each species is a table of all the site visits (unique combinations of date in 1 km^2) between 1970 and 2009 for the taxonomic group in question, with data on the list length (the number of species recorded) and whether the focal species was recorded (1) or not (0). These data were then filtered for data quality, first removing all visits with list lengths shorter than the median for the taxonomic group in question. At the second filtering step, grid cells that had visits in less than three years were excluded. The time series for each species was then estimated from a generalized linear mixed effects model, with year as the covariate and grid cell as a random effect (following (*97*)).

We fitted this model to data on 1026 species in four taxonomic orders (Table S2). The following organizations contributed data for this analysis: Bees, Wasps and Ants Recording Society, British Dragonfly Society, Butterfly Conservation (*25*), the Ground Beetle Recording Scheme and the UK Ladybird Survey.

For each species we extracted the fitted values from the model for the first and last years in the dataset and expressed the change over this period as a percentage of the initial value. Technically, these fitted values are the probability that the focal species was recorded on an average visit in the year in question. A key assumption of the well-sampled sites model is that species' detectability has not changed over time. The relevant recording schemes were therefore consulted, and we excluded species for which this assumption is unsupportable.

<u>Calculating an index of change in invertebrate abundance:</u>

To gather time-series data on invertebrate populations, we reviewed the published literature for studies of long-term invertebrate population change. While we would have ideally used randomly subsampled populations across taxa, these data do not exist. Instead we searched for any published studies using the ISI Web of Knowledge database with the following search terms: (arthropod* OR invertebrate* OR insect* OR hymenoptera OR bee* OR ant* OR coleoptera OR beetle* OR Lepidoptera OR butterfl* OR pollinator* OR odonata OR dragonfl*) AND (population* OR species OR communit*). We used references of all papers identified through this search to find additional papers.

Following the techniques and selection criteria developed by (*21, 98*), studies were included if they included terrestrial or semi-terrestrial invertebrate populations, if the study examined change in absolute or relative abundance using the same methods over time for a minimum of three years, and if they included information on the methods of collection, the locations of collection, and the units of measurement. We excluded species and studies focusing on non-native populations. When studies included only data on range change or species richness, or when raw data were not available, the authors were contacted for unpublished information on population abundance during the study period. If no further information was

obtained, the study was excluded from our analysis. The data were examined at the lowest taxonomic level possible, usually to species, and sometimes to population level (i.e. a species for which multiple distinct populations were reported from one study would be aggregated to the species level). Our final database consisted of 29 studies (*21, 98-125*).

Our dataset included 3,249 estimates of population size for 466 populations of 452 unique species across eight orders (Aphididae, Coleoptera, Diptera, Hemiptera, Hymenoptera, Lepidoptera, Odonata, and Rhabditida) and all continents except South America (Fig S2). The time series data spanned the period 1820 – 2013, with the majority of the data spanning 1960-2012. The mean dataset length was 36.53 years.

We created an index of abundance for all species using the chain method detailed by (*98*), and calculated confidence limits as detailed in (*21*). While alternative methods for modeling trends in population data are available, such as Generalized Additive Models (see (*21*)), the data did not support their use. To calculate an index, we calculated the logarithm of the ratio of population measures for successive years of each time series, imputing missing values with log-linear interpolation. For species with more than one population time series, a mean value for each year was calculated across all time series for that species. Species-specific values were then combined, with all species weighted equally. An index was then calculated by setting the first index value to 1 (in 1970), and chaining subsequent years. For full details, see (*21*).

Due to the dominance of Lepidoptera in our dataset, we evaluated differences in trends between Lepidoptera and non-Lepidoptera.

<u>Meta-analysis of effects of disturbance on Lepidoptera species richness and abundance</u>

Meta-analysis Methods: We reviewed the published literature for studies of Lepidoptera species richness in disturbed and undisturbed habitats, using the ISI Web of Knowledge with the following search terms: (Lepidoptera OR butterfl* OR pollinator) AND (populations OR communit*) AND (disturbance OR logging OR grazing OR urbanization OR fragmentation OR "edge effect" OR (agriculture OR cultivation OR farming OR ranching OR plantation*). We also searched reference lists of all studies identified as usable from the initial search.

Studies were included if they met the following criteria: 1) presented data on Lepidoptera richness in at least two habitat types: low disturbance (control) and anthropogenically disturbed (treatment); 2) included replication within both habitats; 3) included P value, standard error, standard deviation, or other statistics (Z, F, t, r, r^2, χ^2); 4) reported the sample size; 5) included study location, sampling protocol, and number of sampling periods. For data that were reported only as statistically significant, without an actual P value we assumed P =0.05. Disturbance types included forestry, agriculture, fragmentation, grazing, and prevalence of invasive species. Studies were excluded if we were unable to determine the extent

or type of disturbance from the author's description. If data from multiple sampling methods or multiple time-points were reported separately from the sites, data were pooled to generate a single effect size.

We also conducted an analysis of the effect of anthropogenic disturbance on Lepidoptera abundance using the same search results and selection criteria, except substituting abundance for richness in criteria. In both disturbance and richness analyses, we calculated effect sizes (Hedge's g) using Comprehensive Meta-analysis software, ver 2.0. A meta-regression of the effect of latitude was performed for species richness, but not abundance, due to the low number of studies available. To test for publication bias, we examined funnel plots and conducted Duval and Tweedie's trim and fill analysis.

In total we calculated 52 diversity effect sizes from 15 studies (*126-140*) that met our criteria for inclusion in the meta-analysis (Fig S3). The meta-analysis revealed an overall negative effect ($Z = 5.91$, $P < 0.0001$) with a large mean effect estimate of 1.02 (95% CI 0.68 to 0.1.36). Visual examination of funnel plots suggested missing studies and D suggested there were nine missing studies due to possible publication bias. Using Duval and Tweedie's trim and fill analysis to impute missing studies (9 identified), we still find significant overall effects although they are smaller (point effect estimate = 0.55, 95% CI 0.15 to 0.96, Q-value = 1305.1). Meta-regression examining effects of latitude on species richness effect found a positive but very small effect of decreasing effect size at lower latitudes (slope = -0.014, SE = 0.003, $P < 0.0001$, $Z = -5.032$, Tau-squared= 1.25; Fig S4).

In total we calculated 23 abundance effect sizes from 8 studies that met our criteria for inclusion in the meta-analysis. One study showed significant positive effects of disturbance on Lepidoptera abundance, three showed a positive but insignificant effect, one showed no effect, and three showed a negative effect (Fig S5). The meta-analysis revealed a moderate overall negative effect (point effect estimate= 0.42, $Z = 2.880$, $P = 0.004$, 95% CI 0.135 to 0.7).

<u>Differential defaunation by body mass from Pleistocene to Anthropocene</u>

We examined difference in body mass of mammals that went extinct in the Pleistocene with those that went extinct in the Holocene and Anthropocene; and within the Anthropocene we also examined differences in body mass between threatened and not threatened species. To this effect we used species lists and body mass data for all mammals present in Pleistocene and Anthropocene. These lists were compiled from (*141*); to these lists we then added new species recently described and incorporated all IUCN categories for all mammalian species (www.redlist.org). In general we used boundary definitions provided in (*141*) to define the boundaries of the Pleistocene. Although some megafauna extinct species in the Pleistocene survived up to early Holocene in South America (*142*), we considered all of them as "Pleistocene extinct". Differences in distributions of threatened and not threatened in Anthropocene were tested using a Kolmogorov-Smirnov two-sample test, which resulted in a statistically significant difference ($P<0.001$). While direct comparisons of extinctions between modern to fossil datasets are extremely challenging, as there are many biases in the likelihood of an

animal fossilizing, they are still the best way to assess long-term changes in faunal communities. This particular comparison is limited by the quality of the fossil record from the Pleistocene as well as quality of modern species records. For this reason, our statistical analysis is conducted only within threatened and non-threatened species (data-deficient species excluded). However, while both comparisons of modern and fossil records are difficult and both records clearly have biases towards a better understanding of extinction and threat in larger species (e.g (*143*)), mammals are considered one of the best taxa for fossil comparisons due to relatively complete records and extensive cave deposits have provided a particularly rich sampling of small mammals from Pleistocene periods making this a particularly robust dataset (*144*). Similarly, on the large end of the spectrum we note that the very largest animals on all continents were lost (*145*), including a large number of animals larger than any species present today, a pattern which is clearly robust to sampling biases. Examining the distributions of animals using only those about 2 kg yields qualitatively very similar patterns.

Animal biodiversity-ecosystem function relationships

Most quantitative meta-analyses of biodiversity ecosystem function relationships have focused exclusively on plant biodiversity ecosystem function relationships. Those few that have addressed biodiversity-ecosystem function relationships across both producers and consumers (e.g. (*50, 51*)) have included relatively few terrestrial animals, and almost no terrestrial vertebrates, despite the fact that individual species are well known to have large effects on their ecosystems. However, given the continuing growth of interest in these relationships, we replicated searches used from one of the largest meta-analyses to date (*51*) to see if this gap has now been addressed.

Specifically, we conducted a search of the ISI Web of Knowledge database using the keyword sequence *species AND (diversity OR richness) AND (community OR ecosystem) AND (function OR functioning OR production OR productivity OR biomass OR predation OR decomposition OR herbivory).* To be included, a study had to focus on terrestrial animals (invertebrate or vertebrate), and meet all 8 criteria used by (*51*).

In 2014 we found 19, 015 results from initial search criteria. We refined these results by eliminating marine and aquatic ecosystems, and constraining the time period between 2006 and 2014. This reduced results to 863 papers, of which only 12 included terrestrial animals and also met the 8 criteria detailed by (*51*). Of these 12 studies, 6 were exclosure experiments, which did not quantifiably describe the diversity of the vertebrate communities that were experimentally removed, but which presumably excluded more than three species ((*51*) criteria three); they must be considered only marginally appropriate for these analyses.

While it seems clear that there is rising interest in studying biodiversity ecosystem function relationships in animals (Fig S6), there are still relatively few studies on terrestrial animal biodiversity ecosystem function relationships (in comparison to the

>600 studies on other taxa, predominantly plants, identified in the original 2006 search by (*51*)).

Defaunation and Ecosystem Function

Data sources used in producing Fig 7 are as follows: seed dispersal (*146*), litter respiration and decomposition (*147*), carrion removal (*148*), herbivory (*149*), water quality and stream respiration (*150*), trampling (*151*), dung removal (*152*), pollination and plant recruitment (*55*), carbon cycling (*103*), and soil erosion and cattle fodder (*153*).

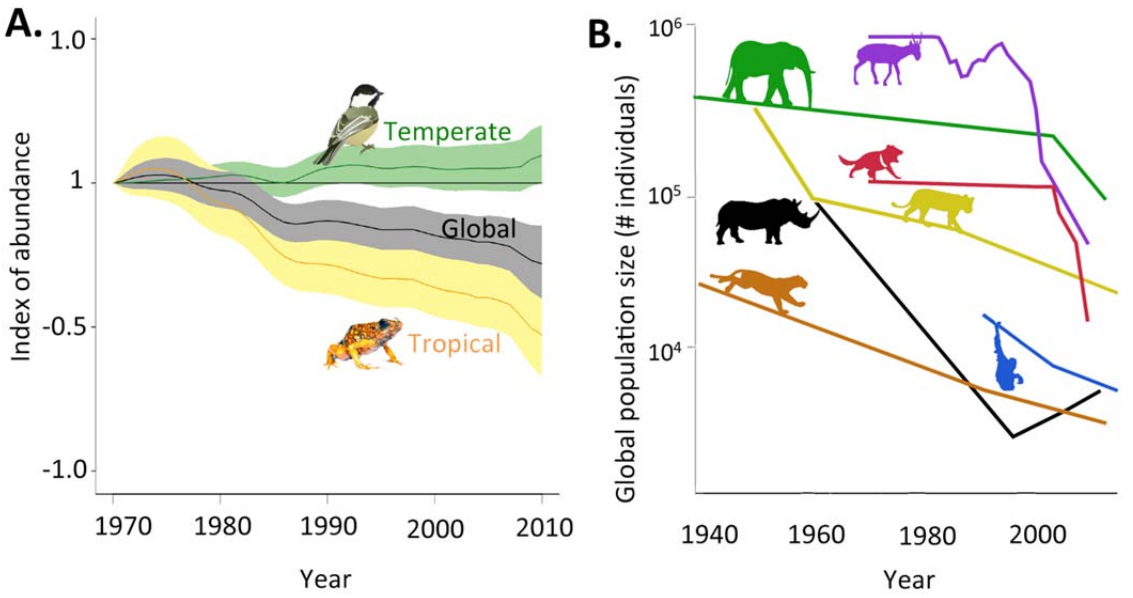

Fig. S1.
Terrestrial vertebrate population declines. (A) We used an integrated abundance index based on aggregating population trends of all species where population data is available globally. Vertebrate populations have declined nearly 25% since 1970, with most of the declines concentrated in the tropics, which drive the global pattern (*21*). For many of the best studied species the declines have been even more precipitous (*21, 22*). (B) Here we show population declines of six well-studied iconic species (population size for all species on log scale). Purple: saiga (*Saiga tatarica*); green: forest elephant (*Loxodonta cyclotis*); yellow: lion (*Panthera leo*); black: black rhino (*Diceros bicornis*); orange: tiger (*Panthera tigris*); red: Tasmanian devil (*Sarcophilus harrisii*); and blue: Sumatran orangutan (*Pongo abelii).* Populations of many of these species were already greatly reduced by the time monitoring began; however population trends since that time have declined towards near total collapse (*83-91*).

Fig. S2.

Map of locations of all sources of invertebrate abundance time series data. The size of the circle is relative to the number of species studied in a given location.

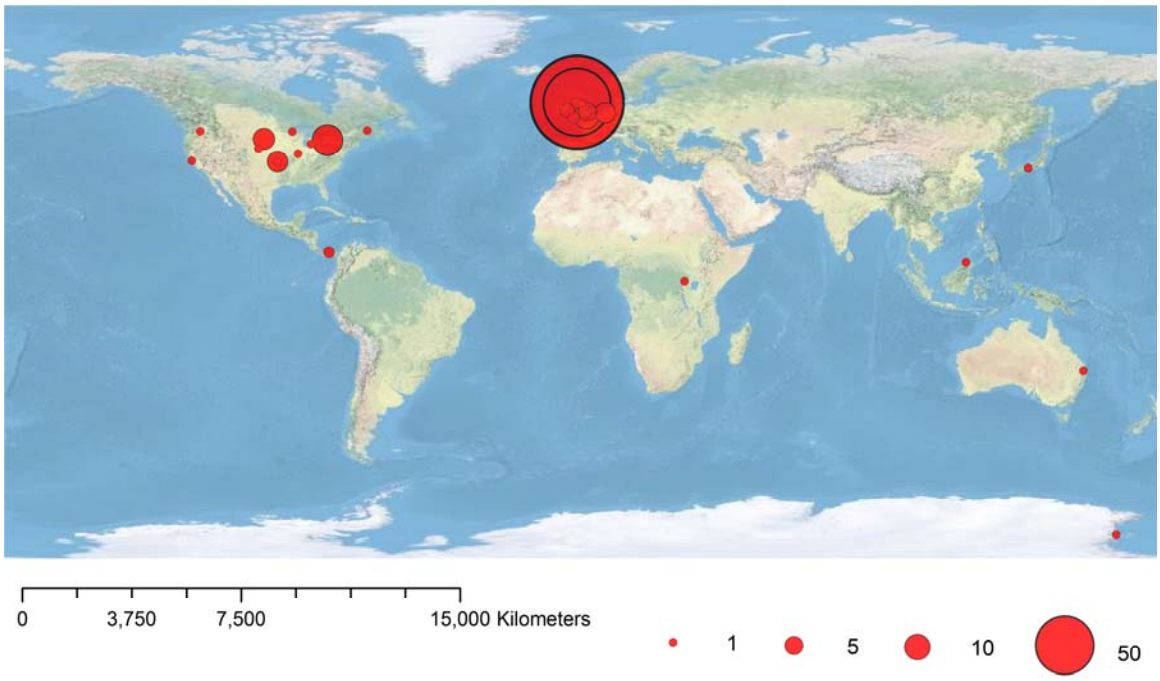

Fig. S3

The majority of studies on disturbance effects on Lepidoptera that met study criteria for meta-analysis are located in tropical regions. The size of the circle is representative of the number of samples in the study while the color of the circle represents the effect size observed.

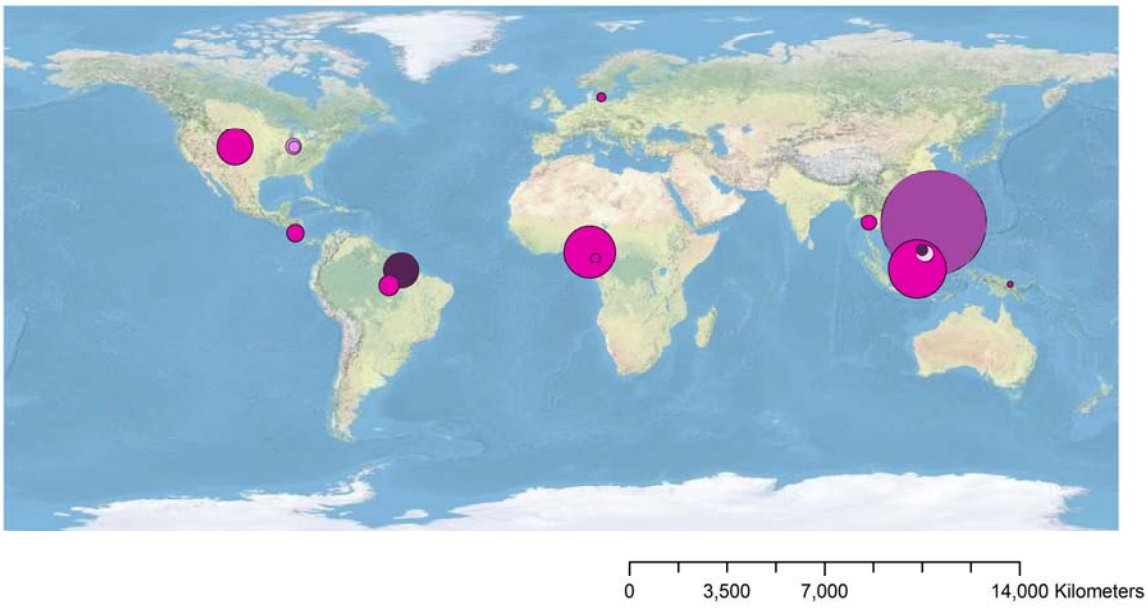

Fig. S4

A fixed-effect regression shows a small but significant decrease in magnitude of effect of disturbance on Lepidoptera abundance at lower latitudes.

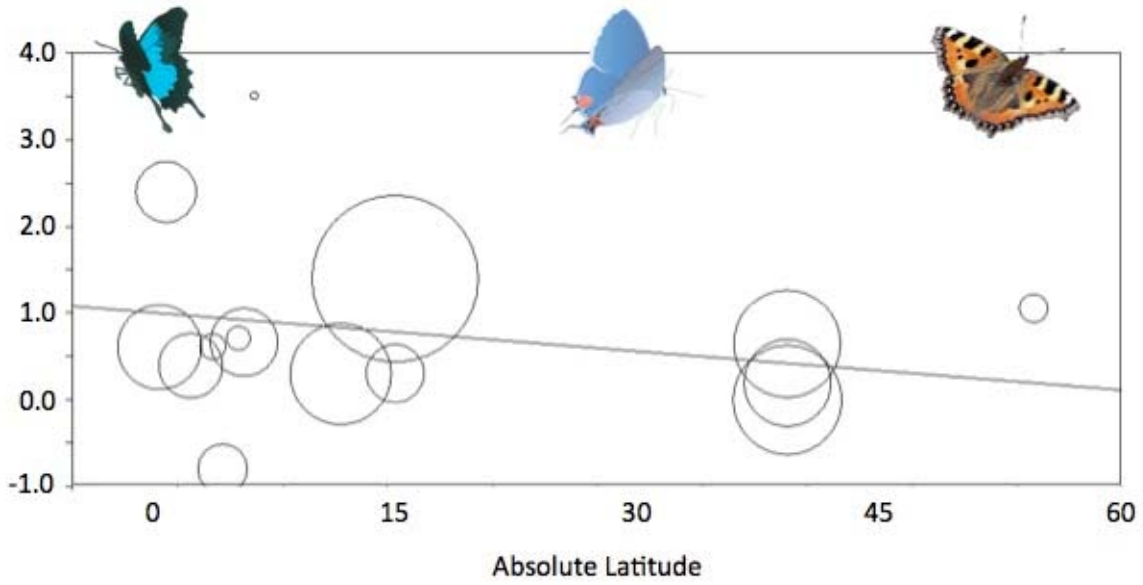

Fig S5.
Disturbance drives systematic declines in Lepidoptera abundance (Hedge's g). Error lines are 95% confidence intervals.

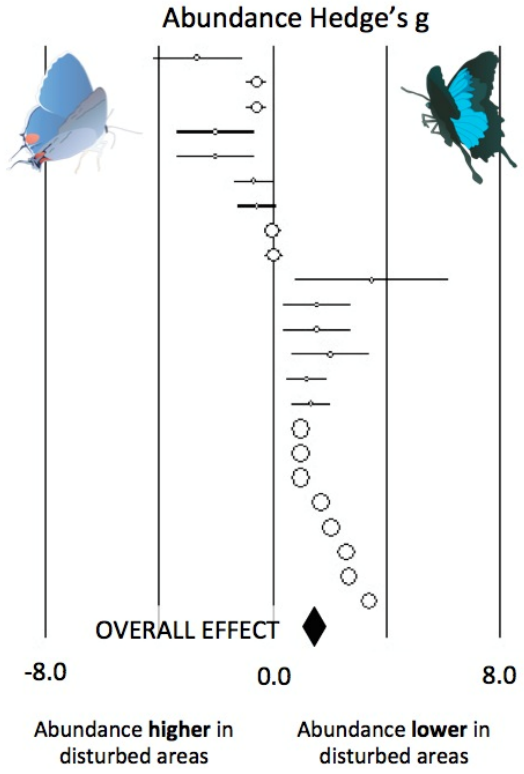

Fig S6

Number of biodiversity ecosystem function relationships found on terrestrial animals over time (see supplementary methods). This histogram includes studies from exclosure experiments that did not quantify diversity of species removed.

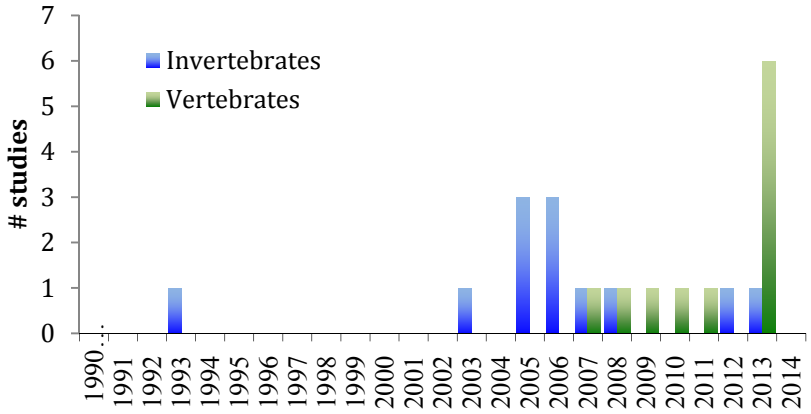

Table S1.

Data on species extinction by taxonomic grouping is provided here; data were taken from (*8, 17*).

	Since 1500	**Since 1900**
Mammalia	77	35
Aves	130	50
Reptilia	21	10
Amphibia	34	34
Fishes	60	60
Total Vertebrates	322	189

Table S2.
Summary of the UK Insect Data used in establishing range contractions across invertebrates.

Order	**Number of species**	**Number of visits**
Coleoptera	258	14,081
Hymenoptera	383	27,488
Lepidoptera	648	513,976
Odonata	38	78,992

Table S3

The Kenya long term exclosure experiment (KLEE) is a multifactorial replicated exclosure experiment that excludes various combinations of all large wildlife, livestock, and mega-wildlife only (*154*). For the purpose of clarity, the figure in main text focuses only on those treatments that remove all large wildlife and the treatments that allow access to all large wildlife. Whenever possible, given data available, we used data from 0 plots (no fences, both wildlife and cattle species allowed free access) and MW plots (electrified fences exclude all large wildlife, but low densities of cattle are allowed) to isolate the effect of wildlife removal from livestock effects. However, in some cases MWC plots (which exclude both large wildlife and cattle) were used instead of MW plots, or MW and MWC plots were pooled; thus these include the effects of all large animal (including both wildlife and livestock). A table of treatments used for each data source and study (*70, 154-167*) is provided below. The figure highlights aspects of the community that are affected by wildlife loss, and thus only those responses reported as significant across wildlife treatments in the original study are depicted in the figure. The units, and details of response metric used are also provided below.

Panel	Code	Ref	Treatments used	Response units	Notes on metric
C	He	(*162*)	0/C and MW/MWC	Percent of shoots eaten	
C	SL	(*162*)	0/C and MW/MWC	Mean thorn length (cm)	
B	B-A	(*155*)	0/C and MW/MWC	Granivorous bird abundance	Data for 0/C and MW/MWC plots was pooled prior to original analysis
B	B-R	(*155*)	0/C and MW/MWC	Bird species richness	Data for 0/C and MW/MWC plots was pooled prior to original analysis
B	I	(*155*)	0/C and MW/MWC	Insect abundance (pitfall trapping)	Data for 0/C and MW/MWC plots was pooled prior to original analysis
B	C	(*156*)	0 and MWC	Coleoptera density (individuals^{-1})	
B	G	(*156*)	0 and MWC	Lizard density (individuals ha^{-1})	
B	F	(*158*)	0 and MWC	Number of fleas/ha	Average across all seasons and years
B	S	(*157*)	0 and MWC	Sightings of *P. mossambicus*/ha	MW plots were not surveyed
B	T	(*159*)	0 and MW	Number of ticks 400 m^{-1}	Sum of all age classes and species of ticks
C	AD	(*161*)	0 and MWC	Number of workers recruiting following experimental disturbance	Other ant species showed no differences in levels of defense

C	FP	(*160*)	0 and MW	Seeds per tree	Averaged across all years
D	A\F	(*166*)	0 and MWC	AMF infectivity (% colonization) off termite mounts	Raw soil; effects were not significant overall but herbivory by mound interaction was significant
D	C-D	(*164*)	C and MWC	Cattle weight gain (kg^{-1} $animal^{-1}$ day^{-1}) in dry season	As cattle weight gain was the response metric, MWC and C plots were used instead of MW and 0 plots
D	C-W	(*164*)	C and MWC	Cattle weight gain (kg^{-1} $animal^{-1}$ day^{-1}) in wet season	As cattle weight gain was the response metric, MWC and C plots were used instead of MW and 0 plots
D	Di	(*70*)	0 and MWC	Number of *Bartonella* infected fleas ha^{-1}	Average across all seasons and years
D	Fi	(*164*)	0 and MW	Minimum fire temperature	
C	NP	(*163*)	0 and MWC	Number of nectaries/ 5 leaves	
C	TP	(*163*)	0 and MWC	Number of swollen thorns / 60 cm	
D	Ph	(*167*)	0 and MW	Photosynthetic rates (µmol CO_2 $m^{-2}s^{-1}$)	values presented are averages for the *A. drepanolobium* for the four different ant species in the dry season
D	Tr	(*167*)	0 and MW	Transpiration rates (mmol H_2O $m^{-2}s^{-1}$)	values presented are averages for the *A. drepanolobium* for the four different ant species in the dry season
A	--	(*162*)	0 and MW	Dung piles of large wildlife 600 m^{-2}	Large wildlife are species > 15 kg

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